**Supplementary table 2**: Host molecular markers summarized from eligible studies in the systematic review.

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **Molecular Marker** | | | | | | | |
| **Host** | **Class** | **Name** | **Function** | **Region** | | **Position (cM)** | **Genotype** | **Authors** |
| *Theobroma cacao* L.  . | SSR | mTcCIR21 | Resistance  WBD | Nuclear | | 24 | TSH 1188  CCN 51 | Santos et al. 2007\* |
| mTcCIR24 | 31 |
| mTcCIR29 | 20 |
| mTcCIR30 | 28 |
| mTcCIR33 | 13 |
| mTcCIR35 | 23 |
| RAPD | r AV14.940 | Resistance WBD | NA | | ~8,7 | F2 (Sca-6 x ICS-1) | Queiroz et al 2003\* |
| EST- SSR | msEstTsh-1 | Resistance WBD | ND | | NA | F2 (Sca-6 x ICS-1) | Lima et al. 2008\* |
| msEstTsh-2 | 5′ UTR | |
| msEstTsh-3 | ORF | |
| msEstTsh-4 | ORF | |
| msEstTsh-5 | ORF | |
| msEstTsh-6 | ND | |
| msEstTsh-7 | ND | |
| msEstTsh-8 | ORF | |
| msEstTsh-9 | ND | |
| msEstTsh-10 | 5' UTR | |
| msEstTsh-11 | 3' UTR | |
| SNP | NA | Deformed branches WBD | NA | | 9 e 29 | Criollo | Osorio-Guarín et al. 2020\* |
| Flower cushion broom WBD | 1; 770 e 4 |
| Harvested healthy pods | 10 e 21 |
| Deformed branches WBD | 9 e 27 | Matina |
| Flower cushion broom WBD | 1; 794 e 4 |
| Harvested healthy pods | 9; 8 e 9 |
| SSR | Y16983 | Resistance WBD | Nuclear | | NA | FO37-09  FO36-11  FO85-09  FO32-10  FO36-10  FO35-09  FO51-06  FO29-09 | Lima et al. 2013\* |
| Y16987 |
| AJ271945 |
| Y16 883 |
| Y16984 |
| AJ271827 |
| AJ271944 |
| AJ271946 |
| AJ271953 |
| Y16980 |
| AJ271956 |
| Y16981 |
| Y16978 |
| GWAS-SNP | NA | Chirimoya Pod | Cromossomo I; II; VI e VII | | NA | Progênies (Wild types x Known clones x Nacional) | McElroy et al. 2018\* |
| Cushion Broom | Cromossomo I; VII e X | |
| Vegetative Broom | Cromossomo VIII E IX | |
| SNP | Tcm003s33466269 | Resistance WBD | Cromossomo III | | 81.5 | Progênies (THS 1188 x CCN 51) | Royaert et al. 2016\* |
| Tcm004s00110232 | Cromossomo IV | | 0.55 |
| Tcm006s19715703 | Cromossomo VI | | 31.01 |
| Tcm006s25375496 | Cromossomo VI | | 61.73 |
| Tcm007s10302466 | Cromossomo VII | | 47.55 |
| Tcm009s02031341 | Cromossomo IX | | 13.73 |
| Tcm009s08066239 | Cromossomo IX | | 44.36 |
| SSR | mTcCIR | Resistance WBD | NA | | ~2.6 | Progênies de autofecundação de TSH 516 | Brown et al. 2005\* |
| SHRSTc |
| RGH |
| WRKY |
| EST-SSR | mTcCIR 292 | Defense-related protein | 5′UTR | | 1.3 | LAN28  SCA6  MAT 1–6  SA16  SNA1001  SNA1003  UPA402  UF676 | Fouet et al. 2011\* |
| mTcCIR 293 | Pathogenesis-related protein | 3′UTR | |
| mTcCIR 294 | Protein kinase | 5′UTR | |
| mTcCIR 297 | Oleosin low molecular weight isoform | 3′UTR | |
| mTcCIR 298 | Aspartyl protease family protein | 3′UTR | |
| mTcCIR 299 | Transducin family protein wd-40 repeat family protein | 5′UTR | |
| mTcCIR 301 | Leucine-rich receptor-like protein kinase | 3′UTR | |
| mTcCIR 302 | Calcium-dependent protein kinase CP4 | 3′UTR | |
| mTcCIR 303 | Serine threonine protein | 5′UTR | |
| mTcCIR 304 | 7S vicilin | CDS | |
| mTcCIR 305 | Chloroplast acyl-acp thioesterase | 5′UTR | |
| mTcCIR 306 | 3-ketoacyl-ACP synthase | 5′UTR | |
| mTcCIR 308 | SNARE protein | 5′UTR | |
| mTcCIR 309 | Glutelin | CDS | |
| mTcCIR 310 | 24-sterol C-methyltransferase | 5′UTR | |
| mTcCIR 312 | UDP-glucose pyrophosphorylase | 5′UTR | |
| mTcCIR 314 | MADS-box protein | 3′UTR | |
| mTcCIR 315 | Nucleic acid binding | 3′UTR | |
| mTcCIR 316 | myb-like transcription factor 2 | 5′UTR | |
| mTcCIR 317 | Transcription factor IIa large subunit | 5′UTR | |
| mTcCIR 318 | Floral homeotic protein apetala1 | 5′UTR | |
| mTcCIR 319 | bZIP transcription factor | 5′UTR | |
| mTcCIR 320 | AP2/EREBP transcription factor | 5′UTR | |
| mTcCIR 322 | Phantastica transcription factor A | 5′UTR | |
| mTcCIR 324 | Scarecrow-like transcription factor 8 | 5′UTR | |
| mTcCIR 325 | Urease accessory protein G | 5′UTR | |
| mTcCIR 326 | Phosphate phosphoenolpyruvate translocator-like protein | 3′UTR | |
| mTcCIR 327 | Phosphoenolpyruvate carboxylase | 5′UTR | |
| mTcCIR 329 | Lysine and histidine specific transporter protein | 3′UTR | |
| mTcCIR 331 | Homeodomain-leucine zipper protein 56 | 5′UTR | |
| mTcCIR 333 | Nucleotide sugar epimerase-like protein | 5′UTR | |
| mTcCIR 336 | Plastid-lipid associated protein | CDS | |
| mTcCIR 337 | Fibrillin precursor-like protein | CDS | |
| mTcCIR 339 | GL1 protein | 5′UTR | |
| mTcCIR 341 | Guanine nucleotide exchange factor P532 | 5′UTR | |
| mTcCIR 342 | 3-methyl-2-oxobutanoate hydroxymethyltransferase | 5′UTR | |
| mTcCIR 343 | Protein arginine N-methyltransferase family protein | 5′UTR | |
| mTcCIR 344 | Late embryogenesis-abundant protein | 5′UTR | |
| mTcCIR 348 | One-helix protein | CDS | |
| mTcCIR 349 | Arabinogalactan protein 2 | 3′UTR | |
| mTcCIR 350 | Unnamed protein product (G. hirsutum SSR) | CDS | |
| mTcCIR 351 | Lipoxygenase | 3′UTR | |
| mTcCIR 352 | Unnamed protein product (G. hirsutum SSR) | 5′UTR | |
| mTcCIR 353 | Progesterone-binding protein homolog | 3′UTR | |
| mTcCIR 354 | Tyrosine specific protein phosphatase family protein | 5′UTR | |
| mTcCIR 355 | Glycosyl transferase family 17 protein | 5′UTR | |
| mTcCIR 356 | Auxin-induