

Chapter 2: Trends in Tree Improvement Methods: From Classical Breeding to Genomic Technologies

Swapam Chakrabarty

College of Forest Resource and Environmental Science, Michigan Technological University,

Houghton, MI 49931, USA

Supplementary Information 2.1

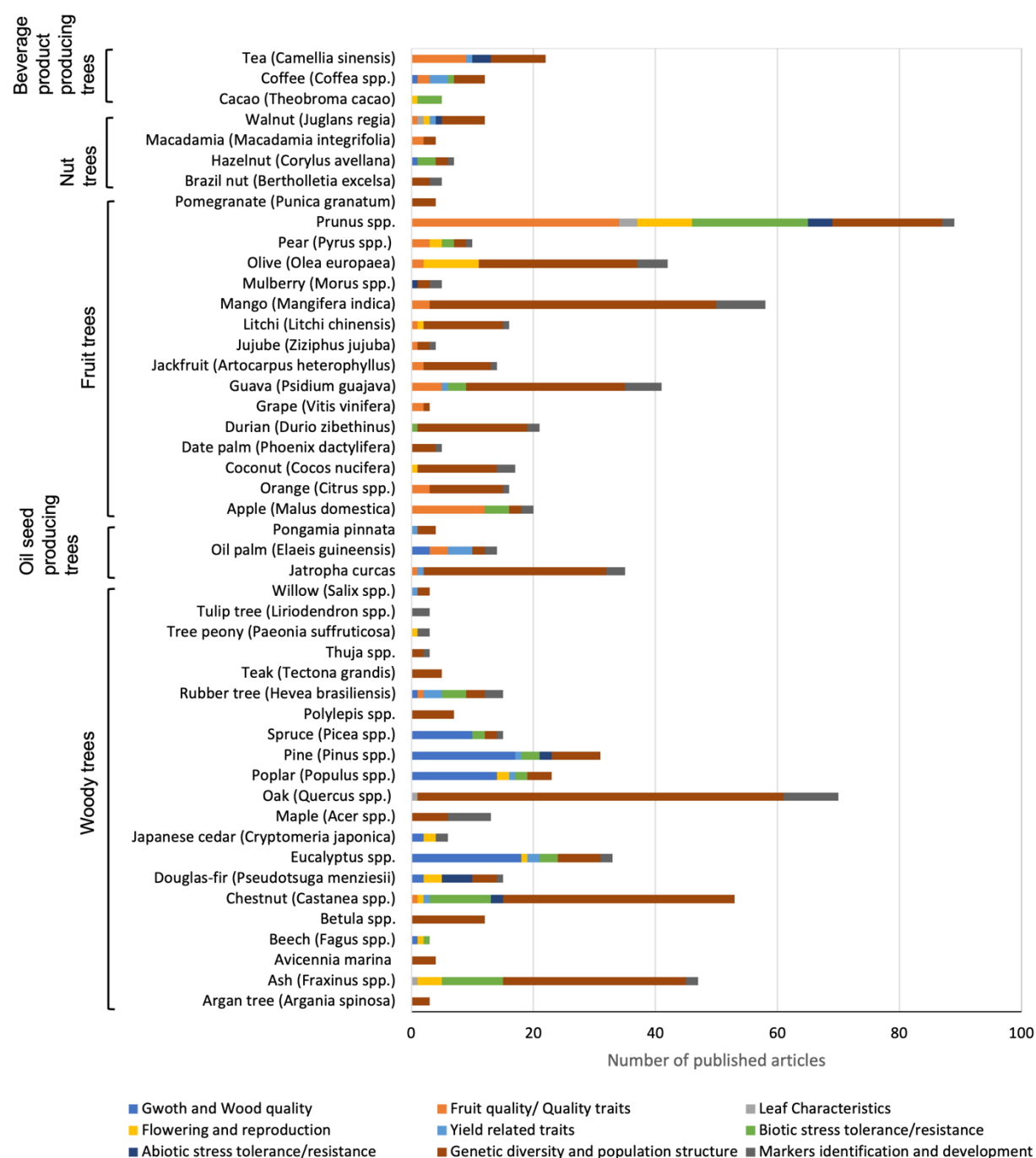


Figure S1. Tree species considered for genetic improvement by genomic selection or marker assisted selection (GS/MAS). Tree species having only one article has been excluded from the figure. See the Supplementary Tables S1 for details.

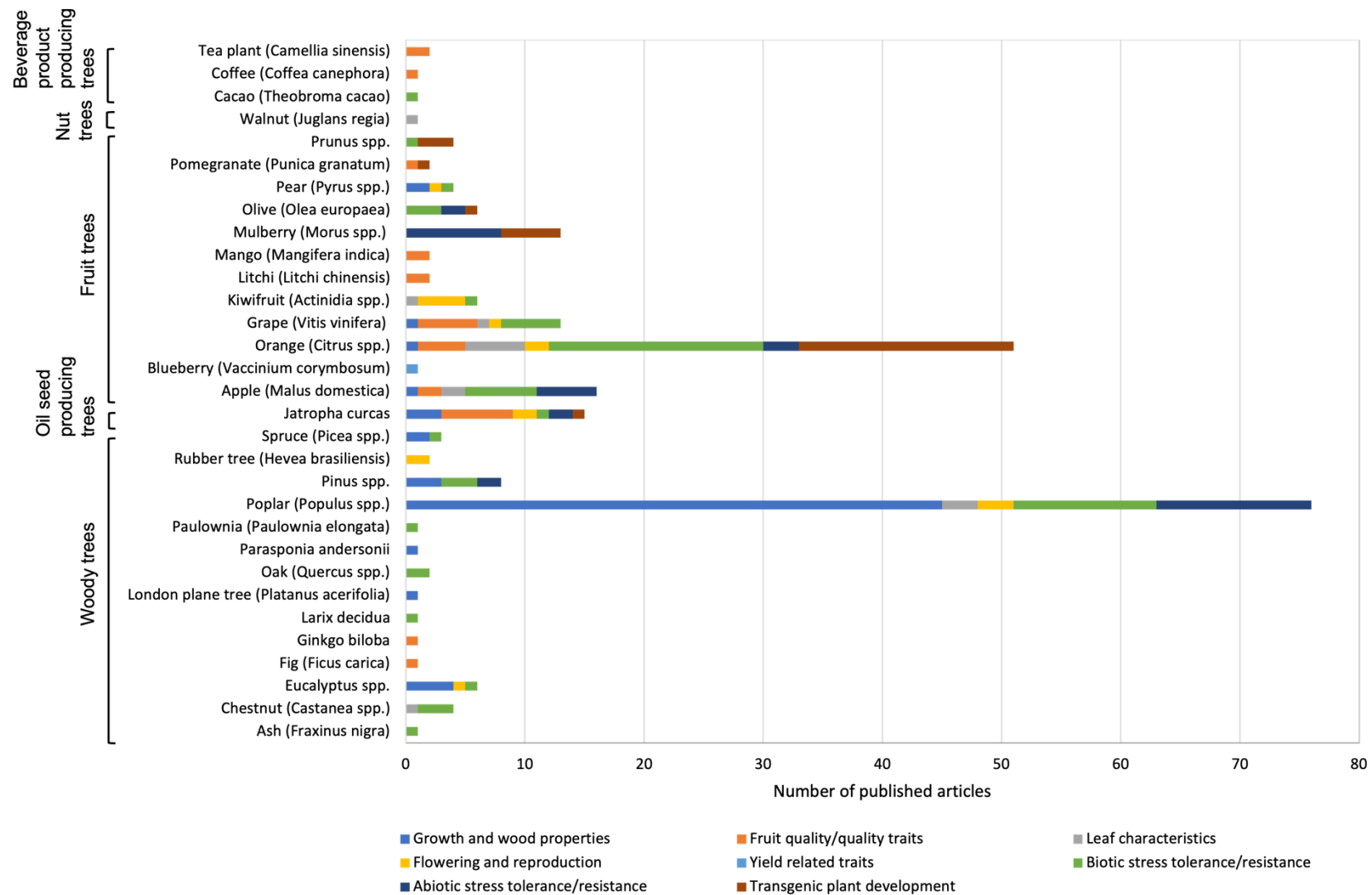


Figure S2. Tree species considered for genetic improvement by genetic engineering or genetic modification (GE/GM).

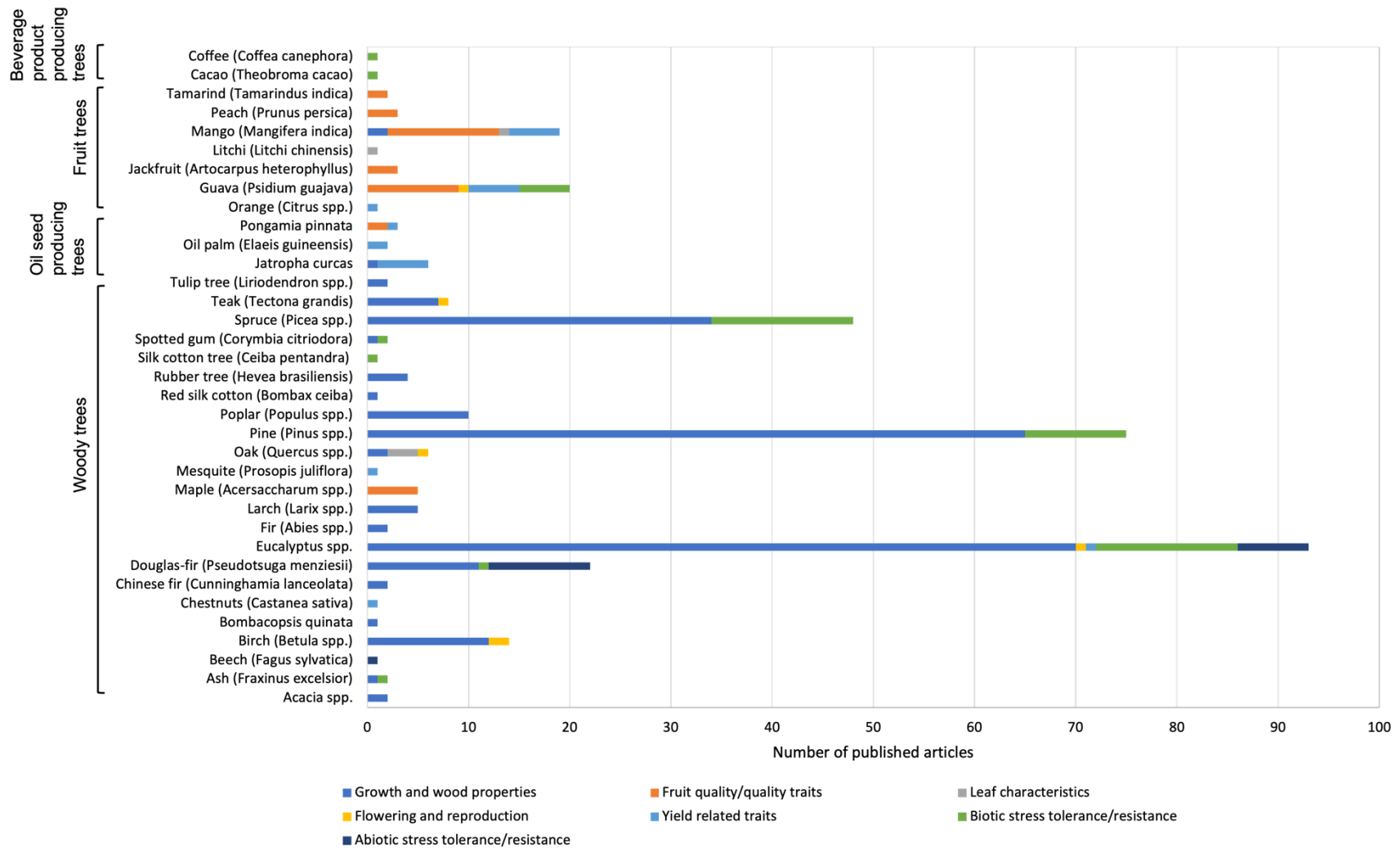


Figure S3. Tree species considered for genetic improvement by classical or conventional breeding (CB).

Table S1. List of tree genetic improvement events using genomic selection or marker assisted selection (GS/MAS)				
	Tree species/texta	Traits studied	Marker used/developed	References
Woody trees	<i>Acacia spp.</i>	Growth and wood properties	SNP	(1)
		Genetic diversity/structure/linkage	SSR	(2)
	Argan tree (<i>Argania spinosa</i>)	Genetic diversity/structure/linkage	SRAP and REMAP	(3-5)
	Ash (<i>Fraxinus spp.</i>)	Leaf characteristics	SSR	(6)
		Flowering and reproduction	SSR	(7-10)
		Biotic stress tolerance/resistance	SSR, RAMS, SNP	(11-20)
		Genetic diversity/structure/linkage	SSR, RFLP, allozyme	(21-50)
		Marker development	SSR, RAPD, SCAR	(51, 52)
	<i>Avicennia marina</i>	Genetic diversity/structure/linkage	SSR, AFLP	(53-56)
	Beech (<i>Fagus spp.</i>)	Growth and wood properties	SNP	(57)
		Flowering and reproduction	SNP	(58)
		Biotic stress tolerance/resistance	SNP	(59)
	<i>Betula spp.</i>	Genetic diversity/structure/linkage	AFLP, RFLP, SSR, RAPD	(60-71)
	<i>Cariniana estrellensis</i>	Genetic diversity/structure/linkage	SNP	(72)
	<i>Casuarina spp.</i>	Marker development	SSR	(73)
	Chestnut (<i>Castanea spp.</i>)	Fruit quality/quality traits	SNP	(74)
		Flowering and reproduction	SSR	(75)
		Yield related traits	SNP, SSR	(76)
		Biotic stress tolerance/resistance	SNP, SSR, AFLP, RFLP, RAPD, isozyme	(77-86)
		Abiotic stress tolerance/resistance	SSR	(87, 88)
		Genetic diversity/structure/linkage	SNP, SSR, ISSR, AFLP, RFLP, RAPD, allozyme, isozyme	(89-126)
	Chinese sweetgum (<i>Liquidambar formosana</i>)	Genetic diversity/structure/linkage	SSR	(127)
	Chinese fir (<i>Cunninghamia lanceolata</i>)	Growth and wood properties	SNPs	(128)

		Marker development	SRAP	(129)
	<i>Commiphora spp.</i>	Marker development	SCAR	(130)
	<i>Dalbergia odorifera</i>	Genetic diversity/structure/linkage	SSR	(131)
		Marker development	SSR	(132)
	<i>Derris trifoliata</i>	Genetic diversity/structure/linkage	ISSR	(133)
	Dog- wood (<i>Cornus xorida</i>)	Genetic diversity/structure/linkage	SSR	(134)
	Douglas-fir (<i>Pseudotsuga menziesii</i>)	Growth and wood properties	SNP	(135, 136)
		Flowering and reproduction	RAPD, RFLP	(137-139)
		Abiotic stress tolerance/resistance	SNP, RFLP, SSR	(140-144)
		Genetic diversity/structure/linkage	RAPD, allozyme	(145-148)
		Marker development	SSR	(149)
	<i>Eucalyptus spp.</i>	Growth and wood properties	SNP, DAiT, RAPD, SSR	(150-167)
		Flowering and reproduction	SSR	(168)
		Yield related traits	SNP	(169, 170)
		Biotic stress tolerance/resistance	SNP	(171-173)
		Genetic diversity/structure/linkage	RAPD, ISSR, SSR	(174-180)
		Marker development	SNP, DAiT	(181, 182)
	<i>Excoecaria agallocha</i>	Genetic diversity/structure/linkage	ISSR	(183)
	Fig (<i>Ficus carica</i>)	Genetic diversity/structure/linkage	SSR, AFLP	(184)
		Marker development	SSR, RAPD	(185)
	<i>Foetidia mauritiana</i>	Genetic diversity/structure/linkage	SNP	(186)
		Marker development	SSR	(187)
	<i>Garcinia kola</i>	Genetic diversity/structure/linkage	RAPD	(188)
	Hawthorn (<i>Crataegus spp.</i>)	Genetic diversity/structure/linkage	SSR	(189)
	Japanese cedar (<i>Cryptomeria japonica</i>)	Growth and wood properties	SNP	(190, 191)
		Flowering and reproduction	SNP, PCR marker	(192, 193)
		Marker development	SNP	(194, 195)
	<i>Kandelia obovata</i>	Growth and wood properties	SNP	(196)

		Genetic diversity/structure/linkage	AFLP	(197)
	<i>Lagerstroemia spp.</i>	Genetic diversity/structure/linkage	AFLP, SSR	(198)
	Larch (<i>Larix spp.</i>)	Genetic diversity/structure/linkage	RAPD	(199)
	Loquat (<i>Eriobotrya japonica</i>)	Marker development	SSR	(200)
	<i>Magnolia stellata</i>	Genetic diversity/structure/linkage	SSR	(201)
	Maple (<i>Acer spp.</i>)	Genetic diversity/structure/linkage	SSR, allozyme	(202-207)
		Marker development	SSR	(208-214)
	<i>Michelia shiluensis</i>	Genetic diversity/structure/linkage	SSR	(215)
		Marker development	SSR	(216)
	Oak (<i>Quercus spp.</i>)	Leaf Characteristics	ISSR	(217)
		Genetic diversity/structure/linkage	SNP, SSR, ISSR, RFLP, AFLP, RAPD, IRAP, SCoT, allozyme	(218-277)
		Marker development	SSR	(278-286)
	Poplar (<i>Populus spp.</i>)	Growth and wood properties	SNP, SSR, AFLP	(287-300)
		Flowering and reproduction	SNP	(301, 302)
		Yield related traits	SNP	(303)
		Biotic stress tolerance/resistance	SNP	(304, 305)
		Genetic diversity/structure/linkage	SSR, AFLP, RAPD, ISSR, SNP	(306-309)
	Pine (<i>Pinus spp.</i>)	Growth and wood properties	SNP, RAPD	(290, 310-325)
		Yield related traits	SSR, ISSR and AFLP	(326)
		Biotic stress tolerance/resistance	SNP, RAPD	(327-329)
		Abiotic stress tolerance/resistance	SNP, RAPD	(330, 331)
		Genetic diversity/structure/linkage	SNP, SSR, ISSR, AFLP, RAPD	(332-339)
	Spruce (<i>Picea spp.</i>)	Growth and wood properties	SNP	(340-349)
		Biotic stress tolerance/resistance	SNP	(350, 351)
		Genetic diversity/structure/linkage	RAPD	(352, 353)
		Marker development	SNP	(354)
	<i>Polylepis spp.</i>	Genetic diversity/structure/linkage	ISSR, AFLP, RAPD, allozyme	(355-361)

	<i>Rhizophora apiculata</i>	Genetic diversity/structure/linkage	SSR	(362)
	Rubber tree (<i>Hevea brasiliensis</i>)	Growth and wood properties	SNP	(363)
		Fruit quality/quality traits	SNP	(364)
		Yield related traits	SNP, SSR	(365-367)
		Biotic stress tolerance/resistance	SNP, SSR, AFLP, RFLP, isozymes	(368-371)
		Genetic diversity/structure/linkage	SNP, ISSR, RFLP	(372-374)
		Marker development	SNP, SSR	(375-377)
	Red silk cotton (<i>Bombax ceiba</i>)	Marker development	SSR	(378, 379)
	<i>Salvadora persica</i>	Genetic diversity/structure/linkage	ISSR	(380)
	Sandalwood (<i>Osyris lanceolata</i>)	Genetic diversity/structure/linkage	ISSR	(381)
	Teak (<i>Tectona grandis</i>)	Genetic diversity/structure/linkage	SNP, SSR, ISSR, AFLP, RAPD	(382-386)
	<i>Terminalia arjuna</i>	Genetic diversity/structure/linkage	AFLP, SAMPL	(387)
	<i>Thuja spp.</i>	Genetic diversity/structure/linkage	SSR	(388, 389)
		Marker development	SSR	(390)
	Tree peony (<i>Paeonia suffruticosa</i>)	Flowering and reproduction	SNP	(391)
		Marker development	SSR	(392, 393)
	<i>Torreya grandis</i>	Growth and wood properties	AFLP, RAPD	(394)
	Tulip tree (<i>Liriodendron spp.</i>)	Marker development	SSR	(395-397)
	Willow (<i>Salix spp.</i>)	Yield related traits	SNP	(398)
		Genetic diversity/structure/linkage	AFLP, RAPD, ISSR	(399, 400)
	<i>Uapaca kirkiana</i>	Genetic diversity/structure/linkage	AFLP	(401)
Oil seed	<i>Jatropha curcas</i>	Fruit quality/quality traits	SNP	(402)
		Yield related traits	SNP, DAiT	(403)
		Genetic diversity/structure/linkage	SNP, SSR, ISSR, AFLP, RAPD, SCAR, DAMD	(404-434)
		Marker development	SSR, AFLP, RAPD, SCAR	(435-437)
	Oil palm (<i>Elaeis guineensis</i>)	Growth and wood properties	SNP, SSR	(438-440)
		Fruit quality/quality traits	SNP	(441-443)

		Yield related traits	SNP, SSR	(444-447)
		Genetic diversity/structure/linkage	ISSR, RFLP, AFLP, SSR	(448, 449)
		Marker development	SNP	(450, 451)
	<i>Pongamia pinnata</i>	Yield related traits	RAPD	(452)
		Genetic diversity/structure/linkage	ISSR, AFLP, RAPD	(453-455)
Fruit trees	Apple (<i>Malus domestica</i>)	Fruit quality/quality traits	SNP, SSR	(456-467)
		Biotic stress tolerance/resistance	SNP, SSR, SCAR, CAPS	(468-471)
		Genetic diversity/structure/linkage	SNP, SSR	(472, 473)
		Marker development	SNP	(474, 475)
	Avocado (<i>Persea americana</i>)	Abiotic stress tolerance/resistance	SNP	(476)
	Blueberries (<i>Vaccinium spp.</i>)	Fruit quality/quality traits	SSR	(477)
	Orange (<i>Citrus spp.</i>)	Fruit quality/quality traits	SNP, DAiT	(478-480)
		Genetic diversity/structure/linkage	SNP, SSR, ISSR, DAiT, AFLP, RAPD, SSAP, SAMPL, SRAP, CAPS-SNP, POGP, RGA	(481-492)
		Marker development	DAiT	(493)
	Coconut (<i>Cocos nucifera</i>)	Flowering and reproduction	AFLP, RAPD, ISSR	(494)
		Genetic diversity/structure/linkage	SSR, AFLP, RFLP, RAPD, SCoT, SRAP	(495-507)
		Marker development	SSR	(508-510)
	Date palm (<i>Phoenix dactylifera</i>)	Genetic diversity/structure/linkage	SSR, ISSR, RAPD, RFLP, AFLP	(511-514)
		Marker development	SSR	(515)
	Durian (<i>Durio zibethinus</i>)	Biotic stress tolerance/resistance	SCAR	(516)
		Genetic diversity/structure/linkage	SSR, ISSR, RAPD, SCAR, RBCL	(517-534)
		Marker development	SSR	(534, 535)
	Grape (<i>Vitis vinifera</i>)	Fruit quality/quality traits	SNP	(536, 537)
		Genetic diversity/structure/linkage	SNP	(538)
	Guava (<i>Psidium guajava</i>)	Fruit quality/quality traits	SSR, RAPD, SSAP	(539-543)

		Yield related traits	SNP	(544)
		Biotic stress tolerance/resistance	SSR, SCAR, RGA	(545-547)
		Genetic diversity/structure/linkage	SSR, AFLP, RAPD, SRAP	(548-573)
		Marker development	SNP/InDel, SSR, AFLP	(574-579)
	Jackfruit (<i>Artocarpus heterophyllus</i>)	Fruit quality/quality traits	SSR, RAPD	(580, 581)
		Genetic diversity/structure/linkage	SSR, AFLP, RFLP, RAPD, SRAP, isozyme	(582-592)
		Marker development	SSR	(593)
	Jujube (<i>Ziziphus jujuba</i>)	Fruit quality/quality traits	ISSR	(594)
		Genetic diversity/structure/linkage	SNP, ISSR	(595, 596)
		Marker development	SSR	(597)
	Litchi (<i>Litchi chinensis</i>)	Fruit quality/quality traits	SNP	(598)
		Flowering and reproduction	SSR	(599)
		Genetic diversity/structure/linkage	SNP, SSR, ISSR, AFLP, RAPD, isozyme	(600-612)
		Marker development	SSR	(613)
	Mango (<i>Mangifera indica</i>)	Fruit quality/quality traits	SNP, SSR	(614-616)
		Genetic diversity/structure/linkage	SNP, SSR, ISSR, AFLP, RAPD, SCoT, SRAP, DAMD, CBDP	(617-663)
		Marker development	SNP, SSR	(664-671)
	Mulberry (<i>Morus spp.</i>)	Abiotic stress tolerance/resistance	SNP	(672)
		Genetic diversity/structure/linkage	ISSR	(673, 674)
		Marker development	SSR, ISSR, RAPD	(675, 676)
	Olive (<i>Olea europaea</i>)	Fruit quality/quality traits	SNP	(677, 678)
		Flowering and reproduction	SNP, SSR	(679-687)
		Genetic diversity/structure/linkage	SNP, SSR, ISSR, AFLP, RAPD, SCAR, CAPS	(688-713)
		Marker development	SSR, DaT, SASPL	(714-718)
	Passion fruit (<i>Passiflora edulis</i>)	Genetic diversity/structure/linkage	ISSR, RAPD	(719)

	Persimmons (<i>Diospyros kaki</i>)	Fruit quality/quality traits	SNP, SSR	(720)
		Genetic diversity/structure/linkage	SCAR	(721)
	Pear (<i>Pyrus spp.</i>)	Fruit quality/quality traits	SNP	(722-724)
		Flowering and reproduction	SNP	(725, 726)
		Biotic stress tolerance/resistance	SSR, RAPD, STS	(727, 728)
		Genetic diversity/structure/linkage	SSR, ISSR, RAPD	(729-731)
		Marker development	SNP	(732)
	<i>Prunus spp.</i>	Fruit quality/quality traits	SNP, SSR, AFLP, RFLP, RAPD, SCAR	(733-766)
		Leaf characteristics	SSR, RFLP, RAPD	(767-769)
		Flowering and reproduction	SSR, AFLP, RFLP, RAPD	(770-778)
		Biotic stress tolerance/resistance	SNP, SSR, AFLP, RAPD, SCAR, SRAP, STS	(779-797)
		Abiotic stress tolerance/resistance	SNP, SSR, AFLP	(798-801)
		Genetic diversity/structure/linkage	SNP, SSR, RFLP, RAPD	(802-819)
		Marker development	SSR	(820, 821)
	Pomegranate (<i>Punica granatum</i>)	Genetic diversity/structure/linkage	SSR, ISSR, AFLP, RAPD, ISTR, SRAP, DAMD	(822-825)
Nuts	Brazil nut (<i>Bertholletia excelsa</i>)	Genetic diversity/structure/linkage	SSR, isozyme	(826-828)
		Marker development	SSR	(829, 830)
	Cashew nut (<i>Anacardium spp.</i>)	Genetic diversity/structure/linkage	SSR	(831, 832)
	Hazelnut (<i>Corylus avellana</i>)	Growth and wood properties	SSR	(833)
		Biotic stress tolerance/resistance	SSR, RAPD	(834-836)
		Genetic diversity/structure/linkage	SSR	(837, 838)
		Marker development	SSR	(839)
	Macadamia (<i>Macadamia integrifolia</i>)	Fruit quality/quality traits	SNP	(840, 841)
		Genetic diversity/structure/linkage	SNP, DArT	(842, 843)
	Pecan (<i>Carya illinoensis</i>)	Flowering and reproduction	SNP	(844)
	Pistachio (<i>Pistacia vera</i>)	Genetic diversity/structure/linkage	CDDP	(845)

	Walnut (<i>Juglans regia</i>)	Fruit quality/quality traits	SNP	(846)
		Leaf characteristics	SNP	(847)
		Flowering and reproduction	SNP	(848)
		Yield related traits	SNP	(849)
		Abiotic stress tolerance/resistance	SNP	(850)
		Genetic diversity/structure/linkage	SNP, SSR, ISSR	(851-857)
Beverage	Cacao (<i>Theobroma cacao</i>)	Flowering and reproduction	SNP	(858)
		Biotic stress tolerance/resistance	SNP, SSR	(859-862)
	Coffee (<i>Coffea spp.</i>)	Growth and wood properties	SNP	(863)
		Fruit quality/quality traits	SNP	(864, 865)
		Yield related traits	SNP	(866-868)
		Biotic stress tolerance/resistance	SNP	(869)
		Genetic diversity/structure/linkage	SNP, SSR, AFLP, RAPD, SRAP, SCoT	(870-875)
	Tea (<i>Camellia sinensis</i>)	Fruit quality/quality traits	SNP, InDel, SSR, CAPS	(876-884)
		Yield related traits	SSR, AFLP, RAPD	(885)
		Abiotic stress tolerance/resistance	AFLP, RAPD	(886-888)
		Genetic diversity/structure/linkage	SNP, SSR, ISSR, AFLP, RAPD, CAPS, STS	(889-897)

Table S2. List of tree genetic improvement events using genetic engineering or genetic modification (GE/GM) approaches				
	Tree species/texta	Traits studied	Main GM/GE method used	References
Woody trees	Ash (<i>Fraxinus nigra</i>)	Biotic stress tolerance/resistance	CRISPR/Cas system	(898)
	Chestnut (<i>Castanea spp.</i>)	Biotic stress tolerance/resistance	Agrobacterium-mediated transformation	(899-901)
		Leaf characteristics	CRISPR/Cas system	(902)
	<i>Eucalyptus spp.</i>	Growth and wood properties	Agrobacterium-mediated transformation	(903, 904)
			CRISPR/Cas system	(905, 906)
		Flowering and reproduction	Agrobacterium-mediated transformation	(907)
		Biotic stress tolerance/resistance	Agrobacterium-mediated transformation	(908)
	Fig (<i>Ficus carica</i>)	Fruit quality/quality traits	CRISPR/Cas9 system	(909)
	<i>Ginkgo biloba</i>	Fruit quality/quality traits	Agrobacterium-mediated transformation	(910)
	<i>Larix decidua</i>	Biotic stress tolerance/resistance	Agrobacterium-mediated transformation	(911)
	London plane tree (<i>Platanus acerifolia</i>)	Growth and wood properties	Agrobacterium-mediated transformation	(912)
	Oak (<i>Quercus spp.</i>)	Biotic stress tolerance/resistance	Agrobacterium-mediated transformation	(913, 914)
	<i>Parasponia andersonii</i>	Growth and wood properties	CRISPR/Cas system	(915)
	Paulownia (<i>Paulownia elongata</i>)	Biotic stress tolerance/resistance	Biolistic transformation	(916)
	Poplar (<i>Populus spp.</i>)	Growth and wood properties	Agrobacterium-mediated transformation	(917-933)
			Antisense inhibition	(934-940)
			CRISPR/Cas system	(941-955)
			RNA interference	(956-961)
		Leaf characteristics	CRISPR/Cas system	(962-964)

		Flowering and reproduction	Agrobacterium-mediated transformation	(965, 966)
			CRISPR/Cas system	(967)
		Biotic stress tolerance/resistance	Agrobacterium-mediated transformation	(968-976)
			CRISPR/Cas system	(977-979)
		Abiotic stress tolerance/resistance	Agrobacterium-mediated transformation	(980-988)
			CRISPR/Cas system	(989, 990)
			Biolistic transformation	(991)
	<i>Pinus spp.</i>	Growth and wood properties	CRISPR/Cas system	(992)
			Biolistic transformation	(993)
			RNA interference	(994)
		Biotic stress tolerance/resistance	Agrobacterium-mediated transformation	(995)
			Biolistic transformation	(996, 997)
		Abiotic stress tolerance/resistance	Agrobacterium-mediated transformation	(998, 999)
	Rubber tree (<i>Hevea brasiliensis</i>)	Flowering and reproduction	CRISPR/Cas system	(1000, 1001)
	Spruce (<i>Picea spp.</i>)	Growth and wood properties	Biolistic transformation	(1002)
			RNA interference	(1003)
		Biotic stress tolerance/resistance	Biolistic transformation	(1004)
Oil seed	<i>Jatropha curcas</i>	Growth and wood properties	Agrobacterium-mediated transformation	(1005, 1006)
			CRISPR/Cas system	(1007)
		Fruit quality/quality traits	Agrobacterium-mediated transformation	(1008, 1009)
			Biolistic transformation	(1010)
			RNA interference	(1011-1013)
		Flowering and reproduction	Agrobacterium-mediated transformation	(1014, 1015)

		Biotic stress tolerance/resistance	RNA interference	(1016)
		Abiotic stress tolerance/resistance	Agrobacterium-mediated transformation	(1017)
			Biostatic transformation	(1018)
		Transgenic plant development	Agrobacterium-mediated transformation	(1019)
	Fruit trees	Apple (<i>Malus domestica</i>)	Growth and wood properties	Agrobacterium-mediated transformation (1020)
			Fruit quality/quality traits	Agrobacterium-mediated transformation (1021, 1022)
			Leaf characteristics	CRISPR/Cas system (1023, 1024)
			Biotic stress tolerance/resistance	Agrobacterium-mediated transformation (1025-1028)
				CRISPR/Cas system (1029, 1030)
			Abiotic stress tolerance/resistance	Agrobacterium-mediated transformation (1031-1035)
		Blueberry (<i>Vaccinium corymbosum</i>)	Yield related traits	Agrobacterium-mediated transformation (1036)
		Orange (<i>Citrus spp.</i>)	Growth and wood properties	Agrobacterium-mediated transformation (1037)
			Fruit quality/quality traits	Agrobacterium-mediated transformation (1038-1041)
			Leaf characteristics	Agrobacterium-mediated transformation (1042, 1043)
				CRISPR/Cas system (1044-1046)
			Flowering and reproduction	Agrobacterium-mediated transformation (1047, 1048)
			Biotic stress tolerance/resistance	Agrobacterium-mediated transformation (1049-1061)
				CRISPR/Cas system (1062-1066)
			Abiotic stress tolerance/resistance	Agrobacterium-mediated transformation (1067-1069)
			Transgenic plant development	Agrobacterium-mediated transformation (1070-1085)

			Biolistic transformation	(1086, 1087)
	Grape (<i>Vitis vinifera</i>)	Growth and wood properties	CRISPR/Cas system	(1088)
		Fruit quality/quality traits	Agrobacterium-mediated transformation	(1021, 1089, 1090)
			CRISPR/Cas system	(1091, 1092)
		Leaf characteristics	CRISPR/Cas system	(1093)
		Flowering and reproduction	Agrobacterium-mediated transformation	(1094)
		Biotic stress tolerance/resistance	Agrobacterium-mediated transformation	(1095, 1096)
			CRISPR/Cas system	(1029, 1097, 1098)
	Kiwifruit (<i>Actinidia spp.</i>)	Leaf characteristics	CRISPR/Cas system	(1099)
		Flowering and reproduction	Agrobacterium-mediated transformation	(1100-1102)
			CRISPR/Cas system	(1103)
		Biotic stress tolerance/resistance	Agrobacterium-mediated transformation	(1104)
	Litchi (<i>Litchi chinensis</i>)	Fruit quality/quality traits	Agrobacterium-mediated transformation	(1105, 1106)
	Mango (<i>Mangifera indica</i>)	Fruit quality/quality traits	Agrobacterium-mediated transformation	(1107, 1108)
	Mulberry (<i>Morus spp.</i>)	Abiotic stress tolerance/resistance	Agrobacterium-mediated transformation	(1109-1116)
		Transgenic plant development	Agrobacterium-mediated transformation	(1117-1119)
			Biolistic transformation	(1120)
			Protoplast electroporation	(1121)
	Pear (<i>Pyrus spp.</i>)	Growth and wood properties	Agrobacterium-mediated transformation	(1122, 1123)
		Flowering and reproduction	CRISPR/Cas system	(1024)
		Biotic stress tolerance/resistance	CRISPR/Cas system	(1030)

	Pomegranate (<i>Punica granatum</i>)	Fruit quality/quality traits	CRISPR/Cas system	(1124)
		Transgenic plant development	Agrobacterium-mediated transformation	(1125)
	<i>Prunus spp.</i>	Biotic stress tolerance/resistance	Agrobacterium-mediated transformation	(1126)
		Transgenic plant development	Agrobacterium-mediated transformation	(1127-1129)
	Olive (<i>Olea europaea</i>)	Biotic stress tolerance/resistance	Agrobacterium-mediated transformation	(1130-1132)
		Abiotic stress tolerance/resistance	Agrobacterium-mediated transformation	(1133, 1134)
		Transgenic plant development	Agrobacterium-mediated transformation	(1135)
Nut	Walnut (<i>Juglans regia</i>)	Leaf characteristics	CRISPR/Cas system	(1136)
Beverage	Cacao (<i>Theobroma cacao</i>)	Biotic stress tolerance/resistance	CRISPR/Cas system	(1137)
	Coffee (<i>Coffea canephora</i>)	Fruit quality/quality traits	CRISPR/Cas system	(1138)
	Tea plant (<i>Camellia sinensis</i>)	Fruit quality/quality traits	CRISPR/Cas system	(1139, 1140)

Table S3. List of tree genetic improvement events using classical or conventional breeding (CB) approaches				
	Tree species/Texa	Traits studied	Study focused on	References
Woody trees	<i>Acacia spp.</i>	Growth and wood properties	Genetic diversity/variation/variability	(1141, 1142)
	<i>Ash (Fraxinus excelsior)</i>	Growth and wood properties	Genetic diversity/variation/variability	(1143)
		Biotic stress tolerance/resistance	Hybridization and genetic effects	(1144)
	<i>Beech (Fagus sylvatica)</i>	Abiotic stress tolerance/resistance	Genetic diversity/variation/variability	(1145)
	<i>Birch (Betula spp.)</i>	Growth and wood properties	Genetic diversity/variation/variability	(1146-1149)
			Genetic selection/characterization/evaluation	(1150)
			Hybridization and genetic effects	(1151-1153)
			Heritability and genetic correlation	(1154-1157)
		Flowering and reproduction	Hybridization and genetic effects	(1158, 1159)
	<i>Bombacopsis quinata</i>	Growth and wood properties	Genetic diversity/variation/variability	(1160)
	<i>Chestnuts (Castanea sativa)</i>	Yield related traits	Genetic diversity/variation/variability	(1161)
	<i>Chinese fir (Cunninghamia lanceolata)</i>	Growth and wood properties	Heritability and genetic correlation	(1162)
			G x E interaction and genetic stability	(1163)
	<i>Douglas-fir (Pseudotsuga menziesii)</i>	Growth and wood properties	Genetic diversity/variation/variability	(1164-1167)
			Genetic selection/characterization/evaluation	(1168-1170)
			Hybridization and genetic effects	(1171)
			G x E interaction and genetic stability	(1172-1174)
		Biotic stress tolerance/resistance	Genetic diversity/variation/variability	(1175)
		Abiotic stress tolerance/resistance	Genetic diversity/variation/variability	(1176-1181)
			Genetic selection/characterization/evaluation	(1182)
			Heritability and genetic correlation	(1183)
			Hybridization and genetic effects	(1184, 1185)

	<i>Eucalyptus spp.</i>	Growth and wood properties	Genetic diversity/variation/variability	(1186-1206)
			Genetic selection/characterization/evaluation	(1207-1215)
			Heritability and genetic correlation	(1216-1235)
			Hybridization and genetic effects	(1236-1251)
			G x E interaction and genetic stability	(1252-1256)
		Flowering and reproduction	Heritability and genetic correlation	(1257)
		Yield related traits	Heritability and genetic correlation	(1258)
		Biotic stress tolerance/resistance	Genetic diversity/variation/variability	(1259-1265)
			Heritability and genetic correlation	(1266-1268)
			Hybridization and genetic effects	(1269-1271)
			G x E interaction and genetic stability	(1272)
		Abiotic stress tolerance/resistance	Genetic diversity/variation/variability	(1273-1277)
			Heritability and genetic correlation	(1278, 1279)
	Fir (<i>Abies spp.</i>)	Growth and wood properties	Genetic diversity/variation/variability	(1280)
			Heritability and genetic correlation	(1281)
	Larch (<i>Larix spp.</i>)	Growth and wood properties	Genetic diversity/variation/variability	(1282, 1283)
			Heritability and genetic correlation	(1284)
			Hybridization and genetic effects	(1285, 1286)
	Maple (<i>Acer saccharum spp.</i>)	Fruit quality/quality traits	Genetic diversity/variation/variability	(1287)
			Genetic selection/characterization/evaluation	(1288-1291)
	Mesquite (<i>Prosopis juliflora</i>)	Yield related traits	Genetic selection/characterization/evaluation	(1292)
	Oak (<i>Quercus spp.</i>)	Growth and wood properties	Genetic diversity/variation/variability	(1293, 1294)
		Leaf characteristics	Genetic diversity/variation/variability	(1295, 1296)
			Hybridization and genetic effects	(1297)
		Flowering and reproduction	Hybridization and genetic effects	(1298)
	Pine (<i>Pinus spp.</i>)	Growth and wood properties	Genetic diversity/variation/variability	(1299-1308)

			Genetic selection/characterization/evaluation	(1309-1315)
			Heritability and genetic correlation	(1316-1346)
			Hybridization and genetic effects	(1347-1349)
			G x E interaction and genetic stability	(1350-1364)
		Biotic stress tolerance/resistance	Genetic diversity/variation/variability	(1365-1367)
			Genetic selection/characterization/evaluation	(1368, 1369)
			Heritability and genetic correlation	(1370-1373)
			G x E interaction and genetic stability	(1374)
	Poplar (<i>Populus spp.</i>)	Growth and wood properties	Genetic diversity/variation/variability	(1375-1379)
			Heritability and genetic correlation	(1380)
			Hybridization and genetic effects	(1381-1384)
	Red silk cotton (<i>Bombax ceiba</i>)	Growth and wood properties	Genetic diversity/variation/variability	(1385)
	Rubber tree (<i>Hevea brasiliensis</i>)	Growth and wood properties	Genetic diversity/variation/variability	(1386, 1387)
			Heritability and genetic correlation	(1388, 1389)
	Silk cotton tree (<i>Ceiba pentandra</i>)	Biotic stress tolerance/resistance	Heritability and genetic correlation	(1390)
	Spotted gum (<i>Corymbia citriodora</i>)	Growth and wood properties	Genetic selection/characterization/evaluation	(1391)
		Biotic stress tolerance/resistance	Heritability and genetic correlation	(1392)
	Spruce (<i>Picea spp.</i>)	Growth and wood properties	Genetic diversity/variation/variability	(1393-1402)
			Genetic selection/characterization/evaluation	(1403-1405)
			Heritability and genetic correlation	(1406-1420)
			Hybridization and genetic effects	(1421, 1422)
			G x E interaction and genetic stability	(1423-1426)
		Biotic stress tolerance/resistance	Genetic diversity/variation/variability	(1427-1437)
			Heritability and genetic correlation	(1438-1440)

	Teak (<i>Tectona grandis</i>)	Growth and wood properties	Genetic diversity/variation/variability	(1441-1444)
			Genetic selection/characterization/evaluation	(1445, 1446)
			Heritability and genetic correlation	(1447)
	Tulip tree (<i>Liriodendron spp.</i>)	Flowering and reproduction	Genetic diversity/variation/variability	(1448)
		Growth and wood properties	Hybridization and genetic effects	(1449, 1450)
Oil seed	<i>Jatropha curcas</i>	Growth and wood properties	Genetic diversity/variation/variability	(1451)
		Yield related traits	Genetic diversity/variation/variability	(1452-1456)
	Oil palm (<i>Elaeis guineensis</i>)	Yield related traits	Genetic selection/characterization/evaluation	(1457)
			Hybridization and genetic effects	(1458)
	<i>Pongamia pinnata</i>	Fruit quality/quality traits	Genetic diversity/variation/variability	(1459, 1460)
		Yield related traits	Genetic diversity/variation/variability	(1461)
Fruit trees	Orange (<i>Citrus spp.</i>)	Yield related traits	Heritability and genetic correlation	(1462)
	Guava (<i>Psidium guajava</i>)	Fruit quality/quality traits	Genetic diversity/variation/variability	(1463-1467)
			Genetic selection/characterization/evaluation	(1468, 1469)
			Heritability and genetic correlation	(1470, 1471)
		Flowering and reproduction	Genetic diversity/variation/variability	(1472)
		Yield related traits	Genetic diversity/variation/variability	(1473, 1474)
			Heritability and genetic correlation	(1475-1477)
		Biotic stress tolerance/resistance	Genetic selection/characterization/evaluation	(1478-1480)
			Heritability and genetic correlation	(1481)
			Hybridization and genetic effects	(1482)
	Jackfruit (<i>Artocarpus heterophyllus</i>)	Fruit quality/quality traits	Genetic diversity/variation/variability	(1483, 1484)
			Genetic selection/characterization/evaluation	(1485)
	Litchi (<i>Litchi chinensis</i>)	Leaf characteristics	Genetic diversity/variation/variability	(1486)
	Mango (<i>Mangifera indica</i>)	Growth and wood properties	Genetic diversity/variation/variability	(1487, 1488)

		Fruit quality/quality traits	Genetic diversity/variation/variability	(1489-1494)
			Genetic selection/characterization/evaluation	(1495-1497)
			Heritability and genetic correlation	(1498, 1499)
		Leaf characteristics	Genetic diversity/variation/variability	(1500)
		Yield related traits	Genetic diversity/variation/variability	(1501-1503)
	Genetic selection/characterization/evaluation		(1504, 1505)	
	Peach (<i>Prunus persica</i>)	Fruit quality/quality traits	Genetic diversity/variation/variability	(1506-1508)
			Heritability and genetic correlation	(1509)
	Tamarind (<i>Tamarindus indica</i>)	Fruit quality/quality traits	Genetic diversity/variation/variability	(1510, 1511)
	Beverage	Cacao (<i>Theobroma cacao</i>)	Biotic stress tolerance/resistance	Hybridization and genetic effects
Coffee (<i>Coffea canephora</i>)		Biotic stress tolerance/resistance	Hybridization and genetic effects	(1513)

References

1. Muhammad AJ, Choong CY, Wong M, Abdullah MZ, Norwati M, Wickneswari R. Genetic mapping and QTL analysis of important traits based on single nucleotide polymorphisms in Acacia hybrid population. *Acta Ecologica Sinica*. 2021.
2. Tchatchoua TD, Poethig RS, Doody E, Weathers TC, Swartz K, Mathieson I, et al. Genetic diversity of *Faidherbia albida* populations in the Sudano Sahelian region of Cameroon, using simple sequence repeat (SSR) markers. *African Journal of Biotechnology*. 2020;19(7):415-25.
3. El Mousadik A, Petit R. High level of genetic differentiation for allelic richness among populations of the argan tree [*Argania spinosa* (L.) Skeels] endemic to Morocco. *Theoretical and applied genetics*. 1996;92(7):832-9.
4. Pakhrou O, Medraoui L, Belkadi B, Rachidi F, Errahmani H, Alami M, et al. Using two retrotransposon-based marker systems (SRAP and REMAP) for genetic diversity analysis of Moroccan Argan tree. *Molecular Biology Research Communications*. 2020;9(3):93.
5. Ait Aabd N, Bouharroud R, Tahiri A, Wifaya A, Mimouni A, El Mousadik A. Genetic diversity and breeding of argan tree (*Argania spinosa* L. Skeels). *Advances in plant breeding strategies: nut and beverage crops*: Springer; 2019. p. 31-56.
6. Thomasset M, Fernandez-Manjarrés JF, Douglas GC, Frascaria-Lacoste N, Raquin C, Hodgkinson TR. Molecular and morphological characterization of reciprocal F1 hybrid ash (*Fraxinus excelsior* × *Fraxinus angustifolia*, Oleaceae) and parental species reveals asymmetric character inheritance. *International Journal of Plant Sciences*. 2011;172(3):423-33.
7. Gérard PR, Klein EK, Austerlitz F, Fernández-Manjarrés JF, Frascaria-Lacoste N. Assortative mating and differential male mating success in an ash hybrid zone population. *BMC Evolutionary Biology*. 2006;6(1):1-14.
8. Semizer-Cuming D, Chybicki IJ, Finkeldey R, Kjær ED. Gene flow and reproductive success in ash (*Fraxinus excelsior* L.) in the face of ash dieback: restoration and conservation. *Ann Forest Sci*. 2021;78(1):1-15.
9. Goto S, Shimatani K, Yoshimaru H, Takahashi Y. Fat-tailed gene flow in the dioecious canopy tree species *Fraxinus mandshurica* var. *japonica* revealed by microsatellites. *Molecular Ecology*. 2006;15(10):2985-96.
10. Bacles CF, Ennos RA. Paternity analysis of pollen-mediated gene flow for *Fraxinus excelsior* L. in a chronically fragmented landscape. *Heredity*. 2008;101(4):368-80.
11. Sønstebo JH, Vivian-Smith A, Adamson K, Drenkhan R, Solheim H, Hietala AM. Genome-wide population diversity in *Hymenoscyphus fraxineus* points to an eastern Russian origin of European Ash dieback. *BioRxiv*. 2017:154492.
12. Semizer-Cuming D, Kjaer ED, Finkeldey R. Gene flow of common ash (*Fraxinus excelsior* L.) in a fragmented landscape. *Plos One*. 2017;12(10).
13. Fussi B, Konnert M. Genetic analysis of European common ash (*Fraxinus excelsior* L.) populations affected by ash dieback. *Silvae Genet*. 2014;63:198-212.

14. Wohlmuth A, Essl F, Heinze B. Genetic analysis of inherited reduced susceptibility of *Fraxinus excelsior* L. seedlings in Austria to ash dieback. *Forestry: An International Journal of Forest Research*. 2018;91(4):514-25.
15. Hausman CE, Bertke MM, Jaeger JF, Rocha OJ. Genetic structure of green ash (*Fraxinus pennsylvanica*): implications for the establishment of ex situ conservation protocols in light of the invasion of the emerald ash borer. *Plant Genetic Resources*. 2014;12(3):286-97.
16. Held JB. Assessment of Genetic Diversity and Relatedness in an Emerald Ash Borer-Resistant Green Ash Population: Ohio University; 2017.
17. Koch J, Carey D, Mason M, Poland T, Knight K. Intraspecific variation in *Fraxinus pennsylvanica* responses to emerald ash borer (*Agrilus planipennis*). *New Forest*. 2015;46(5):995-1011.
18. Noakes AG, Best T, Staton ME, Koch J, Romero-Severson J. Cross amplification of 15 EST-SSR markers in the genus *Fraxinus*. *Conserv Genet Resour*. 2014;6(4):969-70.
19. Kraj W, Zarek M, Kowalski T. Genetic variability of *Chalara fraxinea*, dieback cause of European ash (*Fraxinus excelsior* L.). *Mycological Progress*. 2012;11(1):37-45.
20. Stocks JJ, Metheringham CL, Plumb WJ, Lee SJ, Kelly LJ, Nichols RA, et al. Genomic basis of European ash tree resistance to ash dieback fungus. *Nature ecology & evolution*. 2019;3(12):1686-96.
21. Heinze B, Fussi B. Pre-disease Levels of Genetic Diversity and Differentiation among Common Ash (*Fraxinus excelsior* L.) Seedlots in Austria. *Baltic Forestry*. 2017;23(1):198-208.
22. Tollefsrud MM, Myking T, Sonstebo JH, Lygis V, Hietala AM, Heuertz M. Genetic Structure in the Northern Range Margins of Common Ash, *Fraxinus excelsior* L. *Plos One*. 2016;11(12).
23. Beatty GE, Brown JA, Cassidy EM, Finlay C, McKendrick L, Montgomery WI, et al. Lack of genetic structure and evidence for long-distance dispersal in ash (*Fraxinus excelsior*) populations under threat from an emergent fungal pathogen: implications for restorative planting. *Tree Genetics & Genomes*. 2015;11(3):1-13.
24. Rungis D, Korica A, Gailite A, Puspure I, Veinberga I, editors. Analysis of the genetic diversity and population structure of Latvian ash (*Fraxinus excelsior* L.) stands using nuclear and chloroplast SSR markers. *Proceedings of the Latvian Academy of Sciences*; 2016: De Gruyter Poland.
25. Ferrazzini D, Monteleone I, Belletti P. Genetic variability and divergence among Italian populations of common ash (*Fraxinus excelsior* L.). *Ann Forest Sci*. 2007;64(2):159-68.
26. Sutherland B, Belaj A, Nier S, Cottrell J, P VAUGHAN S, Hubert J, et al. Molecular biodiversity and population structure in common ash (*Fraxinus excelsior* L.) in Britain: implications for conservation. *Molecular Ecology*. 2010;19(11):2196-211.
27. Heuertz M, Hausman JF, Hardy OJ, Vendramin GG, Frascaria-Lacoste N, Vekemans X. Nuclear microsatellites reveal contrasting patterns of genetic structure between western and southeastern European populations of the common ash (*Fraxinus excelsior* L.). *Evolution*. 2004;58(5):976-88.

28. Heuertz M, Fineschi S, Anzidei M, Pastorelli R, Salvini D, Paule L, et al. Chloroplast DNA variation and postglacial recolonization of common ash (*Fraxinus excelsior* L.) in Europe. *Molecular ecology*. 2004;13(11):3437-52.
29. FERNANDEZ-MANJARRES JF, Gérard PR, Dufour J, Raquin C, FRASCARIA-LACOSTE N. Differential patterns of morphological and molecular hybridization between *Fraxinus excelsior* L. and *Fraxinus angustifolia* Vahl (Oleaceae) in eastern and western France. *Molecular ecology*. 2006;15(11):3245-57.
30. Gömöry D, Paule L, Krajmerová D, ROMSÁKOVÁ I, Piecka J. Gene exchange across a postglacial contact zone in *Fraxinus excelsior* L. *Silvae Genet*. 2012;61(1-2):18-27.
31. Heuertz M, Carnevale S, Fineschi S, Sebastiani F, Hausman J, Paule L, et al. Chloroplast DNA phylogeography of European ashes, *Fraxinus* sp.(Oleaceae): roles of hybridization and life history traits. *Molecular ecology*. 2006;15(8):2131-40.
32. Morand ME, Brachet S, Rossignol P, Dufour J, Frascaria-Lacoste N. A generalized heterozygote deficiency assessed with microsatellites in French common ash populations. *Molecular Ecology*. 2002;11(3):377-85.
33. Bacles CF, Burczyk J, Lowe AJ, Ennos RA. HISTORICAL AND CONTEMPORARY MATING PATTERNS IN REMNANT POPULATIONS OF THE FOREST TREE *FRAXINUS EXCELSIOR* L. *Evolution*. 2005;59(5):979-90.
34. Hebel I, Haas R, Dounavi A. Genetic variation of common ash (*Fraxinus excelsior* L.) populations from provenance regions in southern Germany by using nuclear and chloroplast microsatellites. *Silvae Genet*. 2006;55(1):38-43.
35. Dacasa Rüdinger M, Glaeser J, Hebel I, Dounavi A. Genetic structures of common ash (*Fraxinus excelsior*) populations in Germany at sites differing in water regimes. *Canadian journal of forest research*. 2008;38(5):1199-210.
36. Holtken A, Tahtinen J, Pappinen A. Effects of discontinuous marginal habitats on the genetic structure of common ash (*Fraxinus excelsior* L.). *Silvae Genet*. 2003;52(5-6):206-11.
37. Ballian D, Monteleone I, Ferrazzini D, Kajba D, Belletti P. Genetic characterization of common ash (*Fraxinus excelsior* L.) populations in Bosnia and Herzegovina. *Periodicum biologorum*. 2008;110(4):323-8.
38. Hu LJ, Uchiyama K, Shen HL, Saito Y, Tsuda Y, Ide Y. Nuclear DNA microsatellites reveal genetic variation but a lack of phylogeographical structure in an endangered species, *Fraxinus mandshurica*, across north-east China. *Ann Bot-London*. 2008;102(2):195-205.
39. Heuertz M, Hausman JF, Tsvetkov I, Frascaria-Lacoste N, Vekemans X. Assessment of genetic structure within and among Bulgarian populations of the common ash (*Fraxinus excelsior* L.). *Molecular Ecology*. 2001;10(7):1615-23.
40. Thomasset M, Hodkinson T, Restoux G, Frascaria-Lacoste N, Douglas G, Fernández-Manjarrés J. Thank you for not flowering: conservation genetics and gene flow analysis of native and non-native populations of *Fraxinus* (Oleaceae) in Ireland. *Heredity*. 2014;112(6):596-606.
41. Thomasset M, Fernández-Manjarrés JF, Douglas GC, Bertolino P, Frascaria-Lacoste N, Hodkinson TR. Assignment testing reveals multiple introduced source populations including potential ash hybrids (*Fraxinus excelsior* × *F. angustifolia*) in Ireland. *Eur J Forest Res*. 2013;132(2):195-209.

42. Gerard PR, FERNANDEZ-MANJARRES JF, FRASCARIA-LACOSTE N. Temporal cline in a hybrid zone population between *Fraxinus excelsior* L. and *Fraxinus angustifolia* Vahl. *Molecular Ecology*. 2006;15(12):3655-67.
43. Morand-Prieur M, Vedel F, Raquin C, Brachet S, Sihachakr D, Frascaria-Lacoste N. Maternal inheritance of a chloroplast microsatellite marker in controlled hybrids between *Fraxinus excelsior* and *Fraxinus angustifolia*. *Molecular ecology*. 2002;11(3):613-7.
44. Abbate L, Mercati F, Di Noto G, Heuertz M, Carimi F, Fatta del Bosco S, et al. Genetic distinctiveness highlights the conservation value of a sicilian manna ash germplasm collection assigned to *Fraxinus angustifolia* (Oleaceae). *Plants*. 2020;9(8):1035.
45. Temunović M, Franjić J, Satovic Z, Grgurev M, Frascaria-Lacoste N, Fernández-Manjarrés JF. Environmental heterogeneity explains the genetic structure of continental and Mediterranean populations of *Fraxinus angustifolia* Vahl. 2012.
46. Papi R, Spanos K, Kyriakidis D. Genetic variation of *Fraxinus angustifolia* natural populations in Greece based on nuclear and chloroplast microsatellite markers. *Eur J Forest Res*. 2012;131(4):1151-61.
47. Lee HS, Chang C-S, Kim H, Choi DY. A preliminary population genetic study of an overlooked endemic ash, *Fraxinus chiisanensis* in Korea using allozyme variation. *Journal of Korean Society of Forest Science*. 2009;98(5):531-8.
48. Hu LJ, Uchiyama K, Saito Y, Ide Y. Contrasting patterns of nuclear microsatellite genetic structure of *Fraxinus mandshurica* var. *japonica* between northern and southern populations in Japan. *Journal of Biogeography*. 2010;37(6):1131-43.
49. Hu L-J, Uchiyama K, Shen H-L, Ide Y. Multiple-scaled spatial genetic structures of *Fraxinus mandshurica* over a riparian–mountain landscape in Northeast China. *Conserv Genet*. 2010;11(1):77-87.
50. Ishida K, Hiura T. Mating system and population genetic structure of an androdioecious tree, *Fraxinus lanuginosa* Koidz.(Oleaceae) in northern Japan. *Heredity*. 2002;88(4):296-301.
51. Harbourne M, Douglas G, Waldren S, Hodgkinson T. Characterization and primer development for amplification of chloroplast microsatellite regions of *Fraxinus excelsior*. *Journal of Plant Research*. 2005;118(5):339-41.
52. Gérard PR, Fernández-Manjarrés JF, Bertolino P, Dufour J, Raquin C, Frascaria-Lacoste N. New insights in the recognition of the European ash species *Fraxinus excelsior* L. and *Fraxinus angustifolia* Vahl as useful tools for forest management. *Ann Forest Sci*. 2006;63(7):733-8.
53. Maguire TL, Saenger P, Baverstock P, Henry R. Microsatellite analysis of genetic structure in the mangrove species *Avicennia marina* (Forsk.) Vierh.(Avicenniaceae). *Molecular Ecology*. 2000;9(11):1853-62.
54. Maguire T, Peakall R, Saenger P. Comparative analysis of genetic diversity in the mangrove species *Avicennia marina* (Forsk.) Vierh.(Avicenniaceae) detected by AFLPs and SSRs. *Theoretical and applied Genetics*. 2002;104(2):388-98.
55. Le HG, Hong PN, Tuan MS, Harada K. Genetic variation of *Avicennia marina* (Forsk.) Vierh.(Avicenniaceae) in Vietnam revealed by microsatellite and AFLP markers. *Genes & genetic systems*. 2003;78(6):399-407.
56. ARNAUD-HAOND S, Teixeira S, Massa SI, Billot C, Saenger P, Coupland G, et al. Genetic structure at range edge: low diversity and high inbreeding in Southeast Asian mangrove (*Avicennia marina*) populations. *Molecular Ecology*. 2006;15(12):3515-25.

57. Lalagüe H, Csilléry K, Oddou-Muratorio S, Safrana J, De Quattro C, Fady B, et al. Nucleotide diversity and linkage disequilibrium at 58 stress response and phenology candidate genes in a European beech (*Fagus sylvatica* L.) population from southeastern France. *Tree genetics & genomes*. 2014;10(1):15-26.
58. Müller M, Seifert S, Finkeldey R. A candidate gene-based association study reveals SNPs significantly associated with bud burst in European beech (*Fagus sylvatica* L.). *Tree Genetics & Genomes*. 2015;11(6):1-13.
59. Čalić I, Koch J, Carey D, Addo-Quaye C, Carlson JE, Neale DB. Genome-wide association study identifies a major gene for beech bark disease resistance in American beech (*Fagus grandifolia* Ehrh.). *BMC genomics*. 2017;18(1):1-14.
60. Wang HY, Yin X, Yin DX, Li L, Xiao HX. Population genetic structures of two ecologically distinct species *Betula platyphylla* and *B. ermanii* inferred based on nuclear and chloroplast DNA markers. *Ecol Evol*. 2019;9(19):11406-19.
61. Tsuda Y, Semerikov V, Sebastiani F, Vendramin GG, Lascoux M. Multispecies genetic structure and hybridization in the *Betula* genus across Eurasia. *Molecular Ecology*. 2017;26(2):589-605.
62. Tsuda Y, Nakao K, Ide Y, Tsumura Y. The population demography of *Betula maximowicziana*, a cool-temperate tree species in Japan, in relation to the last glacial period: its admixture-like genetic structure is the result of simple population splitting not admixing. *Molecular Ecology*. 2015;24(7):1403-18.
63. Tsuda Y, Ide Y. Wide-range analysis of genetic structure of *Betula maximowicziana*, a long-lived pioneer tree species and noble hardwood in the cool temperate zone of Japan. *Molecular Ecology*. 2005;14(13):3929-41.
64. Hu YN, Zhao L, Buggs RJA, Zhang XM, Li J, Wang N. Population structure of *Betula albosinensis* and *Betula platyphylla*: evidence for hybridization and a cryptic lineage. *Ann Bot-London*. 2019;123(7):1179-89.
65. Czernicka M, Plawiak J, Muras P. Genetic diversity of F1 and F2 interspecific hybrids between dwarf birch (*Betula nana* L.) and Himalayan birch (*B. utilis* var. *jacquemontii* (Spach) Winkl. 'Doorenbos') using RAPD-PCR markers and ploidy analysis. *Acta Biochim Pol*. 2014;61(2):195-9.
66. Zohren J, Wang NA, Kardailsky I, Borrell JS, Joecker A, Nichols RA, et al. Unidirectional diploid-tetraploid introgression among British birch trees with shifting ranges shown by restriction site-associated markers. *Molecular Ecology*. 2016;25(11):2413-26.
67. Palme AE, Su Q, Palsson S, Lascoux M. Extensive sharing of chloroplast haplotypes among European birches indicates hybridization among *Betula pendula*, *B. pubescens* and *B. nana*. *Molecular Ecology*. 2004;13(1):167-78.
68. Eidesen PB, Alsos IG, Brochmann C. Comparative analyses of plastid and AFLP data suggest different colonization history and asymmetric hybridization between *Betula pubescens* and *B. nana*. *Molecular Ecology*. 2015;24(15):3993-4009.
69. Linda R, Kuneš I, Baláš M. Genetic and morphometric variability between populations of *Betula* × *oycoviensis* from Poland and Czechia: A revised view of the taxonomic treatment of the Ojców birch. *Plos One*. 2020;15(12):e0243310.
70. de Dato GD, Teani A, Mattioni C, Aravanopoulos F, Avramidou EV, Stojnic S, et al. Genetic Analysis by nuSSR Markers of Silver Birch (*Betula pendula* Roth) Populations in Their Southern European Distribution Range. *Frontiers in Plant Science*. 2020;11.
71. Zeng J, Zou Y, Bai J, Zheng H. RAPD analysis of genetic variation in natural populations of *Betula alnoides* from Guangxi, China. *Euphytica*. 2003;134(1):33-41.

72. Guidugli M, Nazareno A, Feres J, Contel E, Mestriner M, Alzate-Marin A. Small but not isolated: a population genetic survey of the tropical tree *Cariniana estrellensis* (Lecythidaceae) in a highly fragmented habitat. *Heredity*. 2016;116(3):339-47.
73. Kullán A, Kulkarni A, Kumar RS, Rajkumar R. Development of microsatellite markers and their use in genetic diversity and population structure analysis in *Casuarina*. *Tree Genetics & Genomes*. 2016;12(3):1-12.
74. Kang M-J, Shin A-Y, Shin Y, Lee S-A, Lee H-R, Kim T-D, et al. Identification of transcriptome-wide, nut weight-associated SNPs in *Castanea crenata*. *Scientific reports*. 2019;9(1):1-10.
75. Medina-Mora C. Pollination biology and simple sequence repeat (SSR) genetic identification of chestnut cultivars and their progeny: Michigan State University; 2015.
76. Nishio S, Terakami S, Matsumoto T, Yamamoto T, Takada N, Kato H, et al. Identification of QTLs for agronomic traits in the Japanese chestnut (*Castanea crenata* Sieb. Et Zucc.) breeding. *The Horticulture Journal*. 2018;87(1):43-54.
77. Kubisiak TL, Hebard F, Nelson CD, Zhang J, Bernatzky R, Huang H, et al. Molecular mapping of resistance to blight in an interspecific cross in the genus *Castanea*. *Phytopathology*. 1997;87(7):751-9.
78. Bernatzky R, Mulcahy DL. Marker-aided selection in a backcross breeding program for resistance to chestnut blight in the American chestnut. *Canadian Journal of Forest Research*. 1992;22(7):1031-5.
79. Westbrook JW, Zhang Q, Mandal MK, Jenkins EV, Barth LE, Jenkins JW, et al. Optimizing genomic selection for blight resistance in American chestnut backcross populations: A trade-off with American chestnut ancestry implies resistance is polygenic. *Evolutionary applications*. 2020;13(1):31-47.
80. Torello Marinoni D, Nishio S, Valentini N, Shirasawa K, Acquadro A, Portis E, et al. Development of High-Density Genetic Linkage Maps and Identification of Loci for Chestnut Gall Wasp Resistance in *Castanea* spp. *Plants*. 2020;9(8):1048.
81. Zhebentyayeva TN, Sisco PH, Georgi LL, Jeffers SN, Perkins MT, James JB, et al. Dissecting resistance to *Phytophthora cinnamomi* in interspecific hybrid chestnut crosses using sequence-based genotyping and QTL mapping. *Phytopathology*. 2019;109(9):1594-604.
82. Santos C, Zhebentyayeva T, Serrazina S, Nelson CD, Costa R. Development and characterization of EST-SSR markers for mapping reaction to *Phytophthora cinnamomi* in *Castanea* spp. *Scientia Horticulturae*. 2015;194:181-7.
83. Santos C, Nelson CD, Zhebentyayeva T, Machado H, Gomes-Laranjo J, Costa RL. First interspecific genetic linkage map for *Castanea sativa* x *Castanea crenata* revealed QTLs for resistance to *Phytophthora cinnamomi*. *Plos One*. 2017;12(9):e0184381.
84. Bowles ME. Interactions Between *Phytophthora* spp. and *Castanea* spp. and the Creation of a Genetic Linkage Map for the F1 Parent in a First-Generation Backcross Family of *Castanea* spp. 2006.
85. Abbott A, Staton M, Olukolu B, Hebard F, Georgi L, Jeffers S, et al., editors. Genetic and genomic resources for mapping resistance to *Phytophthora cinnamomi* in chestnut. V International Chestnut Symposium 1019; 2012.
86. González MV, Cuenca B, López M, Prado MJ, Rey M. Molecular characterization of chestnut plants selected for putative resistance to *Phytophthora cinnamomi* using SSR markers. *Scientia horticulturae*. 2011;130(2):459-67.
87. Müller M, Nelson CD, Gailing O. Analysis of environment-marker associations in American chestnut. *Forests*. 2018;9(11):695.

88. Alcaide F, Solla A, Mattioni C, Castellana S, Martín MÁ. Adaptive diversity and drought tolerance in *Castanea sativa* assessed through EST-SSR genic markers. *Forestry: An International Journal of Forest Research*. 2019;92(3):287-96.
89. Gailing O, Nelson CD. Genetic variation patterns of American chestnut populations at EST-SSRs. *Botany*. 2017;95(8):799-807.
90. Sandercock A, Westbrook J, Zhang Q, Johnson H, Saielli T, Scrivani J, et al. Whole-genome resequencing reveals the population structure, genomic diversity, and demographic history of American chestnut (*Castanea dentata*). *bioRxiv*. 2022.
91. Kubisiak TL, Roberds JH, editors. Genetic structure of American chestnut populations based on neutral DNA markers. In: *Restoration of American Chestnut to Forest Lands: proceedings of a conference and workshop held at The North Carolina Arboretum, Asheville, North Carolina, USA, May 4–6, 2004* Natural Resources Report NPS/NCR/CUE/NRR–2006/001[Washington, DC]: US Dept of the Interior, National Park Service, National Capital Region, Center for Urban Ecology, 2006: 109-122; 2006.
92. Kubisiak T, Nelson C, Staton M, Zhebentyayeva T, Smith C, Olukolu B, et al. A transcriptome-based genetic map of Chinese chestnut (*Castanea mollissima*) and identification of regions of segmental homology with peach (*Prunus persica*). *Tree Genetics & Genomes*. 2013;9(2):557-71.
93. Huang g, Dane F, Kubisiak TL. Allozyme and RAPD analysis of the genetic diversity and geographic variation in wild populations of the American chestnut (Fagaceae). *American Journal of Botany*. 1998;85(7):1013-21.
94. Huang H, Dane F, Norton JD. Genetic analysis of 11 polymorphic isozyme loci in chestnut species and characterization of chestnut cultivars by multi-locus allozyme genotypes. *Journal of the American Society for Horticultural Science*. 1994;119(4):840-9.
95. Huang H, Dane F, Norton J, Weaver D, Hebard F. Linkage relationships of isozymes and morphological traits in interspecific chestnut crosses. *HortScience*. 1996;31(3):419-20.
96. Huang H, Dane F, Norton J. Allozyme diversity in Chinese, Seguin and American chestnut (*Castanea* spp.). *Theoretical and Applied Genetics*. 1994;88(8):981-5.
97. Pereira-Lorenzo S, Costa RML, Ramos-Cabrer AM, Ribeiro CAM, da Silva MFS, Manzano G, et al. Variation in grafted European chestnut and hybrids by microsatellites reveals two main origins in the Iberian Peninsula. *Tree Genetics & Genomes*. 2010;6(5):701-15.
98. Martin M, Alvarez J, Mattioni C, Cherubini M, Villani F, Martin L. Identification and characterisation of traditional chestnut varieties of southern Spain using morphological and simple sequence repeat (SSRs) markers. *Annals of Applied Biology*. 2009;154(3):389-98.
99. Abdelhamid S, Lê C-L, Conedera M, Kuepfer P. The assessment of genetic diversity of *Castanea* species by RAPD, AFLP, ISSR, and SSR markers. *Turkish Journal of Botany*. 2014;38(5):835-50.
100. Torello Marinoni D, Akkak A, Beltramo C, Guaraldo P, Boccacci P, Bounous G, et al. Genetic and morphological characterization of chestnut (*Castanea sativa* Mill.) germplasm in Piedmont (north-western Italy). *Tree genetics & genomes*. 2013;9(4):1017-30.
101. Fernández-Cruz J, Fernández-López J. Genetic structure of wild sweet chestnut (*Castanea sativa* Mill.) populations in northwest of Spain and their differences with other European stands. *Conserv Genet*. 2016;17(4):949-67.

102. Fineschi S, Turchini D, Villani F, Vendramin G. Chloroplast DNA polymorphism reveals little geographical structure in *Castanea sativa* Mill.(Fagaceae) throughout southern European countries. *Molecular Ecology*. 2000;9(10):1495-503.
103. Fineschi S, Malvolti M, Morgante M, Vendramin G. Allozyme variation within and among cultivated varieties of sweet chestnut (*Castanea sativa*). *Canadian Journal of Forest Research*. 1994;24(6):1160-5.
104. Villani F, Pigliucci i, Benedettelli S, Cherubini M. Genetic differentiation among Turkish chestnut (*Castanea sativa* Mill.) populations. *Heredity*. 1991;66(1):131-6.
105. Abdelhamid S, Omri A, Araouiki A, Sghair A. Molecular Characterization of Swiss Chestnut Cultivars (*Castanea Sativa* Mill.) Using RAPD, AFLP and ISSR Markers.
106. Ramos-Cabrer A, Pereira-Lorenzo S. Genetic relationship between *Castanea sativa* Mill. trees from north-western to south Spain based on morphological traits and isoenzymes. *Genet Resour Crop Ev*. 2005;52(7):879-90.
107. Casasoli M, Mattioni C, Cherubini M, Villani F. A genetic linkage map of European chestnut (*Castanea sativa* Mill.) based on RAPD, ISSR and isozyme markers. *Theoretical and applied genetics*. 2001;102(8):1190-9.
108. Sisco P, Kubisiak T, Casasoli M, Barreneche T, Kremer A, Clark C, et al., editors. An improved genetic map for *Castanea mollissima*/*Castanea dentata* and its relationship to the genetic map of *Castanea sativa*. In: Abreu, CG; Rosa, E; Monteiro, AA, eds *Proceedings of the III International Chestnut Congress Acta Horticulturae 693* Leuven,[Belgium]: ISHS, 2005: 491-495; 2005.
109. Poljak I, Idžojić M, Šatović Z, Ježić M, Ćurković-Perica M, Simovski B, et al. Genetic diversity of the sweet chestnut (*Castanea sativa* Mill.) in Central Europe and the western part of the Balkan Peninsula and evidence of marron genotype introgression into wild populations. *Tree Genetics & Genomes*. 2017;13(1):1-13.
110. Lusini I, Velichkov I, Pollegioni P, Chiocchini F, Hinkov G, Zlatanov T, et al. Estimating the genetic diversity and spatial structure of Bulgarian *Castanea sativa* populations by SSRs: implications for conservation. *Conserv Genet*. 2014;15(2):283-93.
111. Bouffartigue C, Debille S, Fabreguettes O, Cabrer AR, Pereira-Lorenzo S, Flutre T, et al. Two main genetic clusters with high admixture between forest and cultivated chestnut (*Castanea sativa* Mill.) in France. *Ann Forest Sci*. 2020;77(3):1-16.
112. Mattioni C, Martin MA, Pollegioni P, Cherubini M, Villani F. Microsatellite markers reveal a strong geographical structure in European populations of *Castanea sativa* (Fagaceae): evidence for multiple glacial refugia. *American Journal of Botany*. 2013;100(5):951-61.
113. Mattioni C, Martin MA, Chiocchini F, Cherubini M, Gaudet M, Pollegioni P, et al. Landscape genetics structure of European sweet chestnut (*Castanea sativa* Mill): indications for conservation priorities. *Tree Genetics & Genomes*. 2017;13(2):1-14.
114. Alessandri S, Krznar M, Ajolfi D, Ramos Cabrer AM, Pereira-Lorenzo S, Dondini L. Genetic Diversity of *Castanea sativa* Mill. Accessions from the Tuscan-Emilian Apennines and Emilia Romagna Region (Italy). *Agronomy*. 2020;10(9):1319.
115. Cavallini M, Lombardo G, Binelli G, Cantini C. Assessing the Genetic Identity of Tuscan Sweet Chestnut (*Castanea sativa* Mill.). *Forests*. 2022;13(7):967.
116. Martín M, Mattioni C, Cherubini M, Turchini D, Villani F. Genetic characterisation of traditional chestnut varieties in Italy using microsatellites (simple sequence repeats) markers. *Annals of Applied Biology*. 2010;157(1):37-44.

117. Nishio S, Takada N, Terakami S, Takeuchi Y, Kimura MK, Isoda K, et al. Genetic structure analysis of cultivated and wild chestnut populations reveals gene flow from cultivars to natural stands. *Scientific Reports*. 2021;11(1):1-13.
118. Perkins MT, Zhebentyayeva T, Sisco PH, Craddock JH. Genome-wide sequence-based genotyping supports a nonhybrid origin of *Castanea alabamensis*. *Systematic Botany*. 2021;46(4):973-84.
119. Martín MA, Mattioni C, Molina JR, Alvarez JB, Cherubini M, Herrera MA, et al. Landscape genetic structure of chestnut (*Castanea sativa* Mill.) in Spain. *Tree genetics & genomes*. 2012;8(1):127-36.
120. Tanaka T, Yamamoto T, Suzuki M. Genetic diversity of *Castanea crenata* in northern Japan assessed by SSR markers. *Breeding Science*. 2005;55(3):271-7.
121. Jiang X, Tang D, Gong B. Genetic diversity and association analysis of Chinese chestnut (*Castanea mollissima* Blume) cultivars based on SSR markers. *Brazilian Journal of Botany*. 2017;40(1):235-46.
122. Dane F, Hawkins LK, Huang H. Genetic variation and population structure of *Castanea pumila* var. *ozarkensis*. *Journal of the American Society for Horticultural Science*. 1999;124(6):666-70.
123. Fu Y, Dane F. Allozyme variation in endangered *Castanea pumila* var. *pumila*. *Ann Bot-London*. 2003;92(2):223-30.
124. Fang G-C, Blackmon BP, Staton ME, Nelson CD, Kubisiak TL, Olukolu BA, et al. A physical map of the Chinese chestnut (*Castanea mollissima*) genome and its integration with the genetic map. *Tree genetics & genomes*. 2013;9(2):525-37.
125. Ji F, Wei W, Liu Y, Wang G, Zhang Q, Xing Y, et al. Construction of a SNP-based high-density genetic map using genotyping by sequencing (GBS) and QTL analysis of nut traits in Chinese chestnut (*Castanea mollissima* Blume). *Frontiers in plant science*. 2018;9:816.
126. NIE X-h, WANG Z-h, LIU N-w, Li S, YAN B-q, Yu X, et al. Fingerprinting 146 Chinese chestnut (*Castanea mollissima* Blume) accessions and selecting a core collection using SSR markers. *Journal of Integrative Agriculture*. 2021;20(5):1277-86.
127. Sun R, Lin F, Huang P, Zheng Y. Moderate genetic diversity and genetic differentiation in the relict tree *Liquidambar formosana* Hance revealed by genic simple sequence repeat markers. *Frontiers in plant science*. 2016;7:1411.
128. Cao S, Duan H, Sun Y, Hu R, Wu B, Lin J, et al. Genome-wide association study with growth-related traits and secondary metabolite contents in red-and white-heart Chinese fir. *Frontiers in Plant Science*. 2022;13.
129. Zheng H, Duan H, Hu D, Wei R, Li Y. Sequence-related amplified polymorphism primer screening on Chinese fir (*Cunninghamia lanceolata* (Lamb.) Hook). *J Forestry Res*. 2015;26(1):101-6.
130. Sairkar PK, Sharma A, Shukla N. SCAR marker for identification and discrimination of *Commiphora wightii* and *C. myrrha*. *Molecular Biology International*. 2016;2016.
131. Liu F, Hong Z, Xu D, Jia H, Zhang N, Liu X, et al. Genetic diversity of the endangered *Dalbergia odorifera* revealed by SSR markers. *Forests*. 2019;10(3):225.
132. Liu F, Hong Z, Yang Z, Zhang N, Liu X, Xu D. De novo transcriptome analysis of *Dalbergia odorifera* and transferability of SSR markers developed from the transcriptome. *Forests* 10 (2): 98. 2019.

133. Wu B, Geng S-L, Shu B. Genetic variation and the conservation of isolated populations of *Derris trifoliata* (Leguminosae), a mangrove-associated vine, in southern China. *Biochemical Systematics and Ecology*. 2012;40:118-25.
134. Wang X, Wadl PA, Rinehart TA, Scheffler BE, Windham MT, Spiers JM, et al. A linkage map for flowering dogwood (*Cornus florida* L.) based on microsatellite markers. *Euphytica*. 2009;165(1):165-75.
135. Thistlethwaite FR, Ratcliffe B, Klápště J, Porth I, Chen C, Stoeckl MU, et al. Genomic prediction accuracies in space and time for height and wood density of Douglas-fir using exome capture as the genotyping platform. *BMC genomics*. 2017;18(1):1-16.
136. Thistlethwaite FR, El-Dien OG, Ratcliffe B, Klapste J, Porth I, Chen C, et al. Linkage disequilibrium vs. pedigree: Genomic selection prediction accuracy in conifer species. *Plos One*. 2020;15(6).
137. Jermstad KD, Reem AM, Henifin JR, Wheeler NC, Neale DB. Inheritance of Restriction-Fragment-Length-Polymorphisms and Random Amplified Polymorphic Dnas in Coastal Douglas-Fir. *Theoretical and Applied Genetics*. 1994;89(6):758-66.
138. Jermstad KD, Bassoni DL, Wheeler NC, Neale DB. A sex-averaged genetic linkage map in coastal Douglas-fir (*Pseudotsuga menziesii* [Mirb.] Franco var 'menziesii') based on RFLP and RAPD markers. *Theoretical and Applied Genetics*. 1998;97(5-6):762-70.
139. Jermstad KD, Bassoni DL, Jech KS, Wheeler NC, Neale DB. Mapping of quantitative trait loci controlling adaptive traits in coastal Douglas-fir. I. Timing of vegetative bud flush. *Theoretical and Applied Genetics*. 2001;102(8):1142-51.
140. Jermstad KD, Bassoni DL, Wheeler NC, Anekonda TS, Aitken SN, Adams WT, et al. Mapping of quantitative trait loci controlling adaptive traits in coastal Douglas-fir. II. Spring and fall cold-hardiness. *Theoretical and Applied Genetics*. 2001;102(8):1152-8.
141. Jermstad KD, Bassoni DL, Jech KS, Ritchie GA, Wheeler NC, Neale DB. Mapping of quantitative trait loci controlling adaptive traits in coastal Douglas fir. III. Quantitative trait loci-by-environment interactions. *Genetics*. 2003;165(3):1489-506.
142. Eckert AJ, Bower AD, Wegrzyn JL, Pande B, Jermstad KD, Krutovsky KV, et al. Association genetics of coastal Douglas fir (*Pseudotsuga menziesii* var. *menziesii*, Pinaceae). I. Cold-hardiness related traits. *Genetics*. 2009;182(4):1289-302.
143. Wheeler NC, Jermstad KD, Krutovsky K, Aitken SN, Howe GT, Krakowski J, et al. Mapping of quantitative trait loci controlling adaptive traits in coastal Douglas-fir. IV. Cold-hardiness QTL verification and candidate gene mapping. *Molecular Breeding*. 2005;15(2):145-56.
144. Krutovsky KV, Neale DB. Nucleotide diversity and linkage disequilibrium in cold-hardiness- and wood quality-related candidate genes in Douglas fir. *Genetics*. 2005;171(4):2029-41.
145. Viard F, El-Kassaby Y, Ritland K. Diversity and genetic structure in populations of *Pseudotsuga menziesii* (Pinaceae) at chloroplast microsatellite loci. *Genome*. 2001;44(3):336-44.
146. Aagaard JE, Krutovskii KV, Strauss SH. RAPDs and allozymes exhibit similar levels of diversity and differentiation among populations and races of Douglas-fir. *Heredity*. 1998;81(1):69-78.
147. Krutovsky KV, Clair JBS, Saich R, Hipkins VD, Neale DB. Estimation of population structure in coastal Douglas-fir [*Pseudotsuga menziesii* (Mirb.) Franco var. *menziesii*] using allozyme and microsatellite markers. *Tree Genetics & Genomes*. 2009;5(4):641-58.

148. Slavov GT, Howe GT, Yakovlev I, Edwards KJ, Krutovskii KV, Tuskan GA, et al. Highly variable SSR markers in Douglas-fir: Mendelian inheritance and map locations. *Theoretical and Applied Genetics*. 2004;108(5):873-80.
149. Amarasinghe V, Carlson JE. The development of microsatellite DNA markers for genetic analysis in Douglas-fir. *Canadian journal of forest research*. 2002;32(11):1904-15.
150. Gan S, Shi J, Li M, Wu K, Wu J, Bai J. Moderate-density molecular maps of *Eucalyptus urophylla* ST Blake and *E. tereticornis* Smith genomes based on RAPD markers. *Genetica*. 2003;118(1):59-67.
151. Cappa EP, de Lima BM, da Silva-Junior OB, Garcia CC, Mansfield SD, Grattapaglia D. Improving genomic prediction of growth and wood traits in *Eucalyptus* using phenotypes from non-genotyped trees by single-step GBLUP. *Plant Science*. 2019;284:9-15.
152. Verhaegen D, Plomion C, Gion J-M, Poitel M, Costa P, Kremer A. Quantitative trait dissection analysis in *Eucalyptus* using RAPD markers: 1. Detection of QTL in interspecific hybrid progeny, stability of QTL expression across different ages. *Theoretical and Applied Genetics*. 1997;95(4):597-608.
153. Resende R, Resende M, Silva F, Azevedo C, Takahashi E, Silva-Junior O, et al. Assessing the expected response to genomic selection of individuals and families in *Eucalyptus* breeding with an additive-dominant model. *Heredity*. 2017;119(4):245-55.
154. Resende MD, Resende MF, Sansaloni CP, Petroli CD, Missiaggia AA, Aguiar AM, et al. Genomic selection for growth and wood quality in *Eucalyptus*: capturing the missing heritability and accelerating breeding for complex traits in forest trees. *New Phytologist*. 2012;194(1):116-28.
155. Tan B, Grattapaglia D, Martins GS, Ferreira KZ, Sundberg B, Ingvarsson PK. Evaluating the accuracy of genomic prediction of growth and wood traits in two *Eucalyptus* species and their F 1 hybrids. *BMC plant biology*. 2017;17(1):1-15.
156. Denis M, Bouvet J-M. Efficiency of genomic selection with models including dominance effect in the context of *Eucalyptus* breeding. *Tree Genetics & Genomes*. 2013;9(1):37-51.
157. Grattapaglia D, Bertolucci FL, Penchel R, Sederoff RR. Genetic mapping of quantitative trait loci controlling growth and wood quality traits in *Eucalyptus grandis* using a maternal half-sib family and RAPD markers. *Genetics*. 1996;144(3):1205-14.
158. Ballesta P, Serra N, Guerra FP, Hasbún R, Mora F. Genomic prediction of growth and stem quality traits in *Eucalyptus globulus* Labill. at its southernmost distribution limit in Chile. *Forests*. 2018;9(12):779.
159. Freeman JS, Potts BM, Downes GM, Pilbeam D, Thavamanikumar S, Vaillancourt RE. Stability of quantitative trait loci for growth and wood properties across multiple pedigrees and environments in *Eucalyptus globulus*. *New Phytologist*. 2013;198(4):1121-34.
160. Ballesta P, Maldonado C, Pérez-Rodríguez P, Mora F. SNP and haplotype-based genomic selection of quantitative traits in *Eucalyptus globulus*. *Plants*. 2019;8(9):331.
161. Cappa EP, El-Kassaby YA, Garcia MN, Acuña C, Borralho NM, Grattapaglia D, et al. Impacts of population structure and analytical models in genome-wide association studies of complex traits in forest trees: a case study in *Eucalyptus globulus*. *Plos One*. 2013;8(11):e81267.

162. Thavamanikumar S, McManus LJ, Ades PK, Bossinger G, Stackpole DJ, Kerr R, et al. Association mapping for wood quality and growth traits in *Eucalyptus globulus* ssp. *globulus* Labill identifies nine stable marker-trait associations for seven traits. *Tree Genetics & Genomes*. 2014;10(6):1661-78.
163. Suontama M, Klápště J, Telfer E, Graham N, Stovold T, Low C, et al. Efficiency of genomic prediction across two *Eucalyptus nitens* seed orchards with different selection histories. *Heredity*. 2019;122(3):370-9.
164. Resende RT, Resende MDV, Silva FF, Azevedo CF, Takahashi EK, Silva-Junior OB, et al. Regional heritability mapping and genome-wide association identify loci for complex growth, wood and disease resistance traits in *Eucalyptus*. *New Phytologist*. 2017;213(3):1287-300.
165. Müller BS, de Almeida Filho JE, Lima BM, Garcia CC, Missiaggia A, Aguiar AM, et al. Independent and Joint-GWAS for growth traits in *Eucalyptus* by assembling genome-wide data for 3373 individuals across four breeding populations. *New Phytologist*. 2019;221(2):818-33.
166. Marco de Lima B, Cappa EP, Silva-Junior OB, Garcia C, Mansfield SD, Grattapaglia D. Quantitative genetic parameters for growth and wood properties in *Eucalyptus* “urograndis” hybrid using near-infrared phenotyping and genome-wide SNP-based relationships. *Plos One*. 2019;14(6):e0218747.
167. Ballesta P, Bush D, Silva FF, Mora F. Genomic predictions using low-density SNP markers, pedigree and GWAS information: a case study with the non-model species *Eucalyptus cladocalyx*. *Plants*. 2020;9(1):99.
168. Grattapaglia D, Ribeiro V, Rezende GDS. Retrospective selection of elite parent trees using paternity testing with microsatellite markers: an alternative short term breeding tactic for *Eucalyptus*. *Theoretical and Applied Genetics*. 2004;109(1):192-9.
169. Kainer D, Padovan A, Degenhardt J, Krause S, Mondal P, Foley WJ, et al. High marker density GWAS provides novel insights into the genomic architecture of terpene oil yield in *Eucalyptus*. *New Phytologist*. 2019;223(3):1489-504.
170. Padovan A, Webb H, Mazanec R, Grayling P, Bartle J, Foley WJ, et al. Association genetics of essential oil traits in *Eucalyptus loxophleba*: explaining variation in oil yield. *Molecular Breeding*. 2017;37(6):73.
171. Naidoo S, Oates C, Mhoswa L, Neil MO, Acosta J, Christie N, et al. Factors underpinning resistance against the galling pest, *Leptocybe invasa* in *Eucalyptus grandis*. In: Publication: Gen Tech Rep SRS-252 Asheville, NC: US Department of Agriculture Forest Service Southern Research Station. 2020:52-.
172. Mhoswa L, O'Neill MM, Mphahlele MM, Oates CN, Payn KG, Slippers B, et al. A genome-wide association study for resistance to the insect pest *Leptocybe invasa* in *Eucalyptus grandis* reveals genomic regions and positional candidate defense genes. *Plant and Cell Physiology*. 2020;61(7):1285-96.
173. Kainer D, Stone EA, Padovan A, Foley WJ, Külheim C. Accuracy of genomic prediction for foliar terpene traits in *Eucalyptus polybractea*. *G3: Genes, Genomes, Genetics*. 2018;8(8):2573-83.
174. Acuña CV, Fernandez P, Villalba PV, García MN, Hopp HE, Marcucci Poltri SN. Discovery, validation, and in silico functional characterization of EST-SSR markers in *Eucalyptus globulus*. *Tree Genetics & Genomes*. 2012;8(2):289-301.

175. Grattapaglia D, Sederoff R. Genetic linkage maps of *Eucalyptus grandis* and *Eucalyptus urophylla* using a pseudo-testcross: mapping strategy and RAPD markers. *Genetics*. 1994;137(4):1121-37.
176. Baril C, Verhaegen D, Vigneron P, Bouvet J-M, Kremer A. Structure of the specific combining ability between two species of *Eucalyptus*. I. RAPD data. *Theoretical and Applied Genetics*. 1997;94(6):796-803.
177. Chezian P, Yasodha R, Ghosh M. Genetic diversity analysis in a seed orchard of *Eucalyptus tereticornis*. *New Forest*. 2010;40(1):85-99.
178. Yost JM, Wise SL, Love NL, Steane DA, Jones RC, Ritter MK, et al. Origins, diversity and naturalization of *Eucalyptus globulus* (Myrtaceae) in California. *Forests*. 2021;12(8):1129.
179. Tan B, Ingvarsson PK. Integrating genome-wide association mapping of additive and dominance genetic effects to improve genomic prediction accuracy in *Eucalyptus*. *The Plant Genome*. 2022;15(2):e20208.
180. Ishii K. DNA Markers in *Eucalyptus* with emphasis on species identification. *Environmental Control in Biology*. 2009;47(1):1-11.
181. Silva-Junior OB, Faria DA, Grattapaglia D. A flexible multi-species genome-wide 60K SNP chip developed from pooled resequencing of 240 *Eucalyptus* tree genomes across 12 species. *New Phytologist*. 2015;206(4):1527-40.
182. Steane DA, Nicolle D, Sansaloni CP, Petroli CD, Carling J, Kilian A, et al. Population genetic analysis and phylogeny reconstruction in *Eucalyptus* (Myrtaceae) using high-throughput, genome-wide genotyping. *Molecular phylogenetics and evolution*. 2011;59(1):206-24.
183. Zhang Z, Zhou R, Tang T, Huang Y, Zhong Y, Shi S. Genetic variation in central and peripheral populations of *Excoecaria agallocha* from Indo-West Pacific. *Aquatic Botany*. 2008;89(1):57-62.
184. Baraket G, Chatti K, Saddoud O, Abdelkarim AB, Mars M, Trifi M, et al. Comparative assessment of SSR and AFLP markers for evaluation of genetic diversity and conservation of fig, *Ficus carica* L., genetic resources in Tunisia. *Plant Molecular Biology Reporter*. 2011;29(1):171-84.
185. Zhang X, Hu Y, Liu L, Wang X, Wang W, Liu Y, et al., editors. Classification and phylogenetic relationship of 10 fig varieties by RAPD and SSR molecular markers. *IOP Conference Series: Earth and Environmental Science*; 2019: IOP Publishing.
186. Cuénin N, Flores O, Rivière E, Lebreton G, Reynaud B, Martos F. Great genetic diversity but high selfing rates and short-distance gene flow characterize populations of a tree (*Foetidia*; *Lecythidaceae*) in the fragmented tropical dry forest of the Mascarene Islands. *Journal of Heredity*. 2019;110(3):287-99.
187. Martos F, Lebreton G, Riviere E, Humeau L, Chevallier MH. Microsatellites in the Tree *Foetidia Mauritanica* (*Lecythidaceae*) and Utility in Other *Foetidia* Taxa from the Mascarene Islands. *Appl Plant Sci*. 2016;4(8).
188. Olawuyi OJ, Azeez AA. Molecular evaluation of *Garcinia kola* Heckel accessions using RAPD markers. *American Journal of Molecular Biology*. 2019;9(2):41-51.
189. Güney M, Kafkas S, Keles H, Aras S, Ercişli S. Characterization of hawthorn (*Crataegus* spp.) genotypes by SSR markers. *Physiology and molecular biology of plants*. 2018;24(6):1221-30.

190. Hiraoka Y, Fukatsu E, Mishima K, Hirao T, Teshima KM, Tamura M, et al. Potential of genome-wide studies in unrelated plus trees of a coniferous species, *Cryptomeria japonica* (Japanese cedar). *Frontiers in plant science*. 2018;9:1322.
191. Uchiyama K, Iwata H, Moriguchi Y, Ujino-Ihara T, Ueno S, Taguchi Y, et al. Demonstration of genome-wide association studies for identifying markers for wood property and male strobili traits in *Cryptomeria japonica*. *Plos One*. 2013;8(11):e79866.
192. Moriguchi Y, Ueno S, Saito M, Higuchi Y, Miyajima D, Ito S, et al. A simple allele-specific PCR marker for identifying male-sterile trees: Towards DNA marker-assisted selection in the *Cryptomeria japonica* breeding program. *Tree genetics & genomes*. 2014;10(4):1069-77.
193. Mishima K, Hirao T, Tsubomura M, Tamura M, Kurita M, Nose M, et al. Identification of novel putative causative genes and genetic marker for male sterility in Japanese cedar (*Cryptomeria japonica* D. Don). *Bmc Genomics*. 2018;19(1):1-16.
194. Uchiyama K, Ujino-Ihara T, Ueno S, Taguchi Y, Futamura N, Shinohara K, et al. Single nucleotide polymorphisms in *Cryptomeria japonica*: their discovery and validation for genome mapping and diversity studies. *Tree Genetics & Genomes*. 2012;8(6):1213-22.
195. Hasegawa Y, Ueno S, Matsumoto A, Ujino-Ihara T, Uchiyama K, Totsuka S, et al. Fine mapping of the male-sterile genes (MS1, MS2, MS3, and MS4) and development of SNP markers for marker-assisted selection in Japanese cedar (*Cryptomeria japonica* D. Don). *Plos One*. 2018;13(11):e0206695.
196. Hao S, Hu W, Ye C, Shen Y, Li QQ. Plastid development of albino viviparous propagules in woody mangrove *Kandelia obovata*. *Tree Physiol*. 2022.
197. Harada K, Okaura T, Van Huan N, Iwasaki M, Nitasaka E. A novel microsatellite locus isolated from an AFLP fragment in the mangrove species *Kandelia obovata* (Rhizophoraceae). *Journal of plant research*. 2005;118(1):49-51.
198. Zhou Y, Ye Y, Feng L, Zhang Y, Lin Q, Liu J, et al. A Genetic Linkage Map of BC2 Population Reveals QTL Associated with Plant Architecture Traits in *Lagerstroemia*. *Forests*. 2021;12(3):322.
199. Arcade A, Faivre-Rampant P, Le Guerroué B, Pâques L, Prat D. Heterozygosity and hybrid performance in larch. *Theoretical and applied genetics*. 1996;93(8):1274-81.
200. Wen G, Dang J, Xie Z, Wang J, Jiang P, Guo Q, et al. Molecular karyotypes of loquat (*Eriobotrya japonica*) aneuploids can be detected by using SSR markers combined with quantitative PCR irrespective of heterozygosity. *Plant methods*. 2020;16(1):1-16.
201. Ueno S, Setsuko S, Kawahara T, Yoshimaru H. Genetic diversity and differentiation of the endangered Japanese endemic tree *Magnolia stellata* using nuclear and chloroplast microsatellite markers. *Conserv Genet*. 2005;6(4):563-74.
202. Young AG, Merriam HG. Effects of Forest Fragmentation on the Spatial Genetic-Structure of *Acer-Saccharum* Marsh (Sugar Maple) Populations. *Heredity*. 1994;72:201-8.
203. Young A, Warwick S, Merriam H. Genetic variation and structure at three spatial scales for *Acer saccharum* (sugar maple) in Canada and the implications for conservation. *Canadian Journal of Forest Research*. 1993;23(12):2568-78.
204. Perry D, Knowles P. Spatial genetic structure within three sugar maple (*Acer saccharum* Marsh.) stands. *Heredity*. 1991;66(1):137-42.

205. Takayama K, Sun BY, Stuessy TF. Genetic consequences of anagenetic speciation in *Acer okamotoanum* (Sapindaceae) on Ullung Island, Korea. *Ann Bot-London*. 2012;109(2):321-30.
206. Ye H, Wu JH, Wang Z, Hou HM, Gao Y, Han W, et al. Population genetic variation characterization of the boreal tree *Acer ginnala* in Northern China. *Scientific Reports*. 2020;10(1).
207. Liu CP, Tsuda Y, Shen HL, Hu LJ, Saito Y, Ide Y. Genetic Structure and Hierarchical Population Divergence History of *Acer mono* var. *mono* in South and Northeast China. *Plos One*. 2014;9(1).
208. Harmon M, Lane T, Staton M, Coggeshall MV, Best T, Chen C-C, et al. Development of novel genic microsatellite markers from transcriptome sequencing in sugar maple (*Acer saccharum* Marsh.). *BMC research notes*. 2017;10(1):1-7.
209. Graignic N, Tremblay F, Bergeron Y. Development of polymorphic nuclear microsatellite markers in sugar maple (*Acer saccharum* Marsh.) using cross-species transfer and SSR-enriched shotgun pyrosequencing. *Conserv Genet Resour*. 2013;5(3):845-8.
210. Khodwekar S, Staton M, Coggeshall MV, Carlson JE, Gailing O. Nuclear microsatellite markers for population genetic studies in sugar maple (*Acer saccharum* Marsh.). *Ann for Res*. 2015;58(2):193-204.
211. Kikuchi S, Shibata M. Development of polymorphic microsatellite markers in *Acer mono* Maxim. *Molecular Ecology Resources*. 2008;8(2):339-41.
212. Pandey M, Gailing O, Fischer D, Hattemer H, Finkeldey R. Characterization of microsatellite markers in sycamore (*Acer pseudoplatanus* L.). *Molecular Ecology Notes*. 2004;4(2):253-5.
213. Segarra-Moragues JG, Gleiser G, Gonzalez-Candelas F. Isolation and characterization of microsatellite loci in *Acer opalus* (Aceraceae), a sexually-polymorphic tree, through an enriched genomic library. *Conserv Genet*. 2008;9(4):1059-62.
214. Zhao LL, Sun WB, Yang JB. Development and Characterization of Microsatellite Markers in the Critically Endangered Species *Acer Yangbiense* (Aceraceae). *American Journal of Botany*. 2011;98(9):E247-E9.
215. Deng Y, Liu T, Xie Y, Wei Y, Xie Z, Shi Y, et al. High genetic diversity and low differentiation in *Michelia shiluensis*, an endangered Magnolia species in south China. *Forests*. 2020;11(4):469.
216. Deng Y, Luo Y, He Y, Qin X, Li C, Deng X. Complete chloroplast genome of *Michelia shiluensis* and a comparative analysis with four Magnoliaceae species. *Forests*. 2020;11(3):267.
217. Rubio de Casas R, Vargas P, Pérez-Corona E, Cano E, Manrique E, García-Verdugo C, et al. Variation in sclerophylly among Iberian populations of *Quercus coccifera* L. is associated with genetic differentiation across contrasting environments. *Plant Biology*. 2009;11(3):464-72.
218. Pettenkofer T, Burkardt K, Ammer C, Vor T, Finkeldey R, Müller M, et al. Genetic diversity and differentiation of introduced red oak (*Quercus rubra*) in Germany in comparison with reference native North American populations. *Eur J Forest Res*. 2019;138(2):275-85.
219. Romero-Severson J, Aldrich P, Feng Y, Sun W, Michler C. Chloroplast DNA variation of northern red oak (*Quercus rubra* L.) in Indiana. *New Forest*. 2003;26(1):43-9.

220. Magni C, Ducouso A, Caron H, Petit R, Kremer A. Chloroplast DNA variation of *Quercus rubra* L. in North America and comparison with other Fagaceae. *Molecular ecology*. 2005;14(2):513-24.
221. Borkowski DS, Hoban SM, Chatwin W, Romero-Severson J. Rangewide population differentiation and population substructure in *Quercus rubra* L. *Tree Genetics & Genomes*. 2017;13(3):1-11.
222. Sork V, Huang S, Wiener E, editors. Macrogeographic and fine-scale genetic structure in a North American oak species, *Quercus rubra* L. *Ann Sci Forest*; 1993: EDP Sciences.
223. Götz J, Krutovsky KV, Leinemann L, Müller M, Rajora OP, Gailing O. Chloroplast Haplotypes of Northern Red Oak (*Quercus rubra* L.) Stands in Germany Suggest Their Origin from Northeastern Canada. *Forests*. 2020;11(9):1025.
224. Mohammad-Panah N, Shabanian N, Khadivi A, Rahmani M-S, Emami A. Genetic structure of gall oak (*Quercus infectoria*) characterized by nuclear and chloroplast SSR markers. *Tree Genetics & Genomes*. 2017;13(3):1-12.
225. Rahmani M-S, Alikhani L, Shabanian N, Khadivi-Khub A. Genetic differentiation in *Quercus infectoria* from northwest of Iran revealed by different nuclear markers. *Tree genetics & genomes*. 2015;11(1):1-9.
226. Lumaret R, Mir C, Michaud H, Raynal V. Phylogeographical variation of chloroplast DNA in holm oak (*Quercus ilex* L.). *Molecular Ecology*. 2002;11(11):2327-36.
227. Fernández i Martí A, Romero-Rodríguez C, Navarro-Cerrillo RM, Abril N, Jorrín-Novo JV, Dodd RS. Population genetic diversity of *Quercus ilex* subsp. *ballota* (Desf.) Samp. reveals divergence in recent and evolutionary migration rates in the Spanish dehesas. *Forests*. 2018;9(6):337.
228. Kesić L, Cseke K, Orlović S, Stojanović DB, Kostić S, Benke A, et al. Genetic Diversity and Differentiation of Pedunculate Oak (*Quercus robur* L.) Populations at the Southern Margin of Its Distribution Range—Implications for Conservation. *Diversity*. 2021;13(8):371.
229. Padutov VE, Baranov OY, Kagan DI, Razumova OA, Veinberga I, Baumanis I, et al., editors. Analysis of Latvian and Belarusian Oak (*Quercus robur* L.) Population Provenance and Genetic Structure Using Chloroplast Markers. *Proceedings of the Latvian Academy of Sciences*; 2021: De Gruyter Poland.
230. Degen B, Yanbaev Y, Ianbaev R, Bakhtina S, Tagirova A. Genetic diversity and differentiation among populations of the pedunculate oak (*Quercus robur*) at the eastern margin of its range based on a new set of 95 SNP loci. *J Forestry Res*. 2021;32(5):2237-43.
231. Yakovlev I, Kleinschmidt J. Genetic differentiation of pedunculate oak *Quercus robur* L. in the European part of Russia based on RAPD markers. *Russian Journal of Genetics*. 2002;38(2):148-55.
232. Temunović M, Garnier-Géré P, Morić M, Franjić J, Ivanković M, Bogdan S, et al. Candidate gene SNP variation in floodplain populations of pedunculate oak (*Quercus robur* L.) near the species' southern range margin: Weak differentiation yet distinct associations with water availability. *Molecular Ecology*. 2020;29(13):2359-78.
233. Zanetto A, Kremer A. Geographical structure of gene diversity in *Quercus petraea* (Matt.) Liebl. I. Monolocus patterns of variation. *Heredity*. 1995;75(5):506-17.

234. Kremer A, Zanetto A. Geographical structure of gene diversity in *Quercus petraea* (Matt.) Liebl. II: Multilocus patterns of variation. *Heredity*. 1997;78(5):476-89.
235. Bruschi P, Vendramin GG, Bussotti F, Grossoni P. Morphological and molecular diversity among Italian populations of *Quercus petraea* (Fagaceae). *Ann Bot-London*. 2003;91(6):707-16.
236. Bruschi P, Vendramin GG, Bussotti F, Grossoni P. Morphological and molecular differentiation between *Quercus petraea* (Matt.) Liebl. and *Quercus pubescens* Willd.(Fagaceae) in northern and central Italy. *Ann Bot-London*. 2000;85(3):325-33.
237. Lupini A, Aci MM, Mauceri A, Luzzi G, Bagnato S, Menguzzato G, et al. Genetic diversity in old populations of sessile oak from Calabria assessed by nuclear and chloroplast SSR. *Journal of Mountain Science*. 2019;16(5):1111-20.
238. Le Corre V, Roussel G, Zanetto A, Kremer A. Geographical structure of gene diversity in *Quercus petraea* (Matt.) Liebl. III. Patterns of variation identified by geostatistical analyses. *Heredity*. 1998;80(4):464-73.
239. Le Corre V, Dumolin-Lapègue S, Kremer A. Genetic variation at allozyme and RAPD loci in sessile oak *Quercus petraea* (Matt.) Liebl.: the role of history and geography. *Molecular Ecology*. 1997;6(6):519-29.
240. Guo B, Hao X, Han L, Zhai Y, Zhou S, Chen S, et al. Unraveling the genetic diversity and structure of *Quercus liaotungensis* population through analysis of microsatellite markers. *PeerJ*. 2021;9:e10922.
241. Wang J, Wei Q, Lu S, Chen Y, Wang Y. Genetic diversity of *Quercus liaotungensis* Koidz populations at different altitudes. *Scientific Research and Essays*. 2014;9(8):249-56.
242. Zhang YY, Fang YM, Yu MK, Li XX, Xia T. Molecular characterization and genetic structure of *Quercus acutissima* germplasm in China using microsatellites. *Molecular Biology Reports*. 2013;40(6):4083-90.
243. Saito Y, Tsuda Y, Uchiyama K, Fukuda T, Seto Y, Kim P-G, et al. Genetic variation in *Quercus acutissima* Carruth., in traditional Japanese rural forests and agricultural landscapes, revealed by chloroplast microsatellite markers. *Forests*. 2017;8(11):451.
244. Alikhani L, Rahmani M-S, Shabanian N, Badakhshan H, Khadivi-Khub A. Genetic variability and structure of *Quercus brantii* assessed by ISSR, IRAP and SCoT markers. *Gene*. 2014;552(1):176-83.
245. Shiran B, Mashayekhi S, Jahanbazi H, Soltani A, Bruschi P. Morphological and molecular diversity among populations of *Quercus brantii* Lindl. in western forest of Iran. *Plant Biosystems-An International Journal Dealing with all Aspects of Plant Biology*. 2011;145(2):452-60.
246. Deacon NJ, Cavender-Bares J. Limited pollen dispersal contributes to population genetic structure but not local adaptation in *Quercus oleoides* forests of Costa Rica. *Plos One*. 2015;10(9):e0138783.
247. Li Y, Zhang X, Fang Y. Landscape features and climatic forces shape the genetic structure and evolutionary history of an oak species (*Quercus chenii*) in East China. *Frontiers in Plant Science*. 2019;10:1060.
248. Ohsawa T, Tsuda Y, Saito Y, Ide Y. The genetic structure of *Quercus crispula* in northeastern Japan as revealed by nuclear simple sequence repeat loci. *Journal of plant research*. 2011;124(6):645-54.
249. Mayes SG, McGinley MA, Werth CR. Clonal population structure and genetic variation in sand-shinnery oak, *Quercus havardii* (Fagaceae). *American Journal of Botany*. 1998;85(11):1609-17.

250. Zhang X, Korpelainen H, Li C. Microsatellite variation of *Quercus aquifolioides* populations at varying altitudes in the Wolong Natural Reserve of China. *Silva Fenn.* 2007;40(3):407.
251. Shi X, Wen Q, Cao M, Guo X, Xu L-a. Genetic diversity and structure of natural *Quercus variabilis* population in China as revealed by microsatellites markers. *Forests.* 2017;8(12):495.
252. López-Aljorna A, Bueno MÁ, Aguinagalde I, Martín JP. Fingerprinting and genetic variability in cork oak (*Quercus suber* L.) elite trees using ISSR and SSR markers. *Ann Forest Sci.* 2007;64(7):773-9.
253. Isagi Y, Suhandono S. PCR primers amplifying microsatellite loci of *Quercus myrsinifolia* Blume and their conservation between oak species. *Molecular Ecology.* 1997;6(9):897-9.
254. Pakkad G, Ueno S, Yoshimaru H. Genetic diversity and differentiation of *Quercus semiserrata* Roxb. in northern Thailand revealed by nuclear and chloroplast microsatellite markers. *Forest Ecol Manag.* 2008;255(3-4):1067-77.
255. Valencia-Cuevas L, Piñero D, Mussali-Galante P, Valencia-Ávalos S, Tovar-Sánchez E. Effect of a red oak species gradient on genetic structure and diversity of *Quercus castanea* (Fagaceae) in Mexico. *Tree Genetics & Genomes.* 2014;10(3):641-52.
256. Chen X-D, Yang J, Guo Y-F, Zhao Y-M, Zhou T, Zhang X, et al. Spatial genetic structure and demographic history of the dominant forest oak *Quercus fabri* hance in subtropical China. *Frontiers in plant science.* 2021;11:583284.
257. Jurkšienė G, Baranov OY, Kagan DI, Kovalevič-Razumova OA, Baliuckas V. Genetic diversity and differentiation of pedunculate (*Quercus robur*) and sessile (*Q. petraea*) oaks. *J Forestry Res.* 2020;31(6):2445-52.
258. Antonecchia G, Fortini P, Lepais O, Gerber S, Legér P, Scippa GS, et al. Genetic structure of a natural oak community in central Italy: evidence of gene flow between three sympatric white oak species (*Quercus*, Fagaceae). *Ann for Res.* 2015;58(2):205-16.
259. Mariette S, Cottrell J, Csaikl UM, Goikoechea P, König A, Lowe AJ, et al. Comparison of levels of genetic diversity detected with AFLP and microsatellite markers within and among mixed *Q. petraea* (Matt.) Liebl. and *Q. robur* L. stands. *Silvae Genet.* 2002;51(2-3):72-9.
260. González-Rodríguez A, Arias DM, Oyama K. Genetic variation and differentiation of populations within the *Quercus affinis* *Quercus laurina* (Fagaceae) complex analyzed with RAPD markers. *Canadian Journal of Botany.* 2005;83(2):155-62.
261. Curtu AL, Gailing O, Finkeldey R. Evidence for hybridization and introgression within a species-rich oak (*Quercus* spp.) community. *BMC Evolutionary Biology.* 2007;7(1):1-15.
262. Curtu A, Gailing O, Leinemann L, Finkeldey R. Genetic variation and differentiation within a natural community of five oak species (*Quercus* spp.). *Plant Biology.* 2007;9(01):116-26.
263. Deguilloux M-F, Pemonge M-H, Petit RJ. Use of chloroplast microsatellites to differentiate oak populations. *Ann Forest Sci.* 2004;61(8):825-30.
264. Hokanson SC, Isebrands J, Jensen RJ, Hancock JF. Isozyme variation in oaks of the Apostle Islands in Wisconsin: genetic structure and levels of inbreeding in *Quercus rubra* and *Q. ellipsoidalis* (Fagaceae). *American Journal of Botany.* 1993;80(11):1349-57.
265. Lind-Riehl JF. Genetic variation, local adaptation and population structure in North American red oak species, *Quercus rubra* L. and *Q. ellipsoidalis* EJ Hill: Michigan Technological University; 2014.

266. Neophytou C, Aravanopoulos FA, Fink S, Dounavi A. Detecting interspecific and geographic differentiation patterns in two interfertile oak species (*Quercus petraea* (Matt.) Liebl. and *Q. robur* L.) using small sets of microsatellite markers. *Forest Ecol Manag.* 2010;259(10):2026-35.
267. Kremer A, Petit R-J, editors. Gene diversity in natural populations of oak species. *Ann Sci Forest*; 1993: EDP Sciences.
268. YÜCEDAĞ C, Gailing O. Morphological and genetic variation within and among four *Quercus petraea* and *Q. robur* natural populations. *Turkish Journal of Botany.* 2013;37(4):619-29.
269. Scotti-Saintagne C, Mariette S, Porth I, Goicoechea PG, Barreneche T, Bodénes C, et al. Genome scanning for interspecific differentiation between two closely related oak species [*Quercus robur* L. and *Q. petraea* (Matt.) Liebl.]. *Genetics.* 2004;168(3):1615-26.
270. Muir G, Schloetterer C. Evidence for shared ancestral polymorphism rather than recurrent gene flow at microsatellite loci differentiating two hybridizing oaks (*Quercus* spp.). *Molecular ecology.* 2005;14(2):549-61.
271. Lang T, Abadie P, Léger V, Decourcelle T, Frigerio J-M, Burban C, et al. High-quality SNPs from genic regions highlight introgression patterns among European white oaks (*Quercus petraea* and *Q. robur*). *bioRxiv.* 2021:388447.
272. Coelho AC, Lima M, Neves D, Cravador A. Genetic diversity of two evergreen oaks [*Quercus suber* (L.) and *Quercus ilex* subsp *rotundifolia* (Lam.)] in Portugal using AFLP markers. *Silvae Genet.* 2006;55(3):105-18.
273. Lind JF, Gailing O. Genetic structure of *Quercus rubra* L. and *Quercus ellipsoidalis* EJ Hill populations at gene-based EST-SSR and nuclear SSR markers. *Tree genetics & genomes.* 2013;9(3):707-22.
274. Streiff R, Labbe T, Bacilieri R, Steinkellner H, GLÖSSL J, Kremer A. Within-population genetic structure in *Quercus robur* L. and *Quercus petraea* (Matt.) Liebl. assessed with isozymes and microsatellites. *Molecular Ecology.* 1998;7(3):317-28.
275. VALBUENA-CARABANA M, GONZÁLEZ-MARTÍNEZ SC, Hardy OJ, Gil L. Fine-scale spatial genetic structure in mixed oak stands with different levels of hybridization. *Molecular Ecology.* 2007;16(6):1207-19.
276. Valbuena-Carabana M, González-Martínez SC, Sork V, Collada C, Soto A, Goicoechea P, et al. Gene flow and hybridisation in a mixed oak forest (*Quercus pyrenaica* Willd. and *Quercus petraea* (Matts.) Liebl.) in central Spain. *Heredity.* 2005;95(6):457-65.
277. Chen X-D, Zhang X, Zhang H, Zhou T, Zhao Y-M, Yang J, et al. Genetic Differentiation and Demographic History of Three *Cerris* Oak Species in China Based on Nuclear Microsatellite Makers. *Forests.* 2021;12(9):1164.
278. Aldrich PR, Michler CH, Sun W, Romero-Severson J. Microsatellite markers for northern red oak (Fagaceae: *Quercus rubra*). *Molecular Ecology Notes.* 2002;2(4):472-4.
279. Kampfer S, Lexer C, Glossl J, Steinkellner H. Brief report characterization of (GA) n microsatellite loci from *Quercus robur*. *Hereditas.* 1998;129(183):1-86.
280. Fluch S, Turetschek E, Lexer C, Streiff R, Kremer A, Burg K, et al. Identification and characterization of (GA/CT) n-microsatellite loci from *Quercus petraea*. *Plant Molecular Biology.* 1997;33(6):1093-6.
281. Ueno S, Tsumura Y. Development of ten microsatellite markers for *Quercus mongolica* var. *crispula* by database mining. *Conserv Genet.* 2008;9(4):1083-5.

282. Mishima K, Watanabe A, Isoda K, Ubukata M, Takata K. Isolation and characterization of microsatellite loci from *Quercus mongolica* var. *crispula*. *Molecular Ecology Notes*. 2006;6(3):695-7.
283. Chatwin WB, Carpenter KK, Jimenez FR, Elzinga DB, Johnson LA, Maughan PJ. Microsatellite primer development for post oak, *Quercus stellata* (Fagaceae). *Appl Plant Sci*. 2014;2(10):1400070.
284. Deguilloux MF, Dumolin-Lapègue S, Gielly L, Grivet D, Petit R. A set of primers for the amplification of chloroplast microsatellites in *Quercus*. *Molecular Ecology Notes*. 2003;3(1):24-7.
285. Sullivan AR, Lind JF, McCleary TS, Romero-Severson J, Gailing O. Development and characterization of genomic and gene-based microsatellite markers in North American red oak species. *Plant Molecular Biology Reporter*. 2013;31(1):231-9.
286. Soto A, Lorenzo Z, Gil L. Nuclear microsatellite markers for the identification of *Quercus ilex* L. and *Q. suber* L. hybrids. *Silvae Genet*. 2003;52(2):63-6.
287. Du Q, Pan W, Tian J, Li B, Zhang D. The UDP-glucuronate decarboxylase gene family in *Populus*: structure, expression, and association genetics. *Plos One*. 2013;8(4):e60880.
288. Tschaplinski TJ, Tuskan GA, Sewell MM, Gebre GM, Todd DE, Pendley CD. Phenotypic variation and quantitative trait locus identification for osmotic potential in an interspecific hybrid inbred F2 poplar pedigree grown in contrasting environments. *Tree Physiol*. 2006;26(5):595-604.
289. El-Kassaby YA, Klápště J, Guy RD. Breeding without breeding: selection using the genomic best linear unbiased predictor method (GBLUP). *New Forest*. 2012;43(5-6):631-7.
290. Kaplan A. Genomic Selection and Genome-Wide Association Study in *Populus trichocarpa* and *Pinus taeda*: Virginia Tech; 2016.
291. Chhetri HB, Macaya-Sanz D, Kainer D, Biswal AK, Evans LM, Chen JG, et al. Multitrait genome-wide association analysis of *Populus trichocarpa* identifies key polymorphisms controlling morphological and physiological traits. *New Phytologist*. 2019;223(1):293-309.
292. Bdeir R, Muchero W, Yordanov Y, Tuskan GA, Busov V, Gailing O. Genome-wide association studies of bark texture in *Populus trichocarpa*. *Tree Genetics & Genomes*. 2019;15(1):1-14.
293. Porth I, Klápště J, McKown AD, La Mantia J, Guy RD, Ingvarsson PK, et al. Evolutionary quantitative genomics of *Populus trichocarpa*. *Plos One*. 2015;10(11):e0142864.
294. McKown AD, Klápště J, Guy RD, Geraldles A, Porth I, Hannemann J, et al. Genome-wide association implicates numerous genes underlying ecological trait variation in natural populations of *Populus trichocarpa*. *New Phytologist*. 2014;203(2):535-53.
295. McKown AD, Guy RD, Quamme L, Klápště J, La Mantia J, Constabel C, et al. Association genetics, geography and ecophysiology link stomatal patterning in *Populus trichocarpa* with carbon gain and disease resistance trade-offs. *Molecular ecology*. 2014;23(23):5771-90.
296. Guerra FP, Wegrzyn JL, Sykes R, Davis MF, Stanton BJ, Neale DB. Association genetics of chemical wood properties in black poplar (*Populus nigra*). *New Phytologist*. 2013;197(1):162-76.

297. Guerra FP, Suren H, Holliday J, Richards JH, Fiehn O, Famula R, et al. Exome resequencing and GWAS for growth, ecophysiology, and chemical and metabolomic composition of wood of *Populus trichocarpa*. *BMC genomics*. 2019;20(1):1-14.
298. Fahrenkrog AM, Neves LG, Resende Jr MF, Vazquez AI, de Los Campos G, Dervinis C, et al. Genome-wide association study reveals putative regulators of bioenergy traits in *Populus deltoides*. *New Phytologist*. 2017;213(2):799-811.
299. Porth I, Klapšte J, Skyba O, Hannemann J, McKown AD, Guy RD, et al. Genome-wide association mapping for wood characteristics in *Populus* identifies an array of candidate single nucleotide polymorphisms. *New Phytologist*. 2013;200(3):710-26.
300. Zhang B, Tong C, Yin T, Zhang X, Zhuge Q, Huang M, et al. Detection of quantitative trait loci influencing growth trajectories of adventitious roots in *Populus* using functional mapping. *Tree genetics & genomes*. 2009;5(3):539-52.
301. McKown AD, Klápště J, Guy RD, Soolanayakanahally RY, La Mantia J, Porth I, et al. Sexual homomorphism in dioecious trees: extensive tests fail to detect sexual dimorphism in *Populus*. *Scientific Reports*. 2017;7(1):1-14.
302. McKown AD, Klápště J, Guy RD, El-Kassaby YA, Mansfield SD. Ecological genomics of variation in bud-break phenology and mechanisms of response to climate warming in *Populus trichocarpa*. *New Phytologist*. 2018;220(1):300-16.
303. Allwright MR, Payne A, Emiliani G, Milner S, Viger M, Rouse F, et al. Biomass traits and candidate genes for bioenergy revealed through association genetics in coppiced European *Populus nigra* (L.). *Biotechnology for biofuels*. 2016;9(1):1-22.
304. Carletti G, Carra A, Allegro G, Vietto L, Desiderio F, Bagnaresi P, et al. QTLs for woolly poplar aphid (*Phloeomyzus passerinii* L.) resistance detected in an inter-specific *Populus deltoides* x *P. nigra* mapping population. *Plos One*. 2016;11(3):e0152569.
305. Suarez-Gonzalez A, Hefer CA, Lexer C, Cronk QC, Douglas CJ. Scale and direction of adaptive introgression between black cottonwood (*Populus trichocarpa*) and balsam poplar (*P. balsamifera*). *Molecular ecology*. 2018;27(7):1667-80.
306. Gaudet M. Molecular approach to dissect adaptive traits in native European *Populus nigra* L.: construction of a genetic linkage map based on AFLP, SSR and SNP markers: Tuscia University; 2006.
307. Muraguri MS. Genetic diversity of *Populus ilicifolia* populations in Kenya using amplified fragment length polymorphism (AFLP) markers: Kenyatta University; 2015.
308. Wang Y, Sun X, Tan B, Zhang B, Xu L-a, Huang M, et al. A genetic linkage map of *Populus adenopoda* Maxim. x *P. alba* L. hybrid based on SSR and SRAP markers. *Euphytica*. 2010;173(2):193-205.
309. Ke C, Xiuqing J, Peng R, Jianqing L. Genetic relationships of poplar species in section *Tacamahaca* based on cpDNA and ISSR. *Scientific Research and Essays*. 2011;6(19):4048-54.
310. Resende Jr M, Munoz P, Acosta J, Peter G, Davis J, Grattapaglia D, et al. Accelerating the domestication of trees using genomic selection: accuracy of prediction models across ages and environments. *New Phytologist*. 2012;193(3):617-24.
311. Zapata-Valenzuela J, Whetten RW, Neale D, McKeand S, Isik F. Genomic estimated breeding values using genomic relationship matrices in a cloned population of loblolly pine. *G3: Genes, Genomes, Genetics*. 2013;3(5):909-16.
312. Zapata-Valenzuela J, Isik F, Maltecca C, Wegrzyn J, Neale D, McKeand S, et al. SNP markers trace familial linkages in a cloned population of *Pinus taeda*—prospects for genomic selection. *Tree Genetics & Genomes*. 2012;8(6):1307-18.

313. Xiong JS, McKeand SE, Isik F, Wegrzyn J, Neale DB, Zeng Z-B, et al. Quantitative trait loci influencing forking defects in an outbred pedigree of loblolly pine. *BMC genetics*. 2016;17(1):1-11.
314. MacKay JJ, O'Malley DM, Presnell T, Booker FL, Campbell MM, Whetten RW, et al. Inheritance, gene expression, and lignin characterization in a mutant pine deficient in cinnamyl alcohol dehydrogenase. *Proceedings of the National Academy of Sciences*. 1997;94(15):8255-60.
315. Lu M, Krutovsky KV, Nelson CD, West JB, Reilly NA, Loopstra CA. Association genetics of growth and adaptive traits in loblolly pine (*Pinus taeda* L.) using whole-exome-discovered polymorphisms. *Tree Genetics & Genomes*. 2017;13(3):57.
316. Resende Jr M, Muñoz P, Resende MD, Garrick DJ, Fernando RL, Davis JM, et al. Accuracy of genomic selection methods in a standard data set of loblolly pine (*Pinus taeda* L.). *Genetics*. 2012;190(4):1503-10.
317. Chhatre VE. Population structure, association mapping of economic traits and landscape genomics of east Texas loblolly pine (*Pinus taeda* L.): Texas A&M University; 2013.
318. Cumbie W, Eckert A, Wegrzyn J, Whetten R, Neale D, Goldfarb B. Association genetics of carbon isotope discrimination, height and foliar nitrogen in a natural population of *Pinus taeda* L. *Heredity*. 2011;107(2):105-14.
319. González-Martínez SC, Wheeler NC, Ersoz E, Nelson CD, Neale DB. Association genetics in *Pinus taeda* LI Wood property traits. *Genetics*. 2007;175(1):399-409.
320. Isik F, Bartholomé J, Farjat A, Chancerel E, Raffin A, Sanchez L, et al. Genomic selection in maritime pine. *Plant Science*. 2016;242:108-19.
321. Calleja-Rodriguez A, Pan J, Funda T, Chen Z-Q, Baisón J, Isik F, et al. Genomic prediction accuracies and abilities for growth and wood quality traits of Scots pine, using genotyping-by-sequencing (GBS) data. *bioRxiv*. 2019:607648.
322. Calleja-Rodriguez A, Pan J, Funda T, Chen Z, Baisón J, Isik F, et al. Evaluation of the efficiency of genomic versus pedigree predictions for growth and wood quality traits in Scots pine. *BMC genomics*. 2020;21(1):1-17.
323. Zhang Y, Yang Q, Zhou Z, Jin G. Divergence among masson pine parents revealed by geographical origins and SSR markers and their relationships with progeny performance. *New Forest*. 2013;44(3):341-55.
324. Dillon S, Nolan M, Li W, Bell C, Wu H, Southerton S. Allelic variation in cell wall candidate genes affecting solid wood properties in natural populations and land races of *Pinus radiata*. *Genetics*. 2010;185(4):1477-87.
325. Lepoittevin C, Harvengt L, Plomion C, Garnier-Géré P. Association mapping for growth, straightness and wood chemistry traits in the *Pinus pinaster* Aquitaine breeding population. *Tree Genetics & Genomes*. 2012;8(1):113-26.
326. Rawat A, Barthwal S, Ginwal H. Comparative assessment of SSR, ISSR and AFLP markers for characterization of selected genotypes of Himalayan Chir pine (*Pinus roxburghii* Sarg.) based on resin yield. *Silvae Genet*. 2014;63(1-6):94-108.
327. Cumbie WP, Huber DA, Steel VC, Rottmann W, Cannistra C, Pearson L, et al. Marker associations for fusiform rust resistance in a clonal population of loblolly pine (*Pinus taeda*, L.). *Tree Genetics & Genomes*. 2020;16(6):1-15.
328. Devey ME, Delfino-Mix A, Kinloch BB, Neale DB. Random amplified polymorphic DNA markers tightly linked to a gene for resistance to white pine blister rust in sugar pine. *Proceedings of the National Academy of Sciences*. 1995;92(6):2066-70.

329. Liu J-J, Snieszko RA, Sissons R, Krakowski J, Alger G, Schoettle AW, et al. Association mapping and development of marker-assisted selection tools for the resistance to white pine blister rust in the Alberta limber pine populations. *Frontiers in Plant Science*. 2020;11:1404.
330. De La Torre AR, Wilhite B, Neale DB. Environmental genome-wide association reveals climate adaptation is shaped by subtle to moderate allele frequency shifts in loblolly pine. *Genome biology and evolution*. 2019;11(10):2976-89.
331. Schiller G, Korol L, Shklar G. Habitat effects on adaptive genetic variation in *Pinus halepensis* Mill. provenances. *Forest Genetics*. 2004;11(3/4):325.
332. Parchman TL, Gompert Z, Mudge J, Schilkey FD, Benkman CW, Buerkle CA. Genome-wide association genetics of an adaptive trait in lodgepole pine. *Molecular ecology*. 2012;21(12):2991-3005.
333. Liwaksaneeyanawin C. Genetic evaluation of natural and domesticated lodgepole pine populations using molecular markers: University of British Columbia; 2006.
334. Fernandes L, Rocheta M, Cordeiro J, Pereira S, Gerber S, Oliveira MM, et al. Genetic variation, mating patterns and gene flow in a *Pinus pinaster* Aiton clonal seed orchard. *Ann Forest Sci*. 2008;65(7).
335. Rajora OP, Rahman MH, Buchert GP, Dancik BP. Microsatellite DNA analysis of genetic effects of harvesting in old-growth eastern white pine (*Pinus strobus*) in Ontario, Canada. *Molecular Ecology*. 2000;9(3):339-48.
336. Cengel B, Tayanç Y, Kandemir G, Velioglu E, Alan M, Kaya Z. Magnitude and efficiency of genetic diversity captured from seed stands of *Pinus nigra* (Arnold) subsp. *pallasiana* in established seed orchards and plantations. *New Forest*. 2012;43(3):303-17.
337. Yang H-x, Luo R, Zhao F-c, Liu T-y, Liu C-x, Huang S-w. Constructing genetic linkage maps for *Pinus elliottii* var. *elliottii* and *Pinus caribaea* var. *hondurensis* using SRAP, SSR, EST and ISSR markers. *Trees*. 2013;27(5):1429-42.
338. Rawat A, Barthwal S, Ginwal H, Tripathi S. Association mapping for identification of ISSR and AFLP markers linked with resin yield in Himalayan Chir Pine (*Pinus roxburghii* Sarg. *Silvae Genet*. 2015;64(1-6):220-39.
339. Sakaguchi S, Sugino T, Tsumura Y, Ito M, Crisp MD, Bowman DM, et al. High-throughput linkage mapping of Australian white cypress pine (*Callitris glaucophylla*) and map transferability to related species. *Tree Genetics & Genomes*. 2015;11(6):1-12.
340. El-Dien OG, Ratcliffe B, Klápště J, Chen C, Porth I, El-Kassaby YA. Prediction accuracies for growth and wood attributes of interior spruce in space using genotyping-by-sequencing. *BMC genomics*. 2015;16(1):1-16.
341. El-Dien OG, Ratcliffe B, Klápště J, Porth I, Chen C, El-Kassaby YA. Multienvironment genomic variance decomposition analysis of open-pollinated Interior spruce (*Picea glauca* x *engelmannii*). *Molecular breeding*. 2018;38(3):1-16.
342. Ratcliffe B, El-Dien OG, Klapste J, Porth I, Chen C, Jaquish B, et al. A comparison of genomic selection models across time in interior spruce (*Picea engelmannii* x *glauca*) using unordered SNP imputation methods. *Heredity*. 2015;115(6):547-55.
343. Beaulieu J, Doerksen TK, MacKay J, Rainville A, Bousquet J. Genomic selection accuracies within and between environments and small breeding groups in white spruce. *BMC genomics*. 2014;15(1):1-16.
344. Beaulieu J, Doerksen T, Clément S, MacKay J, Bousquet J. Accuracy of genomic selection models in a large population of open-pollinated families in white spruce. *Heredity*. 2014;113(4):343-52.

345. Lenz PR, Nadeau S, Azaiez A, Gérardi S, Deslauriers M, Perron M, et al. Genomic prediction for hastening and improving efficiency of forward selection in conifer polycross mating designs: an example from white spruce. *Heredity*. 2020;124(4):562-78.
346. Lenz PR, Beaulieu J, Mansfield SD, Clément S, Despons M, Bousquet J. Factors affecting the accuracy of genomic selection for growth and wood quality traits in an advanced-breeding population of black spruce (*Picea mariana*). *BMC genomics*. 2017;18(1):1-17.
347. Lamara M, Raherison E, Lenz P, Beaulieu J, Bousquet J, MacKay J. Genetic architecture of wood properties based on association analysis and co-expression networks in white spruce. *New Phytologist*. 2016;210(1):240-55.
348. Fuentes-Utrilla P, Goswami C, Cottrell J, Pong-Wong R, Law A, A'Hara S, et al. QTL analysis and genomic selection using RADseq derived markers in Sitka spruce: the potential utility of within family data. *Tree Genetics & Genomes*. 2017;13(2):33.
349. Baison J, Vidalis A, Zhou L, Chen ZQ, Li Z, Sillanpää MJ, et al. Genome-wide association study identified novel candidate loci affecting wood formation in Norway spruce. *The Plant Journal*. 2019;100(1):83-100.
350. Elfstrand M, Baison J, Lundén K, Zhou L, Vos I, Capador HD, et al. Association genetics identifies a specifically regulated Norway spruce laccase gene, PaLAC5, linked to *Heterobasidion parviporum* resistance. *Plant, Cell & Environment*. 2020;43(7):1779-91.
351. Mukrimin M, Kovalchuk A, Neves LG, Jaber EH, Haapanen M, Kirst M, et al. Genome-wide exon-capture approach identifies genetic variants of Norway spruce genes associated with susceptibility to *Heterobasidion parviporum* infection. *Frontiers in plant science*. 2018;9:793.
352. Rajora OP, Mann IK, Shi Y-Z. Genetic diversity and population structure of boreal white spruce (*Picea glauca*) in pristine conifer-dominated and mixedwood forest stands. *Botany*. 2005;83(9):1096-105.
353. Isabel N, Beaulieu J, Bousquet J. Complete Congruence between Gene Diversity Estimates Derived from Genotypic Data at Enzyme and Random Amplified Polymorphic DNA Loci in Black Spruce. *P Natl Acad Sci USA*. 1995;92(14):6369-73.
354. Bernhardsson C, Zan Y, Chen Z, Ingvarsson PK, Wu HX. Development of a highly efficient 50K single nucleotide polymorphism genotyping array for the large and complex genome of Norway spruce (*Picea abies* L. Karst) by whole genome resequencing and its transferability to other spruce species. *Molecular ecology resources*. 2021;21(3):880-96.
355. Julio N, Rondan Dueñas J, Renison D, Hensen I. Genetic structure and diversity of *Polylepis australis* (Rosaceae) tree populations from central Argentina: Implications for forest conservation. *Silvae Genet*. 2011;60(2):55.
356. Julio N, Sobral A, Duenas JR, Di Rienzo J, Renison D, Hensen I. RAPD and ISSR markers indicate diminished gene flow due to recent fragmentation of *Polylepis australis* woodlands in central Argentina. *Biochemical Systematics and Ecology*. 2008;36(5-6):329-35.
357. Hensen I, Teich I, Hirsch H, von Wehrden H, Renison D. Range-wide genetic structure and diversity of the endemic tree line species *Polylepis australis* (Rosaceae) in Argentina. *American Journal of Botany*. 2011;98(11):1825-33.
358. Peng Y, Morales L, Hensen I, Renison D. No effect of elevation and fragmentation on genetic diversity and structure in *Polylepis australis* trees from central Argentina. *Austral Ecology*. 2017;42(3):288-96.

359. Quinteros-Casaverde N, Flores-Negrón CF, Williams DA. Low genetic diversity and fragmentation effects in a wind-pollinated tree, *Polylepis multijuga* Plige (Rosaceae) in the high Andes. *Conserv Genet.* 2012;13(2):593-603.
360. Aragundi S, Hamrick J, Parker KC. Genetic insights into the historical distribution of *Polylepis pauta* (Rosaceae) in the northeastern Cordillera Oriental of Ecuador. *Conserv Genet.* 2011;12(3):607-18.
361. Bastidas-León EW, Espinel-Ortiz DA, Romoleroux K. Population genetic analysis of two *Polylepis microphylla* (Wedd.) Bitter (Rosaceae) forests in Ecuador. *Neotropical Biodiversity.* 2021;7(1):184-97.
362. Yahya AF, Hyun JO, Lee JH, Kim YY, Lee KM, Hong KN, et al. Genetic variation and population genetic structure of *Rhizophora apiculata* (Rhizophoraceae) in the greater Sunda Islands, Indonesia using microsatellite markers. *Journal of plant research.* 2014;127(2):287-97.
363. Souza LM, Francisco FR, Gonçalves PS, Scaloppi Junior EJ, Le Guen V, Fritsche-Neto R, et al. Genomic selection in rubber tree breeding: a comparison of models and methods for managing G×E interactions. *Frontiers in plant science.* 2019;10:1353.
364. Bini K, Saha T, Radhakrishnan S, Ravindran M, Uthup TK. Development of Novel Markers for Yield in *Hevea brasiliensis* Muell. Arg. Based on Candidate Genes from Biosynthetic Pathways Associated with Latex Production. *Biochem Genet.* 2022:1-29.
365. Cros D, Mbo-Nkoulou L, Bell JM, Oum J, Masson A, Soumahoro M, et al. Within-family genomic selection in rubber tree (*Hevea brasiliensis*) increases genetic gain for rubber production. *Industrial Crops and Products.* 2019;138:111464.
366. Chanroj V, Rattanawong R, Phumichai T, Tangphatsornruang S, Ukoskit K. Genome-wide association mapping of latex yield and girth in Amazonian accessions of *Hevea brasiliensis* grown in a suboptimal climate zone. *Genomics.* 2017;109(5-6):475-84.
367. An Z, Zhao Y, Zhang X, Huang X, Hu Y, Cheng H, et al. A high-density genetic map and QTL mapping on growth and latex yield-related traits in *Hevea brasiliensis* Müll. Arg. *Industrial Crops and Products.* 2019;132:440-8.
368. Li D, Deng Z, Qin B, Liu X, Men Z. De novo assembly and characterization of bark transcriptome using Illumina sequencing and development of EST-SSR markers in rubber tree (*Hevea brasiliensis* Muell. Arg.). *BMC genomics.* 2012;13(1):1-14.
369. Le Guen V, Garcia D, Doare F, Mattos CRR, Condina V, Couturier C, et al. A rubber tree's durable resistance to *Microcyclus ulei* is conferred by a qualitative gene and a major quantitative resistance factor. *Tree Genetics & Genomes.* 2011;7(5):877-89.
370. Tran DM, Clément-Demange A, Deon M, Garcia D, Le Guen V, Clément-Vidal A, et al. Genetic determinism of sensitivity to *Corynespora cassiicola* exudates in rubber tree (*Hevea brasiliensis*). *Plos One.* 2016;11(10):e0162807.
371. Lespinasse D, Grivet L, Troispoux V, Rodier-Goud M, Pinard F, Seguin M. Identification of QTLs involved in the resistance to South American leaf blight (*Microcyclus ulei*) in the rubber tree. *Theoretical and Applied Genetics.* 2000;100(6):975-84.
372. Besse P, Seguin M, Lebrun P, Chevallier M, Nicolas D, Lanaud C. Genetic diversity among wild and cultivated populations of *Hevea brasiliensis* assessed by nuclear RFLP analysis. *Theoretical and applied genetics.* 1994;88(2):199-207.
373. Saithong K, Hong KW, Fu-Cheng L, Kevin DH, Kasem S. Genetic variation among isolates of *Rigidoporus microporus* causing white root disease of rubber trees in southern Thailand revealed by ISSR markers and pathogenicity. *African Journal of Microbiology Research.* 2009;3(10):641-8.

374. De Souza LM, Dos Santos LH, Rosa JR, Da Silva CC, Mantello CC, Conson AR, et al. Linkage disequilibrium and population structure in wild and cultivated populations of rubber tree (*Hevea brasiliensis*). *Frontiers in Plant Science*. 2018;9:815.
375. Yu F, Wang B-H, Feng S-P, Wang J-Y, Li W-G, Wu Y-T. Development, characterization, and cross-species/genera transferability of SSR markers for rubber tree (*Hevea brasiliensis*). *Plant cell reports*. 2011;30(3):335-44.
376. Pootakham W, Ruang-Areerate P, Jomchai N, Sonthirod C, Sangrakru D, Yoocha T, et al. Construction of a high-density integrated genetic linkage map of rubber tree (*Hevea brasiliensis*) using genotyping-by-sequencing (GBS). *Frontiers in plant science*. 2015;6:367.
377. Le Guen V, Gay C, Xiong TC, Souza LM, Rodier-Goud M, Seguin M. Development and characterization of 296 new polymorphic microsatellite markers for rubber tree (*Hevea brasiliensis*). *Plant Breeding*. 2011;130(2):294-6.
378. Ju MM, Ma HC, Xin PY, Zhou ZL, Tian B. Development and Characterization of Est-Ssr Markers in *Bombax Ceiba* (Malvaceae). *Appl Plant Sci*. 2015;3(4).
379. Tian B, Tian X, Xu Y, Ma H. Developing SSR primers in *Bombax ceiba* (Bombacaceae). *Guangxi Zhiwu/Guihaia*. 2013;33(4):465-7.
380. Monfared MA, Samsampour D, Sharifi-Sirchi GR, Sadeghi F. Assessment of genetic diversity in *Salvadora persica* L. based on inter simple sequence repeat (ISSR) genetic marker. *Journal of Genetic Engineering and biotechnology*. 2018;16(2):661-7.
381. Andiego K, Dangasuk O, Odee D, Omondi F, Otieno D, Balozi B. Genetic diversity of endangered sandalwood (*Osyris lanceolata*) populations in Kenya using ISSR molecular markers. *East African Agricultural and Forestry Journal*. 2019;83(2):80-93.
382. Fofana IJ, Ofori D, Poitel M, Verhaegen D. Diversity and genetic structure of teak (*Tectona grandis* Lf) in its natural range using DNA microsatellite markers. *New Forest*. 2009;37(2):175-95.
383. Win TT. Genetic Diversity and Population Genetic Structure of Teak. *The Teak Genome*: Springer; 2021. p. 181-90.
384. THWE TW. Geographic variation and genetic structure of teak (*Tectona grandis*) in Myanmar revealed by cpSNP and nrSSR markers: The University of Tokyo; 2015.
385. Vaishnav V, Mohammad N, Wali SA, Kumar R, Tripathi SB, Negi MS, et al. AFLP markers for analysis of genetic diversity and structure of teak (*Tectona grandis*) in India. *Canadian Journal of Forest Research*. 2015;45(3):297-306.
386. Hossain MMRMZ. Review on the application of molecular approaches for the genetic analysis of teak (*Tectona grandis* Lf) populations. 2022.
387. Sarwat M, Das S, Srivastava P. AFLP and SAMPL markers for characterization of genetic diversity in *Terminalia arjuna*: a backbone tree of Tasar silk industry. *Plant Systematics and Evolution*. 2011;293(1):13-23.
388. Worth JR, Tamaki I, Tsuyama I, Harrison PA, Sugai K, Sakio H, et al. Genetic Distinctiveness but Low Diversity Characterizes Rear-Edge *Thuja standishii* (Gordon) Carr.(Cupressaceae) Populations in Southwest Japan. *Diversity*. 2021;13(5):185.
389. Qin A, Ding Y, Jian Z, Ma F, Worth JR, Pei S, et al. Low genetic diversity and population differentiation in *Thuja sutchuenensis* Franch., an extremely endangered rediscovered conifer species in southwestern China. *Global Ecology and Conservation*. 2021;25:e01430.

390. Worth JR, Chang K, Ha Y-H, Qin A. Development of microsatellite markers for the Japanese endemic conifer *Thuja standishii* and transfer to other East Asian species. *BMC research notes*. 2019;12(1):1-5.
391. Hou X, Guo Q, Wei W, Guo L, Guo D, Zhang L. Screening of genes related to early and late flowering in tree peony based on bulked segregant RNA sequencing and verification by quantitative real-time PCR. *Molecules*. 2018;23(3):689.
392. Li C, Wu J, Li Q, Yang Y, Zhang K. Development of Simple Sequence Repeat Markers from Functional Genes and Establishment of Molecular Identity for Tree Peony. *Journal of Plant Biochemistry and Biotechnology*. 2022;31(1):22-36.
393. Wu J, Cai C, Cheng F, Cui H, Zhou H. Characterisation and development of EST-SSR markers in tree peony using transcriptome sequences. *Molecular breeding*. 2014;34(4):1853-66.
394. Zeng Y, Ye S, Yu W, Wu S, Hou W, Wu R, et al., editors. Genetic linkage map construction and QTL identification of juvenile growth traits in *Torreya grandis*. *BMC genetics*; 2014: Springer.
395. Zhang X. Development of Liriodendron EST-SSR markers and genetic composition of two *Liriodendron tulipifera* L. Orchards: Clemson University; 2013.
396. Xu M, Sun YG, Li HG. EST-SSRs development and paternity analysis for *Liriodendron* spp. *New Forest*. 2010;40(3):361-82.
397. Long XF, Weng YH, Liu SQ, Hao ZD, Sheng Y, Guan LH, et al. Genetic Diversity and Differentiation of Relict Plant *Liriodendron* Populations Based on 29 Novel EST-SSR Markers. *Forests*. 2019;10(4).
398. Carlson CH, Gouker FE, Crowell CR, Evans L, DiFazio SP, Smart CD, et al. Joint linkage and association mapping of complex traits in shrub willow (*Salix purpurea* L.). *Ann Bot-London*. 2019;124(4):701-15.
399. Sulima P, Prinz K, Przyborowski JA. Genetic diversity and genetic relationships of purple willow (*Salix purpurea* L.) from natural locations. *International journal of molecular sciences*. 2017;19(1):105.
400. Ngantcha AC. DNA fingerprinting and genetic relationships among willow (*Salix* spp.) 2010.
401. Mwase WF, Akinnifesi F, Stedje B, Kwapata M, Bjørnstad Å. Genetic diversity within and among southern African provenances of *Uapaca kirkiana* Müell. Arg using morphological and AFLP markers. *New Forest*. 2010;40(3):383-99.
402. Trebbi D, Ravi S, Broccanello C, Chiodi C, Francis G, Oliver J, et al. Identification and validation of SNP markers linked to seed toxicity in *Jatropha curcas* L. *Scientific reports*. 2019;9(1):1-7.
403. Azevedo Peixoto Ld, Laviola BG, Alves AA, Rosado TB, Bhering LL. Breeding *Jatropha curcas* by genomic selection: A pilot assessment of the accuracy of predictive models. *Plos One*. 2017;12(3):e0173368.
404. Dhakshanamoorthy D, Selvaraj R, Chidambaram A. Utility of RAPD marker for genetic diversity analysis in gamma rays and ethyl methane sulphonate (EMS)-treated *Jatropha curcas* plants. *Comptes rendus biologiques*. 2015;338(2):75-82.
405. Pamidimarri DS, Mastan SG, Rahman H, Reddy MP. Molecular characterization and genetic diversity analysis of *Jatropha curcas* L. in India using RAPD and AFLP analysis. *Molecular biology reports*. 2010;37(5):2249-57.
406. Mastan SG, Sudheer PD, Rahman H, Ghosh A, Rathore MS, Prakash CR, et al. Molecular characterization of intra-population variability of *Jatropha curcas* L. using DNA based molecular markers. *Molecular Biology Reports*. 2012;39(4):4383-90.

407. Vásquez-Mayorga M, Fuchs EJ, Hernández EJ, Herrera F, Hernández J, Moreira I, et al. Molecular characterization and genetic diversity of *Jatropha curcas* L. in Costa Rica. *PeerJ*. 2017;5:e2931.
408. Anggraeni TDA, Satyawati D, Kang YJ, Ha J, Kim MY, Chitikineni A, et al. Genetic diversity of *Jatropha curcas* collections from different islands in Indonesia. *Plant Genet Resour-C*. 2018;16(4):334-42.
409. Gupta P, Idris A, Mantri S, Asif MH, Yadav HK, Roy JK, et al. Discovery and use of single nucleotide polymorphic (SNP) markers in *Jatropha curcas* L. *Molecular Breeding*. 2012;30(3):1325-35.
410. Na-ek Y, Wongkaew A, Phumichai T, Kongsiri N, Kaveeta R, Phumichai C. Genetic diversity of physic nut (*Jatropha curcas* L.) revealed by SSR markers. *Journal of Crop Science and Biotechnology*. 2011;14(2):105-10.
411. Machua J, Muturi G, Omondi SF, Gicheru J. Genetic diversity of *Jatropha curcas* L. populations in Kenya using RAPD molecular markers: Implication to plantation establishment. *African Journal of Biotechnology*. 2011;10(16):3062-9.
412. Tatikonda L, Wani SP, Kannan S, Beerelli N, Sreedevi TK, Hoisington DA, et al. AFLP-based molecular characterization of an elite germplasm collection of *Jatropha curcas* L., a biofuel plant. *Plant Science*. 2009;176(4):505-13.
413. Mavuso C, Wu YP, Chen FC, Huang BH, Lin SJ. Genetic diversity analysis of *Jatropha curcas* L. accessions cultivated in Taiwan using inter simple sequence repeats (ISSR) markers. *Agroforest Syst*. 2016;90(3):417-31.
414. Vijayanand V, Senthil N, Vellaikumar S, Paramathma M. Genetic diversity of Indian *Jatropha* species as revealed by morphological and ISSR markers. *Journal of Crop Science and Biotechnology*. 2009;12(3):115.
415. Kumar RS, Parthiban KT, Rao MG. Molecular characterization of *Jatropha* genetic resources through inter-simple sequence repeat (ISSR) markers. *Molecular Biology Reports*. 2009;36(7):1951-6.
416. Ram SG, Parthiban KT, Kumar RS, Thiruvengadam V, Paramathma M. Genetic diversity among *Jatropha* species as revealed by RAPD markers. *Genet Resour Crop Ev*. 2008;55(6):803-9.
417. Basha SD, Sujatha M. Inter and intra-population variability of *Jatropha curcas* (L.) characterized by RAPD and ISSR markers and development of population-specific SCAR markers. *Euphytica*. 2007;156(3):375-86.
418. Sun QB, Li LF, Li Y, Wu GJ, Ge XJ. SSR and AFLP markers reveal low genetic diversity in the biofuel plant *Jatropha curcas* in China. *Crop Sci*. 2008;48(5):1865-71.
419. Shen JL, Jia XN, Ni HQ, Sun PG, Niu SH, Chen XY. AFLP analysis of genetic diversity of *Jatropha curcas* grown in Hainan, China. *Trees-Struct Funct*. 2010;24(3):455-62.
420. Rosado TB, Laviola BG, Faria DA, Pappas MR, Bhering LL, Quirino B, et al. Molecular Markers Reveal Limited Genetic Diversity in a Large Germplasm Collection of the Biofuel Crop *Jatropha curcas* L. in Brazil. *Crop Sci*. 2010;50(6):2372-82.
421. Rafii MY, Shabanimofrad M, Edaroyati MWP, Latif MA. Analysis of the genetic diversity of physic nut, *Jatropha curcas* L. accessions using RAPD markers. *Molecular Biology Reports*. 2012;39(6):6505-11.
422. Danquah EO, Akromah R, Quashie-Sam SJ, Oduro W, Falk D, Thevathasan NV, et al. The genetic diversity of *Jatropha Curcas* (L.) germplasm in Ghana as revealed by random amplified polymorphic DNA (RAPD) primers. *Agroforest Syst*. 2012;86(3):443-50.

423. Ovando-Medina I, Sánchez-Gutiérrez A, Adriano-Anaya L, Espinosa-García F, Núñez-Farfán J, Salvador-Figueroa M. Genetic diversity in *Jatropha curcas* populations in the State of Chiapas, Mexico. *Diversity*. 2011;3(4):641-59.
424. Ouattara B, Ndir KN, Gueye MC, Diédhiou I, Barnaud A, Fonceka D, et al. Genetic diversity of *Jatropha curcas* L. in Senegal compared with exotic accessions based on microsatellite markers. *Genet Resour Crop Ev*. 2014;61(6):1039-45.
425. Kumar S, Kumaria S, Sharma SK, Rao SR, Tandon P. Genetic diversity assessment of *Jatropha curcas* L. germplasm from Northeast India. *Biomass Bioenerg*. 2011;35(7):3063-70.
426. Kumar RV, Tripathi YK, Shukla P, Ahlawat SP, Gupta VK. Genetic diversity and relationships among germplasm of *Jatropha curcas* L. revealed by RAPDs. *Trees-Struct Funct*. 2009;23(5):1075-9.
427. Chen K, Ren P, Ying CY, Jiang Q, Jia XQ. Genetic relationships among *Jatropha curcas* L. clones from Panzhihua, China as revealed by RAPD and ISSR. *Afr J Agr Res*. 2011;6(11):2582-5.
428. Camellia NN, Lee AT, Abdullah N. Genetic relationships and diversity of *Jatropha curcas* accessions in Malaysia. *African Journal of Biotechnology*. 2012;11(13):3048-54.
429. Montes JM, Technow F, Martin M, Becker K. Genetic diversity in *Jatropha curcas* L. assessed with SSR and SNP markers. *Diversity*. 2014;6(3):551-66.
430. Oliveira VD, Rabbani ARC, da Silva AVC, Ledo AD. Genetic variability in physic nuts cultivated in Northeastern Brazil. *Cienc Rural*. 2013;43(6):978-84.
431. Tanya P, Taeprayoon P, Hadkam Y, Srinives P. Genetic Diversity Among *Jatropha* and *Jatropha*-Related Species Based on ISSR Markers. *Plant Molecular Biology Reporter*. 2011;29(1):252-64.
432. Rampadarath S, Puchooa D, Bal S, Jeewon R. Application of rep-PCR as a molecular tool for the genetic diversity assessment of *Jatropha curcas*. *African Journal of Biotechnology*. 2016;15(7):172-9.
433. Pecina-Quintero V, Anaya-López JL, Colmenero AZ, García NM, Colín CAN, Bonilla JLS, et al. Molecular characterisation of *Jatropha curcas* L. genetic resources from Chiapas, México through AFLP markers. *biomass and bioenergy*. 2011;35(5):1897-905.
434. Mergeai G. Genetic analysis of twenty two selected genotypes of *Jatropha curcas* L.(physic nut) from Africa, Asia and America using SSR and AFLP markers. *International Journal of Genetics and Molecular Biology*. 2020.
435. Pamidimarri DVNS, Singh S, Mastan SG, Patel J, Reddy MP. Molecular characterization and identification of markers for toxic and non-toxic varieties of *Jatropha curcas* L. using RAPD, AFLP and SSR markers. *Molecular Biology Reports*. 2009;36(6):1357-64.
436. Mastan SG, Sudheer PDVN, Rahman H, Reddy MP, Chikara J. Development of SCAR Marker Specific to Non-Toxic *Jatropha curcas* L. and Designing a Novel Multiplexing PCR Along with nrDNA ITS Primers to Circumvent the False Negative Detection. *Mol Biotechnol*. 2012;50(1):57-61.
437. Wen M, Wang H, Xia Z, Zou M, Lu C, Wang W. Development of EST-SSR and genomic-SSR markers to assess genetic diversity in *Jatropha Curcas* L. *BMC research notes*. 2010;3(1):1-8.

438. Osorio-Guarín JA, Garzón-Martínez GA, Delgadillo-Duran P, Bastidas S, Moreno LP, Enciso-Rodríguez FE, et al. Genome-wide association study (GWAS) for morphological and yield-related traits in an oil palm hybrid (*Elaeis oleifera* x *Elaeis guineensis*) population. *BMC Plant Biology*. 2019;19(1):1-11.
439. Babu BK, Mathur R, Ravichandran G, Venu M. Genome-wide association study (GWAS) for stem height increment in oil palm (*Elaeis guineensis*) germplasm using SNP markers. *Tree Genetics & Genomes*. 2019;15(3):1-8.
440. Lee M, Xia JH, Zou Z, Ye J, Alfiko Y, Jin J, et al. A consensus linkage map of oil palm and a major QTL for stem height. *Scientific reports*. 2015;5(1):1-7.
441. Kwong QB, Teh CK, Ong AL, Heng HY, Lee HL, Mohamed M, et al. Development and validation of a high-density SNP genotyping array for African oil palm. *Molecular plant*. 2016;9(8):1132-41.
442. Xia W, Luo T, Dou Y, Zhang W, Mason AS, Huang D, et al. Identification and validation of candidate genes involved in fatty acid content in oil palm by genome-wide association analysis. *Frontiers in Plant Science*. 2019;10:1263.
443. Teh C-K, Ong A-L, Kwong Q-B, Apparow S, Chew F-T, Mayes S, et al. Genome-wide association study identifies three key loci for high mesocarp oil content in perennial crop oil palm. *Scientific reports*. 2016;6(1):1-7.
444. Cros D, Denis M, Sánchez L, Cochard B, Flori A, Durand-Gasselin T, et al. Genomic selection prediction accuracy in a perennial crop: case study of oil palm (*Elaeis guineensis* Jacq.). *Theoretical and applied genetics*. 2015;128(3):397-410.
445. Cros D, Bocs S, Riou V, Ortega-Abboud E, Tisné S, Argout X, et al. Genomic preselection with genotyping-by-sequencing increases performance of commercial oil palm hybrid crosses. *BMC genomics*. 2017;18(1):1-17.
446. Marchal A, Legarra A, Tisne S, Carasco-Lacombe C, Manez A, Suryana E, et al. Multivariate genomic model improves analysis of oil palm (*Elaeis guineensis* Jacq.) progeny tests. *Molecular Breeding*. 2016;36(1):2.
447. Ithnin M, Xu Y, Marjuni M, Serdari NM, Amiruddin MD, Low E-TL, et al. Multiple locus genome-wide association studies for important economic traits of oil palm. *Tree Genetics & Genomes*. 2017;13(5):1-14.
448. Xia W, Luo T, Zhang W, Mason AS, Huang D, Huang X, et al. Development of high-density SNP markers and their application in evaluating genetic diversity and population structure in *Elaeis guineensis*. *Frontiers in plant science*. 2019;10:130.
449. Nordiana H, Ngoot-Chin T, Singh R, Clyde M, Madon M. Evaluation of inter simple sequence repeat (ISSR) markers for genetic mapping of an oil palm interspecific hybrid mapping population. *Journal of oil Palm Research, Kuala Lumpur*. 2014;26(3):214-25.
450. Pootakham W, Uthapaisanwong P, Sangsrakru D, Yoocha T, Tragoonrung S, Tangphatsornruang S. Development and characterization of single-nucleotide polymorphism markers from 454 transcriptome sequences in oil palm (*E. laeis guineensis*). *Plant Breeding*. 2013;132(6):711-7.
451. Bai B, Wang L, Zhang YJ, Lee M, Rahmadsyah R, Alfiko Y, et al. Developing genome-wide SNPs and constructing an ultrahigh-density linkage map in oil palm. *Scientific reports*. 2018;8(1):1-7.
452. Kesari V, Rangan L. Genetic diversity analysis by RAPD markers in candidate plus trees of *Pongamia pinnata*, a promising source of bioenergy. *Biomass and Bioenergy*. 2011;35(7):3123-8.

453. Kesari V, Madurai Sathyanarayana V, Parida A, Rangan L. Molecular marker-based characterization in candidate plus trees of *Pongamia pinnata*, a potential biodiesel legume. *AoB Plants*. 2010;2010.
454. Sharma SS, Negi MS, Sinha P, Kumar K, Tripathi SB. Assessment of genetic diversity of biodiesel species *Pongamia pinnata* accessions using AFLP and three endonuclease-AFLP. *Plant Molecular Biology Reporter*. 2011;29(1):12-8.
455. Pavithra H, Shivanna M, Chandrika K, Prasanna K, Gowda B. Genetic analysis of *Pongamia pinnata* (L.) Pierre populations using AFLP markers. *Tree genetics & genomes*. 2014;10(1):173-88.
456. Muranty H, Troggio M, Sadok IB, Al Rifai M, Auwerkerken A, Banchi E, et al. Accuracy and responses of genomic selection on key traits in apple breeding. *Horticulture research*. 2015;2(1):1-12.
457. Kumar S, Garrick DJ, Bink MC, Whitworth C, Chagné D, Volz RK. Novel genomic approaches unravel genetic architecture of complex traits in apple. *BMC genomics*. 2013;14(1):1-13.
458. Roth M, Muranty H, Di Guardo M, Guerra W, Patocchi A, Costa F. Genomic prediction of fruit texture and training population optimization towards the application of genomic selection in apple. *Horticulture research*. 2020;7(1):1-14.
459. Longhi S, Cappellin L, Guerra W, Costa F. Validation of a functional molecular marker suitable for marker-assisted breeding for fruit texture in apple (*Malus* × *domestica* Borkh.). *Molecular Breeding*. 2013;32(4):841-52.
460. Kumar S, Chagné D, Bink MC, Volz RK, Whitworth C, Carlisle C. Genomic selection for fruit quality traits in apple (*Malus* × *domestica* Borkh.). *Plos One*. 2012;7(5):e36674.
461. McClure KA, Gardner KM, Toivonen PM, Hampson CR, Song J, Forney CF, et al. QTL analysis of soft scald in two apple populations. *Horticulture research*. 2016;3(1):1-7.
462. McClure KA, Gardner KM, Douglas GM, Song J, Forney CF, DeLong J, et al. A genome-wide association study of apple quality and scab resistance. *The plant genome*. 2018;11(1):170075.
463. Gardner KM, Brown P, Cooke TF, Cann S, Costa F, Bustamante C, et al. Fast and cost-effective genetic mapping in apple using next-generation sequencing. *G3: Genes, Genomes, Genetics*. 2014;4(9):1681-7.
464. Larsen B, Migicovsky Z, Jeppesen AA, Gardner KM, Toldam-Andersen TB, Myles S, et al. Genome-wide association studies in apple reveal loci for aroma volatiles, sugar composition, and harvest date. *The Plant Genome*. 2019;12(2):180104.
465. Kumar S, Raulier P, Chagné D, Whitworth C. Molecular-level and trait-level differentiation between the cultivated apple (*Malus* × *domestica* Borkh.) and its main progenitor *Malus sieversii*. *Plant Genetic Resources*. 2014;12(3):330-40.
466. Farneti B, Di Guardo M, Khomenko I, Cappellin L, Biasioli F, Velasco R, et al. Genome-wide association study unravels the genetic control of the apple volatilome and its interplay with fruit texture. *Journal of experimental botany*. 2017;68(7):1467-78.
467. Di Guardo M, Bink MC, Guerra W, Letschka T, Lozano L, Busatto N, et al. Deciphering the genetic control of fruit texture in apple by multiple family-based analysis and genome-wide association. *Journal of experimental botany*. 2017;68(7):1451-66.
468. Luo F, Norelli JL, Howard NP, Wisniewski M, Flachowsky H, Hanke M-V, et al. Introgressing blue mold resistance into elite apple germplasm by rapid cycle breeding and foreground and background DNA-informed selection. *Tree Genetics & Genomes*. 2020;16(2):1-15.

469. Kellerhals M, Franck L, Baumgartner I, Patocchi A, Frey J, editors. Breeding for fire blight resistance in apple. XII International Workshop on Fire Blight 896; 2010.
470. Soriano JM, Madduri M, Schaart JG, van der Burgh A, van Kaauwen MP, Tomic L, et al. Fine mapping of the gene Rvi18 (V25) for broad-spectrum resistance to apple scab, and development of a linked SSR marker suitable for marker-assisted breeding. *Molecular breeding*. 2014;34(4):2021-32.
471. Tartarini S, Sansavini S, Vinatzer B, Gennari F, Domizi C, editors. Efficiency of marker assisted selection (MAS) for the Vf scab resistance gene. *Eucarpia symposium on Fruit Breeding and Genetics* 538; 1999.
472. Federico M, Busconi M, Camangi F, Fogher C, Stefani A, Sebastiani L. Ancient Pomoideae (*Malus domestica* Borkh. and *Pyrus communis* L.) cultivars in “Appenino Toscano”(Tuscany, Italy): molecular (SSR) and morphological characterization. *Caryologia*. 2008;61(3):320-31.
473. Larsen B, Gardner K, Pedersen C, Ørgaard M, Migicovsky Z, Myles S, et al. Population structure, relatedness and ploidy levels in an apple gene bank revealed through genotyping-by-sequencing. *Plos One*. 2018;13(8):e0201889.
474. Goulão L, Oliveira CM. Molecular characterisation of cultivars of apple (*Malus*× *domestica* Borkh.) using microsatellite (SSR and ISSR) markers. *Euphytica*. 2001;122(1):81-9.
475. Bianco L, Cestaro A, Sargent DJ, Banchi E, Derdak S, Di Guardo M, et al. Development and validation of a 20K single nucleotide polymorphism (SNP) whole genome genotyping array for apple (*Malus*× *domestica* Borkh). *Plos One*. 2014;9(10):e110377.
476. Kuhn DN, Livingstone III DS, Richards JH, Manosalva P, Van den Berg N, Chambers AH. Application of genomic tools to avocado (*Persea americana*) breeding: SNP discovery for genotyping and germplasm characterization. *Scientia Horticulturae*. 2019;246:1-11.
477. Bhatt DS. Use of molecular markers and antioxidant properties to study biodiversity and to discriminate blueberries: Memorial University of Newfoundland; 2021.
478. Gois I, Borém A, Cristofani-Yaly M, De Resende M, Azevedo C, Bastianel M, et al. Genome wide selection in citrus breeding. *Embrapa Florestas-Artigo em periódico indexado (ALICE)*. 2016.
479. Minamikawa MF, Nonaka K, Kaminuma E, Kajiya-Kanegae H, Onogi A, Goto S, et al. Genome-wide association study and genomic prediction in citrus: potential of genomics-assisted breeding for fruit quality traits. *Scientific reports*. 2017;7(1):1-13.
480. Imai A, Nonaka K, Kuniga T, Yoshioka T, Hayashi T. Genome-wide association mapping of fruit-quality traits using genotyping-by-sequencing approach in citrus landraces, modern cultivars, and breeding lines in Japan. *Tree genetics & genomes*. 2018;14(2):1-15.
481. Yu H, Yang X, Guo F, Jiang X, Deng X, Xu Q. Genetic diversity and population structure of pummelo (*Citrus maxima*) germplasm in China. *Tree Genetics & Genomes*. 2017;13(3):1-10.
482. Ollitrault P, Terol J, Garcia-Lor A, Bérard A, Chauveau A, Froelicher Y, et al. SNP mining in *C. clementina* BAC end sequences; transferability in the Citrus genus (Rutaceae), phylogenetic inferences and perspectives for genetic mapping. *BMC genomics*. 2012;13(1):1-19.

483. Hazarika T, Hazarika B, Shukla A. Genetic variability and phylogenetic relationships studies of genus *Citrus* L. with the application of molecular markers. *Genet Resour Crop Ev.* 2014;61(8):1441-54.
484. Gulsen O, Uzun A, Canan I, Seday U, Canihos E. A new citrus linkage map based on SRAP, SSR, ISSR, POGP, RGA and RAPD markers. *Euphytica.* 2010;173(2):265-77.
485. Distefano G, La Malfa S, Gentile A, Wu S-B. EST-SNP genotyping of citrus species using high-resolution melting curve analysis. *Tree genetics & genomes.* 2013;9(5):1271-81.
486. Biswas MK, Chai L, Amar MH, Zhang X, Deng X-x. Comparative analysis of genetic diversity in *Citrus* germplasm collection using AFLP, SSAP, SAMPL and SSR markers. *Scientia Horticulturae.* 2011;129(4):798-803.
487. Amar MH, Biswas MK, Zhang Z, Guo W-W. Exploitation of SSR, SRAP and CAPS-SNP markers for genetic diversity of *Citrus* germplasm collection. *Scientia Horticulturae.* 2011;128(3):220-7.
488. Al-Mouei R, Choumane W. Assessment of genetic variability within the genus *Citrus* in Syria using SSR markers. *American Journal of Experimental Agriculture.* 2014;4(8):939-50.
489. Curtolo M, Soratto TAT, Gazaffi R, Takita MA, Machado MA, Cristofani-Yaly M. High-density linkage maps for *Citrus sunki* and *Poncirus trifoliata* using DArTseq markers. *Tree genetics & genomes.* 2018;14(1):1-10.
490. Chen C, Bowman KD, Choi YA, Dang PM, Rao MN, Huang S, et al. EST-SSR genetic maps for *Citrus sinensis* and *Poncirus trifoliata*. *Tree Genetics & Genomes.* 2008;4(1):1-10.
491. Zhu S, Wang F, Shen W, Jiang D, Hong Q, Zhao X. Genetic diversity of *Poncirus* and phylogenetic relationships with its relatives revealed by SSR and SNP/InDel markers. *Acta Physiologiae Plantarum.* 2015;37(7):1-11.
492. Salis C, Papadakis IE, Kintzios S, Hagidimitriou M. In vitro propagation and assessment of genetic relationships of citrus rootstocks using ISSR molecular markers. *Notulae Botanicae Horti Agrobotanici Cluj-Napoca.* 2017;45(2):383-91.
493. Liu X, Tang L, Wu H, Xi W, Yu J, Zhou Z. Development of DArT markers and evaluation of phylogenetic relationship of key *Citrus* species. *Genet Resour Crop Ev.* 2016;63(8):1307-18.
494. Herran A, Estioko L, Becker D, Rodriguez M, Rohde W, Ritter E. Linkage mapping and QTL analysis in coconut (*Cocos nucifera* L.). *Theoretical and Applied Genetics.* 2000;101(1):292-300.
495. Teulat B, Aldam C, Trehin R, Lebrun P, Barker JH, Arnold G, et al. An analysis of genetic diversity in coconut (*Cocos nucifera*) populations from across the geographic range using sequence-tagged microsatellites (SSRs) and AFLPs. *Theoretical and applied genetics.* 2000;100(5):764-71.
496. Perera L, Russell J, Provan J, Powell W. Use of microsatellite DNA markers to investigate the level of genetic diversity and population genetic structure of coconut (*Cocos nucifera* L.). *Genome.* 2000;43(1):15-21.
497. Meerow AW, Wisser RJ, Brown SJ, Kuhn DN, Schnell RJ, Broschat TK. Analysis of genetic diversity and population structure within Florida coconut (*Cocos nucifera* L.) germplasm using microsatellite DNA, with special emphasis on the Fiji Dwarf cultivar. *Theoretical and Applied Genetics.* 2003;106(4):715-26.

498. Rianguwong K, Wanchana S, Aesomnuk W, Saensuk C, Nubankoh P, Ruanjaichon V, et al. Mining and validation of novel genotyping-by-sequencing (GBS)-based simple sequence repeats (SSRs) and their application for the estimation of the genetic diversity and population structure of coconuts (*Cocos nucifera* L.) in Thailand. *Horticulture research*. 2020;7(1):1-16.
499. Rajesh M, Sabana A, Rachana K, Rahman S, Jerard B, Karun A. Genetic relationship and diversity among coconut (*Cocos nucifera* L.) accessions revealed through SCoT analysis. *3 Biotech*. 2015;5(6):999-1006.
500. Loiola CM, Azevedo AON, Diniz LE, Aragao WM, Azevedo CDdO, Santos PHA, et al. Genetic relationships among tall coconut palm (*Cocos nucifera* L.) accessions of the International Coconut Genebank for Latin America and the Caribbean (ICG-LAC), evaluated using microsatellite markers (SSRs). *Plos One*. 2016;11(3):e0151309.
501. Lebrun P, N'cho Y-P, Seguin M, Grivet L, Baudouin L. Genetic diversity in coconut (*Cocos nucifera* L.) revealed by restriction fragment length polymorphism (RFLP) markers. *Euphytica*. 1998;101(1):103-8.
502. Rajesh M, Samsudeen K, Rejusha P, Manjula C, Rahman S, Karun A. Characterization of Annur and Bedakam ecotypes of coconut from Kerala state, India, using microsatellite markers. 2014.
503. Martinez RT, Baudouin L, Berger A, Dollet M. Characterization of the genetic diversity of the Tall coconut (*Cocos nucifera* L.) in the Dominican Republic using microsatellite (SSR) markers. *Tree Genetics & Genomes*. 2010;6(1):73-81.
504. Daher RF, Pereira MG, Tupinambá EA, do Amaral Junior AT, Aragão WM, Ribeiro FE, et al. Assessment of coconut tree genetic divergence by compound sample RAPD marker analysis. *Crop Breeding and Applied Biotechnology*. 2002;2(3).
505. Ribeiro FE, Baudouin L, Lebrun P, Chaves LJ, Brondani C, Zucchi MI, et al. Population structures of Brazilian tall coconut (*Cocos nucifera* L.) by microsatellite markers. *Genetics and Molecular Biology*. 2010;33(4):696-702.
506. Xuan DTK, Nguyen QT, Khang NHM, Mai HNX, Trung DDM, Chau NNB, et al. Molecular characterization of coconut (*Cocos nucifera* L.) varieties in Vietnam using sequence-related amplified polymorphism (SRAP) markers. *Biologia*. 2022;1-11.
507. Rahayu MS, Setiawan A, Maskromo I, Purwito A, Sudarsono S. Genetic diversity analysis of Puan Kalianda kopyor coconuts (*Cocos nucifera*) from South Lampung, Indonesia based on SSR markers. *Biodiversitas Journal of Biological Diversity*. 2022;23(1).
508. Rivera R, Edwards KJ, Barker JHA, Arnold GM, Ayad G, Hodgkin T, et al. Isolation and characterization of polymorphic microsatellites in *Cocos nucifera* L. *Genome*. 1999;42(4):668-75.
509. Wu Y, Yang Y, Qadri R, Iqbal A, Li J, Fan H, et al. Development of SSR markers for coconut (*Cocos nucifera* L.) by selectively amplified microsatellite (SAM) and its applications. *Tropical Plant Biology*. 2019;12(1):32-43.
510. Preethi P, Rahman S, Naganeeswaran S, Sabana AA, Gangaraj KP, Jerard BA, et al. Development of EST-SSR markers for genetic diversity analysis in coconut (*Cocos nucifera* L.). *Molecular Biology Reports*. 2020;47(12):9385-97.
511. Takele D, Tsegaw M, Indracanti M. Genetic diversity assessment in some landraces and varieties of date palm (*Phoenix dactylifera* L.) from Afar Region, Ethiopia, using ISSR markers. *Ecological Genetics and Genomics*. 2021;19:100085.
512. Ibrahim IA, Hashem MH, Hemeida AA, Hassan MM, Maksoud AI. Characterization of genetic diversity of Date palm (*Phoenix dactylifera* L.) cultivars collected from New Valley governorate (El-Kharga and Dakhleh) based on morphological variability and molecular markers. *Life Sci J*. 2014;11(11):879-89.

513. Emoghene BO, Asemota O, Idu M, Eke CR. Molecular characterization of some date palms in Nigeria using RAPD markers. *Journal of Applied Biology and Biotechnology*. 2015;3(5):0-3.
514. Al-Khalifah NS, Shanavaskhan A. Molecular identification of date palm cultivars using Random Amplified Polymorphic DNA (RAPD) markers. *Date Palm Biotechnology Protocols Volume II*: Springer; 2017. p. 185-96.
515. Zhao Y, Williams R, Prakash C, He G. Identification and characterization of gene-based SSR markers in date palm (*Phoenix dactylifera* L.). *BMC plant biology*. 2012;12(1):1-8.
516. Noor Camellia N, Salma I, Mohd Norfaizal G. Development of SCAR markers for rapid identification of resistance to phytophthora in durian using inter simple sequence repeat markers. *Asian J Adv Basic Sci*. 2019;7(1):30-4.
517. Vanijajiva O. The application of ISSR markers in genetic variance detection among Durian (*Durio zibethinus* Murr.) cultivars in the Nonthaburi province, Thailand. *Procedia Engineering*. 2012;32:155-9.
518. Vanijajiva O. Genetic variability among durian (*Durio zibethinus* Murr.) cultivars in the Nonthaburi province, Thailand detected by RAPD analysis. *Journal of Agricultural Technology*. 2011;7(4):1107-16.
519. Hannum S, Wahyuningsih H, Sinaga R, Pasaribu N, Hartanto A. Genetic diversity among durian (*Durio zibethinus* Murr.) Populations From Nias Island, Indonesia using RAPD markers. *APPLIED ECOLOGY AND ENVIRONMENTAL RESEARCH*. 2020;18(5):7337-51.
520. Sundari S, Arumingtyas EL, Hakim L, Azrianingsih R, Wahyudi D. Genetic variability of local durian (*Durio zibethinus* Murr.) in Ternate Island based on RAPD markers. *Plant Cell Biotechnology and Molecular Biology*. 2017;18(1-2):68-75.
521. Prakoso CNY, Retnoningsih A. Molecular based genetic diversity of Brongkol's superior durian germplasm of Semarang, Indonesia. *Biodiversitas Journal of Biological Diversity*. 2021;22(12).
522. Yulita KS, Murnianjari M. KERAGAMAN GENETIK BEBERAPA KLON DURIAN (*Durio zibethinus* Murray) ASAL JAWA BARAT BERDASARKAN SIDIK RANDOM AMPLIFIED POLIMORPHIC DNA. *Berita Biologi*. 2010;10(3):269-75.
523. Yulita KDS. Identifikasi molekuler pohon induk beberapa varietas durian asal Jepara menggunakan Random Amplified Polymorphic DNA. 2013.
524. RUWAIDA IP, SUPRIYADI S, PARJANTO P. Variability analysis of Sukun durian plant (*Durio zibethinus*) based on RAPD marker. *Nusantara Bioscience*. 2009;1(2).
525. Siew GY, Ng WL, Tan SW, Alitheen NB, Tan SG, Yeap SK. Genetic variation and DNA fingerprinting of durian types in Malaysia using simple sequence repeat (SSR) markers. *PeerJ*. 2018;6:e4266.
526. Siew GY, Ng WL, Salleh MF, Tan SW, Ky H, Alitheen NBM, et al. Assessment of the Genetic Variation of Malaysian Durian Varieties using Inter-Simple Sequence Repeat Markers and Chloroplast DNA Sequences. *Pertanika Journal of Tropical Agricultural Science*. 2018;41(1).
527. Prihatini R, Ihsan F, Indriyani NLP. Genomic profiling of F1 hybrids of durian (*Durio zibethinus*) revealed by RAPD-PCR. *Journal of Horticultural Research*. 2016;24(2).

528. Nasrika E, Retnoningsih A. Inter Simple Sequence Repeat molecular markers to reveal the genetic diversity of superior durian of Gunungpati, Semarang, Indonesia. *Biodiversitas Journal of Biological Diversity*. 2021;22(9).
529. Songnuan W, Pichakum A, Traiperm P, Rungjangsuwan E-o, Siriwattanakul U, Leeratsuwan N, et al. Diversity of durian (*Durio zibethinus* L.) from Nonthaburi, Thailand based on morpho-palatability characteristics and simple sequence repeat markers. *Agriculture and Natural Resources*. 2019;53(3):218-27.
530. Thinhuatoey N, Poeaim A, Vanijajiva O, Youryon P, Poeaim S. Genetic Diversity of Durian (*Durio Zibethinus* Murray) Based on SRAP Marker. *International Journal of Agricultural Technology*. 2016;12(7.1):1483-91.
531. Hariyati T, Kusnadi J, Arumingtyas EL. Genetic diversity of hybrid durian resulted from cross breeding between *Durio kutejensis* and *Durio zibethinus* based on random amplified polymorphic DNAs (RAPDs). 2013.
532. Mursyidin DH, Makruf MI, Noor A. Molecular diversity of exotic durian (*Durio* spp.) germplasm: a case study of Kalimantan, Indonesia. *Journal of Genetic Engineering and Biotechnology*. 2022;20(1):1-13.
533. Riupassa PA, Chikmawati T. The Molecular diversity-based ISSR of *Durio tanjungpurensis* originating from West Kalimantan, Indonesia. *Makara Journal of Science*. 2015;19(1):5.
534. HANDAYANI F, RAHAYU SP. Assessment of genetic diversity in Lai (*Durio kutejensis*) local cultivars of Batuah (Indonesia) using ISSR marker. *Biodiversitas Journal of Biological Diversity*. 2017;18(2):525-9.
535. Santoso PJ, Pancoro A, Suhandono S, Aryantha INP. Development of simple-sequence repeats markers from Durian (*Durio zibethinus* Murr. cultv. Matahari) genomic library. *AGRIVITA, Journal of Agricultural Science*. 2017;39(3):257-65.
536. Zhang H, Fan X, Zhang Y, Jiang J, Liu C. Identification of favorable SNP alleles and candidate genes for seedlessness in *Vitis vinifera* L. using genome-wide association mapping. *Euphytica*. 2017;213(7):1-13.
537. Guo D-L, Zhao H-L, Li Q, Zhang G-H, Jiang J-F, Liu C-H, et al. Genome-wide association study of berry-related traits in grape [*Vitis vinifera* L.] based on genotyping-by-sequencing markers. *Horticulture research*. 2019;6.
538. Laucou V, Launay A, Bacilieri R, Lacombe T, Adam-Blondon A-F, Berard A, et al. Extended diversity analysis of cultivated grapevine *Vitis vinifera* with 10K genome-wide SNPs. *Plos One*. 2018;13(2):e0192540.
539. Feng C, Feng C, Lin X, Liu S, Li Y, Kang M. A chromosome-level genome assembly provides insights into ascorbic acid accumulation and fruit softening in guava (*Psidium guajava*). *Plant biotechnology journal*. 2021;19(4):717-30.
540. Feria-Romero I, Astudillo-De la Vega H, Chavez-Soto M, Rivera-Arce E, Lopez M, Serrano H, et al. RAPD markers associated with quercetin accumulation in *Psidium guajava*. *Biologia plantarum*. 2009;53(1):125-8.
541. Padmakar B, Sailaja D, Aswath C. Molecular exploration of guava (*Psidium guajava* L.) genome using SSR and RAPD markers: a step towards establishing linkage map. *Journal of Horticultural Sciences*. 2015;10(2):130-5.
542. Padmakar B, Kanupriya C, Latha PM, Vasugi C, Dinesh M, Sailaja D, et al. Enrichment of genetic linkage maps and mapping QTLs specific to seed strength-hardness/softness-in guava (*Psidium guajava* L.). *Journal of Horticultural Sciences*. 2016;11(1):13-20.

543. Campos-Rivero G, Cazáres-Sánchez E, Tamayo-Ordóñez M, Tamayo-Ordóñez Y, Padilla-Ramrez J, Quiroz-Moreno A, et al. Application of sequence specific amplified polymorphism (SSAP) and simple sequence repeat (SSR) markers for variability and molecular assisted selection (MAS) studies of the Mexican guava. *Afr J Agr Res*. 2017;12(29):2372-87.
544. Ritter E, Rodríguez-Medina N, Velásquez B, Rivero D, Rodríguez J, Martínez F, et al., editors. QTL (Quantitative Trait Loci) analysis in guava. II International Symposium on Guava and other Myrtaceae 849; 2008.
545. Tigano M, De Siqueira K, Castagnone-Sereno P, Mulet K, Queiroz P, Dos Santos M, et al. Genetic diversity of the root-knot nematode *Meloidogyne enterolobii* and development of a SCAR marker for this guava-damaging species. *Plant pathology*. 2010;59(6):1054-61.
546. Santos RM, Viana AP, Santos EA, SOUZA RM, ALMEIDA OF, Gomes VM, et al. Genetic structuring of segregating populations of *Psidium* spp resistant to the southern root-knot nematode by Bayesian approach as basis for the guava breeding program. *Anais da Academia Brasileira de Ciências*. 2020;92.
547. Noia L, Tuler A, Ferreira A, Ferreira M. Relationship between *Psidium* species (Myrtaceae) by resistance gene analog markers: Focus on nematode resistance. *Genetics and Molecular Research*. 2017;16(1):1-13.
548. Urquía D, Gutierrez B, Pozo G, Pozo MJ, Torres MdL. Origin and dispersion pathways of guava in the Galapagos Islands inferred through genetics and historical records. *Ecol Evol*. 2021;11(21):15111-31.
549. Urquía D, Gutierrez B, Pozo G, Pozo MJ, Espín A, Torres MdL. *Psidium guajava* in the Galapagos Islands: population genetics and history of an invasive species. *Plos One*. 2019;14(3):e0203737.
550. Sitther V, Zhang D, Harris D, Yadav A, Zee F, Meinhardt L, et al. Genetic characterization of guava (*Psidium guajava* L.) germplasm in the United States using microsatellite markers. *Genet Resour Crop Ev*. 2014;61(4):829-39.
551. Aranguren Y, Briceño A, Fermin G, editors. Assessment of the variability of Venezuelan guava landraces by microsatellites. II International Symposium on Guava and other Myrtaceae 849; 2008.
552. Nogueira A, Ferreira M, Guilhen J, Ferreira A. Multivariate analysis in a genetic divergence study of *Psidium guajava*. *Genetics and Molecular Research*. 2014;13(4):10657-68.
553. Coser SM, da Silva Ferreira MF, Ferreira A, Mitre LK, Carvalho CR, Clarindo WR. Assessment of genetic diversity in *Psidium guajava* L. using different approaches. *Scientia Horticulturae*. 2012;148:223-9.
554. Mehmood A, Luo S, Ahmad N, Dong C, Mahmood T, Sajjad Y, et al. Molecular variability and phylogenetic relationships of guava (*Psidium guajava* L.) cultivars using inter-primer binding site (iPBS) and microsatellite (SSR) markers. *Genet Resour Crop Ev*. 2016;63(8):1345-61.
555. Valdés-Infante Herrero J, Rodríguez Medina NN, Bautista Alor M, Margarita Ortíz García M, Quiroz Moreno A, Sánchez Teye LF, et al. Microsatellites developed in guava (*Psidium guajava* L.) and their usefulness in evaluating diversity in the Myrtaceae family. *Revista Colombiana de Biotecnología*. 2010;12(1):64-76.
556. Rodríguez N, Valdés-Infante J, Becker D, Velásques B, Coto O, Rohde W, et al. Morphological, agronomic and molecular characterization of Cuban accessions of guava (*Psidium guajava* L.). *Journal of Genetics and Breeding (Italy)*. 2004.

557. Kherwar D, Usha K, Mithra S, Singh B. Microsatellite (SSR) marker assisted assessment of population structure and genetic diversity for morpho-physiological traits in guava (*Psidium guajava* L.). *Journal of Plant Biochemistry and Biotechnology*. 2018;27(3):284-92.
558. Ma Z, Liu S, Liang Z, Xu S, Hu W. Analysis of genetic diversity of 45 guava germplasm evaluated using SSR markers. *International Journal of Fruit Science*. 2020;20(3):385-93.
559. Viji G, Harris D, Yadav A, Zee F. Use of microsatellite markers to characterize genetic diversity of selected accessions of guava (*Psidium guajava*) in the United States. *Acta horticulturae*. 2010(859):169-76.
560. Kanupriya, Latha PM, Aswath C, Reddy L, Padmakar B, Vasugi C, et al. Cultivar identification and genetic fingerprinting of guava (*Psidium guajava*) using microsatellite markers. *International Journal of Fruit Science*. 2011;11(2):184-96.
561. Ritter E, Herran A, Valdés-Infante J, RODRÍGUEZ-MEDINA M, Briceño A, Fermin G, et al. Comparative linkage mapping in three guava mapping populations and construction of an integrated reference map in guava. *Embrapa Semiárido-Artigo em periódico indexado (ALICE)*. 2010.
562. Padmakar B, Kanupriya C, Latha PM, Prashant K, Dinesh M, Sailaja D, et al. Development of SRAP and SSR marker-based genetic linkage maps of guava (*Psidium guajava* L.). *Scientia Horticulturae*. 2015;192:158-65.
563. Rodríguez NN, Valdés J, Rodríguez JA, Velásquez JB, Rivero D, Martínez F, et al. Genetic resources and breeding of guava (*Psidium guajava* L.) in Cuba. *Biotecnología Aplicada*. 2010;27(3):238-40.
564. Ahmed B, Mannan M, Hossain S. Molecular characterization of guava (*Psidium guajava* L.) germplasm by RAPD analysis. *International Journal of Natural Sciences*. 2011;1(3):62-7.
565. Rodríguez N, Valdés-Infante J, Becker D, Velásquez B, González G, Sourd D, et al., editors. Characterization of guava accessions by SSR markers, extension of the molecular linkage map, and mapping of QTLs for vegetative and reproductive characters. *I International Guava Symposium* 735; 2005.
566. Chen T-W, Ng C-C, Wang C-Y, Shyu Y-T. Molecular identification and analysis of *Psidium guajava* L. from indigenous tribes of Taiwan. *Journal of Food and Drug Analysis*. 2007;15(1):7.
567. Hernández-Delgado S, Padilla-Ramírez JS, Nava-Cedillo A, Mayek-Pérez N. Morphological and genetic diversity of Mexican guava germplasm. *Plant Genetic Resources*. 2007;5(3):131-41.
568. Gomes Filho A, de Oliveira JG, Viana AP, de Oliveira Siqueira AP, Oliveira MG, Pereira MG. RAPD molecular markers and morphological descriptors in the evaluation of genetic diversity of guava (*Psidium guajava* L.)/Marcadores moleculares RAPD e descritores morfológicos na avaliação da diversidade genética de goiabeiras (*Psidium guajava* L.). *Acta Scientiarum Agronomy*. 2010;32(4):627-34.
569. Thaipong K, Promchot S, Auvuchanon A, Boonprakob U. Genetic analysis of guava germplasm using AFLP Markers. *Int J Agric Technol*. 2017;13:741-52.
570. Da Costa S, Santos C. Allelic database and divergence among *Psidium* accessions by using microsatellite markers. *Embrapa Semiárido-Artigo em periódico indexado (ALICE)*. 2013.

571. Costa S, Santos C. Genetic divergence among *Psidium* accessions based on single nucleotide polymorphisms developed for *Eucalyptus*. *Genetics and Molecular Research*. 2017;16(2):gmr16029566-gmr.
572. Grossi LL, Fernandes M, Silva MA, de Oliveira Bernardes C, Tuler AC, dos Santos PHD, et al. DArTseq-derived SNPs for the genus *Psidium* reveal the high diversity of native species. *Tree Genetics & Genomes*. 2021;17(2):1-13.
573. Valera-Montero L, Muñoz-Rodríguez P, Silos-Espino H, Flores-Benítez S. Análisis morfológico y molecular de la diversidad genética de guayaba (*Psidium guajava* L.) del Centro de México. *Phyton (Buenos Aires)*. 2016;85(2):176-83.
574. Lepitre V, Nansot G, Grangeon R, Pomies V, Rivallan R, Risterucci A-M, et al. The microsatellite (SSR)/AFLP reference linkage map of guava. *Acta horticulturae*. 2010(849):183-92.
575. Tuler A, Carrijo T, Nôia L, Ferreira A, Peixoto A, da Silva Ferreira M. SSR markers: a tool for species identification in *Psidium* (Myrtaceae). *Molecular Biology Reports*. 2015;42(11):1501-13.
576. Kumar C, Kumar R, Singh SK, Goswami AK, Nagaraja A, Paliwal R, et al. Development of novel g-SSR markers in guava (*Psidium guajava* L.) cv. Allahabad Safeda and their application in genetic diversity, population structure and cross species transferability studies. *Plos One*. 2020;15(8):e0237538.
577. Rai MK, Phulwaria M, Shekhawat N. Transferability of simple sequence repeat (SSR) markers developed in guava (*Psidium guajava* L.) to four Myrtaceae species. *Molecular Biology Reports*. 2013;40(8):5067-71.
578. Thakur S, Yadav IS, Jindal M, Sharma PK, Dhillon GS, Boora RS, et al. Development of genome-wide functional markers using draft genome assembly of guava (*Psidium guajava* L.) cv. Allahabad safeda to expedite molecular breeding. *Frontiers in plant science*. 2021;12.
579. Risterucci A-M, Duval M-F, Rohde W, Billotte N. Isolation and characterization of microsatellite loci from *Psidium guajava* L. *Molecular Ecology Notes*. 2005;5(4):745-8.
580. Kavya K, Shyamamma S, Gayatri S. Morphological and molecular genetic diversity analysis using SSR markers in Jackfruit (*Artocarpus heterophyllus* Lam.) genotypes for pulp colour. *Indian J Agric Res*. 2019;53(1):8-16.
581. Pushpakumara D, Harris S. Potential of RAPD markers for identification of fruit types of *Artocarpus*. *Journal of the National Science Foundation of Sri Lanka*. 2007;35(3).
582. Shyamamma S, Chandra S, Hegde M, Naryanswamy P. Evaluation of genetic diversity in jackfruit (*Artocarpus heterophyllus* Lam.) based on amplified fragment length polymorphism markers. *Genetics and Molecular Research*. 2008;7(3):645-56.
583. Li Y-Z, Qi M, Feng F, Ye C-H. Genetic diversity within a jackfruit (*Artocarpus heterophyllus* Lam.) germplasm collection in China using AFLP markers. *Agricultural Sciences in China*. 2010;9(9):1263-70.
584. Nakintu J, Albrecht C, Müller CM, Kagoro-Rugunda G, Andama M, Olet EA, et al. Exploring the genetic diversity of jackfruit (*Artocarpus heterophyllus* Lam.) grown in Uganda based on SSR markers. *Genet Resour Crop Ev*. 2020;67(3):605-19.
585. Palupi D, Rahayu S, Daryono B. Genetic diversity in jackfruit (*Artocarpus Heterophyllus* Lam.) based on molecular characters in Indonesia. *SABRAO Journal of Breeding and Genetics*. 2019;51:57-67.

586. Simon L, Shyamalamma S, Narayanaswamy P. Morphological and molecular analysis of genetic diversity in jackfruit. *The Journal of Horticultural Science and Biotechnology*. 2007;82(5):764-8.
587. Kanzaki S, Yonemori K, Sugiura A, Subhadrabandhu S. Phylogenetic relationships between the jackfruit, the breadfruit and nine other *Artocarpus* spp. from RFLP analysis of an amplified region of cpDNA. *Scientia Horticulturae*. 1997;70(1):57-66.
588. Schnell R, Olano C, Campbell R, Brown J. AFLP analysis of genetic diversity within a jackfruit germplasm collection. *Scientia Horticulturae*. 2001;91(3-4):261-74.
589. Choudhary SB, Gurjar SC, Singh BK, Singh DK, Sharma HK, Horo S, et al. Morphology and genic-SSRs-based diversity analysis and georeferencing of economic traits in natural populations of Jack (*Artocarpus heterophyllus* Lam.) from Eastern India. *Scientia Horticulturae*. 2022;295:110852.
590. Ojwang RA, Muge EK, Nyaboga EN, Mbatia BN, Ogoyi DO. Genetic diversity and relationships among populations of jackfruit, an underutilized nutrient-rich climate-smart fruit tree crop in Kenya and Uganda. *Journal of Crop Improvement*. 2022;36(5):619-37.
591. Witherup C, Zuberi MI, Hossain S, Zerega NJ. Genetic diversity of Bangladeshi jackfruit (*Artocarpus heterophyllus*) over time and across seedling sources. *Economic Botany*. 2019;73(2):233-48.
592. Azad A, Jones J, Haq N. Assessing morphological and isozyme variation of jackfruit (*Artocarpus heterophyllus* Lam.) in Bangladesh. *Agroforest Syst*. 2007;71(2):109-25.
593. Singh DK, Pandey A, Choudhary SB, Kumar S, Tribhuvan KU, Mishra DC, et al. Development of genic-SSR markers and their application in revealing genetic diversity and population structure in an Eastern and North-Eastern Indian collection of Jack (*Artocarpus heterophyllus* Lam.). *Ecological Indicators*. 2021;131:108143.
594. Reche J, García-Martínez S, Carbonell P, Almansa M, Hernández F, Legua P, et al. Relationships between physico-chemical and functional parameters and genetic analysis with ISSR markers in Spanish jujubes (*Ziziphus jujuba* Mill.) cultivars. *Scientia Horticulturae*. 2019;253:390-8.
595. Li S, Guo M, Tian S, Liu H, Zhao X. Genetic diversity and population structure of Chinese jujube (*Ziziphus jujuba* Mill.) and sour jujube (*Ziziphus acidojujuba* Mill.) using inter-simple sequence repeat (ISSR) Markers. *Molecular Plant Breeding*. 2021;12.
596. Chen W, Hou L, Zhang Z, Pang X, Li Y. Genetic diversity, population structure, and linkage disequilibrium of a core collection of *Ziziphus jujuba* assessed with genome-wide SNPs developed by genotyping-by-sequencing and SSR markers. *Frontiers in plant science*. 2017;8:575.
597. Wang S, Liu Y, Ma L, Liu H, Tang Y, Wu L, et al. Isolation and characterization of microsatellite markers and analysis of genetic diversity in Chinese jujube (*Ziziphus jujuba* Mill.). *Plos One*. 2014;9(6):e99842.
598. Liu W, Xiao Z, Fan C, Jiang N, Meng X, Xiang X. Cloning and characterization of a flavonol synthase gene from *Litchi chinensis* and its variation among litchi cultivars with different fruit maturation periods. *Frontiers in plant science*. 2018;9:567.
599. Liu W-W, Kim H-J, Chen H-B, Lu X-Y, Zhou B-Y. Identification of MV-generated ROS responsive EST clones in floral buds of *Litchi chinensis* Sonn. *Plant cell reports*. 2013;32(9):1361-72.

600. Liu W, Xiao Z, Bao X, Yang X, Fang J, Xiang X. Identifying litchi (*Litchi chinensis* Sonn.) cultivars and their genetic relationships using single nucleotide polymorphism (SNP) markers. *Plos One*. 2015;10(8):e0135390.
601. Liu L, Pan D, Zhong F, Wang J. POD isoenzyme and RAPD analysis on litchi in fuqing. *Acta horticulturae*. 2010(863):189-94.
602. Long Y, Cheng J, Mei Z, Zhao L, Wei C, Fu S, et al. Genetic analysis of litchi (*Litchi chinensis* Sonn.) in southern China by improved random amplified polymorphic DNA (RAPD) and inter-simple sequence repeat (ISSR). *Molecular biology reports*. 2015;42(1):159-66.
603. Ding X, Lu L, Chen X, editors. Segregation patterns of RAPD markers in an F1 population of *Litchi chinensis* Sonn. I International Symposium on Litchi and Longan 558; 2000.
604. HU F-c, Zhe C, WANG X-h, WANG J-b, FAN H-y, QIN Y-h, et al. Construction of high-density SNP genetic maps and QTL mapping for dwarf-related traits in *Litchi chinensis* Sonn. *Journal of Integrative Agriculture*. 2021;20(11):2900-13.
605. Tran H, Kanzaki S, Triest L, Hormaza I, Kuk NJ, Ming R, et al. Analysis of genetic diversity of lychee (*Litchi chinensis* Sonn.) and wild forest relatives in the Sapindaceae from Vietnam using microsatellites. *Genet Resour Crop Ev*. 2019;66(8):1653-69.
606. Madhou M, Normand F, Bahorun T, Hormaza JI. Fingerprinting and analysis of genetic diversity of litchi (*Litchi chinensis* Sonn.) accessions from different germplasm collections using microsatellite markers. *Tree Genetics & Genomes*. 2013;9(2):387-96.
607. Tongpamnak P, Patanatar A, Srinives P, Babprasert C. Determiation of Genetic Diversity and Relationships among Thai Litchi Accessions by RAPD and AFLP Markers. *Agriculture and Natural Resources*. 2002;36(4):370-80.
608. Madhou M, Normand F, Bahorun T, Hormaza JI, editors. Comparison of accessions conserved in different litchi germplasm collections using microsatellite markers. IV International Symposium on Lychee, Longan and Other Sapindaceae Fruits 1029; 2012.
609. Degani C, Deng J, Beiles A, El-Batsri R, Goren M, Gazit S. Identifying lychee (*Litchi chinensis* Sonn.) cultivars and their genetic relationships using intersimple sequence repeat (ISSR) markers. *Journal of the American Society for Horticultural Science*. 2003;128(6):838-45.
610. Anuntalabhochai S, Chundet R, Chiangda J, Apavatjirut P. Genetic diversity within lychee (*Litchi chinensis* Sonn.) based on RAPD analysis. *Acta horticulturae*. 2002.
611. Degani C, Beiles A, El-Batsri R, Goren M, Gazit S. Identifying lychee cultivars by isozyme analysis. *Journal of the American Society for Horticultural Science*. 1995;120(2):307-12.
612. Aradhya MK, Zee FT, Manshardt R. Isozyme variation in lychee (*Litchi chinensis* Sonn.). *Scientia horticulturae*. 1995;63(1-2):21-35.
613. Viruel MA, Hormaza J. Development, characterization and variability analysis of microsatellites in lychee (*Litchi chinensis* Sonn., Sapindaceae). *Theoretical and Applied Genetics*. 2004;108(5):896-902.
614. Bally IS, Bombarely A, Chambers AH, Cohen Y, Dillon NL, Innes DJ, et al. The ‘Tommy Atkins’ mango genome reveals candidate genes for fruit quality. *BMC plant biology*. 2021;21(1):1-18.
615. Kuhn DN, Bally IS, Dillon NL, Innes D, Groh AM, Rahaman J, et al. Genetic map of mango: a tool for mango breeding. *Frontiers in plant science*. 2017;8:577.

616. Lal S, Singh AK, Singh SK, Srivastav M, Singh BP, Sharma N, et al. Association analysis for pomological traits in mango (*Mangifera indica* L.) by genic-SSR markers. *Trees*. 2017;31(5):1391-409.
617. Ribeiro IdS, Lima Neto F, Santos C. Allelic database and accession divergence of a Brazilian mango collection based on microsatellite markers. 2012.
618. Nazish T, Shabbir G, Ali A, Sami-ul-Allah S, Naeem M, Javed M, et al. Molecular diversity of Pakistani mango (*Mangifera indica* L.) varieties based on microsatellite markers. *Genetics and Molecular Research*. 2017;16(2).
619. Souza I, Valente S, Britto F, de Souza V, LIMA PdC. RAPD analysis of the genetic diversity of mango (*Mangifera indica*) germplasm in Brazil. *Embrapa Meio-Norte-Artigo em periódico indexado (ALICE)*. 2011.
620. Ravishankar KV, Bommisetty P, Bajpai A, Srivastava N, Mani BH, Vasugi C, et al. Genetic diversity and population structure analysis of mango (*Mangifera indica*) cultivars assessed by microsatellite markers. *Trees*. 2015;29(3):775-83.
621. Sherman A, Rubinstein M, Eshed R, Benita M, Ish-Shalom M, Sharabi-Schwager M, et al. Mango (*Mangifera indica* L.) germplasm diversity based on single nucleotide polymorphisms derived from the transcriptome. *BMC Plant Biology*. 2015;15(1):1-11.
622. Dillon NL, Innes DJ, Bally IS, Wright CL, Devitt LC, Dietzgen RG. Expressed sequence tag-simple sequence repeat (EST-SSR) marker resources for diversity analysis of mango (*Mangifera indica* L.). *Diversity*. 2014;6(1):72-87.
623. Dillon NL, Bally IS, Wright CL, Hucks L, Innes DJ, Dietzgen RG. Genetic diversity of the Australian national mango genebank. *Scientia Horticulturae*. 2013;150:213-26.
624. Kuhn DN, Dillon N, Bally I, Groh A, Rahaman J, Warschefsky E, et al. Estimation of genetic diversity and relatedness in a mango germplasm collection using SNP markers and a simplified visual analysis method. *Scientia Horticulturae*. 2019;252:156-68.
625. Luo C, Shu B, Yao Q, Wu H, Xu W, Wang S. Construction of a high-density genetic map based on large-scale marker development in mango using specific-locus amplified fragment sequencing (SLAF-seq). *Frontiers in plant science*. 2016;7:1310.
626. Dang Z, Chen Y. Construction of a genetic linkage map of mango based on SRAP, AFLP and ISSR markers. *Agricultural Biotechnology*. 2017;6(6):9-16.
627. Jena RC, Chand PK. Multiple DNA marker-assisted diversity analysis of Indian mango (*Mangifera indica* L.) populations. *Scientific reports*. 2021;11(1):1-15.
628. Mansour H, Mekki LE, Hussein MA. Assessment of genetic diversity and relationships among Egyptian mango (*Mangifera indica* L.) cultivars grown in Suez Canal and Sinai region using RAPD markers. *Pakistan Journal of Biological Sciences: PJBS*. 2014;17(1):56-61.
629. Yamanaka S, Hosaka F, Matsumura M, Onoue-Makishi Y, Nashima K, Urasaki N, et al. Genetic diversity and relatedness of mango cultivars assessed by SSR markers. *Breeding science*. 2019;69(2):332-44.
630. Matra DD, Fathoni MAN, Majiidu M, Wicaksono H, Sriyono A, Gunawan G, et al. The genetic variation and relationship among the natural hybrids of *Mangifera casturi* Kosterm. *Scientific Reports*. 2021;11(1):1-10.
631. Ajayi I, Olawuyi O, Ayodele A, Faneye A. Molecular relationship among *Mangifera indica* L.(Mango) varieties using simple sequence repeat (SSR) marker. *J Adv Biol Biotechnol*. 2019;22(4):1-16.

632. Surapaneni M, Vemireddy LR, Begum H, Purushotham Reddy B, Neetasri C, Nagaraju J, et al. Population structure and genetic analysis of different utility types of mango (*Mangifera indica* L.) germplasm of Andhra Pradesh state of India using microsatellite markers. *Plant Systematics and Evolution*. 2013;299(7):1215-29.
633. Zhou L, He X-H, Yu H-X, Chen M-Y, Fan Y, Zhang X-J, et al. Evaluation of the genetic diversity of mango (*Mangifera indica* L.) seedling germplasm resources and their potential parents with start codon targeted (SCoT) markers. *Genet Resour Crop Ev*. 2020;67(1):41-58.
634. Begum H, Reddy M, Malathi S, Reddy B, Narshimulu G, Nagaraju J, et al. Morphological and microsatellite analysis of intravarietal variability in 'Cherukurasam' cultivar of mango (*Mangifera indica* L.). 2014.
635. Anggraheni Y, Mulyaningsih E, editors. Diversity Assessment of Mango (*Mangifera* spp) Plant Collection of Cibinong Germplasm Garden Based on Leaves Morphology and RAPD Markers. IOP Conference Series: Earth and Environmental Science; 2021: IOP Publishing.
636. Gajera H, Bambharolia R, Domadiya RK, Patel S, Golakiya B. Molecular characterization and genetic variability studies associated with fruit quality of indigenous mango (*Mangifera indica* L.) cultivars. *Plant Systematics and Evolution*. 2014;300(5):1011-20.
637. Rajwana IA, Tabbasam N, Malik AU, Malik SA, Zafar Y. Assessment of genetic diversity among mango (*Mangifera indica* L.) genotypes using RAPD markers. *Scientia Horticulturae*. 2008;117(3):297-301.
638. Luo C, He X-H, Chen H, Hu Y, Ou S-J. Genetic relationship and diversity of *Mangifera indica* L.: revealed through SCoT analysis. *Genet Resour Crop Ev*. 2012;59(7):1505-15.
639. Singh S, Bhat K, editors. Molecular characterization and analysis of geographical differentiation of Indian mango (*Mangifera indica* L.) germplasm. I International Symposium on Biotechnology of Fruit Species: BIOTECHFRUIT2008 839; 2008.
640. Duval M-F, Risterucci A-M, Calabre C, Le Bellec F, Bunel J, Sitbon C, editors. Genetic diversity of Caribbean mangoes (*Mangifera indica* L.) using microsatellite markers. VIII International Mango Symposium 820; 2006.
641. Gálvez-López D, Hernández-Delgado S, González-Paz M, Becerra-Leor EN, Salvador-Figueroa M, Mayek-Pérez N. Genetic analysis of mango landraces from Mexico based on molecular markers. *Plant Genetic Resources*. 2009;7(3):244-51.
642. Schnell R, Ronning C, Knight R. Identification of cultivars and validation of genetic relationships in *Mangifera indica* L. using RAPD markers. *Theoretical and Applied Genetics*. 1995;90(2):269-74.
643. Eiadthong W, Yonemori K, Kanzaki S, Sugiura A, Utsunomiya N, Subhadrabandhu S. Amplified fragment length polymorphism analysis for studying genetic relationships among *Mangifera* species in Thailand. *Journal of the American Society for Horticultural Science*. 2000;125(2):160-4.
644. Lopez-Valenzuela J, Martinez O, Paredes-Lopez O. Geographic differentiation and embryo type identification in *Mangifera indica* L. cultivars using RAPD markers. *HortScience*. 1997;32(6):1105-8.
645. Pandit SS, Mitra S, Giri AP, Pujari KH, Patil BP, Jambhale ND, et al. Genetic diversity analysis of mango cultivars using inter simple sequence repeat markers. *Current science*. 2007;1135-41.

646. Himabindu A, Rajasekhar M. Molecular characterization of traditional mango germplasm of coastal Andhra Pradesh using RAPD markers. *Electronic Journal of Plant Breeding*. 2021;12(4):1261-7.
647. Hartana A, Purwoko BS. Diversity of Indonesian mango (*Mangifera indica*) cultivars based on morphological and RAPD markers. *SABRAO Journal of Breeding and Genetics*. 2010;42(2):84-95.
648. HIDAYAT A, RAHAYU ES, ABDULLAH M, Retnoningsih A. Microsatellites to reveal genetic diversity and to distinguish four mangoes of Tegal District, Central Java, Indonesia. *Biodiversitas Journal of Biological Diversity*. 2021;22(8).
649. RASHED M, MAKLAD M. GENETIC RELATIONSHIPS AMONG SIX MANGO (*Mangifera indica* L.) CULTIVARS USING RAPD MARKERS. *Egyptian Journal of Genetics And Cytology*. 2016;45(1):105-12.
650. Xin-Hua H, Yong-Ze G, Yang-rui L, Shi-jin O. Assessment of the genetic relationship and diversity of mango and its relatives by cpISSR marker. *Agricultural Sciences in China*. 2007;6(2):137-42.
651. Ariffin Z, Sah MSM, Idris S, Hashim N. Genetic diversity of selected *Mangifera* species revealed by inter simple sequence repeats markers. *International Journal of Biodiversity*. 2015;2015.
652. Tsai C-C, Chen Y-KH, Chen C-H, Weng I-S, Tsai C-M, Lee S-R, et al. Cultivar identification and genetic relationship of mango (*Mangifera indica*) in Taiwan using 37 SSR markers. *Scientia Horticulturae*. 2013;164:196-201.
653. Razak SA, Azman NHEN, Ismail SN, Yusof MFM, Ariffin MAT, Sabdin ZHM, et al. Assessment of diversity and population structure of mango (*'Mangifera indica'*L.) germplasm based on microsatellite (SSR) markers. *Australian Journal of Crop Science*. 2019;13(2):315-20.
654. Damodaran T, Kannan R, Ahmed I, Srivastava R, Rai R, Umamaheshwari S. Assessing genetic relationships among mango (*Mangifera indica* L.) accessions of Andaman Islands using inter simple sequence repeat markers. *New Zealand Journal of Crop and Horticultural Science*. 2012;40(4):229-40.
655. Kashkush K, Jingui F, Tomer E, Hillel J, Lavi U. Cultivar identification and genetic map of mango (*Mangifera indica*). *Euphytica*. 2001;122(1):129-36.
656. Luo C, He X-H, Chen H, Ou S-J, Gao M-P. Analysis of diversity and relationships among mango cultivars using Start Codon Targeted (SCoT) markers. *Biochemical Systematics and Ecology*. 2010;38(6):1176-84.
657. Al Washahi L, Al Shamsi H, Dillon N, Sharma N, Al Qamashoui B, Al Saadi A, editors. Molecular characterization of local mango (*Mangifera indica* L.) germplasm in Oman. *XI International Mango Symposium* 1183; 2015.
658. Kheshin M, Sayed HA, Allatif A. Morphological and molecular analysis of genetic diversity among some 'Sukkary' mango (*Mangifera indica* L.) genotypes. *Journal of Horticultural Science and Ornamental Plants*. 2016;8(1):1-10.
659. Shamili M, Fatahi R, Hormaza J. Characterization and evaluation of genetic diversity of Iranian mango (*Mangifera indica* L., *Anacardiaceae*) genotypes using microsatellites. *Scientia Horticulturae*. 2012;148:230-4.
660. Archak S, Gaikwad AB, Gautam D. Molecular genetic diversity analysis of commercial mango (*Mangifera indica* L.) cultivars employed as parents in hybrid development in India. *Indian J Plant Gen Res*. 2014;27:209-16.

661. Srivastava N, Bajpai A, Chandra R, Rajan S, Muthukumar M, Srivastava MK. Comparison of PCR based marker systems for genetic analysis in different cultivars of mango. *Journal of environmental biology*. 2012;33(2):159.
662. Cordeiro M, Ramos V, Bellon G, Andrade S, Pinto J, Faleiro F, et al., editors. Genetic variability of mango (*Mangifera indica* L.) cultivars used in the Embrapa Cerrados breeding program using RAPD markers. III International Symposium on Tropical and Subtropical Fruits 864; 2004.
663. Karihaloo J, Dwivedi Y, Archak S, Gaikwad AB. Analysis of genetic diversity of Indian mango cultivars using RAPD markers. *The Journal of Horticultural Science and Biotechnology*. 2003;78(3):285-9.
664. Chiang YC, Tsai CM, Chen YKH, Lee SR, Chen CH, Lin YS, et al. Development and characterization of 20 new polymorphic microsatellite markers from *Mangifera indica* (Anacardiaceae). *American journal of botany*. 2012;99(3):e117-e9.
665. Ravishankar KV, Mani BHR, Anand L, Dinesh MR. Development of new microsatellite markers from Mango (*Mangifera indica*) and cross-species amplification. *American Journal of Botany*. 2011;98(4):e96-e9.
666. Kuhn D, Dillon N, Innes D, Wu L-S, Mockaitis K, editors. Development of single nucleotide polymorphism (SNP) markers from the mango (*Mangifera indica*) transcriptome for mapping and estimation of genetic diversity. XXIX International Horticultural Congress on Horticulture: Sustaining Lives, Livelihoods and Landscapes (IHC2014): IV 1111; 2014.
667. Kumar M, Ponnuswami V, Nagarajan P, Jeyakumar P, Senthil N. Molecular characterization of ten mango cultivars using simple sequences repeat (SSR) markers. *African Journal of Biotechnology*. 2013;12(47):6568-73.
668. Md RM, Iftekhar A, Md AH, Md SI, Md AZC, Dilruba S, et al. Morphological characterization and Simple Sequence Repeats (SSRs) based DNA fingerprinting of selected mango (*Mangifera indica* L.) genotypes in Bangladesh. *Journal of Horticulture and Forestry*. 2019;11(7):104-19.
669. Honsho C, Nishiyama K, Eiadthong W, Yonemori K. Isolation and characterization of new microsatellite markers in mango (*Mangifera indica*). *Molecular Ecology Notes*. 2005;5(1):152-4.
670. Mahato AK, Sharma N, Singh A, Srivastav M, Singh SK, Singh AK, et al. Leaf transcriptome sequencing for identifying genic-SSR markers and SNP heterozygosity in crossbred mango variety 'Amrapali' (*Mangifera indica* L.). *Plos One*. 2016;11(10):e0164325.
671. Chunwongse C, Phumichai C, Tongyoo P, Juejun N, Chunwongse J. Development of di-nucleotide microsatellite markers and construction of genetic linkage map in mango (*Mangifera indica* L.). *Songklanakarin Journal of Science & Technology*. 2015;37(2).
672. Chaitra VN. Identification of Nucleotide Variants to Analyse Quantitative Trait Loci (QTL) in Drought Resistant Mulberry Cultivars.
673. Vijayan K. The emerging role of genomic tools in mulberry (*Morus*) genetic improvement. *Tree Genetics & Genomes*. 2010;6(4):613-25.
674. Vijayan K. Inter simple sequence repeat (ISSR) polymorphism and its application in mulberry genome analysis. *International Journal of Industrial Entomology*. 2005;10(2):79-86.
675. BIMA AKZAD M, NURAENI S, HALIMAH LAREKENG S. DETECTING DNA POLYMORPHISM ON MULBERRY (*Morus* Sp.) USING RAPD AND ISSR MARKERS. *Plant Cell Biotechnology and Molecular Biology*. 2021.

676. Akzad MB, Nuraeni S, Larekeng SH. Detecting DNA polymorphism on mulberry (*Morus* sp) using RAPD and SSR markers. *Plant Cell Biotech Mol Bio*. 2021;22(35&36):106-11.
677. Salimonti A, Carbone F, Romano E, Pellegrino M, Benincasa C, Micali S, et al. Association Study of the 5' UTR Intron of the FAD2-2 Gene With Oleic and Linoleic Acid Content in *Olea europaea* L. *Frontiers in Plant Science*. 2020;11.
678. Kaya HB, Akdemir D, Lozano R, Cetin O, Kaya HS, Sahin M, et al. Genome wide association study of 5 agronomic traits in olive (*Olea europaea* L.). *Scientific Reports*. 2019;9.
679. Mariotti R, Pandolfi S, De Cauwer I, Saumitou-Laprade P, Vernet P, Rossi M, et al. Diallelic self-incompatibility is the main determinant of fertilization patterns in olive orchards. *Evolutionary Applications*. 2021;14(4):983-95.
680. Mariotti R, Fornasiero A, Mousavi S, Cultrera NGM, Brizioli F, Pandolfi S, et al. Genetic Mapping of the Incompatibility Locus in Olive and Development of a Linked Sequence-Tagged Site Marker. *Frontiers in Plant Science*. 2020;10.
681. Beghe D, Piotti A, Satovic Z, de la Rosa R, Belaj A. Pollen-mediated gene flow and fine-scale spatial genetic structure in *Olea europaea* subsp *europaea* var. *sylvestris*. *Ann Bot-London*. 2017;119(4):671-9.
682. Besnard G, Cheptou Po, Debbaoui M, Lafont P, Hugueny B, Dupin J, et al. Paternity tests support a diallelic self-incompatibility system in a wild olive (*Olea europaea* subsp. *laperrinei*, *Oleaceae*). *Ecol Evol*. 2020;10(4):1876-88.
683. Saumitou-Laprade P, Vernet P, Vekemans X, Billiard S, Gallina S, Essalouh L, et al. Elucidation of the genetic architecture of self-incompatibility in olive: Evolutionary consequences and perspectives for orchard management. *Evolutionary applications*. 2017;10(9):867-80.
684. Moreno-Sanz P, Lombardo L, Lorenzi S, Michelotti F, Grando MS. Genetic Resources of *Olea europaea* L. in the Garda Trentino Olive Groves Revealed by Ancient Trees Genotyping and Parentage Analysis of Drupe Embryos. *Genes*. 2020;11(10).
685. Alagna F, Caceres ME, Pandolfi S, Collani S, Mousavi S, Mariotti R, et al. The paradox of self-fertile varieties in the context of self-incompatible genotypes in olive. *Frontiers in plant science*. 2019;10:725.
686. Arbeiter AB, Jakse J, Bandelj D. Paternity Analysis of the Olive Variety "Istrska Belica" and Identification of Pollen Donors by Microsatellite Markers. *Sci World J*. 2014.
687. Mookerjee S, Guerin J, Collins G, Ford C, Sedgley M. Paternity analysis using microsatellite markers to identify pollen donors in an olive grove. *Theoretical and Applied Genetics*. 2005;111(6):1174-82.
688. Ipek A, Yilmaz K, Sikici P, Tangu NA, Oz AT, Bayraktar M, et al. SNP Discovery by GBS in Olive and the Construction of a High-Density Genetic Linkage Map. *Biochem Genet*. 2016;54(3):313-25.
689. Ipek A, Ipek M, Ercisli S, Tangu NA. Transcriptome-based SNP discovery by GBS and the construction of a genetic map for olive. *Funct Integr Genomic*. 2017;17(5):493-501.
690. Kaya HB, Cetin O, Kaya HS, Sahin M, Sefer F, Tanyolac B. Association Mapping in Turkish Olive Cultivars Revealed Significant Markers Related to Some Important Agronomic Traits. *Biochem Genet*. 2016;54(4):506-33.
691. Julca I, Marcet-Houben M, Cruz F, Gomez-Garrido J, Gaut BS, Diez CM, et al. Genomic evidence for recurrent genetic admixture during the domestication of Mediterranean olive trees (*Olea europaea* L.). *Bmc Biol*. 2020;18(1).

692. Kaya HB, Cetin O, Kaya H, Sahin M, Sefer F, Kahraman A, et al. SNP Discovery by Illumina-Based Transcriptome Sequencing of the Olive and the Genetic Characterization of Turkish Olive Genotypes Revealed by AFLP, SSR and SNP Markers. *Plos One*. 2013;8(9).
693. Sakar E, Unver H, Ercisli S. Genetic Diversity Among Historical Olive (*Olea europaea* L.) Genotypes from Southern Anatolia Based on SSR Markers (Publication with Expression of Concern. See vol. 57, pg. 475, 2019). *Biochem Genet*. 2016;54(6):842-53.
694. Sakar E, Unver H, Bakir M, Ulas M, Sakar ZM. Genetic Relationships Among Olive (*Olea europaea* L.) Cultivars Native to Turkey. *Biochem Genet*. 2016;54(4):348-59.
695. Duran ST, Aghayeva S, Akparov Z, Mammadov A, Asgarova R, Uslu OY, et al. Genetic variation and relationships between Azerbaijani and Turkish olive genetic resources. *Molecular Biology Reports*. 2021.
696. Ben Ayed R, Ercişli S, Hanana M, Rebai A, Moreau F. Assessment of population structure, genetic diversity and relationship of Mediterranean olive accessions using SSR markers and computational tools. *Biotechnology Letters*. 2022;44(1):113-27.
697. Roubos K, Moustakas M, Aravanopoulos FA. Molecular identification of Greek olive (*Olea europaea*) cultivars based on microsatellite loci. *Genetics and Molecular Research*. 2010;9(3):1865-76.
698. Debbabi OS, Mnasri SR, Ben Amar F, Ben Naceur M, Montemurro C, Miazzi MM. Applications of Microsatellite Markers for the Characterization of Olive Genetic Resources of Tunisia. *Genes*. 2021;12(2).
699. Mariotti R, Belaj A, De La Rosa R, Leòn L, Brizioli F, Baldoni L, et al. EST–SNP Study of *Olea europaea* L. Uncovers Functional Polymorphisms between Cultivated and Wild Olives. *Genes*. 2020;11(8):916.
700. Bracci T, Busconi M, Fogher C, Sebastiani L. Molecular studies in olive (*Olea europaea* L.): overview on DNA markers applications and recent advances in genome analysis. *Plant cell reports*. 2011;30(4):449-62.
701. Basheer-Salimia RA, Awad MK, Kalaitzis P. Genetic Fingerprinting of Palestinian Olive (*Olea europea* L.) Cultivars Using SNP Markers. *Jordan Journal of Agricultural Sciences*. 2009;5(3):282-94.
702. Ghanbari A, Estaji A. ISSR Analysis for Determination of genetic diversity in 29 olive (*Olea europaea* L.) cultivars. *Iranian Journal of Genetics and Plant Breeding*. 2018;7(1):31-40.
703. Galatali S, Ghafoor NA, Kaya E. Characterization of Olive (*Olea Europaea* L.) Genetic Resources via PCR-Based Molecular Marker Systems. *European Journal of Biology and Biotechnology*. 2021;2(1):26-33.
704. D’Agostino N, Taranto F, Camposeo S, Mangini G, Fanelli V, Gadaleta S, et al. GBS-derived SNP catalogue unveiled wide genetic variability and geographical relationships of Italian olive cultivars. *Scientific reports*. 2018;8(1):1-13.
705. Cordeiro A, Sanchez-Sevilla J, Alvarez-Tinaut M, Gomez-Jimenez M. Genetic diversity assessment in Portugal accessions of *Olea europaea* by RAPD markers. *Biologia plantarum*. 2008;52(4):642-7.
706. Bazakos C, Dulger AO, Uncu AT, Spaniolas S, Spano T, Kalaitzis P. A SNP-based PCR–RFLP capillary electrophoresis analysis for the identification of the varietal origin of olive oils. *Food Chemistry*. 2012;134(4):2411-8.
707. Sion S, Savoia MA, Gadaleta S, Piarulli L, Mascio I, Fanelli V, et al. How to choose a good marker to analyze the olive germplasm (*Olea europaea* L.) and derived products. *Genes*. 2021;12(10):1474.

708. Reale S, Doveri S, Díaz A, Angiolillo A, Lucentini L, Pilla F, et al. SNP-based markers for discriminating olive (*Olea europaea* L.) cultivars. *Genome*. 2006;49(9):1193-205.
709. Kyriakopoulou CI, Kalogianni DP. Genetic identification of the wild form of olive (*Olea europaea* var. *sylvestris*) using allele-specific real-time PCR. *Foods*. 2020;9(4):467.
710. Sesli M, Yegenoglu ED. Genetic relationships in wild olives (*Olea europaea* ssp. *oleaster*) by ISSR and RAPD markers. *Biotechnology & Biotechnological Equipment*. 2017;31(5):897-904.
711. Muzzalupo I, Perri E. Genetic characterization of olive germplasms by molecular markers. *The European Journal of Plant Science and Biotechnology*. 2008;2(1):60-8.
712. Muzzalupo I, Lombardo N, Musacchio A, Noce ME, Pellegrino G, Perri E, et al. DNA sequence analysis of microsatellite markers enhances their efficiency for germplasm management in an Italian olive collection. *Journal of the American Society for Horticultural Science*. 2006;131(3):352-9.
713. Linos A, Nikoloudakis N, Katsiotis A, Hagidimitriou M. Genetic structure of the Greek olive germplasm revealed by RAPD, ISSR and SSR markers. *Scientia Horticulturae*. 2014;175:33-43.
714. Cipriani G, Marrazzo MT, Marconi R, Cimato A, Testolin R. Microsatellite markers isolated in olive (*Olea europaea* L.) are suitable for individual fingerprinting and reveal polymorphism within ancient cultivars. *Theoretical and Applied Genetics*. 2002;104(2-3):223-8.
715. Carriero F, Fontanazza G, Cellini F, Giorio G. Identification of simple sequence repeats (SSRs) in olive (*Olea europaea* L.). *Theoretical and Applied Genetics*. 2002;104(2-3):301-7.
716. Ercisli S, Ipek A, Barut E. SSR Marker-Based DNA Fingerprinting and Cultivar Identification of Olives (*Olea europaea*). *Biochem Genet*. 2011;49(9-10):555-61.
717. Domínguez-García MC, Belaj A, De la Rosa R, Satovic Z, Heller-Uszynska K, Kilian A, et al. Development of DArT markers in olive (*Olea europaea* L.) and usefulness in variability studies and genome mapping. *Scientia horticulturae*. 2012;136:50-60.
718. Alsamman AM, Adawy S, Ibrahim S, Hussein B, Hussein E. Selective Amplification of Start codon Polymorphic Loci (SASPL): a new PCR-based molecular marker in olive. *Plant Omics*. 2017;10(2).
719. Ho V, Ngo T, Phan T, Ta T, Tran T. Genetic diversity among passion fruit (*Passiflora edulis*) accessions of southern vietnam using RAPD and ISSR markers. *Sabroa J Breed Genet*. 2021;53(1):1-14.
720. Mitani N, Kono A, Yamada M, Sato A, Kobayashi S, Ban Y, et al. Practical marker-assisted selection using two SCAR markers for fruit astringency type in crosses of 'Taiten'× PCNA cultivars in persimmon breeding. *Scientia Horticulturae*. 2014;170:219-23.
721. Luo C, Zhang F, Zhang Q, Guo D, Luo Z. Characterization and comparison of EST-SSR and TRAP markers for genetic analysis of the Japanese persimmon *Diospyros kaki*. *Genet Mol Res*. 2013;12(3):2841-51.
722. Minamikawa MF, Takada N, Terakami S, Saito T, Onogi A, Kajiya-Kanegae H, et al. Genome-wide association study and genomic prediction using parental and breeding populations of Japanese pear (*Pyrus pyrifolia* Nakai). *Scientific reports*. 2018;8(1):1-12.

723. Zhang M-Y, Xue C, Hu H, Li J, Xue Y, Wang R, et al. Genome-wide association studies provide insights into the genetic determination of fruit traits of pear. *Nature communications*. 2021;12(1):1-10.
724. Wu J, Li L-T, Li M, Khan MA, Li X-G, Chen H, et al. High-density genetic linkage map construction and identification of fruit-related QTLs in pear using SNP and SSR markers. *Journal of experimental botany*. 2014;65(20):5771-81.
725. Li X, Singh J, Qin M, Li S, Zhang X, Zhang M, et al. Development of an integrated 200K SNP genotyping array and application for genetic mapping, genome assembly improvement and genome wide association studies in pear (*Pyrus*). *Plant biotechnology journal*. 2019;17(8):1582-94.
726. Gabay G, Dahan Y, Izhaki Y, Faigenboim A, Ben-Ari G, Elkind Y, et al. High-resolution genetic linkage map of European pear (*Pyrus communis*) and QTL fine-mapping of vegetative budbreak time. *BMC plant biology*. 2018;18(1):1-13.
727. Iwata H, Hayashi T, Terakami S, Takada N, Sawamura Y, Yamamoto T. Potential assessment of genome-wide association study and genomic selection in Japanese pear *Pyrus pyrifolia*. *Breeding Science*. 2013;63(1):125-40.
728. Gonai T, Terakami S, Nishitani C, Yamamoto T, Kasumi M. The validity of marker-assisted selection using DNA markers linked to a pear scab resistance gene (*Vnk*) in two populations. *Journal of the Japanese Society for Horticultural Science*. 2009;78(1):49-54.
729. Liu Q, Song Y, Liu L, Zhang M, Sun J, Zhang S, et al. Genetic diversity and population structure of pear (*Pyrus* spp.) collections revealed by a set of core genome-wide SSR markers. *Tree genetics & genomes*. 2015;11(6):1-22.
730. Sharma H, Sharma P, Sharma R. Evaluation of Genetic Relatedness Among Temperate Pome Fruit Crops of Family Rosaceae Using Arbitrary Oligonucleotide Markers. *Proceedings of the National Academy of Sciences, India Section B: Biological Sciences*. 2018;88(1):191-8.
731. Shirasawa K, Nishio S, Terakami S, Botta R, Marinoni DT, Isobe S. Chromosome-level genome assembly of Japanese chestnut (*Castanea crenata* Sieb. et Zucc.) reveals conserved chromosomal segments in woody rosids. *DNA Research*. 2021;28(5):dsab016.
732. Terakami S, Nishitani C, Kunihiya M, Shirasawa K, Sato S, Tabata S, et al. Transcriptome-based single nucleotide polymorphism markers for genome mapping in Japanese pear (*Pyrus pyrifolia* Nakai). *Tree genetics & genomes*. 2014;10(4):853-63.
733. Ferik F, Ates D, Ercisli S, Erdogan A, Orhan E, Tanyolac MB. Genome-wide association links candidate genes to fruit firmness, fruit flesh color, flowering time, and soluble solid content in apricot (*Prunus armeniaca* L.). *Molecular Biology Reports*. 2022;49(6):5283-91.
734. Nsibi M, Gouble B, Bureau S, Flutre T, Sauvage C, Audergon J-M, et al. Adoption and Optimization of Genomic Selection To Sustain Breeding for Apricot Fruit Quality. *G3: Genes, Genomes, Genetics*. 2020;10(12):4513-29.
735. Forcada CF, Oraguzie N, Igartua E, Moreno MÁ, Gogorcena Y. Population structure and marker–trait associations for pomological traits in peach and nectarine cultivars. *Tree genetics & genomes*. 2013;9(2):331-49.
736. Mora JRH, Micheletti D, Bink M, Van de Weg E, Cantín C, Nazzicari N, et al. Integrated QTL detection for key breeding traits in multiple peach progenies. *BMC genomics*. 2017;18(1):1-15.
737. Fresnedo-Ramírez J, Bink MC, van de Weg E, Famula TR, Crisosto CH, Frett TJ, et al. QTL mapping of pomological traits in peach and related species breeding germplasm. *Molecular Breeding*. 2015;35(8):1-19.

738. Quilot B, Wu B, Kervella J, Génard M, Foulongne M, Moreau K. QTL analysis of quality traits in an advanced backcross between *Prunus persica* cultivars and the wild relative species *P. davidiana*. *Theoretical and Applied Genetics*. 2004;109(4):884-97.
739. Verde I, Quarta R, Cedrola C, Dettori M. QTL analysis of agronomic traits in a BC1 peach population. *Acta horticulturae*. 2002.
740. Martínez-García PJ, Parfitt DE, Ogundiwin EA, Fass J, Chan HM, Ahmad R, et al. High density SNP mapping and QTL analysis for fruit quality characteristics in peach (*Prunus persica* L.). *Tree Genetics & Genomes*. 2013;9(1):19-36.
741. Cao K, Wang L, Zhu G, Fang W, Chen C, Luo J. Genetic diversity, linkage disequilibrium, and association mapping analyses of peach (*Prunus persica*) landraces in China. *Tree genetics & genomes*. 2012;8(5):975-90.
742. Picañol R, Eduardo I, Aranzana M, Howad W, Batlle I, Iglesias I, et al. Combining linkage and association mapping to search for markers linked to the flat fruit character in peach. *Euphytica*. 2013;190(2):279-88.
743. Bliss FA, Arulsekhar S, Foolad MR, Becerra V, Gillen A, Warburton M, et al. An expanded genetic linkage map of *Prunus* based on an interspecific cross between almond and peach. *Genome*. 2002;45(3):520-9.
744. Etienne C, Rothan C, Moing A, Plomion C, Bodénès C, Svanella-Dumas L, et al. Candidate genes and QTLs for sugar and organic acid content in peach [*Prunus persica* (L.) Batsch]. *Theoretical and Applied Genetics*. 2002;105(1):145-59.
745. da Silva Linge C, Bassi D, Bianco L, Pacheco I, Pirona R, Rossini L. Genetic dissection of fruit weight and size in an F2 peach (*Prunus persica* (L.) Batsch) progeny. *Molecular Breeding*. 2015;35(2):1-19.
746. Biscarini F, Nazzicari N, Bink M, Arús P, Aranzana MJ, Verde I, et al. Genome-enabled predictions for fruit weight and quality from repeated records in European peach progenies. *BMC genomics*. 2017;18(1):1-15.
747. Eduardo I, Pacheco I, Chietera G, Bassi D, Pozzi C, Vecchiatti A, et al. QTL analysis of fruit quality traits in two peach intraspecific populations and importance of maturity date pleiotropic effect. *Tree Genetics & Genomes*. 2011;7(2):323-35.
748. Micheletti D, Dettori MT, Micali S, Aramini V, Pacheco I, Linge CD, et al. Whole-Genome Analysis of Diversity and SNP-Major Gene Association in Peach Germplasm. *Plos One*. 2015;10(9).
749. Cao K, Zhou Z, Wang Q, Guo J, Zhao P, Zhu G, et al. Genome-wide association study of 12 agronomic traits in peach. *Nature Communications*. 2016;7(1):1-10.
750. Cao K, Li Y, Deng CH, Gardiner SE, Zhu G, Fang W, et al. Comparative population genomics identified genomic regions and candidate genes associated with fruit domestication traits in peach. *Plant biotechnology journal*. 2019;17(10):1954-70.
751. Zeballos JL, Abidi W, Giménez R, Monforte AJ, Moreno MÁ, Gogorcena Y. Mapping QTLs associated with fruit quality traits in peach [*Prunus persica* (L.) Batsch] using SNP maps. *Tree Genetics & Genomes*. 2016;12(3):1-17.
752. Cirilli M, Giovannini D, Ciacciulli A, Chiozzotto R, Gattolin S, Rossini L, et al. Integrative genomics approaches validate PpYUC11-like as candidate gene for the stony hard trait in peach (*P. persica* L. Batsch). *BMC plant biology*. 2018;18(1):1-12.
753. Ciacciulli A, Cirilli M, Chiozzotto R, Attanasio G, Linge CDS, Pacheco I, et al. Linkage and association mapping for the slow softening (SwS) trait in peach (*P. persica* L. Batsch) fruit. *Tree Genetics & Genomes*. 2018;14(6):1-10.

754. Eduardo I, Picañol R, Rojas E, Batlle I, Howad W, Aranzana M, et al. Mapping of a major gene for the slow ripening character in peach: co-location with the maturity date gene and development of a candidate gene-based diagnostic marker for its selection. *Euphytica*. 2015;205(2):627-36.
755. Eduardo I, Chietera G, Pirona R, Pacheco I, Troggio M, Banchi E, et al. Genetic dissection of aroma volatile compounds from the essential oil of peach fruit: QTL analysis and identification of candidate genes using dense SNP maps. *Tree Genetics & Genomes*. 2013;9(1):189-204.
756. Abdelghafar A. Enabling Marker Assisted Breeding (MAB) for Phytochemical Compounds in Peach [*Prunus persica* (L.) Batsch]. 2016.
757. Nunez-Lillo G, Balladares C, Pavez C, Urrea C, Sanhueza D, Vendramin E, et al. High-density genetic map and QTL analysis of soluble solid content, maturity date, and mealiness in peach using genotyping by sequencing. *Scientia Horticulturae*. 2019;257.
758. Lambert P, Campoy JA, Pacheco I, Mauroux J-B, Linge CDS, Micheletti D, et al. Identifying SNP markers tightly associated with six major genes in peach [*Prunus persica* (L.) Batsch] using a high-density SNP array with an objective of marker-assisted selection (MAS). *Tree Genetics & Genomes*. 2016;12(6):1-21.
759. Quarta R, Dettori M, Sartori A, Verde I, editors. Genetic linkage map and QTL analysis in peach. XXV International Horticultural Congress, Part 11: Application of Biotechnology and Molecular Biology and Breeding-Gene 521; 1998.
760. Donoso J, Picañol R, Serra O, Howad W, Alegre S, Arús P, et al. Exploring almond genetic variability useful for peach improvement: mapping major genes and QTLs in two interspecific almond× peach populations. *Molecular Breeding*. 2016;36(2):16.
761. Campos CR. Marker assisted selection, fine mapping and identification of candidate genes for three major traits of *Prunus persica* L.(Batsh). 2020.
762. Abbott A, Rajapakse S, Sosinski B, Lu Z, Sossey-Alaoui K, Gannavarapu M, et al., editors. Construction of saturated linkage maps of peach crosses segregating for characters controlling fruit quality, tree architecture and pest resistance. IV International Peach Symposium 465; 1997.
763. Warburton M, Becerra-Velasquez V, Goffreda J, Bliss F. Utility of RAPD markers in identifying genetic linkages to genes of economic interest in peach. *Theoretical and Applied Genetics*. 1996;93(5):920-5.
764. Font i Forcada C, Guajardo V, Chin-Wo SR, Moreno MÁ. Association mapping analysis for fruit quality traits in *Prunus persica* using SNP markers. *Frontiers in plant science*. 2019;9:2005.
765. González M, Salazar E, Castillo J, Morales P, Mura-Jornet I, Maldonado J, et al. Genetic structure based on EST–SSR: a putative tool for fruit color selection in Japanese plum (*Prunus salicina* L.) breeding programs. *Molecular Breeding*. 2016;36(6):68.
766. Arús P, Ballester J, Jáuregui B, Joobeur T, Truco M, Carmen de Vicente M, editors. The European *Prunus* mapping project: update on marker development in almond. *Eucarpia Symposium on Fruit Breeding and Genetics* 484; 1996.
767. Chaparro J, Werner D, O'malley D, Sederoff R. Targeted mapping and linkage analysis of morphological isozyme, and RAPD markers in peach. *Theoretical and Applied Genetics*. 1994;87(7):805-15.

768. Dettori MT, Quarta R, Verde I. A peach linkage map integrating RFLPs, SSRs, RAPDs, and morphological markers. *Genome*. 2001;44(5):783-90.
769. Yamamoto T, Shimada T, Imai T, Yaegaki H, Haji T, Matsuta N, et al. Characterization of morphological traits based on a genetic linkage map in peach. *Breeding Science*. 2001;51(4):271-8.
770. Badenes M, Hurtado M, Sanz F, Archelos D, Burgos L, Egea J, et al. Searching for molecular markers linked to male sterility and self-compatibility in apricot. *Plant Breeding*. 2000;119(2):157-60.
771. Sonneveld T, Robbins T, Bošković R, Tobutt K. Cloning of six cherry self-incompatibility alleles and development of allele-specific PCR detection. *Theoretical and Applied Genetics*. 2001;102(6-7):1046-55.
772. Wang D, Karle R, Iezzoni A. QTL analysis of flower and fruit traits in sour cherry. *Theoretical and Applied Genetics*. 2000;100(3-4):535-44.
773. Sosinski B, Gannavarapu M, Hager L, Beck L, King GJ, Ryder C, et al. Characterization of microsatellite markers in peach [*Prunus persica* (L.) Batsch]. *Theoretical and Applied Genetics*. 2000;101(3):421-8.
774. Dirlewanger E, Moing A, Rothan C, Svanella L, Pronier V, Guye A, et al. Mapping QTLs controlling fruit quality in peach (*Prunus persica* (L.) Batsch). *Theoretical and Applied Genetics*. 1999;98(1):18-31.
775. Zhang Q, Zhang H, Sun L, Fan G, Ye M, Jiang L, et al. The genetic architecture of floral traits in the woody plant *Prunus mume*. *Nature communications*. 2018;9(1):1-12.
776. Tao R, Yamane H, Sassa H, Mori H, Gradziel TM, Dandekar AM, et al. Identification of stylar RNases associated with gametophytic self-incompatibility in almond (*Prunus dulcis*). *Plant and cell physiology*. 1997;38(3):304-11.
777. Ballester J, Socias i Company R, Arus P, De Vicente M. Genetic mapping of a major gene delaying blooming time in almond. *Plant Breeding*. 2001;120(3):268-70.
778. Joobeur T, Viruel M, de Vicente IM, Jauregui B, Ballester J, Dettori M, et al. Construction of a saturated linkage map for *Prunus* using an almond× peach F2 progeny. *Theoretical and Applied Genetics*. 1998;97(7):1034-41.
779. Passaro M, Geuna F, Bassi D, Cirilli M. Development of a high-resolution melting approach for reliable and cost-effective genotyping of PPVres locus in apricot (*P. armeniaca*). *Molecular Breeding*. 2017;37(6):74.
780. Polo-Oltra Á, Romero C, López I, Badenes ML, Zuriaga E. Cost-Effective and Time-Efficient Molecular Assisted Selection for Ppv Resistance in Apricot Based on ParPMC2 Allele-Specific PCR. *Agronomy*. 2020;10(9):1292.
781. Soriano JM, Domingo ML, Zuriaga E, Romero C, Zhebentyayeva T, Abbott AG, et al. Identification of simple sequence repeat markers tightly linked to plum pox virus resistance in apricot. *Molecular breeding*. 2012;30(2):1017-26.
782. Soriano J, Vera-Ruiz EM, Vilanova S, Martínez-Calvo J, Llacer G, Badenes ML, et al. Identification and mapping of a locus conferring plum pox virus resistance in two apricot-improved linkage maps. *Tree Genetics & Genomes*. 2008;4(3):391-402.
783. Hurtado M, Romero C, Vilanova S, Abbott A, Llacer G, Badenes M. Genetic linkage maps of two apricot cultivars (*Prunus armeniaca* L.), and mapping of PPV (sharka) resistance. *Theoretical and Applied Genetics*. 2002;105(2):182-91.

784. Salava J, Wang Y, Krška B, Polak J, Kominek P, Miller W, et al. Identification of molecular markers linked to resistance of apricot (*Prunus armeniaca* L.) to plum pox virus/Identifizierung von molekularen Markern in Verbindung mit der Resistenz von Aprikosen (*Prunus armeniaca* L.) gegen das Plum pox virus. *Zeitschrift für Pflanzenkrankheiten und Pflanzenschutz/Journal of Plant Diseases and Protection*. 2002;64-7.
785. Vilanova S, Romero C, Abbott A, Llacer G, Badenes M. An apricot (*Prunus armeniaca* L.) F2 progeny linkage map based on SSR and AFLP markers, mapping plum pox virus resistance and self-incompatibility traits. *Theoretical and Applied Genetics*. 2003;107(2):239-47.
786. Mariette S, Wong Jun Tai F, Roch G, Barre A, Chague A, Decroocq S, et al. Genome-wide association links candidate genes to resistance to Plum Pox Virus in apricot (*Prunus armeniaca*). *New Phytologist*. 2016;209(2):773-84.
787. Lu Z-X, Sosinski B, Reighard G, Baird W, Abbott A. Construction of a genetic linkage map and identification of AFLP markers for resistance to root-knot nematodes in peach rootstocks. *Genome*. 1998;41(2):199-207.
788. Lu Z-X, Sossey-Alaoui K, Reighard G, Baird WV, Abbott A. Development and characterization of a codominant marker linked to root-knot nematode resistance, and its application to peach rootstock breeding. *Theoretical and Applied Genetics*. 1999;99(1):115-22.
789. Cao K, Wang L, Zhu G, Fang W, Chen C, Zhao P. Construction of a linkage map and identification of resistance gene analog markers for root-knot nematodes in wild peach, *Prunus kansuensis*. *Journal of the American Society for Horticultural Science*. 2011;136(3):190-7.
790. Maquilan MAD, Olmstead MA, Olmstead JW, Dickson DW, Chaparro JX. Genetic analyses of resistance to the peach root-knot nematode (*Meloidogyne floridensis*) using microsatellite markers. *Tree Genetics & Genomes*. 2018;14(4):1-15.
791. Yamamoto T, Hayashi T. New root-knot nematode resistance genes and their STS markers in peach. *Scientia Horticulturae*. 2002;96(1-4):81-90.
792. Pacheco I, Bassi D, Eduardo I, Ciacciulli A, Pirona R, Rossini L, et al. QTL mapping for brown rot (*Monilinia fructigena*) resistance in an intraspecific peach (*Prunus persica* L. Batsch) F1 progeny. *Tree Genetics & Genomes*. 2014;10(5):1223-42.
793. Martínez-García PJ, Parfitt DE, Bostock RM, Fresnedo-Ramirez J, Vazquez-Lobo A, Ogundiwin EA, et al. Application of genomic and quantitative genetic tools to identify candidate resistance genes for brown rot resistance in peach. *Plos One*. 2013;8(11):e78634.
794. Viruel M, Madur D, Dirlwanger E, Pascal T, Kervella J, editors. MAPPING QUANTITATIVE TRAIT LOCI CONTROLLING PEACH LEAF CURL RESISTANCE. IV International Peach Symposium 465; 1997.
795. Cirilli M, Rossini L, Geuna F, Palmisano F, Minafra A, Castrignanò T, et al. Genetic dissection of Sharka disease tolerance in peach (*P. persica* L. Batsch). *BMC plant biology*. 2017;17(1):1-15.
796. Lecouls A-C, Bergougnoux V, Rubio-Cabetas M-J, Bosselut N, Voisin R, Poessel J-L, et al. Marker-assisted selection for the wide-spectrum resistance to root-knot nematodes conferred by the Ma gene from Myrobalan plum (*Prunus cerasifera*) in interspecific *Prunus* material. *Molecular breeding*. 2004;13(2):113-24.

797. Lecouls A, Rubio-Cabetas M, Minot J, Voisin R, Bonnet A, Salesses G, et al. RAPD and SCAR markers linked to the Ma1 root-knot nematode resistance gene in Myrobalan plum (*Prunus cerasifera* Ehr.). *Theoretical and Applied Genetics*. 1999;99(1-2):328-35.
798. Castède S, Campoy JA, García JQ, Le Dantec L, Lafargue M, Barreneche T, et al. Genetic determinism of phenological traits highly affected by climate change in *Prunus avium*: flowering date dissected into chilling and heat requirements. *New Phytologist*. 2014;202(2):703-15.
799. Bielenberg DG, Rauh B, Fan S, Gasic K, Abbott AG, Reighard GL, et al. Genotyping by sequencing for SNP-based linkage map construction and QTL analysis of chilling requirement and bloom date in peach [*Prunus persica* (L.) Batsch]. *Plos One*. 2015;10(10):e0139406.
800. Fan S, Bielenberg DG, Zhebentyayeva TN, Reighard GL, Okie WR, Holland D, et al. Mapping quantitative trait loci associated with chilling requirement, heat requirement and bloom date in peach (*Prunus persica*). *New Phytologist*. 2010;185(4):917-30.
801. Dhanapal AP, Crisosto CH. Association genetics of chilling injury susceptibility in peach (*Prunus persica* (L.) Batsch) across multiple years. *3 Biotech*. 2013;3(6):481-90.
802. Sanchez-Perez R, Ruiz D, Dicenta F, Egea J, Martinez-Gomez P. Application of simple sequence repeat (SSR) markers in apricot breeding: molecular characterization, protection, and genetic relationships. *Scientia Horticulturae*. 2005;103(3):305-15.
803. Dirlewanger E, Cosson P, Tavaud M, Aranzana M, Poizat C, Zanetto A, et al. Development of microsatellite markers in peach [*Prunus persica* (L.) Batsch] and their use in genetic diversity analysis in peach and sweet cherry (*Prunus avium* L.). *Theoretical and Applied Genetics*. 2002;105(1):127-38.
804. Eroglu D, Cakir B. Molecular characterization of sweet cherry genotypes and rootstocks by using *Prunus* SSR sequences. *Austin Journal of Biotechnology & Bioengineering*. 2015;2(3):1044.
805. Cao K, Zheng Z, Wang L, Liu X, Zhu G, Fang W, et al. Comparative population genomics reveals the domestication history of the peach, *Prunus persica*, and human influences on perennial fruit crops. *Genome biology*. 2014;15(7):1-15.
806. Bouhadida M, Moreno MÁ, Gonzalo MJ, Alonso JM, Gogorcena Y. Genetic variability of introduced and local Spanish peach cultivars determined by SSR markers. *Tree genetics & genomes*. 2011;7(2):257-70.
807. Bouhadida M, Martín JP, Eremin G, Pinochet J, Moreno MÁ, Gogorcena Y. Chloroplast DNA diversity in *Prunus* and its implication on genetic relationships. *Journal of the American Society for Horticultural Science*. 2007;132(5):670-9.
808. Bouhadida M, Casas AM, Moreno M, Gogorcena Y. Molecular characterization of Miraflores peach variety and relatives using SSRs. *Scientia horticulturae*. 2007;111(2):140-5.
809. Li XW, Meng XQ, Jia HJ, Yu ML, Ma RJ, Wang LR, et al. Peach genetic resources: diversity, population structure and linkage disequilibrium. *Bmc Genetics*. 2013;14.
810. Yoon JH, Liu DC, Song WS, Liu WS, Zhang AM, Li SH. Genetic diversity and ecogeographical phylogenetic relationships among peach and nectarine cultivars based on simple sequence repeat (SSR) markers. *Journal of the American Society for Horticultural Science*. 2006;131(4):513-21.

811. Xie RJ, Li XW, Chai ML, Song LJ, Jia HJ, Wu DJ, et al. Evaluation of the genetic diversity of Asian peach accessions using a selected set of SSR markers. *Scientia Horticulturae*. 2010;125(4):622-9.
812. Dettori M, Verde I, Marchesi U, Palombi M, Quarta R, editors. Characterization and evaluation of genetic diversity in peach germplasm using RAPD and RFLP markers. *International Symposium on Molecular Markers for Characterizing Genotypes and Identifying Cultivars in Horticulture* 546; 2000.
813. Warburton ML, Bliss FA. Genetic diversity in peach (*Prunus persica* L batch) revealed by randomly amplified polymorphic DNA (RAPD) markers and compared to inbreeding coefficients. *Journal of the American Society for Horticultural Science*. 1996;121(6):1012-9.
814. Dirlewanger E, Graziano E, Joobeur T, Garriga-Calderé F, Cosson P, Howad W, et al. Comparative mapping and marker-assisted selection in Rosaceae fruit crops. *Proceedings of the national academy of sciences*. 2004;101(26):9891-6.
815. Casas A, Igartua E, Balaguer G, Moreno M. Genetic diversity of *Prunus* rootstocks analyzed by RAPD markers. *Euphytica*. 1999;110(2):139-49.
816. Guajardo V, Solís S, Almada R, Saski C, Gasic K, Moreno MÁ. Genome-wide SNP identification in *Prunus* rootstocks germplasm collections using genotyping-by-sequencing: phylogenetic analysis, distribution of SNPs and prediction of their effect on gene function. *Scientific reports*. 2020;10(1):1-14.
817. Arismendi MJ, Hinrichsen P, Almada R, Pimentel P, Pinto M, Sagredo B. Characterization of genetic diversity of stone fruit rootstocks used in Chile by means of microsatellite markers. *Journal of the American Society for Horticultural Science*. 2012;137(5):302-10.
818. da Silva Linge C, Antanaviciute L, Abdelghafar A, Arús P, Bassi D, Rossini L, et al. High-density multi-population consensus genetic linkage map for peach. *Plos One*. 2018;13(11):e0207724.
819. Guerrero BI, Guerra ME, Herrera S, Irisarri P, Pina A, Rodrigo J. Genetic diversity and population structure of Japanese plum-type (Hybrids of *P. salicina*) accessions assessed by SSR markers. *Agronomy*. 2021;11(9):1748.
820. Downey SL, Iezzoni AF. Polymorphic DNA markers in black cherry (*Prunus serotina*) are identified using sequences from sweet cherry, peach, and sour cherry. *Journal of the American Society for Horticultural Science*. 2000;125(1):76-80.
821. Xu Y, Ma R-C, Xie H, Liu J-T, Cao M-Q. Development of SSR markers for the phylogenetic analysis of almond trees from China and the Mediterranean region. *Genome*. 2004;47(6):1091-104.
822. Luo X, Cao S, Hao Z, Hou L, Cao D, Zhang J, et al. Analysis of genetic structure in a large sample of pomegranate (*Punica granatum* L.) using fluorescent SSR markers. *The Journal of Horticultural Science and Biotechnology*. 2018;93(6):659-65.
823. Amar MH, El-Zayat MAS. Utilization of ISTR, ISSR and SRAP molecular markers to reveal and classify Egyptian pomegranates (*Punica granatum* L.). *Plant Omics*. 2017;10(5):237-45.
824. Moslemi M, Zahravi M, Khaniki GB. Genetic diversity and population genetic structure of pomegranate (*Punica granatum* L.) in Iran using AFLP markers. *Scientia Horticulturae*. 2010;126(4):441-7.

825. Narzary D, Rana TS, Ranade SA. Molecular analyses of genetic diversity in Indian pomegranates using RAPD, DAMD and ISSR. *Fruit Veg Cereal Sci Biotechnol*. 2010;4:126-43.
826. Cabral J, Baldoni A, Tonini H, Azevedo V, Giustina L, Tiago A, et al. Diversity and genetic structure of the native Brazil nut tree (*Bertholletia excelsa* Bonpl.) population. *Embrapa Agrossilvipastoril-Artigo em periódico indexado (ALICE)*. 2017.
827. Buckley D, O'malley D, Apsit V, Prance G, Bawa K. Genetics of Brazil nut (*Bertholletia excelsa* Humb. & Bonpl.: Lecythidaceae). *Theoretical and applied genetics*. 1988;76(6):923-8.
828. O'Malley D, Buckley D, Prance G, Bawa K. Genetics of Brazil nut (*Bertholletia excelsa* Humb. & Bonpl.: Lecythidaceae). *Theoretical and Applied Genetics*. 1988;76(6):929-32.
829. Reis AMM, Braga AC, Lemes MR, Gribel R, Collevatti RG. Development and characterization of microsatellite markers for the Brazil nut tree *Bertholletia excelsa* Humb. & Bonpl. (Lecythidaceae). *Molecular Ecology Resources*. 2009;9(3):920-3.
830. Sujii PS, Inglis PW, Ciampi AY, Solferini VN, Azevedo VCR. Isolation and characterization of microsatellite markers for *Bertholletia excelsa* (Lecythidaceae) population genetic analysis. *Genetics and Molecular Research*. 2013;12(4):5278-82.
831. Konate M, Tarpaga WV, Bourgou L, Wonni I. Genetic diversity assessment among 18 elite cashew tree genotypes (*Anacardium occidentale* L) selected in Western Burkina Faso. *Journal of Plant Breeding and Crop Science*. 2022;14(1):1-11.
832. Savadi S, Sowmya K, Megha V, Muralidhara B, Mohana G. Genetic diversity and identification of interspecific hybrids of *Anacardium* species using microsatellites. *Brazilian Journal of Botany*. 2021;44(1):139-48.
833. Beltramo C, Valentini N, Portis E, Torello Marinoni D, Boccacci P, Sandoval Prando MA, et al. Genetic mapping and QTL analysis in European hazelnut (*Corylus avellana* L.). *Molecular Breeding*. 2016;36(3):1-17.
834. Peterschmidt BC. DNA markers and characterization of novel sources of eastern filbert blight resistance in European hazelnut (*Corylus avellana* L.). 2013.
835. Sathuvalli VR. DNA markers linked to novel sources of resistance to eastern filbert blight in European hazelnut (*Corylus avellana* L.). 2007.
836. Bhattarai G. Microsatellite marker development, characterization and mapping in European hazelnut (*Corylus avellana* L.), and investigation of novel sources of eastern filbert blight resistance in *Corylus*. 2015.
837. Martins SCR. Characterization of Portuguese old varieties of hazelnut (*Corylus avellana* L.) by morphological, molecular, biochemical and nutritional parameters: Universidade de Tras-os-Montes e Alto Douro (Portugal); 2017.
838. Zong J-W, Zhao T-T, Ma Q-H, Liang L-S, Wang G-X. Assessment of genetic diversity and population genetic structure of *Corylus mandshurica* in China using SSR markers. *Plos One*. 2015;10(9):e0137528.
839. Sekerli M. Microsatellite marker development, characterization, and mapping and investigation of new sources of resistance to eastern filbert blight (EFB) in European hazelnut (*Corylus avellana*). 2019.
840. O'Connor K, Hayes B, Hardner C, Nock C, Baten A, Alam M, et al. Genome-wide association studies for yield component traits in a macadamia breeding population. *BMC genomics*. 2020;21(1):1-12.

841. O'Connor K, Hayes B, Hardner C, Alam M, Topp B. Selecting for nut characteristics in macadamia using a genome-wide association study. *HortScience*. 2019;54(4):629-32.
842. O'Connor K, Kilian A, Hayes B, Hardner C, Nock C, Baten A, et al. Population structure, genetic diversity and linkage disequilibrium in a macadamia breeding population using SNP and silicoDArT markers. *Tree Genetics & Genomes*. 2019;15(2):1-16.
843. Alam M, Neal J, O'Connor K, Kilian A, Topp B. Ultra-high-throughput DArTseq-based silicoDArT and SNP markers for genomic studies in macadamia. *Plos One*. 2018;13(8):e0203465.
844. Bentley N, Grauke L, Klein P. Genotyping by sequencing (GBS) and SNP marker analysis of diverse accessions of pecan (*Carya illinoensis*). *Tree Genetics & Genomes*. 2019;15(1):1-17.
845. Aouadi M, Guenni K, Abdallah D, Louati M, Chatti K, Baraket G, et al. Conserved DNA-derived polymorphism, new markers for genetic diversity analysis of Tunisian *Pistacia vera* L. *Physiology and Molecular Biology of Plants*. 2019;25(5):1211-23.
846. Arab MM, Marrano A, Abdollahi-Arpanahi R, Leslie CA, Askari H, Neale DB, et al. Genome-wide patterns of population structure and association mapping of nut-related traits in Persian walnut populations from Iran using the Axiom J. regia 700K SNP array. *Scientific reports*. 2019;9(1):1-14.
847. Famula RA, Richards JH, Famula TR, Neale DB. Association genetics of carbon isotope discrimination and leaf morphology in a breeding population of *Juglans regia* L. *Tree Genetics & Genomes*. 2019;15(1):1-13.
848. Bernard A, Marrano A, Donkpegan A, Brown PJ, Leslie CA, Neale DB, et al. Association and linkage mapping to unravel genetic architecture of phenological traits and lateral bearing in Persian walnut (*Juglans regia* L.). *BMC genomics*. 2020;21(1):1-25.
849. Marrano A, Sideli GM, Leslie CA, Cheng H, Neale DB. Deciphering of the genetic control of phenology, yield, and pellicle color in Persian walnut (*Juglans regia* L.). *Frontiers in plant science*. 2019;10:1140.
850. Arab MM, Marrano A, Abdollahi-Arpanahi R, Leslie CA, Cheng H, Neale DB, et al. Combining phenotype, genotype, and environment to uncover genetic components underlying water use efficiency in Persian walnut. *Journal of experimental botany*. 2020;71(3):1107-27.
851. Ahmed N, Mir J, Mir RR, Rather NA, Rashid R, Wani S, et al. SSR and RAPD analysis of genetic diversity in walnut (*Juglans regia* L.) genotypes from Jammu and Kashmir, India. *Physiology and Molecular Biology of Plants*. 2012;18(2):149-60.
852. Sütyemez M, BOYACI S, KUŞÇUOĞLU N, ÖZCAN A, BÜKÜCÜ ŞB, YILDIRIM E, et al. A research on the determination of phenological and molecular characterization in open-pollinated genotypes in walnut. *Harran Tarım ve Gıda Bilimleri Dergisi*. 2021;25(4):418-37.
853. Kefayati S, Ikhsan AS, Sutyemez M, Paizila A, Topçu H, Bükücü ŞB, et al. First simple sequence repeat-based genetic linkage map reveals a major QTL for leafing time in walnut (*Juglans regia* L.). *Tree Genetics & Genomes*. 2019;15(1):1-12.
854. Sideli GM, Marrano A, Montanari S, Leslie CA, Allen BJ, Cheng H, et al. Quantitative phenotyping of shell suture strength in walnut (*Juglans regia* L.) enhances precision for detection of QTL and genome-wide association mapping. *Plos One*. 2020;15(4):e0231144.

855. Shah UN, Mir J, Ahmed N, Fazili KM. Assessment of germplasm diversity and genetic relationships among walnut (*Juglans regia* L.) genotypes through microsatellite markers. *Journal of the Saudi Society of Agricultural Sciences*. 2018;17(4):339-50.
856. Houmanat K, Abdellah K, Hssaini L, Razouk R, Hanine H, Jaafary S, et al. Molecular diversity of walnut (*Juglans regia* L.) among two major areas in Morocco in contrast with foreign varieties. *International Journal of Fruit Science*. 2021;21(1):180-92.
857. Kabiri G, Bouda S, Elhansali M, Haddioui A. Genetic diversity and structure of walnut (*Juglans regia* L.) genotypes from Middle and High Atlas mountains of Morocco as investigated by Inter-Simple Sequence Repeat (ISSR) markers. *Australian Journal of Crop Science*. 2019;13(12):1983-91.
858. Da Silva MR, Clément D, Gramacho KP, Monteiro WR, Argout X, Lanaud C, et al. Genome-wide association mapping of sexual incompatibility genes in cacao (*Theobroma cacao* L.). *Tree Genetics & Genomes*. 2016;12(3):1-13.
859. McElroy MS, Navarro AJ, Mustiga G, Stack C, Gezan S, Peña G, et al. Prediction of cacao (*Theobroma cacao*) resistance to *Moniliophthora* spp. diseases via genome-wide association analysis and genomic selection. *Frontiers in plant science*. 2018;9:343.
860. Allegre M, Argout X, Boccara M, Fouet O, Roguet Y, Bérard A, et al. Discovery and mapping of a new expressed sequence tag-single nucleotide polymorphism and simple sequence repeat panel for large-scale genetic studies and breeding of *Theobroma cacao* L. DNA research. 2012;19(1):23-35.
861. Gutiérrez OA, Puig AS, Phillips-Mora W, Bailey BA, Ali SS, Mockaitis K, et al. SNP markers associated with resistance to frosty pod and black pod rot diseases in an F1 population of *Theobroma cacao* L. *Tree Genetics & Genomes*. 2021;17(3):1-19.
862. Chandrakant ES, Tulshiram WS, Mathew D, Minimol J, Jose S, Kurian SP, et al. Microsatellite and inter-microsatellite markers linked with resistance to vascular streak dieback in cocoa (*Theobroma cacao* L.). *The Journal of Horticultural Science and Biotechnology*. 2020;95(3):294-302.
863. Sousa TV, Caixeta ET, Alkimim ER, Oliveira ACB, Pereira AA, Sakiyama NS, et al. Early selection enabled by the implementation of genomic selection in *Coffea arabica* breeding. *Frontiers in Plant Science*. 2019;9:1934.
864. Tran H, Furtado A, Vargas CAC, Smyth H, Slade Lee L, Henry R. SNP in the *Coffea arabica* genome associated with coffee quality. *Tree Genetics & Genomes*. 2018;14(5):1-15.
865. Sant'Ana GC, Pereira LF, Pot D, Ivamoto ST, Domingues DS, Ferreira RV, et al. Genome-wide association study reveals candidate genes influencing lipids and diterpenes contents in *Coffea arabica* L. *Scientific reports*. 2018;8(1):1-12.
866. Ferrão LFV, Ferrão RG, Ferrão MAG, Francisco A, Garcia AAF. A mixed model to multiple harvest-location trials applied to genomic prediction in *Coffea canephora*. *Tree Genetics & Genomes*. 2017;13(5):1-13.
867. Ferrão LFV, Ferrão RG, Ferrão MAG, Fonseca A, Carbonetto P, Stephens M, et al. Accurate genomic prediction of *Coffea canephora* in multiple environments using whole-genome statistical models. *Heredity*. 2019;122(3):261-75.
868. Fanelli Carvalho H, Galli G, Venterim Ferrão LF, Vieira Almeida Nonato J, Padilha L, Perez Maluf M, et al. The effect of bienniality on genomic prediction of yield in Arabica coffee. *Euphytica*. 2020;216:1-16.

869. Gimase JM, Thagana WM, Omondi CO, Cheserek JJ, Gichimu BM, Gichuru EK, et al. Genome-Wide Association Study identify the genetic loci conferring resistance to Coffee Berry Disease (*Colletotrichum kahawae*) in *Coffea arabica* var. Rume Sudan. *Euphytica*. 2020;216(6):1-17.
870. Ferrão LFV, Caixeta ET, Souza FdF, Zambolim EM, Cruz CD, Zambolim L, et al. Comparative study of different molecular markers for classifying and establishing genetic relationships in *Coffea canephora*. *Plant systematics and evolution*. 2013;299(1):225-38.
871. Bikila BA. Estimation of genetic parameters and SNPs based molecular diversity of *Coffea canephora*. 2015.
872. Huded AKC, Jingade P, Bychappa M, Mishra MK. Genetic diversity and population structure analysis of Coffee (*Coffea canephora*) germplasm collections in Indian Gene Bank employing SRAP and SCoT markers. *International Journal of Fruit Science*. 2020;20(sup2):S757-S84.
873. Jingade P, Huded AK, Kosaraju B, Mishra MK. Diversity genotyping of Indian coffee (*Coffea arabica* L.) germplasm accessions by using SRAP markers. *Journal of Crop Improvement*. 2019;33(3):327-45.
874. Motta LB, Soares TCB, Ferrão MAG, Caixeta ET, Lorenzoni RM, Souza Neto JDd. Molecular characterization of arabica and Conilon coffee plants genotypes by SSR and ISSR markers. *Brazilian archives of biology and technology*. 2014;57:728-35.
875. Mishra MK, Huded AKC, Jingade P, Bychappa M. Molecular characterization and genetic structure analysis of *Coffea arabica* and *Coffea canephora* cultivars from India using SCoT markers. *Ecological Genetics and Genomics*. 2022;23:100117.
876. Tan L-Q, Wang L-Y, Xu L-Y, Wu L-Y, Peng M, Zhang C-C, et al. SSR-based genetic mapping and QTL analysis for timing of spring bud flush, young shoot color, and mature leaf size in tea plant (*Camellia sinensis*). *Tree Genetics & Genomes*. 2016;12(3):52.
877. Chen L, editor A high density genetic map for underlying the QTLs associated with the main quality and functional components such as catechins, caffeine in tea plant (*Camellia sinensis*). Joint Conference on 8th World Congress on Agriculture and Horticulture and 16th Euro Global Summit on Food and Beverages, J Food Process Technol, Amsterdam, Netherlands; 2017.
878. Yamashita H, Uchida T, Tanaka Y, Katai H, Nagano AJ, Morita A, et al. Genomic predictions and genome-wide association studies based on RAD-seq of quality-related metabolites for the genomics-assisted breeding of tea plants. *Scientific reports*. 2020;10(1):1-10.
879. Lubanga N, Massawe F, Mayes S. Genomic and pedigree-based predictive ability for quality traits in tea (*Camellia sinensis* (L.) O. Kuntze). *Euphytica*. 2021;217(3):1-15.
880. Xu L-Y, Wang L-Y, Wei K, Tan L-Q, Su J-J, Cheng H. High-density SNP linkage map construction and QTL mapping for flavonoid-related traits in a tea plant (*Camellia sinensis*) using 2b-RAD sequencing. *BMC genomics*. 2018;19(1):1-11.
881. Ma J-Q, Yao M-Z, Ma C-L, Wang X-C, Jin J-Q, Wang X-M, et al. Construction of a SSR-based genetic map and identification of QTLs for catechins content in tea plant (*Camellia sinensis*). *Plos One*. 2014;9(3):e93131.
882. Elangbam M, Misra A. Development of CAPS markers to identify Indian tea (*Camellia sinensis*) clones with high catechin content. *Genet Mol Res*. 2016;15(2):1-13.

883. Fang K, Xia Z, Li H, Jiang X, Qin D, Wang Q, et al. Genome-wide association analysis identified molecular markers associated with important tea flavor-related metabolites. *Horticulture research*. 2021;8.
884. Liu S, An Y, Tong W, Qin X, Samarina L, Guo R, et al. Characterization of genome-wide genetic variations between two varieties of tea plant (*Camellia sinensis*) and development of InDel markers for genetic research. *BMC genomics*. 2019;20(1):1-16.
885. Kamunya S, Wachira F, Pathak R, Korir R, Sharma V, Kumar R, et al. Genomic mapping and testing for quantitative trait loci in tea (*Camellia sinensis* (L.) O. Kuntze). *Tree genetics & genomes*. 2010;6(6):915-29.
886. Mphangwe NI, Vorster J, Steyn JM, Nyirenda HE, Taylor NJ, Apostolides Z. Screening of tea (*Camellia sinensis*) for trait-associated molecular markers. *Applied biochemistry and biotechnology*. 2013;171(2):437-49.
887. Bali S, Mamgain A, Raina SN, Yadava SK, Bhat V, Das S, et al. Construction of a genetic linkage map and mapping of drought tolerance trait in Indian beverage tea. *Molecular Breeding*. 2015;35(5):1-20.
888. Mishra RK, Sen-Mandi S. Molecular profiling and development of DNA marker associated with drought tolerance in tea clones growing in Darjeeling. *Current Science*. 2004;60-6.
889. Taniguchi F, Kimura K, Saba T, Ogino A, Yamaguchi S, Tanaka J. Worldwide core collections of tea (*Camellia sinensis*) based on SSR markers. *Tree genetics & genomes*. 2014;10(6):1555-65.
890. Wang X, Zheng H, Zheng W, Ao C, Jin H, Zhao L, et al. RAPD-based genetic diversities and correlation with morphological traits in *Camellia* (Theaceae) cultivars in China. *Genetics and Molecular Research*. 2011;10(2):849-59.
891. Wambulwa MC, Meegahakumbura M, Chalo R, Kamunya S, Muchugi A, Xu J, et al. Nuclear microsatellites reveal the genetic architecture and breeding history of tea germplasm of East Africa. *Tree Genetics & Genomes*. 2016;12(1):1-10.
892. Niu S, Song Q, Koiwa H, Qiao D, Zhao D, Chen Z, et al. Genetic diversity, linkage disequilibrium, and population structure analysis of the tea plant (*Camellia sinensis*) from an origin center, Guizhou plateau, using genome-wide SNPs developed by genotyping-by-sequencing. *BMC Plant Biology*. 2019;19(1):1-12.
893. Maangi JA. Characterization of gene flow and genetic diversity of interspecific tea (*Camellia sinensis* (L.) O. Kuntze) hybrids using Simple Sequence Repeat markers: JKUAT-COHES; 2022.
894. Liu S, Liu H, Wu A, Hou Y, An Y, Wei C. Construction of fingerprinting for tea plant (*Camellia sinensis*) accessions using new genomic SSR markers. *Molecular Breeding*. 2017;37(8):1-14.
895. Hu C-Y, Lee T-C, Tsai H-T, Tsai Y-Z, Lin S-F. Construction of an integrated genetic map based on maternal and paternal lineages of tea (*Camellia sinensis*). *Euphytica*. 2013;191(1):141-52.
896. Devi AM, Goel S, Misra AK. Generation of silver stained TE-AFLP markers in tea (*Camellia sinensis*) and their assessment in filling gaps with construction of a genetic linkage map. *Scientia Horticulturae*. 2015;192:293-301.
897. Fang W, Cheng H, Duan Y, Jiang X, Li X. Genetic diversity and relationship of clonal tea (*Camellia sinensis*) cultivars in China as revealed by SSR markers. *Plant Systematics and Evolution*. 2012;298(2):469-83.
898. Lee J. Development of Transgenic Black Ash (*Fraxinus nigra*) for Resistance to the Emerald Ash Borer, and Genome Editing for Reproductive Sterility: Purdue University; 2017.

899. Andrade GM, Nairn CJ, Le HT, Merkle SA. Sexually mature transgenic American chestnut trees via embryogenic suspension-based transformation. *Plant Cell Reports*. 2009;28(9):1385-97.
900. Newhouse AE, Polin-McGuigan LD, Baier KA, Valletta KE, Rottmann WH, Tschaplinski TJ, et al. Transgenic American chestnuts show enhanced blight resistance and transmit the trait to T1 progeny. *Plant Science*. 2014;228:88-97.
901. Newhouse AE, Oakes AD, Pilkey HC, Roden HE, Horton TR, Powell WA. Transgenic American chestnuts do not inhibit germination of native seeds or colonization of mycorrhizal fungi. *Frontiers in Plant Science*. 2018;9:1046.
902. Pavese V, Moglia A, Corredoira E, Martínez MT, Torello Marinoni D, Botta R. First report of CRISPR/Cas9 gene editing in *Castanea sativa* Mill. *Frontiers in plant science*. 2021;12:728516.
903. Wang X, Luo P, Qiu Z, Li X, Zeng B, Fan C. Adventitious bud regeneration and *Agrobacterium tumefaciens*-mediated genetic transformation of *Eucalyptus urophylla* × *E. tereticornis* interspecific hybrid. *In Vitro Cellular & Developmental Biology-Plant*. 2021:1-11.
904. Prakash M, Gurumurthi K. Genetic transformation and regeneration of transgenic plants from precultured cotyledon and hypocotyl explants of *Eucalyptus tereticornis* Sm. using *Agrobacterium tumefaciens*. *In Vitro Cellular & Developmental Biology-Plant*. 2009;45(4):429-34.
905. Dai Y, Hu G, Dupas A, Medina L, Blandels N, Clemente HS, et al. Implementing the CRISPR/Cas9 technology in *Eucalyptus* hairy roots using wood-related genes. *International journal of molecular sciences*. 2020;21(10):3408.
906. Nahata SS. Sequence Analysis and Vegetative Growth in Transgenic *Eucalyptus* with CRISPR-Cas9-induced Mutations in the *Eucalyptus* Homologs of the Floral Genes EMBRYO DEVELOPMENT ARREST 33 (EDA33) and TAPETAL DEVELOPMENT AND FUNCTION1 (TDF1). 2020.
907. Klocko AL, Ma C, Robertson S, Esfandiari E, Nilsson O, Strauss SH. FT overexpression induces precocious flowering and normal reproductive development in *Eucalyptus*. *Plant Biotechnology Journal*. 2016;14(2):808-19.
908. Harcourt R, Kyojuka J, Floyd R, Bateman K, Tanaka H, Decroocq V, et al. Insect-and herbicide-resistant transgenic eucalypts. *Molecular Breeding*. 2000;6(3):307-15.
909. Flaishman M, Peer R, Raz A, Cohen O, Izhaki K, Bocobza S, et al., editors. Advanced molecular tools for breeding in Mediterranean fruit trees: genome editing approach of *Ficus carica* L. XXX International Horticultural Congress IHC2018: International Symposium on Nuts and Mediterranean Climate Fruits, Carob and X 1280; 2018.
910. Wu Y, Wang T, Xin Y, Wang G, Xu L-A. Overexpression of GbF3' 5' H1 provides a potential to improve the content of epicatechin and galocatechin. *Molecules*. 2020;25(20):4836.
911. Huang Y, Diner AM, Karnosky DF. *Agrobacterium rhizogenes*-mediated genetic transformation and regeneration of a conifer: *Larix decidua*. *In Vitro Cellular & Developmental Biology-Plant*. 1991;27(4):201-7.
912. Li Z, Fang F, Liu G, Bao M. Stable *Agrobacterium*-mediated genetic transformation of London plane tree (*Platanus acerifolia* Willd.). *Plant cell reports*. 2007;26(5):641-50.

913. Álvarez R, Ordás RJ. Improved genetic transformation protocol for cork oak (*Quercus suber* L.). *Plant cell, tissue and organ culture*. 2007;91(1):45-52.
914. Vidal N, Mallón R, Valladares S, Meijomín AM, Vieitez A. Regeneration of transgenic plants by *Agrobacterium*-mediated transformation of somatic embryos of juvenile and mature *Quercus robur*. *Plant cell reports*. 2010;29(12):1411-22.
915. Van Zeijl A, Wardhani TA, Seifi Kalhor M, Rutten L, Bu F, Hartog M, et al. CRISPR/Cas9-mediated mutagenesis of four putative symbiosis genes of the tropical tree *Parasponia andersonii* reveals novel phenotypes. *Frontiers in plant science*. 2018;9:284.
916. Castellanos-Hernández OA, Rodríguez-Sahagún A, Acevedo-Hernández GJ, Rodríguez-Garay B, Cabrera-Ponce JL, Herrera-Estrella LR. Transgenic *Paulownia elongata* SY Hu plants using biolistic-mediated transformation. *Plant Cell, Tissue and Organ Culture (PCTOC)*. 2009;99(2):175-81.
917. Busov VB, Meilan R, Pearce DW, Ma C, Rood SB, Strauss SH. Activation tagging of a dominant gibberellin catabolism gene (GA 2-oxidase) from poplar that regulates tree stature. *Plant physiology*. 2003;132(3):1283-91.
918. Zhong R, McCarthy RL, Lee C, Ye Z-H. Dissection of the transcriptional program regulating secondary wall biosynthesis during wood formation in poplar. *Plant Physiology*. 2011;157(3):1452-68.
919. Ye Q, Liu X, Bian W, Zhang Z, Zhang H. Over-expression of transcription factor ARK1 gene leads to down-regulation of lignin synthesis related genes in hybrid poplar ‘717’. *Scientific Reports*. 2020;10(1):1-11.
920. Song C, Lu L, Guo Y, Xu H, Li R. Efficient *Agrobacterium*-mediated transformation of the commercial hybrid poplar *Populus Alba* × *Populus glandulosa* Uyeki. *International Journal of Molecular Sciences*. 2019;20(10):2594.
921. Ranocha P, Chabannes M, Chamayou S, Danoun S, Jauneau A, Boudet A-M, et al. Laccase down-regulation causes alterations in phenolic metabolism and cell wall structure in poplar. *Plant Physiology*. 2002;129(1):145-55.
922. Mijnsbrugge KV, Van Montagu M, Inzé D, Boerjan W. Tissue-specific expression conferred by the S-adenosyl-L-methionine synthetase promoter of *Arabidopsis thaliana* in transgenic poplar. *Plant and cell physiology*. 1996;37(8):1108-15.
923. Maheshwari P, Kovalchuk I. *Agrobacterium*-mediated stable genetic transformation of *Populus angustifolia* and *Populus balsamifera*. *Frontiers in plant science*. 2016;7:296.
924. Ma C, Strauss S, Meilan R. *Agrobacterium*-mediated transformation of the genome-sequenced poplar clone, Nisqually-1 (*Populus trichocarpa*). *Plant Molecular Biology Reporter*. 2004;22(3):311a.
925. Huang Y, Gou J, Jia Z, Yang L, Sun Y, Xiao X, et al. Molecular cloning and characterization of two genes encoding dihydroflavonol-4-reductase from *Populus trichocarpa*. *Plos One*. 2012;7(2):e30364.
926. Hancock JE, Loya WM, Giardina CP, Li L, Chiang VL, Pregitzer KS. Plant growth, biomass partitioning and soil carbon formation in response to altered lignin biosynthesis in *Populus tremuloides*. *New Phytologist*. 2007;173(4):732-42.
927. Li L, Zhou Y, Cheng X, Sun J, Marita JM, Ralph J, et al. Combinatorial modification of multiple lignin traits in trees through multigene cotransformation. *Proceedings of the National Academy of Sciences*. 2003;100(8):4939-44.
928. Leple J-C, Dauwe R, Morreel K, Storme V, Lapierre C, Pollet B, et al. Downregulation of cinnamoyl-coenzyme A reductase in poplar: multiple-level phenotyping reveals effects on cell wall polymer metabolism and structure. *The Plant Cell*. 2007;19(11):3669-91.

929. Meyermans H, Morreel K, Lapierre C, Pollet B, De Bruyn A, Busson R, et al. Modifications in lignin and accumulation of phenolic glucosides in poplar xylem upon down-regulation of caffeoyl-coenzyme A O-methyltransferase, an enzyme involved in lignin biosynthesis. *Journal of Biological Chemistry*. 2000;275(47):36899-909.
930. Lu J, Zhao H, Wei J, He Y, Shi C, Wang H, et al. Lignin reduction in transgenic poplars by expressing antisense CCoAOMT gene. *Progress in Natural Science*. 2004;14(12):1060-3.
931. Franke R, McMichael CM, Meyer K, Shirley AM, Cusumano JC, Chapple C. Modified lignin in tobacco and poplar plants over-expressing the Arabidopsis gene encoding ferulate 5-hydroxylase. *The Plant Journal*. 2000;22(3):223-34.
932. Coleman HD, Yan J, Mansfield SD. Sucrose synthase affects carbon partitioning to increase cellulose production and altered cell wall ultrastructure. *Proceedings of the National Academy of Sciences*. 2009;106(31):13118-23.
933. Rauschendorfer J, Yordanov Y, Dobrev P, Vankova R, Sykes R, Kulheim C, et al. Overexpression of a developing xylem cDNA library in transgenic poplar generates high mutation rate specific to wood formation. *Plant Biotechnology Journal*. 2020;18(6):1434-43.
934. Lapierre C, Pollet B, Petit-Conil M, Toval G, Romero J, Pilate G, et al. Structural alterations of lignins in transgenic poplars with depressed cinnamyl alcohol dehydrogenase or caffeic acid O-methyltransferase activity have an opposite impact on the efficiency of industrial kraft pulping. *Plant physiology*. 1999;119(1):153-64.
935. Baucher M, Chabbert B, Pilate G, Van Doorselaere J, Tollier M-T, Petit-Conil M, et al. Red xylem and higher lignin extractability by down-regulating a cinnamyl alcohol dehydrogenase in poplar. *Plant physiology*. 1996;112(4):1479-90.
936. Van Doorselaere J, Baucher M, Chognot E, Chabbert B, Tollier MT, Petit-Conil M, et al. A novel lignin in poplar trees with a reduced caffeic acid/5-hydroxyferulic acid O-methyltransferase activity. *The Plant Journal*. 1995;8(6):855-64.
937. Zhong R, Morrison III WH, Himmelsbach DS, Poole FL, Ye Z-H. Essential role of caffeoyl coenzyme AO-methyltransferase in lignin biosynthesis in woody poplar plants. *Plant Physiology*. 2000;124(2):563-78.
938. Wei J, Wang Y, Wang H, Li R, Lin N, Ma R, et al. Pulp performance of transgenic poplar with depressed caffeoyl-CoA O-methyltransferase. *Chinese Science Bulletin*. 2008;53(22):3553-8.
939. Tian X, Xie J, Zhao Y, Lu H, Liu S, Qu L, et al. Sense-, antisense-and RNAi-4CL1 regulate soluble phenolic acids, cell wall components and growth in transgenic *Populus tomentosa* Carr. *Plant Physiology and Biochemistry*. 2013;65:111-9.
940. Hu W-J, Harding SA, Lung J, Popko JL, Ralph J, Stokke DD, et al. Repression of lignin biosynthesis promotes cellulose accumulation and growth in transgenic trees. *Nature biotechnology*. 1999;17(8):808-12.
941. Shen Y, Li Y, Xu D, Yang C, Li C, Luo K. Molecular cloning and characterization of a brassinosteroid biosynthesis-related gene PtoDWF4 from *Populus tomentosa*. *Tree Physiol*. 2018;38(9):1424-36.
942. Muhr M, Paulat M, Awwanah M, Brinkkötter M, Teichmann T. CRISPR/Cas9-mediated knockout of *Populus* BRANCHED1 and BRANCHED2 orthologs reveals a major function in bud outgrowth control. *Tree Physiol*. 2018;38(10):1588-97.
943. Zhou Y, Zhang Y, Wang X, Han X, An Y, Lin S, et al. Root-specific NF-Y family transcription factor, PdNF-YB21, positively regulates root growth and drought resistance by abscisic acid-mediated indoylacetic acid transport in *Populus*. *New phytologist*. 2020;227(2):407-26.

944. Takata N, Awano T, Nakata MT, Sano Y, Sakamoto S, Mitsuda N, et al. Populus NST/SND orthologs are key regulators of secondary cell wall formation in wood fibers, phloem fibers and xylem ray parenchyma cells. *Tree Physiol.* 2019;39(4):514-25.
945. Liu H, Gao J, Sun J, Li S, Zhang B, Wang Z, et al. Dimerization of PtrMYB074 and PtrWRKY19 mediates transcriptional activation of PtrbHLH186 for secondary xylem development in *Populus trichocarpa*. *The New Phytologist.* 2022;234(3):918.
946. Kiryushkin AS, Ilina EL, Guseva ED, Pawlowski K, Demchenko KN. Hairy CRISPR: genome editing in plants using hairy root transformation. *Plants.* 2021;11(1):51.
947. Azeez A, Busov V. CRISPR/Cas9-mediated single and biallelic knockout of poplar STERILE APETALA (PopSAP) leads to complete reproductive sterility. *Plant Biotechnology Journal.* 2021;19(1):23-5.
948. Zhou X, Jacobs TB, Xue LJ, Harding SA, Tsai CJ. Exploiting SNPs for biallelic CRISPR mutations in the outcrossing woody perennial *Populus* reveals 4-coumarate: CoA ligase specificity and redundancy. *New Phytologist.* 2015;208(2):298-301.
949. Tsai C-J, Xu P, Xue L-J, Hu H, Nyamdari B, Naran R, et al. Compensatory guaiacyl lignin biosynthesis at the expense of syringyl lignin in 4CL1-knockout poplar. *Plant physiology.* 2020;183(1):123-36.
950. Yang L, Zhao X, Ran L, Li C, Fan D, Luo K. PtoMYB156 is involved in negative regulation of phenylpropanoid metabolism and secondary cell wall biosynthesis during wood formation in poplar. *Scientific reports.* 2017;7(1):1-14.
951. Xu C, Fu X, Liu R, Guo L, Ran L, Li C, et al. PtoMYB170 positively regulates lignin deposition during wood formation in poplar and confers drought tolerance in transgenic *Arabidopsis*. *Tree Physiol.* 2017;37(12):1713-26.
952. Fellenberg C, Corea O, Yan LH, Archinuk F, Piirtola EM, Gordon H, et al. Discovery of salicyl benzoate UDP-glycosyltransferase, a central enzyme in poplar salicinoid phenolic glycoside biosynthesis. *The Plant Journal.* 2020;102(1):99-115.
953. de Vries L, Brouckaert M, Chanoca A, Kim H, Regner MR, Timokhin VI, et al. CRISPR-Cas9 editing of CAFFEYOYL SHIKIMATE ESTERASE 1 and 2 shows their importance and partial redundancy in lignification in *Populus tremula* × *P. alba*. *Plant biotechnology journal.* 2021;19(11):2221-34.
954. Liu B, Liu J, Yu J, Wang Z, Sun Y, Li S, et al. Transcriptional reprogramming of xylem cell wall biosynthesis in tension wood. *Plant physiology.* 2021;186(1):250-69.
955. Fan C, Yu H, Qin S, Li Y, Alam A, Xu C, et al. Brassinosteroid overproduction improves lignocellulose quantity and quality to maximize bioethanol yield under green-like biomass process in transgenic poplar. *Biotechnology for biofuels.* 2020;13(1):1-17.
956. Zhou X, Ren S, Lu M, Zhao S, Chen Z, Zhao R, et al. Preliminary study of cell wall structure and its mechanical properties of C3H and HCT RNAi transgenic poplar sapling. *Scientific Reports.* 2018;8(1):1-10.
957. Li Q, Min D, Wang JP-Y, Peszlen I, Horvath L, Horvath B, et al. Down-regulation of glycosyltransferase 8D genes in *Populus trichocarpa* caused reduced mechanical strength and xylan content in wood. *Tree Physiol.* 2011;31(2):226-36.
958. Kalluri UC, Payyavula RS, Labbé JL, Engle N, Bali G, Jawdy SS, et al. Down-regulation of KORRIGAN-like endo- β -1, 4-glucanase genes impacts carbon partitioning, mycorrhizal colonization and biomass production in *Populus*. *Frontiers in plant science.* 2016;7:1455.

959. Lee C, Teng Q, Huang W, Zhong R, Ye Z-H. Down-regulation of PoGT47C expression in poplar results in a reduced glucuronoxylan content and an increased wood digestibility by cellulase. *Plant and cell physiology*. 2009;50(6):1075-89.
960. Jouanin L, Goujon T, de Nadaï V, Martin M-T, Mila I, Vallet C, et al. Lignification in transgenic poplars with extremely reduced caffeic acid O-methyltransferase activity. *Plant Physiology*. 2000;123(4):1363-74.
961. Coleman HD, Park J-Y, Nair R, Chapple C, Mansfield SD. RNAi-mediated suppression of p-coumaroyl-CoA 3'-hydroxylase in hybrid poplar impacts lignin deposition and soluble secondary metabolism. *Proceedings of the National Academy of Sciences*. 2008;105(11):4501-6.
962. Wang J, Wu H, Chen Y, Yin T. Efficient CRISPR/Cas9-mediated gene editing in an interspecific hybrid poplar with a highly heterozygous genome. *Frontiers in plant science*. 2020;11:996.
963. Fan D, Liu T, Li C, Jiao B, Li S, Hou Y, et al. Efficient CRISPR/Cas9-mediated targeted mutagenesis in *Populus* in the first generation. *Scientific reports*. 2015;5(1):1-7.
964. An Y, Geng Y, Yao J, Fu C, Lu M, Wang C, et al. Efficient genome editing in *Populus* using CRISPR/Cas12a. *Frontiers in plant science*. 2020;11.
965. Xue L, Wu H, Chen Y, Li X, Hou J, Lu J, et al. Evidences for a role of two Y-specific genes in sex determination in *Populus deltoides*. *Nature communications*. 2020;11(1):1-12.
966. Kersten B, Leite Montalvão AP, Hoenicka H, Vettori C, Paffetti D, Fladung M. Sequencing of two transgenic early-flowering poplar lines confirmed vector-free single-locus T-DNA integration. *Transgenic research*. 2020;29(3):321-37.
967. Elorriaga E, Klocko AL, Ma C, Strauss SH. Variation in mutation spectra among CRISPR/Cas9 mutagenized poplars. *Frontiers in plant science*. 2018;9:594.
968. Fillatti JJ, Sellmer J, McCown B, Haissig B, Comai L. *Agrobacterium* mediated transformation and regeneration of *Populus*. *Molecular and General Genetics MGG*. 1987;206(2):192-9.
969. Wang P, Wei H, Sun W, Li L, Zhou P, Li D, et al. Effects of Bt-Cry1Ah1 transgenic poplar on target and non-target pests and their parasitic natural enemy in field and laboratory trials. *Forests*. 2020;11(12):1255.
970. Liang H, Maynard CA, Allen RD, Powell WA. Increased *Septoria musiva* resistance in transgenic hybrid poplar leaves expressing a wheat oxalate oxidase gene. *Plant molecular biology*. 2001;45(6):619-29.
971. Gill RI, Ellis BE, Isman MB. Tryptamine-induced resistance in tryptophan decarboxylase transgenic poplar and tobacco plants against their specific herbivores. *Journal of chemical ecology*. 2003;29(4):779-93.
972. Zhou X, Dong Y, Zhang Q, Xiao D, Yang M, Wang J. Expression of multiple exogenous insect resistance and salt tolerance genes in *Populus nigra* L. *Frontiers in Plant Science*. 2020;11:1123.
973. Yuan L, Wang L, Han Z, Jiang Y, Zhao L, Liu H, et al. Molecular cloning and characterization of PtrLAR3, a gene encoding leucoanthocyanidin reductase from *Populus trichocarpa*, and its constitutive expression enhances fungal resistance in transgenic plants. *Journal of experimental botany*. 2012;63(7):2513-24.

974. Movahedi A, Zhang J, Amirian R, Zhuge Q. An efficient *Agrobacterium*-mediated transformation system for poplar. *International Journal of Molecular Sciences*. 2014;15(6):10780-93.
975. Jiang Y, Duan Y, Yin J, Ye S, Zhu J, Zhang F, et al. Genome-wide identification and characterization of the *Populus* WRKY transcription factor family and analysis of their expression in response to biotic and abiotic stresses. *Journal of Experimental Botany*. 2014;65(22):6629-44.
976. Klocko AL, Meilan R, James RR, Viswanath V, Ma C, Payne P, et al. Bt-Cry3Aa transgene expression reduces insect damage and improves growth in field-grown hybrid poplar. *Canadian journal of forest research*. 2014;44(1):28-35.
977. Jiang Y, Guo L, Ma X, Zhao X, Jiao B, Li C, et al. The WRKY transcription factors PtrWRKY18 and PtrWRKY35 promote *Melampsora* resistance in *Populus*. *Tree Physiol*. 2017;37(5):665-75.
978. Wan S, Li C, Ma X, Luo K. PtrMYB57 contributes to the negative regulation of anthocyanin and proanthocyanidin biosynthesis in poplar. *Plant cell reports*. 2017;36(8):1263-76.
979. Wang L, Ran L, Hou Y, Tian Q, Li C, Liu R, et al. The transcription factor MYB115 contributes to the regulation of proanthocyanidin biosynthesis and enhances fungal resistance in poplar. *New Phytologist*. 2017;215(1):351-67.
980. Li Y, Su X, Zhang B, Huang Q, Zhang X, Huang R. Expression of jasmonic ethylene responsive factor gene in transgenic poplar tree leads to increased salt tolerance. *Tree Physiol*. 2009;29(2):273-9.
981. Xu M, Chen C, Cai H, Wu L. Overexpression of PeHKT1; 1 improves salt tolerance in populus. *Genes*. 2018;9(10):475.
982. Wang Y-M, Zhang Y-M, Zhang X, Zhao X, Zhang Y, Wang C, et al. Poplar PsnICE1 enhances cold tolerance by binding to different cis-acting elements to improve reactive oxygen species-scavenging capability. *Tree Physiol*. 2021.
983. Doty SL, James CA, Moore AL, Vajzovic A, Singleton GL, Ma C, et al. Enhanced phytoremediation of volatile environmental pollutants with transgenic trees. *Proceedings of the National Academy of Sciences*. 2007;104(43):16816-21.
984. Yu J, Yang L, Liu X, Tang R, Wang Y, Ge H, et al. Overexpression of poplar pyrabactin resistance-like abscisic acid receptors promotes abscisic acid sensitivity and drought resistance in transgenic *Arabidopsis*. *Plos One*. 2016;11(12):e0168040.
985. Tong S, Wang Y, Chen N, Wang D, Liu B, Wang W, et al. PtoNF-YC9-SRMT-PtoRD26 module regulates the high saline tolerance of a triploid poplar. *Genome biology*. 2022;23(1):1-28.
986. Benedict C, Skinner JS, Meng R, Chang Y, Bhalerao R, Huner NP, et al. The CBF1-dependent low temperature signalling pathway, regulon and increase in freeze tolerance are conserved in *Populus* spp. *Plant, Cell & Environment*. 2006;29(7):1259-72.
987. Liu Y, Yao X, Zhang L, Lu L, Liu R. Overexpression of DBF-interactor protein 6 containing an R3H domain enhances drought tolerance in *Populus L.*(*Populus tomentosa*). *Frontiers in plant science*. 2021;12:601585.
988. Hu L, Lu H, Liu Q, Chen X, Jiang X. Overexpression of mtl D gene in transgenic *Populus tomentosa* improves salt tolerance through accumulation of mannitol. *Tree Physiol*. 2005;25(10):1273-81.
989. Park SJ, Choi Y-I, Jang HA, Kim S-G, Choi H, Kang B-C, et al. Genome editing of hybrid poplar (*Populus alba*× *P. glandulosa*) protoplasts using Cas9/gRNA ribonucleoprotein. *Journal of Plant Biotechnology*. 2021;48(1):34-43.

990. Jiang Y, Tong S, Chen N, Liu B, Bai Q, Chen Y, et al. The PalWRKY77 transcription factor negatively regulates salt tolerance and abscisic acid signaling in *Populus*. *The Plant Journal*. 2021;105(5):1258-73.
991. Su X, Chu Y, Li H, Hou Y, Zhang B, Huang Q, et al. Expression of multiple resistance genes enhances tolerance to environmental stressors in transgenic poplar (*Populus* × *euramericana* ‘Guariento’). *Plos One*. 2011;6(9):e24614.
992. Poovaiah C, Phillips L, Geddes B, Reeves C, Sorieul M, Thorlby G. Genome editing with CRISPR/Cas9 in *Pinus radiata* (D. Don). *BMC plant biology*. 2021;21(1):1-9.
993. Sederoff R, Campbell M, O’Malley D, Whetten R. Genetic regulation of lignin biosynthesis and the potential modification of wood by genetic engineering in loblolly pine. *Genetic engineering of plant secondary metabolism*: Springer; 1994. p. 313-55.
994. Wagner A, Donaldson L, Kim H, Phillips L, Flint H, Steward D, et al. Suppression of 4-coumarate-CoA ligase in the coniferous gymnosperm *Pinus radiata*. *Plant physiology*. 2009;149(1):370-83.
995. Loopstra CA, Stomp A-M, Sederoff RR. *Agrobacterium*-mediated DNA transfer in sugar pine. *Plant molecular biology*. 1990;15(1):1-9.
996. Grace LJ, Charity JA, Gresham B, Kay N, Walter C. Insect-resistant transgenic *Pinus radiata*. *Plant Cell Reports*. 2005;24(2):103-11.
997. Tang W, Tian Y. Transgenic loblolly pine (*Pinus taeda* L.) plants expressing a modified δ -endotoxin gene of *Bacillus thuringiensis* with enhanced resistance to *Dendrolimus punctatus* Walker and *Crypyothelea formosicola* Staud. *Journal of Experimental Botany*. 2003;54(383):835-44.
998. Tang W, Newton R, Li C, Charles T. Enhanced stress tolerance in transgenic pine expressing the pepper CaPF1 gene is associated with the polyamine biosynthesis. *Plant Cell Reports*. 2007;26(1):115-24.
999. Tang W, Charles TM, Newton RJ. Overexpression of the pepper transcription factor CaPF1 in transgenic Virginia pine (*Pinus virginiana* Mill.) confers multiple stress tolerance and enhances organ growth. *Plant molecular biology*. 2005;59(4):603-17.
1000. Li M, Zhang H, Hu J, Han Y, Tian Y. Study on insect-resistant transgenic poplar plants containing both Bt and PI genes. *Scientia Silvae Sinicae*. 2000;36(2):93-7.
1001. Dai X, Yang X, Wang C, Fan Y, Xin S, Hua Y, et al. CRISPR/Cas9-mediated genome editing in *Hevea brasiliensis*. *Industrial Crops and Products*. 2021;164:113418.
1002. Wadenbäck J, von Arnold S, Egertsdotter U, Walter MH, Grima-Pettenati J, Goffner D, et al. Lignin biosynthesis in transgenic Norway spruce plants harboring an antisense construct for cinnamoyl CoA reductase (CCR). *Transgenic research*. 2008;17(3):379-92.
1003. Maloney VJ, Samuels AL, Mansfield SD. The endo-1, 4- β -glucanase Korrigan exhibits functional conservation between gymnosperms and angiosperms and is required for proper cell wall formation in gymnosperms. *New Phytologist*. 2012;193(4):1076-87.
1004. Lachance D, Hamel L-P, Pelletier F, Valéro J, Bernier-Cardou M, Chapman K, et al. Expression of a *Bacillus thuringiensis* cry1Ab gene in transgenic white spruce and its efficacy against the spruce budworm (*Choristoneura fumiferana*). *Tree Genetics & Genomes*. 2007;3(2):153-67.

1005. Hu Y-X, Tao Y-B, Xu Z-F. Overexpression of *Jatropha* Gibberellin 2-oxidase 6 (JcGA2ox6) induces dwarfism and smaller leaves, flowers and fruits in *Arabidopsis* and *Jatropha*. *Frontiers in plant science*. 2017;8:2103.
1006. Tang M, Bai X, Niu L-J, Chai X, Chen M-S, Xu Z-F. miR172 regulates both vegetative and reproductive development in the perennial woody plant *Jatropha curcas*. *Plant and Cell Physiology*. 2018;59(12):2549-63.
1007. Cai L, Zhang L, Fu Q, Xu Z-F. Identification and expression analysis of cytokinin metabolic genes IPTs, CYP735A and CKXs in the biofuel plant *Jatropha curcas*. *PeerJ*. 2018;6:e4812.
1008. Maravi DK, Kumar S, Sharma PK, Kobayashi Y, Goud VV, Sakurai N, et al. Ectopic expression of AtDGAT1, encoding diacylglycerol O-acyltransferase exclusively committed to TAG biosynthesis, enhances oil accumulation in seeds and leaves of *Jatropha*. *Biotechnology for Biofuels*. 2016;9(1):1-13.
1009. Ye J, Wang C, Sun Y, Qu J, Mao H, Chua N-H. Overexpression of a transcription factor increases lipid content in a woody perennial *Jatropha curcas*. *Frontiers in plant science*. 2018;9:1479.
1010. Khan K, Kumar V, Niranjana A, Shanware A, Sane VA. JcMYB1, a *Jatropha* R2R3MYB transcription factor gene, modulates lipid biosynthesis in transgenic plants. *Plant and Cell Physiology*. 2019;60(2):462-75.
1011. Gu K, Tian D, Mao H, Wu L, Yin Z. Development of marker-free transgenic *Jatropha curcas* producing curcumin-deficient seeds through endosperm-specific RNAi-mediated gene silencing. *BMC Plant Biology*. 2015;15(1):1-10.
1012. Kim MJ, Yang SW, Mao H-Z, Veena SP, Yin J-L, Chua N-H. Gene silencing of Sugar-dependent 1 (JcSDP1), encoding a patatin-domain triacylglycerol lipase, enhances seed oil accumulation in *Jatropha curcas*. *Biotechnology for biofuels*. 2014;7(1):1-16.
1013. Patade VY, Khatri D, Kumar K, Grover A, Kumari M, Gupta SM, et al. RNAi mediated curcumin precursor gene silencing in *Jatropha* (*Jatropha curcas* L.). *Molecular biology reports*. 2014;41(7):4305-12.
1014. Tang M, Tao Y-B, Xu Z-F. Ectopic expression of *Jatropha curcas* APETALA1 (JcAP1) caused early flowering in *Arabidopsis*, but not in *Jatropha*. *PeerJ*. 2016;4:e1969.
1015. Hui W-K, Liu M-Q, Wu G-J, Wang J-Y, Zhong Y, Li H-Y, et al. Ectopic expression of an AGAMOUS homologue gene in *Jatropha curcas* causes early flowering and heterostylous phenotypes. *Gene*. 2021;766:145141.
1016. Ye J, Qu J, Mao H-Z, Ma Z-G, Rahman NE, Bai C, et al. Engineering geminivirus resistance in *Jatropha curcas*. *Biotechnology for biofuels*. 2014;7(1):1-11.
1017. Tsuchimoto S, Cartagena J, Khemkladngoen N, Singkaravanit S, Kohinata T, Wada N, et al. Development of transgenic plants in *jatropha* with drought tolerance. *Plant Biotechnology*. 2012;12.0406 d.
1018. Jha B, Mishra A, Jha A, Joshi M. Developing transgenic *Jatropha* using the SbNHX1 gene from an extreme halophyte for cultivation in saline wasteland. *Plos One*. 2013;8(8):e71136.
1019. Mazumdar P, Basu A, Paul A, Mahanta C, Sahoo L. Age and orientation of the cotyledonary leaf explants determine the efficiency of de novo plant regeneration and *Agrobacterium tumefaciens*-mediated transformation in *Jatropha curcas* L. *South African Journal of Botany*. 2010;76(2):337-44.

1020. You CX, Zhao Q, Wang XF, Xie XB, Feng XM, Zhao LL, et al. A ds RNA-binding protein Md DRB 1 associated with mi RNA biogenesis modifies adventitious rooting and tree architecture in apple. *Plant Biotechnology Journal*. 2014;12(2):183-92.
1021. Osakabe Y, Liang Z, Ren C, Nishitani C, Osakabe K, Wada M, et al. CRISPR–Cas9-mediated genome editing in apple and grapevine. *Nature Protocols*. 2018;13(12):2844-63.
1022. Waltz E. Nonbrowning GM apple cleared for market. *Nature biotechnology*. 2015;33(4):326-8.
1023. Nishitani C, Hirai N, Komori S, Wada M, Okada K, Osakabe K, et al. Efficient genome editing in apple using a CRISPR/Cas9 system. *Scientific reports*. 2016;6(1):1-8.
1024. Charrier A, Vergne E, Dousset N, Richer A, Petiteau A, Chevreau E. Efficient targeted mutagenesis in apple and first time edition of pear using the CRISPR-Cas9 system. *Frontiers in plant science*. 2019;10:40.
1025. Yao J-L, Tomez S, Gleave AP. Transformation of apple (*Malus domestica*) using mutants of apple acetolactate synthase as a selectable marker and analysis of the T-DNA integration sites. *Plant cell reports*. 2013;32(5):703-14.
1026. Pessina S, Angeli D, Martens S, Visser RG, Bai Y, Salamini F, et al. The knock-down of the expression of MdMLO19 reduces susceptibility to powdery mildew (*Podosphaera leucotricha*) in apple (*Malus domestica*). *Plant biotechnology journal*. 2016;14(10):2033-44.
1027. Kost TD, Gessler C, Jänsch M, Flachowsky H, Patocchi A, Broggini GA. Development of the first cisgenic apple with increased resistance to fire blight. *Plos One*. 2015;10(12):e0143980.
1028. Hutabarat OS, Flachowsky H, Regos I, Miosic S, Kaufmann C, Faramarzi S, et al. Transgenic apple plants overexpressing the chalcone 3-hydroxylase gene of *Cosmos sulphureus* show increased levels of 3-hydroxyphloridzin and reduced susceptibility to apple scab and fire blight. *Planta*. 2016;243(5):1213-24.
1029. Malnoy M, Viola R, Jung M-H, Koo O-J, Kim S, Kim J-S, et al. DNA-free genetically edited grapevine and apple protoplast using CRISPR/Cas9 ribonucleoproteins. *Frontiers in plant science*. 2016;7:1904.
1030. Malabarba J, Chevreau E, Dousset N, Veillet F, Moizan J, Vergne E. New strategies to overcome present CRISPR/Cas9 limitations in apple and pear: efficient dechimerization and base editing. *International journal of molecular sciences*. 2020;22(1):319.
1031. Zhao Q, Ren YR, Wang QJ, Yao YX, You CX, Hao YJ. Overexpression of Mdb HLH 104 gene enhances the tolerance to iron deficiency in apple. *Plant biotechnology journal*. 2016;14(7):1633-45.
1032. Artlip TS, Wisniewski ME, Arora R, Norelli JL. An apple rootstock overexpressing a peach CBF gene alters growth and flowering in the scion but does not impact cold hardiness or dormancy. *Horticulture research*. 2016;3.
1033. Wisniewski M, Norelli J, Artlip T. Overexpression of a peach CBF gene in apple: a model for understanding the integration of growth, dormancy, and cold hardiness in woody plants. *Frontiers in Plant Science*. 2015;6:85.
1034. Liao X, Guo X, Wang Q, Wang Y, Zhao D, Yao L, et al. Overexpression of Ms DREB 6.2 results in cytokinin-deficient developmental phenotypes and enhances drought tolerance in transgenic apple plants. *The Plant Journal*. 2017;89(3):510-26.

1035. Wang QJ, Sun H, Dong QL, Sun TY, Jin ZX, Hao YJ, et al. The enhancement of tolerance to salt and cold stresses by modifying the redox state and salicylic acid content via the cytosolic malate dehydrogenase gene in transgenic apple plants. *Plant biotechnology journal*. 2016;14(10):1986-97.
1036. Song G-q, Chen Q. Overexpression of the MADS-box gene K-domain increases the yield potential of blueberry. *Plant Science*. 2018;276:22-31.
1037. Bond J, Roose M. Agrobacterium-mediated transformation of the commercially important citrus cultivar Washington navel orange. *Plant Cell Reports*. 1998;18(3):229-34.
1038. Costa M, Otoni W, Moore G. An evaluation of factors affecting the efficiency of Agrobacterium-mediated transformation of *Citrus paradisi* (Macf.) and production of transgenic plants containing carotenoid biosynthetic genes. *Plant Cell Reports*. 2002;21(4):365-73.
1039. Dutt M, Stanton D, Grosser JW. OrnaCitrus: Development of genetically modified anthocyanin-expressing citrus with both ornamental and fresh fruit potential. *Journal of the American Society for Horticultural Science*. 2016;141(1):54-61.
1040. Li D, Shi W, Deng X. Agrobacterium-mediated transformation of embryogenic calluses of Ponkan mandarin and the regeneration of plants containing the chimeric ribonuclease gene. *Plant Cell Reports*. 2002;21(2):153-6.
1041. Wong WS, Li GG, Ning W, Xu ZF, Hsiao WW, Zhang LY, et al. Repression of chilling-induced ACC accumulation in transgenic citrus by over-production of antisense 1-aminocyclopropane-1-carboxylate synthase RNA. *Plant Science*. 2001;161(5):969-77.
1042. Orbović V, Čalović M, Dutt M, Grosser JW, Barthe G. Production and characterization of transgenic Citrus plants carrying p35 anti-apoptotic gene. *Scientia Horticulturae*. 2015;197:203-11.
1043. Zhu C, Zheng X, Huang Y, Ye J, Chen P, Zhang C, et al. Genome sequencing and CRISPR/Cas9 gene editing of an early flowering Mini-Citrus (*Fortunella hindsii*). *Plant biotechnology journal*. 2019;17(11):2199-210.
1044. Jia H, Xu J, Orbović V, Zhang Y, Wang N. Editing citrus genome via SaCas9/sgRNA system. *Frontiers in plant science*. 2017;8:2135.
1045. Zhang F, LeBlanc C, Irish VF, Jacob Y. Rapid and efficient CRISPR/Cas9 gene editing in Citrus using the YAO promoter. *Plant cell reports*. 2017;36(12):1883-7.
1046. Jia H, Wang N. Targeted genome editing of sweet orange using Cas9/sgRNA. *Plos One*. 2014;9(4):e93806.
1047. Peña L, Martín-Trillo M, Juárez J, Pina JA, Navarro L, Martínez-Zapater JM. Constitutive expression of Arabidopsis LEAFY or APETALA1 genes in citrus reduces their generation time. *Nature biotechnology*. 2001;19(3):263-7.
1048. Duan Y-X, Fan J, Guo W-W. Regeneration and characterization of transgenic kumquat plants containing the Arabidopsis APETALA1 gene. *Plant Cell, Tissue and Organ Culture (PCTOC)*. 2010;100(3):273-81.
1049. Dutt M, Grosser J. An embryogenic suspension cell culture system for Agrobacterium-mediated transformation of citrus. *Plant cell reports*. 2010;29(11):1251-60.

1050. Ananthakrishnan G, Orbović V, Pasquali G, Čalović M, Grosser J. Transfer of citrus tristeza virus (CTV)-derived resistance candidate sequences to four grapefruit cultivars through *Agrobacterium*-mediated genetic transformation. *In Vitro Cellular & Developmental Biology-Plant*. 2007;43(6):593-601.
1051. Barbosa-Mendes JM, Mourão Filho FdAA, Bergamin Filho A, Harakava R, Beer SV, Mendes BMJ. Genetic transformation of *Citrus sinensis* cv. Hamlin with *hrpN* gene from *Erwinia amylovora* and evaluation of the transgenic lines for resistance to citrus canker. *Scientia Horticulturae*. 2009;122(1):109-15.
1052. Cardoso SC, Barbosa-Mendes JM, Boscariol-Camargo RL, Christiano RSC, Vieira MLC, Mendes BMJ, et al. Transgenic sweet orange (*Citrus sinensis* L. Osbeck) expressing the *attacin A* gene for resistance to *Xanthomonas citri* subsp. *citri*. *Plant Molecular Biology Reporter*. 2010;28(2):185-92.
1053. Dutt M, Barthe G, Irely M, Grosser J. Transgenic citrus expressing an *Arabidopsis* NPR1 gene exhibit enhanced resistance against Huanglongbing (HLB; Citrus Greening). *Plos One*. 2015;10(9):e0137134.
1054. Febres V, Niblett C, Lee R, Moore G. Characterization of grapefruit plants (*Citrus paradisi* Macf.) transformed with citrus tristeza closterovirus genes. *Plant Cell Reports*. 2003;21(5):421-8.
1055. Fu X-Z, Chen C-W, Wang Y, Liu J-H, Moriguchi T. Ectopic expression of *MdSPDS1* in sweet orange (*Citrus sinensis* Osbeck) reduces canker susceptibility: involvement of H₂O₂ production and transcriptional alteration. *BMC Plant Biology*. 2011;11(1):1-15.
1056. Kayim M, Ceccardi T, Berretta M, Barthe G, Derrick K. Introduction of a citrus blight-associated gene into Carrizo citrange [*Citrus sinensis* (L.) Osbc. × *Poncirus trifoliata* (L.) Raf.] by *Agrobacterium*-mediated transformation. *Plant Cell Reports*. 2004;23(6):377-85.
1057. LI D-l, Xuan X, GUO W-w. Production of transgenic anliucheng sweet orange (*Citrus sinensis* Osbeck) with *Xa21* gene for potential canker resistance. *Journal of Integrative Agriculture*. 2014;13(11):2370-7.
1058. Mendes BMJ, Cardoso S, Boscariol-Camargo R, Cruz R, Mourão Filho F, Bergamin Filho A. Reduction in susceptibility to *Xanthomonas axonopodis* pv. *citri* in transgenic *Citrus sinensis* expressing the rice *Xa21* gene. *Plant Pathology*. 2010;59(1):68-75.
1059. Miyata LY, Harakava R, Stipp LCL, Mendes BMJ, Appezzato-da-Glória B, de Assis Alves Mourão Filho F. GUS expression in sweet oranges (*Citrus sinensis* L. Osbeck) driven by three different phloem-specific promoters. *Plant cell reports*. 2012;31(11):2005-13.
1060. Muniz F, De Souza A, Stipp LCL, Schinor E, Freitas W, Harakava R, et al. Genetic transformation of *Citrus sinensis* with *Citrus tristeza virus* (CTV) derived sequences and reaction of transgenic lines to CTV infection. *Biologia Plantarum*. 2012;56(1):162-6.
1061. Soler N, Plomer M, Fagoaga C, Moreno P, Navarro L, Flores R, et al. Transformation of Mexican lime with an intron-hairpin construct expressing untranslatable versions of the genes coding for the three silencing suppressors of *Citrus tristeza virus* confers complete resistance to the virus. *Plant Biotechnology Journal*. 2012;10(5):597-608.
1062. Peng A, Chen S, Lei T, Xu L, He Y, Wu L, et al. Engineering canker-resistant plants through CRISPR/Cas9-targeted editing of the susceptibility gene *CsLOB 1* promoter in citrus. *Plant biotechnology journal*. 2017;15(12):1509-19.
1063. Wang L, Chen S, Peng A, Xie Z, He Y, Zou X. CRISPR/Cas9-mediated editing of *CsWRKY22* reduces susceptibility to *Xanthomonas citri* subsp. *citri* in Wanjincheng orange (*Citrus sinensis* (L.) Osbeck). *Plant Biotechnology Reports*. 2019;13(5):501-10.

1064. Jia H, Zhang Y, Orbović V, Xu J, White FF, Jones JB, et al. Genome editing of the disease susceptibility gene Cs LOB 1 in citrus confers resistance to citrus canker. *Plant biotechnology journal*. 2017;15(7):817-23.
1065. Jia H, Orbović V, Wang N. CRISPR-LbCas12a-mediated modification of citrus. *Plant biotechnology journal*. 2019;17(10):1928-37.
1066. Jia H, Orbovic V, Jones JB, Wang N. Modification of the PthA4 effector binding elements in Type I Cs LOB 1 promoter using Cas9/sg RNA to produce transgenic Duncan grapefruit alleviating XccΔpthA4: dCs LOB 1.3 infection. *Plant biotechnology journal*. 2016;14(5):1291-301.
1067. Cervera M, Ortega C, Navarro A, Navarro L, Pena L. Generation of transgenic citrus plants with the tolerance-to-salinity gene HAL2 from yeast. *The Journal of Horticultural Science and Biotechnology*. 2000;75(1):26-30.
1068. Fu X-Z, Khan EU, Hu S-S, Fan Q-J, Liu J-H. Overexpression of the betaine aldehyde dehydrogenase gene from *Atriplex hortensis* enhances salt tolerance in the transgenic trifoliate orange (*Poncirus trifoliata* L. Raf.). *Environmental and Experimental Botany*. 2011;74:106-13.
1069. Huang X-S, Liu J-H, Chen X-J. Overexpression of PtrABF gene, a bZIP transcription factor isolated from *Poncirus trifoliata*, enhances dehydration and drought tolerance in tobacco via scavenging ROS and modulating expression of stress-responsive genes. *BMC plant biology*. 2010;10(1):1-18.
1070. Al Bachchu M, Jin SB, Park JW, Sun HJ, Yun SH, Lee HY, et al. Agrobacterium-mediated transformation using embryogenic calli in satsuma mandarin (*Citrus unshiu* Marc.) cv. Miyagawa Wase. *Horticulture, Environment, and Biotechnology*. 2011;52(2):170-5.
1071. Almeida WA, Mourao Filho FA, Pino LE, Boscariol RL, Rodriguez AP, Mendes BM. Genetic transformation and plant recovery from mature tissues of *Citrus sinensis* L. Osbeck. *Plant Science*. 2003;164(2):203-11.
1072. Cervera M, Pina JA, Juárez J, Navarro L, Pena L. Agrobacterium-mediated transformation of citrange: factors affecting transformation and regeneration. *Plant Cell Reports*. 1998;18(3):271-8.
1073. Çevik B, Lee RF, Niblett CL. Genetic transformation of *Citrus paradisi* with antisense and untranslatable RNA-dependent RNA polymerase genes of *Citrus tristeza closterovirus*. *Turkish journal of agriculture and forestry*. 2006;30(3):173-82.
1074. de Oliveira MLP, Febres VJ, Costa MGC, Moore GA, Otoni WC. High-efficiency Agrobacterium-mediated transformation of citrus via sonication and vacuum infiltration. *Plant cell reports*. 2009;28(3):387-95.
1075. Domínguez A, Guerri J, Cambra M, Navarro L, Moreno P, Pena L. Efficient production of transgenic citrus plants expressing the coat protein gene of citrus tristeza virus. *Plant cell reports*. 2000;19(4):427-33.
1076. Duan Y, Guo W, Meng H, Tao N, Li D, Deng X. High efficient transgenic plant regeneration from embryogenic calluses of *Citrus sinensis*. *Biologia Plantarum*. 2007;51(2):212-6.
1077. Dutt M, Vasconcellos M, Grosser J. Effects of antioxidants on Agrobacterium-mediated transformation and accelerated production of transgenic plants of Mexican lime (*Citrus aurantifolia* Swingle). *Plant Cell, Tissue and Organ Culture (PCTOC)*. 2011;107(1):79-89.

1078. Dutt M, Lee DH, Grosser JW. Bifunctional selection–reporter systems for genetic transformation of citrus: mannose-and kanamycin-based systems. *In Vitro Cellular & Developmental Biology-Plant*. 2010;46(6):467-76.
1079. Dutt M, Grosser J. Evaluation of parameters affecting Agrobacterium-mediated transformation of citrus. *Plant Cell, Tissue and Organ Culture (PCTOC)*. 2009;98(3):331-40.
1080. Khan EU, Fu X-Z, Liu J-H. Agrobacterium-mediated genetic transformation and regeneration of transgenic plants using leaf segments as explants in Valencia sweet orange. *Plant Cell, Tissue and Organ Culture (PCTOC)*. 2012;109(2):383-90.
1081. Khawale R, Singh S, Garg G, Baranwal V, Ajirlo SA. Agrobacterium-mediated genetic transformation of Nagpur mandarin (*Citrus reticulata* Blanco). *Current Science*. 2006:1700-5.
1082. Molinari H, Bessalov J, Kobayashi A, Pereira L, Vieira L. Agrobacterium tumefaciens-mediated transformation of Swingle citrumelo (*Citrus paradisi* Macf. × *Poncirus trifoliata* L. Raf.) using thin epicotyl sections. *Scientia Horticulturae*. 2004;99(3-4):379-85.
1083. Tan B, Li D-L, Xu S-X, Fan G-E, Fan J, Guo W-W. Highly efficient transformation of the GFP and MAC12. 2 genes into precocious trifoliate orange (*Poncirus trifoliata* [L.] Raf), a potential model genotype for functional genomics studies in Citrus. *Tree Genetics & Genomes*. 2009;5(3):529-37.
1084. Wu H, Acanda Y, Shankar A, Peoples M, Hubbard C, Orbovic' V, et al. Genetic transformation of commercially important mature citrus scions. *Crop Sci*. 2015;55(6):2786-97.
1085. Yang L, Xu C-J, Hu G-B, Chen K-S. Establishment of an Agrobacterium-mediated transformation system for *Fortunella crassifolia*. *Biologia plantarum*. 2007;51(3):541-5.
1086. Wu H, Acanda Y, Jia H, Wang N, Zale J. Biolistic transformation of Carrizo citrange (*Citrus sinensis* Osb. × *Poncirus trifoliata* L. Raf.). *Plant cell reports*. 2016;35(9):1955-62.
1087. Yao J-L, Wu J-H, Gleave AP, Morris BA. Transformation of citrus embryogenic cells using particle bombardment and production of transgenic embryos. *Plant Science*. 1996;113(2):175-83.
1088. Ren C, Guo Y, Kong J, Lecourieux F, Dai Z, Li S, et al. Knockout of VvCCD8 gene in grapevine affects shoot branching. *BMC plant biology*. 2020;20(1):1-8.
1089. Salvagnin U, Malnoy M, Thöming G, Tasin M, Carlin S, Martens S, et al. Adjusting the scent ratio: using genetically modified *Vitis vinifera* plants to manipulate European grapevine moth behaviour. *Plant biotechnology journal*. 2018;16(1):264-71.
1090. Salvagnin U, Carlin S, Angeli S, Vrhovsek U, Anfora G, Malnoy M, et al. Homologous and heterologous expression of grapevine E-(β)-caryophyllene synthase (VvGwECar2). *Phytochemistry*. 2016;131:76-83.
1091. Ren C, Liu X, Zhang Z, Wang Y, Duan W, Li S, et al. CRISPR/Cas9-mediated efficient targeted mutagenesis in Chardonnay (*Vitis vinifera* L.). *Scientific reports*. 2016;6(1):1-9.
1092. Ren Q, Zhong Z, Wang Y, You Q, Li Q, Yuan M, et al. Bidirectional promoter-based CRISPR-Cas9 systems for plant genome editing. *Frontiers in Plant Science*. 2019;10:1173.
1093. Nakajima I, Ban Y, Azuma A, Onoue N, Moriguchi T, Yamamoto T, et al. CRISPR/Cas9-mediated targeted mutagenesis in grape. *Plos One*. 2017;12(5):e0177966.

1094. Royo C, Torres-Pérez R, Mauri N, Diestro N, Cabezas JA, Marchal C, et al. The major origin of seedless grapes is associated with a missense mutation in the MADS-box gene *VviAGL11*. *Plant physiology*. 2018;177(3):1234-53.
1095. Mauro M, Toutain S, Walter B, Pinck L, Otten L, Coutos-Thévenot P, et al. High efficiency regeneration of grapevine plants transformed with the GFLV coat protein gene. *Plant Science*. 1995;112(1):97-106.
1096. Pessina S, Lenzi L, Perazzolli M, Campa M, Dalla Costa L, Urso S, et al. Knockdown of MLO genes reduces susceptibility to powdery mildew in grapevine. *Horticulture research*. 2016;3.
1097. Wang X, Tu M, Wang D, Liu J, Li Y, Li Z, et al. CRISPR/Cas9-mediated efficient targeted mutagenesis in grape in the first generation. *Plant biotechnology journal*. 2018;16(4):844-55.
1098. Li M-Y, Jiao Y-T, Wang Y-T, Zhang N, Wang B-B, Liu R-Q, et al. CRISPR/Cas9-mediated *VvPR4b* editing decreases downy mildew resistance in grapevine (*Vitis vinifera* L.). *Horticulture research*. 2020;7.
1099. Wang Z, Wang S, Li D, Zhang Q, Li L, Zhong C, et al. Optimized paired-sgRNA/Cas9 cloning and expression cassette triggers high-efficiency multiplex genome editing in kiwifruit. *Plant biotechnology journal*. 2018;16(8):1424-33.
1100. Wu R, Wang T, McGie T, Voogd C, Allan AC, Hellens RP, et al. Overexpression of the kiwifruit *SVP3* gene affects reproductive development and suppresses anthocyanin biosynthesis in petals, but has no effect on vegetative growth, dormancy, or flowering time. *Journal of experimental botany*. 2014;65(17):4985-95.
1101. Moss SM, Wang T, Voogd C, Brian LA, Wu R, Hellens RP, et al. *Ac FT* promotes kiwifruit in vitro flowering when overexpressed and *Arabidopsis* flowering when expressed in the vasculature under its own promoter. *Plant direct*. 2018;2(7):e00068.
1102. Voogd C, Brian LA, Wang T, Allan AC, Varkonyi-Gasic E. Three *FT* and multiple *CEN* and *BFT* genes regulate maturity, flowering, and vegetative phenology in kiwifruit. *Journal of Experimental Botany*. 2017;68(7):1539-53.
1103. Varkonyi-Gasic E, Wang T, Voogd C, Jeon S, Drummond RS, Gleave AP, et al. Mutagenesis of kiwifruit *CENTRORADIALIS*-like genes transforms a climbing woody perennial with long juvenility and axillary flowering into a compact plant with rapid terminal flowering. *Plant Biotechnology Journal*. 2019;17(5):869-80.
1104. Zhang H, Liu H, Liu X. Production of transgenic kiwifruit plants harboring the *SbtCry1Ac* gene. *Genet Mol Res*. 2015;14:8483-9.
1105. Qin Y, Wang D, Fu J, Zhang Z, Qin Y, Hu G, et al. *Agrobacterium rhizogenes*-mediated hairy root transformation as an efficient system for gene function analysis in *Litchi chinensis*. *Plant Methods*. 2021;17(1):1-9.
1106. Padilla G, Pérez JA, Perea-Arango I, Moon PA, Gómez-Lim MA, Borges AA, et al. *Agrobacterium tumefaciens*-mediated transformation of 'Brewster' ('Chen Tze') litchi (*Litchi chinensis* Sonn.) with the *PISTILLATA* cDNA in antisense. *In Vitro Cellular & Developmental Biology-Plant*. 2013;49(5):510-9.
1107. Rai AC, Halon E, Zemach H, Zviran T, Sisai I, Philosoph-Hadas S, et al. Characterization of two ethephon-induced *IDA*-like genes from mango, and elucidation of their involvement in regulating organ abscission. *Genes*. 2021;12(3):439.
1108. Li L, Shuai L, Sun J, Li C, Yi P, Zhou Z, et al. The role of 1-methylcyclopropene in the regulation of ethylene biosynthesis and ethylene receptor gene expression in *Mangifera indica* L. (Mango Fruit). *Food science & nutrition*. 2020;8(2):1284-94.

1109. Checker VG, Chhibbar AK, Khurana P. Stress-inducible expression of barley Hva1 gene in transgenic mulberry displays enhanced tolerance against drought, salinity and cold stress. *Transgenic Research*. 2012;21(5):939-57.
1110. Das M, Chauhan H, Chhibbar A, Haq R, Mohd Q, Khurana P. High-efficiency transformation and selective tolerance against biotic and abiotic stress in mulberry, *Morus indica* cv. K2, by constitutive and inducible expression of tobacco osmotin. *Transgenic research*. 2011;20(2):231-46.
1111. Lal S, Gulyani V, Khurana P. Overexpression of HVA1 gene from barley generates tolerance to salinity and water stress in transgenic mulberry (*Morus indica*). *Transgenic Research*. 2008;17(4):651-63.
1112. Li R, Liu L, Dominic K, Wang T, Fan T, Hu F, et al. Mulberry (*Morus alba*) MmSK gene enhances tolerance to drought stress in transgenic mulberry. *Plant Physiology and Biochemistry*. 2018;132:603-11.
1113. Li MR, Li Y, Li HQ, Wu GJ. Ectopic expression of FaDREB2 enhances osmotic tolerance in paper mulberry. *Journal of integrative plant biology*. 2011;53(12):951-60.
1114. Li M, Li Y, Li H, Wu G. Improvement of paper mulberry tolerance to abiotic stresses by ectopic expression of tall fescue FaDREB1. *Tree Physiol*. 2012;32(1):104-13.
1115. Saeed B, Das M, Khurana P. Overexpression of β -carotene hydroxylase1 (BCH1) in Indian mulberry, *Morus indica* cv. K2, confers tolerance against UV, high temperature and high irradiance stress induced oxidative damage. *Plant Cell, Tissue and Organ Culture (PCTOC)*. 2015;120(3):1003-14.
1116. Sajeevan R, Nataraja KN, Shivashankara K, Pallavi N, Gurumurthy D, Shivanna M. Expression of Arabidopsis SHN1 in Indian mulberry (*Morus indica* L.) increases leaf surface wax content and reduces post-harvest water loss. *Frontiers in plant science*. 2017;8:418.
1117. Bhatnagar S, Kapur A, Khurana P. Evaluation of parameters for high efficiency gene transfer via *Agrobacterium tumefaciens* and production of transformants in Indian mulberry, *Morus indica* cv. K2. *Plant Biotechnology*. 2004;21(1):1-8.
1118. Chitra DV, Chinthapalli B, Padmaja G. Efficient regeneration system for genetic transformation of mulberry (*Morus indica* L. Cultivar S-36) using in vitro derived shoot meristems. *American Journal of Plant Sciences*. 2014;2014.
1119. OKA S, TEWARY PK. Induction of hairy roots from hypocotyls of mulberry (*Morus indica* L.) by Japanese wild strains of *Agrobacterium rhizogenes*. *The Journal of Sericultural Science of Japan*. 2000;69(1):13-9.
1120. Bhatnagar S, Kapur A, Khurana P. Evaluation of parameters for high efficiency gene transfer via particle bombardment in Indian mulberry. 2002.
1121. SUGINIURA Y, MIYAZAKI J, YONEBAYASHI K, KOTANI E, FURUSAWA T. Gene transfer by electroporation into protoplasts isolated from mulberry calli. *The Journal of Sericultural Science of Japan*. 1999;68(1):49-53.
1122. Lebedev V. The rooting of stem cuttings and the stability of uidA gene expression in generative and vegetative progeny of transgenic pear rootstock in the field. *Plants*. 2019;8(8):291.
1123. Pang H, Yan Q, Zhao S, He F, Xu J, Qi B, et al. Knockout of the S-acyltransferase gene, PbPAT14, confers the dwarf yellowing phenotype in first generation pear by ABA accumulation. *International journal of molecular sciences*. 2019;20(24):6347.

1124. Chang L, Wu S, Tian L. Effective genome editing and identification of a regiospecific gallic acid 4-O-glycosyltransferase in pomegranate (*Punica granatum* L.). *Horticulture research*. 2019;6(1):1-15.
1125. Terakami S, Matsuta N, Yamamoto T, Sugaya S, Gemma H, Soejima J. Agrobacterium-mediated transformation of the dwarf pomegranate (*Punica granatum* L. var. *nana*). *Plant Cell Reports*. 2007;26(8):1243-51.
1126. Petri C, Scorza R, Srinivasan C. Highly efficient transformation protocol for plum (*Prunus domestica* L.). *Transgenic Plants*: Springer; 2012. p. 191-9.
1127. Song G-Q, Sink KC. Optimizing shoot regeneration and transient expression factors for *Agrobacterium tumefaciens* transformation of sour cherry (*Prunus cerasus* L.) cultivar Montmorency. *Scientia Horticulturae*. 2005;106(1):60-9.
1128. Petri C, Wang H, Alburquerque N, Faize M, Burgos L. Agrobacterium-mediated transformation of apricot (*Prunus armeniaca* L.) leaf explants. *Plant cell reports*. 2008;27(8):1317-24.
1129. Liu X, Pijut PM. Agrobacterium-mediated transformation of mature *Prunus serotina* (black cherry) and regeneration of transgenic shoots. *Plant Cell, Tissue and Organ Culture (PCTOC)*. 2010;101(1):49-57.
1130. Rugini E, Gutierrez-Pesce P, Spampinato P, Ciarmiello A, D'Ambrosio C, editors. New perspective for biotechnologies in olive breeding: morphogenesis, in vitro selection and gene transformation. III International Symposium on Olive Growing 474; 1997.
1131. Narváez I, Pliego Prieto C, Palomo-Ríos E, Fresta L, Jiménez-Díaz RM, Trapero-Casas JL, et al. Heterologous expression of the AtNPR1 gene in olive and its effects on fungal tolerance. *Frontiers in plant science*. 2020;11:308.
1132. Narvaez I, Khayreddine T, Pliego C, Cerezo S, Jiménez-Díaz RM, Trapero-Casas JL, et al. Usage of the heterologous expression of the antimicrobial gene *afp* from *Aspergillus giganteus* for increasing fungal resistance in olive. *Frontiers in Plant Science*. 2018;9:680.
1133. Silvestri C, Celletti S, Cristofori V, Astolfi S, Ruggiero B, Rugini E. Olive (*Olea europaea* L.) plants transgenic for tobacco osmotin gene are less sensitive to in vitro-induced drought stress. *Acta Physiologiae Plantarum*. 2017;39(10):1-9.
1134. D'angeli S, Altamura M. Osmotin induces cold protection in olive trees by affecting programmed cell death and cytoskeleton organization. *Planta*. 2007;225(5):1147-63.
1135. Torreblanca R, Cerezo S, Palomo-Ríos E, Mercado JA, Pliego-Alfaro F. Development of a high throughput system for genetic transformation of olive (*Olea europaea* L.) plants. *Plant Cell, Tissue and Organ Culture (PCTOC)*. 2010;103(1):61-9.
1136. Walawage SL, Zaini PA, Mubarik MS, Martinelli F, Balan B, Caruso T, et al. Deploying genome editing tools for dissecting the biology of nut trees. *Frontiers in Sustainable Food Systems*. 2019;3:100.
1137. Fister AS, Landherr L, Maximova SN, Guiltinan MJ. Transient expression of CRISPR/Cas9 machinery targeting *TcNPR3* enhances defense response in *Theobroma cacao*. *Frontiers in plant science*. 2018;9:268.
1138. Breitler J-C, Dechamp E, Campa C, Zebral Rodrigues LA, Guyot R, Marraccini P, et al. CRISPR/Cas9-mediated efficient targeted mutagenesis has the potential to accelerate the domestication of *Coffea canephora*. *Plant Cell, Tissue and Organ Culture (PCTOC)*. 2018;134(3):383-94.
1139. Tang Y, Liu L, Wang R, Chen Y, Liu Z, Liu S. Development of a CRISPR/Cas9 constructed for genome editing of caffeine synthase in *Camellia sinensis*. *Journal of Tea Science*. 2016;36(4):414-26.

1140. Ma W, Kang X, Liu P, Zhang Y, Lin X, Li B, et al. The analysis of transcription factor CsHB1 effects on caffeine accumulation in tea callus through CRISPR/Cas9 mediated gene editing. *Process Biochemistry*. 2021;101:304-11.
1141. Hai PH, Jansson G, Harwood C, Hannrup B, Thinh H, Pinyopusarerk K. Genetic variation in wood basic density and knot index and their relationship with growth traits for *Acacia auriculiformis* in northern Vietnam. *New Zealand Journal of Forestry Science*. 2008;38(1):176-93.
1142. Wanyancha JM, Mills WR, Gwaze DP. Genetic-Variation in *Acacia-Albida* (*Faidherbia-Albida*) and Its Agroforestry Potential in Zimbabwe. *Forest Ecol Manag*. 1994;64(2-3):127-34.
1143. He L, Zeng F, He Z, Li Y, Li S, Zhan Y. Interspecific hybridizations of *Fraxinus L.*(*F. mandshurica*× *F. americana* and *F. mandshurica*× *F. velutina*) and heterosis analysis and selection of F1 progenies. *Canadian Journal of Forest Research*. 2019;49(10):1265-76.
1144. Pliura A, Lygis V, Marčiulyniene D, Suchockas V, Bakys R. Genetic variation of *Fraxinus excelsior* half-sib families in response to ash dieback disease following simulated spring frost and summer drought treatments. *iForest-Biogeosciences and Forestry*. 2015;9(1):12.
1145. Meier IC, Leuschner C. Genotypic variation and phenotypic plasticity in the drought response of fine roots of European beech. *Tree Physiol*. 2008;28(2):297-309.
1146. Mu H, Liu G, Jiang J, Li K, Zhu Z, Liu Z, et al. Variations of growth and fiber properties of half-sib family progeny of *Betula platyphylla*. *Journal of Northeast Forestry University*. 2009;37(3):1-8.
1147. Zhao XY, Xia H, Wang XW, Wang C, Liang DY, Li KL, et al. Variance and stability analyses of growth characters in half-sib *Betula platyphylla* families at three different sites in China. *Euphytica*. 2016;208(1):173-86.
1148. Baliuckienė A, Baliuckas V. Genetic variability of silver birch (*Betula pendula L.*) wood hardness in progeny testing at juvenile age. *Baltic Forestry*. 2006;12(2):134-40.
1149. Liu Y, Xu H, Li Z, Teng W, Zhang L, Zou J, et al. Growth variation and stability analysis of birch crossbreed families. *Bulletin of Botanical Research*. 2015;35(6):937-44.
1150. Liang DY, Zhang XX, Wang C, Wang XW, Li KL, Liu GF, et al. Evaluation of *Betula platyphylla* Families Based on Growth and Wood Property Traits. *Forest Sci*. 2018;64(6):663-70.
1151. Li K-l, Jiang J, Jiang Y, Xia D-a, Yang C-p, Liu G-f. Analysis of the genetic effects of seed and seedling traits of *Betula platyphylla* in a 5 x 5 complete diallel cross design. *JOURNAL-BEIJING FORESTRY UNIVERSITY-CHINESE EDITION*-. 2006;28(4):82.
1152. Zhao XY, Bian XY, Liu MR, Li ZX, Li Y, Zheng M, et al. Analysis of genetic effects on a complete diallel cross test of *Betula platyphylla*. *Euphytica*. 2014;200(2):221-9.
1153. Stener LG, Jansson G. Improvement of *Betula pendula* by clonal and progeny testing of phenotypically selected trees. *Scand J Forest Res*. 2005;20(4):292-303.

1154. Jones G, Liziniewicz M, Adamopoulos S, Lindeberg J. Genetic Parameters of Stem and Wood Traits in Full-Sib Silver Birch Families. *Forests*. 2021;12(2).
1155. Stener LG, Hedenberg O. Genetic parameters of wood, fibre, stem quality and growth traits in a clone test with *Betula pendula*. *Scand J Forest Res*. 2003;18(2):103-10.
1156. Zeltins P, Matisons R, Gailis A, Jansons J, Katrevics J, Jansons A. Genetic Parameters of Growth Traits and Stem Quality of Silver Birch in a Low-Density Clonal Plantation. *Forests*. 2018;9(2).
1157. Gailis A, Zeltins P, Purvins A, Augustovs J, Vindedzis V, Zarina I, et al. Genetic parameters of growth and quality traits in open-pollinated silver birch progeny tests. *Silva Fenn*. 2020;54(2).
1158. Chuanping Y, Guifeng L, Zhigang W, Yueliang W, Yumei Z. Study on intensive breeding technique of accelerating *Betula platyphylla* flowering and seeding early. *Scientia Silvae Sinicae*. 2004;40(6):75-8.
1159. Skroppa T, Solvin TM. Genetic variation and inheritance in a 9 x 9 diallel in silver birch (*Betula pendula*). *Scand J Forest Res*. 2019;34(3):178-88.
1160. Hodge GR, Dvorak WS, Uruena H, Rosales L. Growth, provenance effects and genetic variation of *Bombacopsis quinata* in field tests in Venezuela and Colombia. *Forest Ecol Manag*. 2002;158(1-3):273-89.
1161. Ertan E. Variability in leaf and fruit morphology and in fruit composition of chestnuts (*Castanea sativa* Mill.) in the Nazilli region of Turkey. *Genet Resour Crop Ev*. 2007;54(4):691-9.
1162. Bian LM, Shi JS, Zheng RH, Chen JH, Wu HX. Genetic parameters and genotype-environment interactions of Chinese fir (*Cunninghamia lanceolata*) in Fujian Province. *Canadian Journal of Forest Research*. 2014;44(6):582-92.
1163. Weng Y. Genetic variations of open-pollinated progenies from the second seed orchard and selection of superior families of Chinese fir. *Journal of Nanjing Forestry University*. 2008;32(1):15-8.
1164. Cherry ML, Vikram V, Briggs D, Cress DW, Howe GT. Genetic variation in direct and indirect measures of wood stiffness in coastal Douglas-fir. *Canadian Journal of Forest Research*. 2008;38(9):2476-86.
1165. Johnson GR, Gartner BL. Genetic variation in basic density and modulus of elasticity of coastal Douglas-fir. *Tree Genetics & Genomes*. 2007;3(1):25-33.
1166. Vargashernandez J, Adams WT. Genetic-Variation of Wood Density Components in Young Coastal Douglas-Fir - Implications for Tree Breeding. *Can J Forest Res*. 1991;21(12):1801-7.
1167. St. Clair J. Genetic variation in tree structure and its relation to size in Douglas-fir. I. Biomass partitioning, foliage efficiency, stem form, and wood density. *Canadian Journal of Forest Research*. 1994;24(6):1226-35.
1168. Ye T, Jayawickrama K. Early selection for improving volume growth in coastal Douglas-fir breeding programs. *Silvae Genet*. 2012;61(4-5).
1169. Urhan OS, Kolpak SE, Jayawickrama KJS, Howe GT. Early genetic selection for wood stiffness in juvenile Douglas-fir and western hemlock. *Forest Ecol Manag*. 2014;320:104-17.

1170. Vikram V, Cherry ML, Briggs D, Cress DW, Evans R, Howe GT. Stiffness of Douglas-fir lumber: effects of wood properties and genetics. *Canadian Journal of Forest Research*. 2011;41(6):1160-73.
1171. Ye TZ, Jayawickrama KJS. Efficiency of using spatial analysis in first-generation coastal Douglas-fir progeny tests in the US Pacific Northwest. *Tree Genetics & Genomes*. 2008;4(4):677-92.
1172. Jayawickrama KJS, Ye TZ, Howe GT. Heritabilities, Intertrait Genetic Correlations, G x E Interaction and Predicted Genetic Gains for Acoustic Velocity in Mid-rotation Coastal Douglas fir. *Silvae Genet*. 2011;60(1):8-18.
1173. Stonecypher RW, Piesch RF, Helland GG, Chapman JG, Reno HJ. Results from genetic tests of selected parents of Douglas-fir (*Pseudotsuga menziesii* [Mirb.] Franco) in an applied tree improvement program. *Forest Sci*. 1996;42(2):1-35.
1174. Johnson GR. Site-to-site genetic correlations and their implications on breeding zone size and optimum number of progeny test sites for coastal Douglas-fir. *Silvae Genet*. 1997;46(5):280-5.
1175. Johnson GR. Genetic variation in tolerance of Douglas-fir to Swiss needle cast as assessed by symptom expression. *Silvae Genet*. 2002;51(2-3):80-6.
1176. Anekonda TS, Lomas MC, Adams WT, Kavanagh KL, Aitken SN. Genetic variation in drought hardiness of coastal Douglas-fir seedlings from British Columbia. *Canadian Journal of Forest Research*. 2002;32(10):1701-16.
1177. Balduman LM, Aitken SN, Harmon M, Adams WT. Genetic variation in cold hardiness of Douglas-fir in relation to parent tree environment. *Can J Forest Res*. 1999;29(1):62-72.
1178. Aitken SN, Adams WT, Schermann N, Fuchigami LH. Family variation for fall cold hardiness in two Washington populations of coastal Douglas-fir (*Pseudotsuga menziesii* var *menziesii* (Mirb) Franco). *Forest Ecol Manag*. 1996;80(1-3):187-95.
1179. Anekonda TS, Adams WT, Aitken SN. Influence of second flushing on genetic assessment of cold hardiness in coastal Douglas-fir (*Pseudotsuga menziesii* var. *menziesii* (Mirb.) Franco). *Forest Ecol Manag*. 1998;111(2-3):119-26.
1180. O'Neill GA, Adams WT, Aitken SN. Quantitative genetics of spring and fall cold hardiness in seedlings from two Oregon populations of coastal Douglas-fir. *Forest Ecol Manag*. 2001;149(1-3):305-18.
1181. Clair JB. Genetic variation in fall cold hardiness in coastal Douglas-fir in western Oregon and Washington. *Can J Bot*. 2006;84(7):1110-21.
1182. O'Neill GA, Aitken SN, Adams WT. Genetic selection for cold hardiness in coastal Douglas-fir seedlings and saplings. *Can J Forest Res*. 2000;30(11):1799-807.
1183. Anekonda TS, Adams WT, Aitken SN, Neale DB, Jermstad KD, Wheeler NC. Genetics of cold hardiness in a cloned full-sib family of coastal Douglas-fir. *Can J Forest Res*. 2000;30(5):837-40.
1184. White TL. Drought tolerance of southwestern Oregon Douglas-fir. *Forest Sci*. 1987;33(2):283-93.
1185. Aitken SN, Adams WT. Spring cold hardiness under strong genetic control in Oregon populations of *Pseudotsuga menziesii* var. *menziesii*. *Can J Forest Res*. 1997;27(11):1773-80.
1186. Quilhó T, Pereira H. Within and between-tree variation of bark content and wood density of *Eucalyptus globulus* in commercial plantations. *Iawa Journal*. 2001;22(3):255-65.

1187. Raymond CA, MacDonald AC. Where to shoot your pilodyn: within tree variation in basic density in plantation *Eucalyptus globulus* and *E. nitens* in Tasmania. *New Forest*. 1998;15(3):205-21.
1188. Osorio J, Pereira J. Genotypic differences in water use efficiency and ^{13}C discrimination in *Eucalyptus globulus*. *Tree Physiol*. 1994;14(7-8-9):871-82.
1189. Lopez GA, Potts BM, Dutkowski GW, Apiolaza LA, Gelid P. Genetic variation and inter-trait correlations in *Eucalyptus globulus* base population trials in Argentina. *Forest Genetics*. 2002;9(3):217-31.
1190. McDonald A, Borralho N, Potts B. Genetic variation for growth and wood density in *Eucalyptus globulus* ssp. *globulus* in Tasmania (Australia). *Silvae Genet*. 1997;46(4):236-41.
1191. Miranda I, Pereira H. Variation of pulpwood quality with provenances and site in *Eucalyptus globulus*. *Ann Forest Sci*. 2002;59(3):283-91.
1192. Apiolaza LA, Raymond CA, Yeo BJ. Genetic variation of physical and chemical wood properties of *Eucalyptus globulus*. *Silvae Genet*. 2005;54(4-5):160-6.
1193. Poke FS. Genetic variation in wood chemistry of *Eucalyptus globulus*: University of Tasmania; 2006.
1194. Stackpole DJ, Vaillancourt RE, Alves A, Rodrigues J, Potts BM. Genetic Variation in the Chemical Components of *Eucalyptus globulus* Wood. *G3-Genes Genom Genet*. 2011;1(2):151-9.
1195. Blackburn DP, Hamilton MG, Harwood CE, Baker TG, Potts BM. Assessing genetic variation to improve stem straightness in *Eucalyptus globulus*. *Ann Forest Sci*. 2013;70(5):461-70.
1196. Dutkowski GW, Potts BM. Geographic patterns of genetic variation in *Eucalyptus globulus* ssp *globulus* and a revised racial classification. *Aust J Bot*. 1999;47(2):237-63.
1197. Hamilton MG, Tilyard PA, Williams DR, Vaillancourt RE, Wardlaw TJ, Potts BM. The genetic variation in the timing of heteroblastic transition in *Eucalyptus globulus* is stable across environments. *Aust J Bot*. 2011;59(2):170-5.
1198. Jordan GJ, Potts BM, Chalmers P, Wiltshire RJE. Quantitative genetic evidence that the timing of vegetative phase change in *Eucalyptus globulus* ssp *globulus* is an adaptive trait. *Aust J Bot*. 2000;48(5):561-7.
1199. Hamilton MG, Raymond CA, Harwood CE, Potts BM. Genetic variation in *Eucalyptus nitens* pulpwood and wood shrinkage traits. *Tree Genetics & Genomes*. 2009;5(2):307-16.
1200. Blackburn DP, Hamilton MG, Harwood CE, Innes TC, Potts BM, Williams D. Genetic variation in traits affecting sawn timber recovery in plantation-grown *Eucalyptus nitens*. *Ann Forest Sci*. 2011;68(7):1187-95.
1201. Kien. Genetic variation in wood basic density and pilodyn penetration and their relationships with growth, stem straightness, and branch size for *Eucalyptus urophylla* in Northern Vietnam. *New Zealand Journal of Forestry Science*. 2008;38(1):160-75.
1202. Luo J, Arnold R, Aken K. Genetic variation in growth and typhoon resistance in *Eucalyptus pellita* in south-western China. *Australian forestry*. 2006;69(1):38-47.
1203. Leksono B, Kurinobu S, Ide Y. Realized genetic gains observed in second generation seedling seed orchards of *Eucalyptus pellita* in Indonesia. *J Forest Res-Jpn*. 2008;13(2):110-6.

1204. Griffin AR, Cotterill PP. Genetic-Variation in Growth of Outcrossed, Selfed and Open-Pollinated Progenies of Eucalyptus Regnans and Some Implications for Breeding Strategy. *Silvae Genet.* 1988;37(3-4):124-31.
1205. Mahmood K, Marcar NE, Naqvi MH, Arnold RJ, Crawford DF, Iqbal S, et al. Genetic variation in Eucalyptus camaldulensis Dehnh. for growth and stem straightness in a provenance-family trial on saltland in Pakistan. *Forest Ecol Manag.* 2003;176(1-3):405-16.
1206. Arnold R, Johnson I, Owen J. GENETIC VARIATION IN GROWTH, STEM STRAIGHTNESS AND WOOD PROPERTIES IN EUCALYPTUS DUNNII TRIALS IN NORTHERN NEW SOUTH. 2004.
1207. López GA, Potts BM, Dutkowski GW, Rodriguez Traverso J. Quantitative genetics of Eucalyptus globulus: affinities of land race and native stand localities. *Silvae Genet.* 2001;50(5-6):244-52.
1208. Hodge GR, Volker PW, Potts BM, Owen JV. A comparison of genetic information from open-pollinated and control-pollinated progeny tests in two eucalypt species. *Theoretical and Applied Genetics.* 1996;92(1):53-63.
1209. Sanhueza R, White T, Huber D, Griffin A. Genetic parameters estimates, selection indices and predicted genetic gains from selection of Eucalyptus globulus in Chile. *International Journal of Forest Genetics.* 2002.
1210. Silva JCE, Borralho NMG, Araujo JA, Vaillancourt RE, Potts BM. Genetic parameters for growth, wood density and pulp yield in Eucalyptus globulus. *Tree Genetics & Genomes.* 2009;5(2):291-305.
1211. Araujo JA, Sousa R, Lemos L, Borralho NMG. Estimates of genetic parameters and prediction of breeding values for growth in Eucalyptus globulus combining clonal and full-sib progeny information. *Silvae Genet.* 1996;45(4):223-6.
1212. Kien ND, Quang TH, Jansson G, Harwood C, Clapham D, von Arnold S. Cellulose content as a selection trait in breeding for kraft pulp yield in Eucalyptus urophylla. *Ann Forest Sci.* 2009;66(7).
1213. Leksono B, Kurinobu S, Ide Y. Optimum age for selection based on a time trend of genetic parameters related to diameter growth in seedling seed orchards of Eucalyptus pellita in Indonesia. *J Forest Res-Jpn.* 2006;11(5):359-64.
1214. Hardner CM, Potts BM. Postdispersal selection following mixed mating in Eucalyptus regnans. *Evolution.* 1997;51(1):103-11.
1215. Bouvet JM, Ekomono CGM, Brendel O, Laclau JP, Bouillet JP, Epron D. Selecting for water use efficiency, wood chemical traits and biomass with genomic selection in a Eucalyptus breeding program. *Forest Ecol Manag.* 2020;465.
1216. Stackpole DJ, Vaillancourt RE, de Aguiar M, Potts BM. Age trends in genetic parameters for growth and wood density in Eucalyptus globulus. *Tree Genetics & Genomes.* 2010;6(2):179-93.
1217. Volker PW, Dean CA, Tibbits WN, Ravenwood IC. Genetic-Parameters and Gains Expected from Selection in Eucalyptus-Globulus in Tasmania. *Silvae Genet.* 1990;39(1):18-21.
1218. Raymond CA, Schimleck LR. Development of near infrared reflectance analysis calibrations for estimating genetic parameters for cellulose content in Eucalyptus globulus. *Canadian Journal of Forest Research.* 2002;32(1):170-6.
1219. Poke FS, Potts BM, Vaillancourt RE, Raymond CA. Genetic parameters for lignin, extractives and decay in Eucalyptus globulus. *Ann Forest Sci.* 2006;63(8):813-21.

1220. Hamilton MG, Potts BM, Greaves BL, Dutkowski GW. Genetic correlations between pulpwood and solid-wood selection and objective traits in *Eucalyptus globulus*. *Ann Forest Sci.* 2010;67(5).
1221. Callister AN, England N, Collins S. Genetic analysis of *Eucalyptus globulus* diameter, straightness, branch size, and forking in Western Australia. *Can J Forest Res.* 2011;41(6):1333-43.
1222. Harrand L, Hernandez JJV, Upton JL, Valverde GR. Genetic Parameters of Growth Traits and Wood Density in *Eucalyptus grandis* Progenies Planted in Argentina. *Silvae Genet.* 2009;58(1-2):11-9.
1223. Osorio LF, White TL, Huber DA. Age-age and trait-trait correlations for *Eucalyptus grandis* Hill ex Maiden and their implications for optimal selection age and design of clonal trials. *Theoretical and Applied Genetics.* 2003;106(4):735-43.
1224. Schimleck LR, Kube PD, Raymond CA. Genetic improvement of kraft pulp yield in *Eucalyptus nitens* using cellulose content determined by near infrared spectroscopy. *Canadian Journal of Forest Research.* 2004;34(11):2363-70.
1225. Blackburn D, Farrell R, Hamilton M, Volker P, Harwood C, Williams D, et al. Genetic improvement for pulpwood and peeled veneer in *Eucalyptus nitens*. *Canadian Journal of Forest Research.* 2012;42(9):1724-32.
1226. Blackburn D, Hamilton M, Williams D, Harwood C, Potts B. Acoustic Wave Velocity as a Selection Trait in *Eucalyptus nitens*. *Forests.* 2014;5(4):744-62.
1227. Blackburn D, Hamilton M, Harwood C, Innes T, Potts B, Williams D. Stiffness and checking of *Eucalyptus nitens* sawn boards: genetic variation and potential for genetic improvement. *Tree Genetics & Genomes.* 2010;6(5):757-65.
1228. Ignacio-Sánchez E, Vargas-Hernandez J, Lopez-Upton J, Borja-de la Rosa A. Genetic parameters for growth and wood density in juvenile *Eucalyptus urophylla* ST Blake. *Agrociencia.* 2005.
1229. Brawner JT, Bush DJ, Macdonell PF, Warburton PM, Clegg PA. Genetic parameters of red mahogany breeding populations grown in the tropics. *Australian Forestry.* 2010;73(3):177-83.
1230. Hung TD, Brawner JT, Meder R, Lee DJ, Southerton S, Thinh HH, et al. Estimates of genetic parameters for growth and wood properties in *Eucalyptus pellita* F. Muell. to support tree breeding in Vietnam. *Ann Forest Sci.* 2015;72(2):205-17.
1231. Cappa EP, Pathauer PS, Lopez GA. Provenance variation and genetic parameters of *Eucalyptus viminalis* in Argentina. *Tree Genetics & Genomes.* 2010;6(6):981-94.
1232. Davies NT, Apiolaza LA, Sharma M. Heritability of growth strain in *Eucalyptus bosistoana*: a Bayesian approach with left-censored data. *New Zealand Journal of Forestry Science.* 2017;47.
1233. Chauhan SS, Aggarwal P. Segregation of *Eucalyptus tereticornis* Sm. clones for properties relevant to solid wood products. *Ann Forest Sci.* 2011;68(3):511-21.
1234. Retief ECL, Stanger TK. Genetic parameters of pure and hybrid populations of *Eucalyptus grandis* and *E. urophylla* and implications for hybrid breeding strategy. *South Forests.* 2009;71(2):133-40.
1235. Chen SK, Weng QJ, Li FG, Li M, Zhou CP, Gan SM. Genetic parameters for growth and wood chemical properties in *Eucalyptus urophylla* x *E. tereticornis* hybrids. *Ann Forest Sci.* 2018;75(1).

1236. Stackpole DJ, Vaillancourt RE, Downes GM, Harwood CE, Potts BM. Genetic control of kraft pulp yield in *Eucalyptus globulus*. *Can J Forest Res.* 2010;40(5):917-27.
1237. Whittock SP, Apiolaza LA, Kelly CM, Potts BM. Genetic control of coppice and lignotuber development in *Eucalyptus globulus*. *Aust J Bot.* 2003;51(1):57-67.
1238. Araujo JA, Borralho NMG, Dehon G. The importance and type of non-additive genetic effects for growth in *Eucalyptus globulus*. *Tree Genetics & Genomes.* 2012;8(2):327-37.
1239. BORRALHO NG, Cotterill P, Kanowski P. Genetic control of growth of *Eucalyptus globulus* in Portugal. II: Efficiencies of early selection. *Silvae Genet.* 1992;41(2):70-7.
1240. Lopez GA, Potts BM, Vaillancourt RE, Apiolaza LA. Maternal and carryover effects on early growth of *Eucalyptus globulus*. *Canadian Journal of Forest Research.* 2003;33(11):2108-15.
1241. Hardner CM, Potts BM. Inbreeding Depression and Changes in Variation after Selfing in *Eucalyptus-Globulus Ssp Globulus*. *Silvae Genet.* 1995;44(1):46-54.
1242. Chambers P, Potts B, Borralho N. Genetic analysis of survival in *Eucalyptus globulus ssp. globulus*. *Silvae Genet.* 1996;45(2-3):107-12.
1243. Silva JCE, Potts BM, Lopez GA. Heterosis May Result in Selection Favouring the Products of Long-Distance Pollen Dispersal in *Eucalyptus*. *Plos One.* 2014;9(4).
1244. Li Y, Dutkowski GW, Apiolaza LA, Pilbeam D, Costa e Silva J, Potts BM. The genetic architecture of a *Eucalyptus globulus* full-sib breeding population in Australia. *Forest Genetics.* 2007;12(3):167-79.
1245. Silva JC, Borralho NM, Potts BM. Additive and non-additive genetic parameters from clonally replicated and seedling progenies of *Eucalyptus globulus*. *Theoretical and Applied Genetics.* 2004;108(6):1113-9.
1246. Jordan GJ, Potts BM, Wiltshire RJE. Strong, independent, quantitative genetic control of the timing of vegetative phase change and first flowering in *Eucalyptus globulus ssp globulus* (Tasmanian Blue Gum). *Heredity.* 1999;83:179-87.
1247. Wei X, Borralho NMG. Genetic control of wood basic density and bark thickness and their relationships with growth traits of *Eucalyptus urophylla* in south east China. *Silvae Genet.* 1997;46(4):245-50.
1248. Griffin AR, Potts BM, Vaillancourt RE, Bell JC. Life cycle expression of inbreeding depression in *Eucalyptus regnans* and inter-generational stability of its mixed mating system. *Ann Bot-London.* 2019;124(1):179-87.
1249. Volker PW, Potts BM, Borralho NMG. Genetic parameters of intra- and inter-specific hybrids of *Eucalyptus globulus* and *E-nitens*. *Tree Genetics & Genomes.* 2008;4(3):445-60.
1250. Weng Q, He X, Li F, Li M, Yu X, Shi J, et al. Hybridizing ability and heterosis between *Eucalyptus urophylla* and *E-tereticornis* for growth and wood density over two environments. *Silvae Genet.* 2014;63(1-2):15-24.
1251. Madhibha T, Murepa R, Musokonyi C, Gapare W. Genetic parameter estimates for interspecific *Eucalyptus* hybrids and implications for hybrid breeding strategy. *New Forest.* 2013;44(1):63-84.

1252. Raymond CA, Schimleck LR, Muneri A, Michel A. Genetic parameters and genotype-by-environment interactions for pulp-yield predicted using near infrared reflectance analysis and pulp productivity in *Eucalyptus globulus*. *International Journal of Forest Genetics*. 2001.
1253. Muneri A, Raymond CA. Genetic parameters and genotype-by-environment interactions for basic density, pilodyn penetration and diameter in *Eucalyptus globulus*. *International Journal of Forest Genetics*. 2000.
1254. Osorio LF, White TL, Huber DA. Age trends of heritabilities and genotype-by-environment interactions for growth traits and wood density from clonal trials of *Eucalyptus grandis* HILL ex MAIDEN. *Silvae Genet*. 2001;50(3-4):108-17.
1255. Malan F, Verry S. Effect of genotype-by-environment interaction on the wood properties and qualities of four-year-old *Eucalyptus grandis* and *E. grandis* hybrids. *South African forestry journal*. 1996;176(1):47-53.
1256. Silva JCE, Potts BM, Dutkowski GW. Genotype by environment interaction for growth of *Eucalyptus globulus* in Australia. *Tree Genetics & Genomes*. 2006;2(2):61-75.
1257. Chambers PGS, Potts BM, Tilyard PA. The genetic control of flowering precocity in *Eucalyptus globulus* ssp. *globulus*. *Silvae Genet*. 1997;46(4):207-14.
1258. Doran J, Matheson A. Genetic parameters and expected gains from selection for monoterpene yields in *Petford Eucalyptus camaldulensis*. *New Forest*. 1994;8(2):155-67.
1259. Rapley LP, Allen GR, Potts BM. Genetic variation in *Eucalyptus globulus* in relation to susceptibility from attack by the southern eucalypt leaf beetle, *Chrysophtharta agricola*. *Aust J Bot*. 2004;52(6):747-56.
1260. Milgate AW, Potts BM, Joyce K, Mohammed C, Vaillancourt RE. Genetic variation in *Eucalyptus globulus* for susceptibility to *Mycosphaerella nubilosa* and its association with tree growth. *Australas Plant Path*. 2005;34(1):11-8.
1261. O'Reilly-Wapstra JM, McArthur C, Potts BM. Genetic variation in resistance of *Eucalyptus globulus* to marsupial browsers. *Oecologia*. 2002;130(2):289-96.
1262. Borzak CL, Potts BM, Davies NW, O'Reilly-Wapstra JM. Population divergence in the ontogenetic trajectories of foliar terpenes of a *Eucalyptus* species. *Ann Bot-London*. 2015;115(1):159-70.
1263. O'Reilly-Wapstra JM, Humphreys JR, Potts BM. Stability of genetic-based defensive chemistry across life stages in a *Eucalyptus* species. *Journal of Chemical Ecology*. 2007;33(10):1876-84.
1264. Raymond CA. Genetic-Variation in *Eucalyptus-Regnans* and *Eucalyptus-Nitens* for Levels of Observed Defoliation Caused by the *Eucalyptus* Leaf-Beetle, *Chrysophtharta-Bimaculata* Olivier, in Tasmania. *Forest Ecol Manag*. 1995;72(1):21-9.
1265. Carnegie AJ, Johnson IG, Henson M. Variation among provenances and families of blackbutt (*Eucalyptus pilularis*) in early growth and susceptibility to damage from leaf spot fungi. *Canadian Journal of Forest Research*. 2004;34(11):2314-26.
1266. Soria F, Borralho NMG. The genetics of resistance to *Phoracantha semipunctata* attack in *Eucalyptus globulus* in Spain. *Silvae Genet*. 1997;46(6):365-9.
1267. O'Reilly-Wapstra JM, Potts BM, McArthur C, Davies NW, Tilyard P. Inheritance of resistance to mammalian herbivores and of plant defensive chemistry in an *Eucalyptus* species. *Journal of Chemical Ecology*. 2005;31(2):357-75.

1268. Andrew RL, Wallis IR, Harwood CE, Henson M, Foley WJ. Heritable variation in the foliar secondary metabolite sideroxylonal in *Eucalyptus* confers cross-resistance to herbivores. *Oecologia*. 2007;153(4):891-901.
1269. Dungey H, Potts B, Carnegie A, Ades P. *Mycosphaerella* leaf disease: genetic variation in damage to *Eucalyptus nitens*, *Eucalyptus globulus*, and their F1 hybrid. *Canadian Journal of Forest Research*. 1997;27(5):750-9.
1270. Gan S, Li M, Li F, Wu K, Wu J, Bai J. Genetic analysis of growth and susceptibility to bacterial wilt (*Ralstonia solanacearum*) in *eucalyptus* by interspecific factorial crossing. *Silvae Genet*. 2004;53(5-6):254-8.
1271. Tibbits WN, Potts BM, Savva MH. Inheritance of Freezing Resistance in Interspecific F1 Hybrids of *Eucalyptus*. *Theoretical and Applied Genetics*. 1991;83(1):126-35.
1272. Andrew RL, Wallis IR, Harwood CE, Foley WJ. Genetic and environmental contributions to variation and population divergence in a broad-spectrum foliar defence of *Eucalyptus tricarpa*. *Ann Bot-London*. 2010;105(5):707-17.
1273. Dutkowski G. Genetic variation in drought susceptibility of *Eucalyptus globulus* ssp. *globulus* in plantations in Western Australia. *Eucalypt plantations: improving fibre yield and quality CRC for Temperate Hardwood Forestry*, Hobart. 1995.
1274. Dutkowski GW, Potts BM. Genetic variation in the susceptibility of *Eucalyptus globulus* to drought damage. *Tree Genetics & Genomes*. 2012;8(4):757-73.
1275. Tibbits WN, White TL, Hodge GR, Borralho NMG. Genetic variation in frost resistance of *Eucalyptus globulus* ssp *globulus* assessed by artificial freezing in winter. *Aust J Bot*. 2006;54(6):521-9.
1276. Raymond CA, Owen JV, Ravenwood IC. Genetic-Variation for Frost Tolerance in a Breeding Population of *Eucalyptus-Nitens*. *Silvae Genet*. 1992;41(6):355-62.
1277. Doran J, Kar AK, Larmour J, Reid N. Variation in frost tolerance of the 1, 8-cineole-rich variants of the peppermint eucalypts, *Eucalyptus radiata* and *E. dives*. *Australian Forestry*. 2005;68(2):137-43.
1278. Tibbits W, Hodge G. Genetic parameters for cold hardiness in *Eucalyptus nitens* (Deane & Maiden) Maiden. *Silvae Genet*. 2003;52(3-4):89-96.
1279. He XD, Li FG, Li M, Weng QJ, Shi JS, Mo XY, et al. Quantitative genetics of cold hardiness and growth in *Eucalyptus* as estimated from *E. urophylla* x *E. tereticornis* hybrids. *New Forest*. 2012;43(3):383-94.
1280. Shea KL, Fournier GR. Genetic variation and population structure in central and isolated populations of balsam fir, *Abies balsamea* (Pinaceae). *American journal of botany*. 2002;89(5):783-91.
1281. Doede DL, Adams WT. The genetics of stem volume, stem form, and branch characteristics in sapling noble fir. *Silvae Genet*. 1998;47(4):177-83.
1282. Xia H, Zhao GH, Zhang LS, Sun XY, Yin SP, Liang DY, et al. Genetic and variation analyses of growth traits of half-sib *Larix olgensis* families in northeastern China. *Euphytica*. 2016;212(3):387-97.
1283. Fujimoto T, Akutsu H, Nei M, Kita K, Kuromaru M, Oda K. Genetic variation in wood stiffness and strength properties of hybrid larch (*Larix gmelinii* var. *japonica* x *L kaempferi*). *J Forest Res-Jpn*. 2006;11(5):343-9.

1284. Fujimoto T, Kita K, Uchiyama K, Kuromaru M, Akutsu H, Oda K. Age trends in the genetic parameters of wood density and the relationship with growth rates in hybrid larch (*Larix gmelinii* var. *japonica* × *L. kaempferi*) F 1. *J Forest Res-Jpn*. 2006;11(3):157.
1285. Dong LM, Xie YH, Sun XM. Full-diallel-based analysis of genetic parameters for growth traits in Japanese larch (*Larix kaempferi*). *New Forest*. 2020;51(2):261-71.
1286. Li B, Wyckoff GW. Breeding strategies for *Larix decidua*, *L. leptolepis* and their hybrids in the United States. *Forest genetics*. 1994;1(2):65-72.
1287. Larochelle F, Forget É, Rainville A, Bousquet J. Sources of temporal variation in sap sugar content in a mature sugar maple (*Acer saccharum*) plantation. *Forest Ecol Manag*. 1998;106(2-3):307-13.
1288. Kriebel HB. Genetic improvement of sugar maple for high sap sugar content. II. Relative effectiveness of maternal and biparental selection. *Canadian Journal of Forest Research*. 1990;20(6):837-44.
1289. Kriebel HB. Genetic improvement of sugar maple for high sap sugar content. I. Clone selection and seed orchard development. *Canadian Journal of Forest Research*. 1989;19(7):917-23.
1290. Staats LJ. Progeny testing 10-year old sugar maple families (*Acer saccharum* Marsh.) for sap sugar concentration: State University of New York College of Environmental Science and Forestry; 1992.
1291. Singh AS. Evaluation, Selection and In vitro Propagation of Sugar Maple (*Acer saccharum* Marsh.) 2017.
1292. Goel VL, Behl HM. Genetic selection and improvement of hard wood tree species for fuelwood production on sodic soil with particular reference to *Prosopis juliflora*. *Biomass Bioenerg*. 2001;20(1):9-15.
1293. Sampaio T, Goncalves E, Faria C, Almeida MH. Genetic variation among and within *Quercus suber* L. populations in survival, growth, vigor and plant architecture traits. *Forest Ecol Manag*. 2021;483.
1294. Bogdan S, Ivanković M, Temunović M, Morić M, Franjić J, Bogdan IK. Adaptive genetic variability and differentiation of Croatian and Austrian *Quercus robur* L. populations at a drought prone field trial. *Ann for Res*. 2017;60(1):33-46.
1295. Dupouey J-L, Badeau V, editors. Morphological variability of oaks (*Quercus robur* L, *Quercus petraea* (Matt) Liebl, *Quercus pubescens* Willd) in northeastern France: preliminary results. *Ann Sci Forest*; 1993: EDP Sciences.
1296. Gonzalez-Rodriguez A, Oyama K. Leaf morphometric variation in *Quercus affinis* and *Q. laurina* (Fagaceae), two hybridizing Mexican red oaks. *Botanical Journal of the Linnean society*. 2005;147(4):427-35.
1297. Kremer A, Dupouey JL, Deans JD, Cottrell J, Csaikl U, Finkeldey R, et al. Leaf morphological differentiation between *Quercus robur* and *Quercus petraea* is stable across western European mixed oak stands. *Ann Forest Sci*. 2002;59(7):777-87.
1298. Streiff R, Ducousso A, Lexer C, Steinkellner H, Gloessl J, Kremer A. Pollen dispersal inferred from paternity analysis in a mixed oak stand of *Quercus robur* L. and *Q. petraea*(Matt.) Liebl. *Molecular Ecology*. 1999;8(5):831-41.
1299. Myszewski JH, Bridgwater FE, Lowe WJ, Byram TD, Megraw RA. Genetic variation in the microfibril angle of loblolly pine from two test sites. *Southern Journal of Applied Forestry*. 2004;28(4):196-204.
1300. Gräns D, Isik F, Purnell RC, Peszlen IM, McKeand SE. Genetic Variation and the Effect of Herbicide and Fertilization Treatments on Wood Quality Traits in Loblolly Pine. *Forest Sci*. 2021.

1301. Grans D, Isik F, Purnell RC, McKeand SE. Genetic Variation in Response to Herbicide and Fertilization Treatments for Growth and Form Traits in Loblolly Pine. *Forest Sci.* 2016;62(6):633-40.
1302. Isik F, Mora CR, Schimleck LR. Genetic variation in *Pinus taeda* wood properties predicted using non-destructive techniques. *Ann Forest Sci.* 2011;68(2):283-93.
1303. Walker TD, Isik F, McKeand SE. Genetic Variation in Acoustic Time of Flight and Drill Resistance of Juvenile Wood in a Large Loblolly Pine Breeding Population. *Forest Sci.* 2019;65(4):469-82.
1304. Xiong JS, Isik F, McKeand SE, Whetten RW. Genetic Variation of Stem Forking in Loblolly Pine. *Forest Sci.* 2010;56(5):429-36.
1305. MARZIS D. Variation in growth and quality characters in *Pinus pinaster* provenances grown at seven sites in Greece. *Silvae Genet.* 1982;31:5-6.
1306. Zamudio F, Rozenberg P, Baettig R, Vergara A, Yanez M, Gantz C. Genetic variation of wood density components in a *radiata* pine progeny test located in the south of Chile. *Ann Forest Sci.* 2005;62(2):105-14.
1307. Gulcu S, Celik S. Genetic variation in *Pinus brutia* Ten. seed stands and seed orchards for growth, stem form and crown characteristics. *African Journal of Biotechnology.* 2009;8(18):4387-94.
1308. Lai M, Dong LM, Leng CH, Zhang L, Yi M. Genotypic variation in the basic density, dynamic modulus of elasticity and tracheid traits of *Pinus elliottii* in three progeny trials in southern China. *Holzforschung.* 2020;74(1):1-9.
1309. Byram T, Myszewski J, Gwaze D, Lowe W. Improving wood quality in the western gulf forest tree improvement program: the problem of multiple breeding objectives. *Tree Genetics & Genomes.* 2005;1(3):85-92.
1310. Eckard JT, Isik F, Bullock B, Li BL, Gumpertz M. Selection Efficiency for Solid Wood Traits in *Pinus taeda* using Time-of-Flight Acoustic and Micro-Drill Resistance Methods. *Forest Sci.* 2010;56(3):233-41.
1311. Dean CA, Cotterill PP, Burdon RD. Early selection of *radiata* pine - I. Trends over time in additive and dominance genetic variances and covariances of growth traits. *Silvae Genet.* 2006;55(4-5):182-91.
1312. Li L, Wu HX. Efficiency of early selection for rotation-aged growth and wood density traits in *Pinus radiata*. *Canadian Journal of Forest Research.* 2005;35(8):2019-29.
1313. Wu HX, Powell MB, Yang JL, Ivkovic M, Mcrae TA. Efficiency of early selection for rotation-aged wood quality traits in *radiata* pine. *Ann Forest Sci.* 2007;64(1):1-9.
1314. Missanjo E, Matsumura J. Multiple trait selection index for simultaneous improvement of wood properties and growth traits in *Pinus kesiya* Royle ex Gordon in Malawi. *Forests.* 2017;8(4):96.
1315. Silva JCE, Graudal L. Evaluation of an international series of *Pinus kesiya* provenance trials for growth and wood quality traits. *Forest Ecol Manag.* 2008;255(8-9):3477-88.
1316. McKeand SE, Li B, Grissom J, Isik F, Jayawickrama K. Genetic parameter estimates for growth traits from diallel tests of loblolly pine throughout the southeastern United States. *Silvae Genet.* 2008;57(3):101.

1317. Balocchi C, Bridgwater F, Zobel B, Jahromi S. Age trends in genetic parameters for tree height in a nonselected population of loblolly pine. *Forest Sci.* 1993;39(2):231-51.
1318. Atwood RA, White TL, Huber DA. Genetic parameters and gains for growth and wood properties in Florida source loblolly pine in the southeastern United States. *Can J Forest Res.* 2002;32(6):1025-38.
1319. Gwaze DP, Bridgwater FE, Byram TD, Woolliams JA, Williams CG. Predicting age-age genetic correlations in tree-breeding programs: a case study of *Pinus taeda* L. *Theoretical and Applied Genetics.* 2000;100(2):199-206.
1320. Loo JA, Tauer CG, Vanbuijtenen JP. Juvenile Mature Relationships and Heritability Estimates of Several Traits in Loblolly-Pine (*Pinus-Taeda*). *Can J Forest Res.* 1984;14(6):822-5.
1321. Roberds JH, Strom BL, Hain FP, Gwaze DP, McKeand SE, Lott LH. Estimates of genetic parameters for oleoresin and growth traits in juvenile loblolly pine. *Canadian Journal of Forest Research.* 2003;33(12):2469-76.
1322. Riemenschneider DE. Heritability, age-age correlations, and inferences regarding juvenile selection in jack pine. *Forest Sci.* 1988;34(4):1076-82.
1323. Kusnadar D, Galwey NW, Hertzler GL, Butcher TB. Age trends in variances and heritabilities for diameter and height in maritime pine (*Pinus pinaster* Ait.) in Western Australia. *Silvae Genet.* 1998;47(2-3):136-41.
1324. Fries A. Genetic parameters, genetic gain and correlated responses in growth, fibre dimensions and wood density in a Scots pine breeding population. *Ann Forest Sci.* 2012;69(7):783-94.
1325. Hong Z, Fries A, Wu HX. High negative genetic correlations between growth traits and wood properties suggest incorporating multiple traits selection including economic weights for the future Scots pine breeding programs. *Ann Forest Sci.* 2014;71(4):463-72.
1326. Haapanen M, Velling P, Annala M-L. Progeny trial estimates of genetic parameters for growth and quality traits in Scots pine. 1997.
1327. Weng YH, Lu P, Adams GW, Fullarton MS, Tosh KJ. Genetic parameters of growth and stem quality traits for jack pine second-generation progeny tested in New Brunswick. *Canadian Journal of Forest Research.* 2015;45(1):36-43.
1328. Ericsson T, Fries A. High heritability for heartwood in north Swedish Scots pine. *Theoretical and applied genetics.* 1999;98(5):732-5.
1329. Fries A, Ericsson T, Gref R. High heritability of wood extractives in *Pinus sylvestris* progeny tests. *Canadian journal of forest research.* 2000;30(11):1707-13.
1330. Hannrup B, Wilhelmsson L, Danell O. Time trends for genetic parameters of wood density and growth traits in *Pinus sylvestris* L. *Silvae Genet.* 1998;47(4):214-9.
1331. Fundova I, Hallingback HR, Jansson G, Wu HX. Genetic Improvement of Sawn-Board Stiffness and Strength in Scots Pine (*Pinus sylvestris* L.). *Sensors-Basel.* 2020;20(4).
1332. Espinel S, Aragonés A. Genetic parameter estimates for *Pinus radiata* in Basque country, northern Spain. *NZ J For Sci.* 1997;27(3):272-9.

1333. Baltunis BS, Wu HX, Dungey HS, Brawner JT. Comparisons of genetic parameters and clonal value predictions from clonal trials and seedling base population trials of radiata pine. *Tree genetics & genomes*. 2009;5(1):269-78.
1334. Baltunis BS, Wu HX, Powell MB. Inheritance of density, microfibril angle, and modulus of elasticity in juvenile wood of *Pinus radiata* at two locations in Australia. *Can J Forest Res*. 2007;37(11):2164-74.
1335. Kumar S, Burdon RD. Genetic improvement of stiffness of radiata pine: synthesis of results from acoustic assessments. *New Zealand Journal of Forestry Science* (New Zealand Forest Research Institute Ltd (trading as Scion)). 2010;40.
1336. Kumar S, Lee J. Age-age correlations and early selection for end-of-rotation wood density in radiata pine. *Forest Genetics*. 2002;9(4):323-30.
1337. Kumar S, Dungey HS, Matheson AC. Genetic parameters and strategies for genetic improvement of stiffness in radiata pine. *Silvae Genet*. 2006;55(2):77-84.
1338. Kumar S. Genetic parameter estimates for wood stiffness, strength, internal checking, and resin bleeding for radiata pine. *Can J Forest Res*. 2004;34(12):2601-10.
1339. Kumar S, Jayawickrama K, Lee J, Lausberg M. Direct and indirect measures of stiffness and strength show high heritability in a wind-pollinated radiata pine progeny test in New Zealand. *Silvae Genet*. 2002;51(5-6):256-60.
1340. Dungey HS, Matheson AC, Kain D, Evans R. Genetics of wood stiffness and its component traits in *Pinus radiata*. *Canadian Journal of Forest Research*. 2006;36(5):1165-78.
1341. Hodge GR, Purnell RC. Genetic Parameter Estimates for Wood Density, Transition Age, and Radial Growth in Slash Pine. *Can J Forest Res*. 1993;23(9):1881-91.
1342. Hayatgheibi H, Fries A, Kroon J, Wu HX. Estimation of genetic parameters, provenance performances, and genotype by environment interactions for growth and stiffness in lodgepole pine (*Pinus contorta*). *Scand J Forest Res*. 2019;34(1):1-11.
1343. Hayatgheibi H, Fries A, Kroon J, Wu HX. Genetic analysis of lodgepole pine (*Pinus contorta*) solid-wood quality traits. *Canadian Journal of Forest Research*. 2017;47(10):1303-13.
1344. Xie CY, Ying CC. Heritabilities, age-age correlations, and early selection in lodgepole pine (*Pinus contorta* ssp *Latifolia*). *Silvae Genet*. 1996;45(2-3):101-7.
1345. Hodge GR, Dvorak WS. Genetic parameters and provenance variation of *Pinus caribaea* var. *hondurensis* in 48 international trials. *Can J Forest Res*. 2001;31(3):496-511.
1346. Mutete P, Murepa R, Gapare WJ. Genetic parameters in subtropical pine F1 hybrids: heritabilities, between-trait correlations and genotype-by-environment interactions. *Tree Genetics & Genomes*. 2015;11(5):1-16.
1347. Pot D, Chantre G, Rozenberg P, Rodrigues JC, Jones GL, Pereira H, et al. Genetic control of pulp and timber properties in maritime pine (*Pinus pinaster* Ait.). *Ann Forest Sci*. 2002;59(5-6):563-75.
1348. Wu HX, Matheson AC. General and specific combining ability from partial diallels of radiata pine: implications for utility of SCA in breeding and deployment populations. *Theoretical and Applied Genetics*. 2004;108(8):1503-12.

1349. Li XB, Huber DA, Powell GL, White TL, Peter GF. Breeding for improved growth and juvenile corewood stiffness in slash pine. *Can J Forest Res.* 2007;37(10):1886-93.
1350. McKeand SE, Crook RP, Lee Allen H. Genotypic stability effects on predicted family responses to silvicultural treatments in loblolly pine. *Southern Journal of Applied Forestry.* 1997;21(2):84-9.
1351. McKeand SE, Jokela EJ, Huber DA, Byram TD, Allen HL, Li BL, et al. Performance of improved genotypes of loblolly pine across different soils, climates, and silvicultural inputs. *Forest Ecol Manag.* 2006;227(1-2):178-84.
1352. Sierra-Lucero V, Huber D, McKeand S, White T, Rockwood D. Genotype-by-environment interaction and deployment considerations for families from Florida provenances of loblolly pine. *International Journal of Forest Genetics.* 2003.
1353. Correia I, Alía R, Yan W, David T, Aguiar A, Almeida MH. Genotype× Environment interactions in *Pinus pinaster* at age 10 in a multi-environment trial in Portugal: a maximum likelihood approach. *Ann Forest Sci.* 2010;67(6):612-.
1354. Zas Arregui R, Merlo E, Fernández López J. Genotype x environment interaction in Maritime pine families in Galicia, Northwest Spain. 2004.
1355. al. He. Genotype by environment interaction in *Pinus sylvestris* L. in southern Sweden. *Silvae Genet.* 2008;57(1-6):306-11.
1356. Codesido V, Fernandez-Lopez J. Implication of genotype x site interaction on *Pinus radiata* breeding in Galicia. *New Forest.* 2009;37(1):17-34.
1357. Wu HX, Matheson AC. Genotype by environment interactions in an Australia-wide radiata pine diallel mating experiment: Implications for regionalized breeding. *Forest Sci.* 2005;51(1):29-40.
1358. Ivković M, Gapare W, Yang H, Dutkowski G, Buxton P, Wu H. Pattern of genotype by environment interaction for radiata pine in southern Australia. *Ann Forest Sci.* 2015;72(3):391-401.
1359. Raymond CA. Genotype by environment interactions for *Pinus radiata* in New South Wales, Australia. *Tree Genetics & Genomes.* 2011;7(4):819-33.
1360. Baltunis BS, Gapare WJ, Wu HX. Genetic Parameters and Genotype by Environment Interaction in Radiata Pine for Growth and Wood Quality Traits in Australia. *Silvae Genet.* 2010;59(2-3):113-24.
1361. Wielinga B, Raymond CA, James R, Matheson AC. Genetic Parameters and Genotype by Environment Interactions for Green and Basic Density and Stiffness of *Pinus radiata* D. Don Estimated Using Acoustics. *Silvae Genet.* 2009;58(3):112-22.
1362. Gapare WJ, Ivkovic M, Baltunis BS, Matheson CA, Wu HX. Genetic stability of wood density and diameter in *Pinus radiata* D. Don plantation estate across Australia. *Tree Genetics & Genomes.* 2010;6(1):113-25.
1363. Pagliarini MK, Kieras WS, Moreira JP, Sousa VA, Shimizu JY, Moraes MLT, et al. Adaptability, stability, productivity and genetic parameters in slash pine second-generation families in early age. *Silvae Genet.* 2016;65(1):71-82.
1364. Kanzler A, Hagedorn SF, Hodge GR, Dvorak WS. Genotype by environment interaction for volume growth at 6 years of age in a series of five *Pinus patula* progeny trials in southern Africa. *Southern African Forestry Journal.* 2003;2003(198):3-15.
1365. Zas R, Sampedro L, Moreira X, Martins P. Effect of fertilization and genetic variation on susceptibility of *Pinus radiata* seedlings to *Hylobius abietis* damage. *Canadian Journal of Forest Research.* 2008;38(1):63-72.

1366. Quencez C, Bastien C. Genetic variation within and between populations of *Pinus sylvestris* L.(Scots pine) for susceptibility to *Melampsora pinitorqua* Rostr.(pine twist rust). *Heredity*. 2001;86(1):36-44.
1367. Yanchuk AD, Murphy JC, Wallin KF. Evaluation of genetic variation of attack and resistance in lodgepole pine in the early stages of a mountain pine beetle outbreak. *Tree Genetics & Genomes*. 2008;4(2):171-80.
1368. Vergara R, White TL, Huber DA, Schmidt RA. Realized genetic gains of rust resistant selections of slash pine (*Pinus elliottii* var. *elliottii*) planted in high rust hazard sites. *Silvae Genet*. 2007;56(5):231-42.
1369. Wu HX, Ying CC. Genetic parameters and selection efficiencies in resistance to western gall rust, stalactiform blister rust, needle cast, and sequoia pitch moth in lodgepole pine. *Forest Sci*. 1997;43(4):571-81.
1370. Weng YH, Lu P, Meng QF, Krasowski M. Genetic resistance to western gall rust in jack pine and its relationship with tree height growth. *Canadian Journal of Forest Research*. 2015;45(8):970-7.
1371. Ivković M, Baltunis B, Gapare W, Sasse J, Dutkowski G, Elms S, et al. Breeding against *Dothistroma* needle blight of radiata pine in Australia. *Canadian Journal of Forest Research*. 2010;40(8):1653-60.
1372. Carson S. Selecting *Pinus radiata* for resistance to *Dothistroma* needle blight. *New Zealand Journal of Forestry Science*. 1989;19(1):3-21.
1373. Dieters M, Hodge G, White T. Genetic parameter estimates for resistance to rust (*Cronartium quercuum*) infection from full-sib tests of slash pine (*Pinus elliottii*), modelled as functions of rust incidence. *Silvae Genet*. 1996;45(4):235-41.
1374. Li YJ, Dungey HS, Carson M, Carson S. Genotype by environment interaction for growth and *Dothistroma* resistance and clonal connectivity between environments in radiata pine in New Zealand and Australia. *Plos One*. 2018;13(10).
1375. Clair SB, Mock KE, LaMalfa EM, Campbell RB, Ryel RJ. Genetic Contributions to Phenotypic Variation in Physiology, Growth, and Vigor of Western Aspen (*Populus tremuloides*) Clones. *Forest Sci*. 2010;56(2):222-30.
1376. Kanaga MK, Ryel RJ, Mock KE, Pfreder ME. Quantitative-genetic variation in morphological and physiological traits within a quaking aspen (*Populus tremuloides*) population. *Can J Forest Res*. 2008;38(6):1690-4.
1377. Pliura A, Zhang SY, MacKay J, Bousquet J. Genotypic variation in wood density and growth traits of poplar hybrids at four clonal trials. *Forest Ecol Manag*. 2007;238(1-3):92-106.
1378. Orlovic S, Guzina V, Krstic B, Merkulov L. Genetic variability in anatomical, physiological and growth characteristics of hybrid poplar (*Populus x euramericana* Dode (Guinier)) and eastern cottonwood (*Populus deltoides* Bartr.) clones. *Silvae Genet*. 1998;47(4):183-90.
1379. Zhao X, Li Y, Zhao L, Wu P, Zhang Z. Analysis and evaluation of growth and adaptive performance of white poplar hybrid clones in different sites. *Journal of Beijing Forestry University*. 2013;35(6):7-14.
1380. Ding C, Hamann A, Yang RC, Brouard JS. Genetic parameters of growth and adaptive traits in aspen (*Populus tremuloides*): Implications for tree breeding in a warming world. *Plos One*. 2020;15(3).
1381. Li BL, Wu RL. Heterosis and genotype x environment interactions of juvenile aspens in two contrasting sites. *Can J Forest Res*. 1997;27(10):1525-37.

1382. Li B, Wu R. Genetic causes of heterosis in juvenile aspen: A quantitative comparison across intra- and inter-specific hybrids. *Theoretical and Applied Genetics*. 1996;93(3):380-91.
1383. Wu R-L, Wang M-X, Huang M-R. Quantitative genetics of yield breeding for *Populus* short rotation culture. I. Dynamics of genetic control and selection model of yield traits. *Canadian Journal of Forest Research*. 1992;22(2):175-82.
1384. Hart JF, de Araujo F, Thomas BR, Mansfield SD. Wood Quality and Growth Characterization across Intra- and Inter-Specific Hybrid Aspen Clones. *Forests*. 2013;4(4):786-807.
1385. Chaturvedi OP, Pandey N. Genetic divergence in *Bombax ceiba* L. germplasms. *Silvae Genet*. 2001;50(3-4):99-102.
1386. Goncalves PDS, Silva MD, Gouvea LRL, Scaloppi EJ. Genetic variability for girth growth and rubber yield in *Hevea brasiliensis*. *Scientia Agricola*. 2006;63(3):246-54.
1387. Goncalves PDS, Cardinal ABB, da Costa RB, Bortoletto N, Gouvea LRL. Genetic variability and selection for laticiferous system characters in *Hevea brasiliensis*. *Genetics and Molecular Biology*. 2005;28(3):414-22.
1388. Goncalves PDS, Bortoletto N, Cardinal ABB, Gouvea LRL, da Costa RB, de Moraes MLT. Age-age correlation for early selection of rubber tree genotypes in Sao Paulo State, Brazil. *Genetics and Molecular Biology*. 2005;28(4):758-64.
1389. Silva GAP, Gezan SA, de Carvalho MP, Gouvea LRL, Verardi CK, de Oliveira ALB, et al. Genetic parameters in a rubber tree population: heritabilities, genotype-by-environment interactions and multi-trait correlations. *Tree Genetics & Genomes*. 2014;10(6):1511-8.
1390. Abengmeneng C, Ofori D, Kumapley P, Akromah R, Jamnadass R. Estimation of heritability and genetic gain in height growth in *Ceiba pentandra*. *African Journal of Biotechnology*. 2015;14(22):1880-5.
1391. Brawner JT, Meder R, Dieters M, Lee DJ. Selection of *Corymbia citriodora* for pulp productivity. *South Forests*. 2012;74(2):121-31.
1392. Brawner JT, Lee DJ, Hardner CM, Dieters MJ. Relationships between early growth and Quambalaria shoot blight tolerance in *Corymbia citriodora* progeny trials established in Queensland, Australia. *Tree Genetics & Genomes*. 2011;7(4):759-72.
1393. Rozenberg P, VandeSype H. Genetic variation of the pilodyn-girth relationship in Norway spruce (*Picea abies* L [Karst]). *Ann Sci Forest*. 1996;53(6):1153-66.
1394. Steffenrem A, Lindland F, Skroppa T. Genetic and environmental variation of internodal and whorl branch formation in a progeny trial of *Picea abies*. *Scand J Forest Res*. 2008;23(4):290-8.
1395. Steffenrem A, Kvaalen H, Hoibo OA, Edvardsen OM, Skroppa T. Genetic variation of wood quality traits and relationships with growth in *Picea abies*. *Scand J Forest Res*. 2009;24(1):15-27.
1396. Hyslop G. Genetic variation of wood density and its relationship with growth traits in young Norway spruce. *Silvae Genet*. 1997;46(1):55-&.
1397. Grans D, Hannrup B, Isik F, Lundqvist SO, McKeand S. Genetic variation and relationships to growth traits for microfibril angle, wood density and modulus of elasticity in a *Picea abies* clonal trial in southern Sweden. *Scand J Forest Res*. 2009;24(6):494-503.

1398. Ivkovich M, Namkoong G, Koshy M. Genetic variation in wood properties of interior spruce. I. Growth, latewood percentage, and wood density. *Can J Forest Res.* 2002;32(12):2116-27.
1399. Ivkovich M, Namkoong G, Koshy M. Genetic variation in wood properties of interior spruce. II. Tracheid characteristics. *Canadian Journal of Forest Research.* 2002;32(12):2128-39.
1400. Yanchuk AD, Kiss GK. Genetic-Variation in Growth and Wood Specific-Gravity and Its Utility in the Improvement of Interior Spruce in British-Columbia. *Silvae Genet.* 1993;42(2-3):141-8.
1401. Beaulieu J. Genetic variation in tracheid length and relationships with growth and wood traits in eastern white spruce (*Picea glauca*). *Wood Fiber Sci.* 2003;35(4):609-16.
1402. Zhang SY, Yu QB, Beaulieu J. Genetic variation in veneer quality and its correlation to growth in white spruce. *Canadian Journal of Forest Research.* 2004;34(6):1311-8.
1403. Hallingback HR, Hogberg KA, Sall H, Lindeberg J, Johansson M, Jansson G. Optimal timing of early genetic selection for sawn timber traits in *Picea abies*. *Eur J Forest Res.* 2018;137(4):553-64.
1404. Lenz P, Auty D, Achim A, Beaulieu J, Mackay J. Genetic Improvement of White Spruce Mechanical Wood Traits-Early Screening by Means of Acoustic Velocity. *Forests.* 2013;4(3):575-94.
1405. Despons M, Perron M, DeBlois J. Rapid assessment of wood traits for large-scale breeding selection in *Picea mariana* [Mill.] BSP. *Ann Forest Sci.* 2017;74(3):1-12.
1406. Chen ZQ, Gil MRG, Karlsson B, Lundqvist SO, Olsson L, Wu HX. Inheritance of growth and solid wood quality traits in a large Norway spruce population tested at two locations in southern Sweden. *Tree Genetics & Genomes.* 2014;10(5):1291-303.
1407. Hannerz M, Sonesson J, Ekberg I. Genetic correlations between growth and growth rhythm observed in a short-term test and performance in long- term field trials of Norway spruce. *Can J Forest Res.* 1999;29(6):768-78.
1408. Hogberg KA, Dutkowski GW. Genetic Correlations Among Field Trials of Norway Spruce Clones Representing Different Propagation Cycles. *Silvae Genet.* 2010;59(4):182-9.
1409. Hallingback HR, Jansson G, Hannrup B. Genetic correlations between spiral grain and growth and quality traits in *Picea abies*. *Canadian Journal of Forest Research.* 2010;40(2):173-83.
1410. Hallingback HR, Jansson G, Hannrup B. Genetic parameters for grain angle in 28-year-old Norway spruce progeny trials and their parent seed orchard. *Ann Forest Sci.* 2008;65(3).
1411. Costa E, Silva J, Borralho N, Wellendorf H. Genetic parameter estimates for diameter growth, pilodyn penetration and spiral grain in *Picea abies* (L.) Karst. *Silvae Genet.* 2000;49:29-36.
1412. Hannrup B, Grabner M, Karlsson B, Muller U, Rosner S, Wilhelmsson L, et al. Genetic parameters for spiral-grain angle in two 19-year-old clonal Norway spruce trials. *Ann Forest Sci.* 2002;59(5-6):551-6.
1413. Zhou LH, Chen ZQ, Lundqvist SO, Olsson L, Grahn T, Karlsson B, et al. Genetic analysis of wood quality traits in Norway spruce open-pollinated progenies and their parent plus trees at clonal archives and the evaluation of phenotypic selection of plus trees. *Canadian Journal of Forest Research.* 2019;49(7):810-8.

1414. Hogberg KA, Hallingback HR, Sall H, Johansson M, Jansson G. The potential for the genetic improvement of sawn timber traits in *Picea abies*. *Can J Forest Res*. 2014;44(4):273-80.
1415. Hannrup B, Cahalan C, Chantre G, Grabner M, Karlsson B, Le Bayon I, et al. Genetic parameters of growth and wood quality traits in *Picea abies*. *Scand J Forest Res*. 2004;19(1):14-29.
1416. Coriveau A, Beaulieu J, Daoust G. Heritability and Genetic Correlations of Wood Characters of Upper Ottawa Valley White Spruce Populations Grown in Quebec. *Forest Chron*. 1991;67(6):698-705.
1417. Lu PX, Charrette P. Genetic parameter estimates for growth traits of black spruce in northwestern Ontario. *Can J Forest Res*. 2008;38(12):2994-3001.
1418. Wang JJ, Weng YH, Krasowski M, Yan GH, Fullarton M. Genetic parameters of growth and stem forking for black spruce progeny tested in New Brunswick, Canada. *New Forest*. 2018;49(2):265-77.
1419. Mullin TJ, Park YS. Genetic-Parameters and Age-Age Correlations in a Clonally Replicated Test of Black Spruce after 10 Years. *Can J Forest Res*. 1994;24(12):2330-41.
1420. Kennedy SG, Cameron AD, Lee SJ. Genetic relationships between wood quality traits and diameter growth of juvenile core wood in Sitka spruce. *Canadian Journal of Forest Research*. 2013;43(1):1-6.
1421. Berlin M, Jansson G, Hogberg KA, Helmersson A. Analysis of non-additive genetic effects in Norway spruce. *Tree Genetics & Genomes*. 2019;15(3).
1422. Lenz P, Cloutier A, MacKay J, Beaulieu J. Genetic control of wood properties in *Picea glauca* - an analysis of trends with cambial age. *Canadian Journal of Forest Research*. 2010;40(4):703-15.
1423. Chen ZQ, Harry BK, Wu HX. Patterns of additive genotype-by-environment interaction in tree height of Norway spruce in southern and central Sweden. *Tree Genetics & Genomes*. 2017;13(1).
1424. Berlin M, Jansson G, Hogberg KA. Genotype by environment interaction in the southern Swedish breeding population of *Picea abies* using new climatic indices. *Scand J Forest Res*. 2015;30(2):112-21.
1425. Karlsson B, Wellendorf H, Roulund H, Werner M. Genotype \times trial interaction and stability across sites in 11 combined provenance and clone experiments with *Picea abies* in Denmark and Sweden. *Canadian journal of forest research*. 2001;31(10):1826-36.
1426. Karlsson B, Högberg K. Genotypic parameters and clone \times site interaction in clone tests of Norway spruce (*Picea abies* (L.) Karst.). *Forest Genetics*. 1998;5(1):21-30.
1427. Wellendorf H, Thomsen IM. Genetic Variation in Resistance Against *Heterobasidion annosum* (Fr.) Bref. in *Picea abies* (L.) Karst. Expressed After Inoculation of Neighboring Stumps. *Silvae Genet*. 2008;57(6):312-24.
1428. Swedjemark G, Stenlid J, Karlsson B. Genetic variation among clones of *Picea abies* in resistance to growth of *Heterobasidion annosum*. *Silvae Genet*. 1997;46(6):369-74.
1429. Swedjemark G, Karlsson B. Genotypic variation in susceptibility following artificial *Heterobasidion annosum* inoculation of *Picea abies* clones in a 17-year-old field test. *Scand J Forest Res*. 2004;19(2):103-11.

1430. Swedjemark G, Karlsson B. Variation in incidence and genetic impact on natural infection of *Heterobasidion annosum* in *Picea abies* (L.) Karst. in genetic trials in south Sweden. *Forest Ecol Manag.* 2004;203(1-3):135-45.
1431. Karlsson B, Swedjemark G. Genotypic variation in natural infection frequency of *Heterobasidion* spp. in a *Picea abies* clone trial in southern Sweden. *Scand J Forest Res.* 2006;21(2):108-14.
1432. Skroppa T, Solheim H, Steffenrem A. Genetic variation, inheritance patterns and parent-offspring relationships after artificial inoculations with *Heterobasidion parviporum* and *Ceratocystis polonica* in Norway spruce seed orchards and progeny tests. *Silva Fenn.* 2015;49(1).
1433. Skroppa T, Solheim H, Hietala A. Variation in phloem resistance of Norway spruce clones and families to *Heterobasidion parviporum* and *Ceratocystis polonica* and its relationship to phenology and growth traits. *Scand J Forest Res.* 2015;30(2):103-11.
1434. Arnerup J, Swedjemark G, Elfstrand M, Karlsson B, Stenlid J. Variation in growth of *Heterobasidion parviporum* in a full-sib family of *Picea abies*. *Scand J Forest Res.* 2010;25(2):106-10.
1435. King JN, Yanchuk AD, Kiss GK, Alfaro RI. Genetic and phenotypic relationships between weevil (*Pissodes strobi*) resistance and height growth in spruce populations of British Columbia. *Can J Forest Res.* 1997;27(5):732-9.
1436. Kiss GK, Yanchuk AD. Preliminary Evaluation of Genetic-Variation of Weevil Resistance in Interior Spruce in British-Columbia. *Can J Forest Res.* 1991;21(2):230-4.
1437. Yu QB, Yang DQ, Zhang SY, Beaulieu J, Duchesne I. Genetic variation in decay resistance and its correlation to wood density and growth in white spruce. *Can J Forest Res.* 2003;33(11):2177-83.
1438. Steffenrem A, Solheim H, Skroppa T. Genetic parameters for wood quality traits and resistance to the pathogens *Heterobasidion parviporum* and *Endoconidiophora polonica* in a Norway spruce breeding population. *Eur J Forest Res.* 2016;135(5):815-25.
1439. Swedjemark G, Borg-Karlson A, Karlsson B, editors. Breeding for resistance in Norway spruce to the root and butt rot fungi *Heterobasidion* spp. In: Snieszko, Richard A; Yanchuk, Alvin D; Kliejunas, John T; Palmieri, Katharine M; Alexander, Janice M; Frankel, Susan J, tech coords *Proceedings of the fourth international workshop on the genetics of host-parasite interactions in forestry: Disease and insect resistance in forest trees Gen Tech Rep PSW-GTR-240* Albany, CA: Pacific Southwest Research Station, Forest Service, US Department of Agriculture pp 162-166; 2012.
1440. Bodles WJA, Beckett E, Woodward S. Responses of sitka spruce of different genetic origins to inoculation with *Heterobasidion annosum*: lesion lengths, fungal growth and development of the lignosuberized boundary zone. *Forest Pathol.* 2007;37(3):174-86.
1441. Chaix G, Monteuiis O, Garcia C, Alloysius D, Gidiman J, Bacilieri R, et al. Genetic variation in major phenotypic traits among diverse genetic origins of teak (*Tectona grandis* L.f.) planted in Taliwas, Sabah, East Malaysia. *Ann Forest Sci.* 2011;68(5):1015-26.
1442. Behera M, Bhola N, Parida A, Pradhan T. Assessment of inter-population genetic diversity and preliminary evaluation of suitable clones of teak (*Tectona grandis* Linn. F.). *Journal of Applied and Natural Science.* 2016;8(1):273-8.
1443. Mulyadiana A, Trikoesoemaningtyas, Siregar IZ. Evaluation of early growth performance of 41 clones of teak (*Tectona grandis* Linn. f.) at four microsites in Purwakarta, Indonesia. *J Forestry Res.* 2020;31(3):901-7.

1444. Naranjo SS, Moya R, Chauhan S. Early genetic evaluation of morphology and some wood properties of *Tectona grandis* L. clones. *Silvae Genet.* 2012;61(1-2):58-65.
1445. Bagchi S. Selection differential and predicted genetic gain in *Tectona grandis*. *Indian Forester.* 1995;121(6):482-90.
1446. Palanisamy K, Gireesan K, Nagarajan V, Hegde M. Selection and Clonal Multiplication of Superior Trees of Teak (*Tectona Grandis*) and Preliminary Evaluation of Clones. *J Trop for Sci.* 2009;21(2):168-74.
1447. Goh DKS, Japarudin Y, Alwi A, Lapammu M, Flori A, Monteuuis O. Growth differences and genetic parameter estimates of 15 teak (*Tectona grandis* L.f.) genotypes of various ages clonally propagated by microcuttings and planted under humid tropical conditions. *Silvae Genet.* 2013;62(4-5):196-206.
1448. Vasudeva R, Hanumantha M, Gunaga RP. Genetic variation for floral traits among teak (*Tectona grandis* Linn. f.) clones: Implications to seed orchard fertility. *Current Science.* 2004;87(3):358-62.
1449. Yao JX, Li HG, Ye J, Shi LL. Relationship between parental genetic distance and offspring's heterosis for early growth traits in *Liriodendron*: implication for parent pair selection in cross breeding. *New Forest.* 2016;47(1):163-77.
1450. Xia H, Si W, Hao Z, Zhong W, Zhu S, Tu Z, et al. Dynamic changes in the genetic parameters of growth traits with age and their associations with heterosis in hybrid *Liriodendron*. *Tree Genetics & Genomes.* 2021;17(2):1-18.
1451. Divakara B. Assessing variability and divergence of *Jatropha curcas* Linn. germplasm under ex-situ conditions. *Forest Res.* 2017;6(201):2.
1452. Chakrabarty S, Islam AA, Sultana N, Chakraborty P. Genetic diversity of *Jatropha curcas* L. genotypes: a potential biofuel crop in Bangladesh. *Biofuels.* 2019:1-9.
1453. Kaushik N, Kumar K, Kumar S, Kaushik N, Roy S. Genetic variability and divergence studies in seed traits and oil content of *Jatropha* (*Jatropha curcas* L.) accessions. *Biomass Bioenerg.* 2007;31(7):497-502.
1454. Rao GR, Korwar GR, Shanker AK, Ramakrishna YS. Genetic associations, variability and diversity in seed characters, growth, reproductive phenology and yield in *Jatropha curcas* (L.) accessions. *Trees-Struct Funct.* 2008;22(5):697-709.
1455. Ngugi K, Nabiswa A, Kithinji J, Muchugi A. Genetic divergence in *Jatropha curcas* L., a potential biofuel crop in Kenya. *Biofuels.* 2013;4(3):313-22.
1456. Shabanimofrad M, Rafii MY, Wahab PEM, Biabani AR, Latif MA. Phenotypic, genotypic and genetic divergence found in 48 newly collected Malaysian accessions of *Jatropha curcas* L. *Industrial Crops and Products.* 2013;42:543-51.
1457. Cros D, Tchounke B, Nkague-Nkamba L. Training genomic selection models across several breeding cycles increases genetic gain in oil palm in silico study. *Molecular Breeding.* 2018;38(7):1-12.
1458. Cros D, Denis M, Bouvet J-M, Sánchez L. Long-term genomic selection for heterosis without dominance in multiplicative traits: case study of bunch production in oil palm. *BMC genomics.* 2015;16(1):1-17.
1459. Kaushik N, Kumar S, Kumar K, Beniwal RS, Kaushik N, Roy S. Genetic variability and association studies in pod and seed traits of *Pongamia pinnata* (L.) Pierre in Haryana, India. *Genet Resour Crop Ev.* 2007;54(8):1827-32.

1460. Mukta N, Murthy IYLN, Sripal P. Variability assessment in *Pongamia pinnata* (L.) Pierre germplasm for biodiesel traits. *Industrial Crops and Products*. 2009;29(2-3):536-40.
1461. Rao GR, Shanker AK, Srinivas I, Korwar GR, Venkateswarlu B. Diversity and variability in seed characters and growth of *Pongamia pinnata* (L.) Pierre accessions. *Trees-Struct Funct*. 2011;25(4):725-34.
1462. Verma G, Mahajan P, Sharma A. Correlation and path analysis between yield and different morphological characters in Kinnow Mandarin (C. Noballis Å—C. Deliciosa). *Journal of Applied and Natural Science*. 2018;10(2):759-64.
1463. Rajan S, Yadava L, Kumar R, Saxena S. Genetic divergence in seed characteristics of guava: A basis for parent selection in hybridization. *Indian J Hortic*. 2007;64(3):290-3.
1464. Kherwar D, Usha K. Genetic variations, character association and path analysis studies in guava (*Psidium guajava* L.) for bioactive and antioxidant attributes. *Indian Journal of Plant Physiology*. 2016;21(3):355-61.
1465. Jana B, Munsi P, Mgnna D, Das B. Evaluation of Guava (*Psidium guajava* L.) Genotypes Based on Fruit Morphology, Physico-chemical Properties. and Yield under Eastern Plateau Condition. 2010.
1466. Bose SK, Ahmed S, Howlader P, Ali M. Flowering, Fruiting Behavior and Nutritional Quality of Selected Guava Genotypes. *International Journal of Horticultural Science and Technology*. 2019;6(1):11-25.
1467. Silva CCAd, Vieira HD, Viana AP, Maitan MQ, Santos EA. Phenomics approaches: genetic diversity and variance components in a S 2 guava family by seed traits. *Bragantia*. 2021;80.
1468. Padilla-Ramirez J, Gonzalez-Gaona E, editors. Collection and characterization of Mexican guava (*Psidium guajava* L.) germplasm. II International Symposium on Guava and other Myrtaceae 849; 2008.
1469. Rajan S, Yadava L, Kumar R, Saxena S. Selection possibilities for seed content-a determinant of fresh fruit quality in guava (*Psidium guajava*L.). 2005.
1470. Rajan S, Yadava L, Kumar R, Saxena S. Direct and indirect effects of seed related characters on number of seed in guava (*Psidium guajava* L.) fruits. *Scientia horticulturae*. 2008;116(1):47-51.
1471. Pelea LP, González AS, Fernández E, Rodríguez Medina N, Valdés-Infante Herrero J, Pommer C, editors. Heritability estimates of guava (*Psidium guajava* L.) Agricultural important characters evaluated in three populations. III International Symposium on Guava and other Myrtaceae 959; 2012.
1472. Proença CEB, Tuler AC, Lucas EJ, Vasconcelos TNdC, de Faria JEQ, Staggemeier VG, et al. Diversity, phylogeny and evolution of the rapidly evolving genus *Psidium* L.(Myrtaceae, Myrteae). *Ann Bot-London*. 2022;129(4):367-88.
1473. Ambrósio M, Viana AP, Ribeiro RM, Preisigke SC, Cavalcante NR, Silva FAd, et al. Genotypic superiority of *Psidium guajava* S 1 families using mixed modeling for truncated and simultaneous selection. *Scientia Agricola*. 2020;78.
1474. Patel R, Maiti C, Deka BC, Vermav V, Deshmukh N, Verma M. Genetic variability, character association and path coefficient study in guava (*Psidium guajava* L.) for plant growth, floral and yield attributes. *International Journal of Bio-resource and Stress Management*. 2015;6(4):457-66.

1475. Gupta N, Kour A. Genetic parameters, character association and path analysis for fruit yield and its component characters in guava (*Psidium guajava* L.). *Electronic Journal of Plant Breeding*. 2019;10(1):256-63.
1476. Singh D, Gill M, Boora R, Arora N. Estimates of genetic variability, heritability, genetic advance, correlation coefficients and their prospects for crop improvement in guava (*Psidium guajava* L.). *Journal of Applied Horticulture*. 2015;17(1):76-8.
1477. Sohi HS, Gill M, Singh D, Arora N. Characterization of F1 hybrids of guava (*Psidium Guajava* L.) on the basis of phenotypic and biochemical parameters. *Chemical Science Review and Letters*. 2019;8(32):335-9.
1478. Milan A, editor Collection and evaluation of guava (*Psidium guajava* L.) for nematode resistance in Malaysia. II International Symposium on Guava and other Myrtaceae 849; 2008.
1479. Gomes VM, Ribeiro RM, Viana AP, de Souza RM, Santos EA, Rodrigues DL, et al. Inheritance of resistance to *Meloidogyne enterolobii* and individual selection in segregating populations of *Psidium* spp. *European Journal of Plant Pathology*. 2017;148(3):699-708.
1480. Ribeiro RM, Gomes VM, Viana AP, Souza RMd, Santos PRd. Selection of interspecific *Psidium* spp. hybrids resistant to *Meloidogyne enterolobii*. *Acta Scientiarum Agronomy*. 2019;41.
1481. Da Costa SR, Santos CAF, da Cunha e Castro JM. Inheritance of resistance to *Meloidogyne enterolobii* in *Psidium guajava* x *P. guineense* hybrid. *European Journal of Plant Pathology*. 2017;148(2):405-11.
1482. SS Negi SR, editor Improvement of guava through breeding2007: ISHS *Acta Horticulturae* 735: I International Guava Symposium.
1483. Chhetri A. Appraisalment of Variability and Association among the Jackfruit (*Artocarpus heterophyllus* Lam.) Genotypes Found in North-East India. *Current Journal of Applied Science and Technology*. 2019;33(4):1-13.
1484. Dhakar MK, Das B, Sarkar P, Nath V, Singh A, Bhatt B. Diversity in jackfruit (*Artocarpus heterophyllus* Lam.): insights into fruit characterization for the identification of superior genotypes. *Plant Genetic Resources*. 2020;18(5):307-15.
1485. Miah G, Rahman M, Saha SR, Islam MM, Nayak D, Dhyan S, et al. Morpho-physiological characterization of jackfruit (*Artocarpus heterophyllus* Lam.) accessions in Bangladesh. *Indian Journal of Agroforestry*. 2019;21(1):1-12.
1486. Wu J, Zhang C, Chen J, Cai C, Wang L, Fu D, et al. Morphological diversity within litchi (*Litchi chinensis* Sonn.) based on leaf and branch traits. *Scientia Horticulturae*. 2016;207:21-7.
1487. da Costa Preisigke S, de Campos AL, Souza NS, Neves LG, Barelli MAA, da Luz PB, et al. Genetic divergence in mango and obtaining minimum efficient descriptors. *American Journal of Plant Sciences*. 2013;2013.
1488. Narvariya SS, Singh A. Qualitative Traits, Genetic Variability and Character Association for the Potential Use in Breeding Programme of Mango (*Mangifera indica* L.). *Int J Curr Microbiol App Sci*. 2019;8(2):1752-64.
1489. Zhang C, Xie D, Bai T, Luo X, Zhang F, Ni Z, et al. Diversity of a large collection of natural populations of mango (*Mangifera indica* Linn.) revealed by agro-morphological and quality traits. *Diversity*. 2020;12(1):27.

1490. Akin-Idowu PE, Adebo UG, Egbekunle KO, Olagunju YO, Aderonmu OI, Aduloju AO. Diversity of mango (*Mangifera indica* L.) cultivars based on physicochemical, nutritional, antioxidant, and phytochemical traits in South West Nigeria. *International Journal of Fruit Science*. 2020;20(sup2):S352-S76.
1491. Alcasid CE, Gueco LS, Valencia LD. Diversity analysis based on morphological traits of different mango accessions collected from selected areas in the Philippines. *Asian Journal of Agriculture and Food Sciences*. 2015;3(6).
1492. Krishnapillai N, Wijeratnam RW. Morphometric analysis of mango varieties in Sri Lanka. *Australian Journal of Crop Science*. 2016;10(6):784-92.
1493. Jena RC, Agarwal K, Chand PK. Fruit and leaf diversity of selected Indian mangoes (*Mangifera indica* L.). *Scientia Horticulturae*. 2021;282:109941.
1494. Rodríguez Pleguezuelo C, Durán Zuazo V, Muriel Fernández J, Franco Tarifa D. Physico-chemical quality parameters of mango (*Mangifera indica* L.) fruits grown in a Mediterranean subtropical climate (SE Spain). *Journal of Agricultural Science and Technology*. 2012;14(2):365-74.
1495. Manveen K. An evaluation of mango (*Mangifera indica* L.) germplasm for future breeding programme. *Afr J Agr Res*. 2014;9(20):1530-8.
1496. Sennhenn A, Prinz K, Gebauer J, Whitbread A, Jamnadass R, Kehlenbeck K. Identification of mango (*Mangifera indica* L.) landraces from Eastern and Central Kenya using a morphological and molecular approach. *Genet Resour Crop Ev*. 2014;61(1):7-22.
1497. Hardner C, Bally I, Wright C. Prediction of breeding values for average fruit weight in mango using a multivariate individual mixed model. *Euphytica*. 2012;186(2):463-77.
1498. Bally IS, De Faveri J. Genetic analysis of multiple fruit quality traits in mango across sites and years. *Euphytica*. 2021;217(3):1-18.
1499. Brown JS, Schnell RJ, Ayala-Silva T, Moore JM, Tondo CL, Winterstein MC. Broad-sense heritability estimates for fruit color and morphological traits from open-pollinated half-sib mango families. *Hortscience*. 2009;44(6):1552-6.
1500. Mohamed Z, Ahmed THM. Diversity of Mango (*Mangifera indica* L.) cultivars in Shendi area: morphological leaf characterization. *International Journal of Research in Agricultural Sciences*. 2015;2(4):2348-3997.
1501. Majumder D, Hassan L, Rahim M, Kabir M. Genetic diversity in mango (*Mangifera indica* L.) through multivariate analysis. *Bangladesh Journal of Agricultural Research*. 2013;38(2):343-53.
1502. Majumder D, Hassan L, Rahim M, Kabir M. Genotypic and phenotypic variability in mango (*Mangifera indica* L.). *Bangladesh Journal of Agricultural Research*. 2012;37(4):683-90.
1503. Haseeb GM, Ghounim IE-S, Hmam I, Mustafa MR. EVALUATION OF FOUR NEWLY INTRODUCED MANGO (*MANGIFERAINDICA* L.) CULTIVARS GROWN UNDER EL-GIZA CONDITIONS. *Plant Archives*. 2020;20(2):9405-10.
1504. Igbari A, Nodza G, Adeusi A, Ogundipe O. Morphological characterization of mango (*Mangifera indica* L.) cultivars from South-West Nigeria. *Ife Journal of Science*. 2019;21(1):155-63.

1505. Tewodros BN, Fredah KRW, Wassu MA, Githiri SM, Willis OO. Phenotype characterization and diversity assessment of mango (*Mangifera indica* L.) cultivars in Ethiopia. *Journal of Plant Breeding and Crop Science*. 2019;11(2):55-67.
1506. Cantín CM, Gogorcena Y, Moreno MÁ. Phenotypic diversity and relationships of fruit quality traits in peach and nectarine [*Prunus persica* (L.) Batsch] breeding progenies. *Euphytica*. 2010;171(2):211-26.
1507. i Forcada CF, Gradziel TM, Gogorcena Y, Moreno MÁ. Phenotypic diversity among local Spanish and foreign peach and nectarine [*Prunus persica* (L.) Batsch] accessions. *Euphytica*. 2014;197(2):261-77.
1508. Fresnedo-Ramírez J, Frett TJ, Sandefur PJ, Salgado-Rojas A, Clark JR, Gasic K, et al. QTL mapping and breeding value estimation through pedigree-based analysis of fruit size and weight in four diverse peach breeding programs. *Tree Genetics & Genomes*. 2016;12(2):25.
1509. de Souza VA, Byrne DH, Taylor JF. Heritability, genetic and phenotypic correlations, and predicted selection response of quantitative traits in peach: II. An analysis of several fruit traits. *Journal of the American Society for Horticultural Science*. 1998;123(4):604-11.
1510. Rajamanickam C. Genetic variability, correlation and path analysis in tamarind (*Tamarindus indica* L.). *Journal of Spices & Aromatic Crops*. 2020;29(2).
1511. Singh T, Nandini R. Genetic variability, character associaton and path analysis in the tamarind (*Tamarindus indica* L.) population of Nallur tamarind grove. *SAARC Journal of Agriculture*. 2014;12(1):20-5.
1512. Nyadanu D, Akromah R, Adomako B, Akrofi AY, Dzahini-Obiatey H, Lowor ST, et al. Genetic control, combining ability and heritability of resistance to stem canker in cacao (*Theobroma cacao* L.). *Euphytica*. 2017;213(12).
1513. Montagnon C, Leroy T, Cilas C, Legnate H, Charrier A. Heterozygous genotypes are efficient testers for assessing between-population combining ability in the reciprocal recurrent selection of *Coffea canephora*. *Euphytica*. 2008;160(1):101-10.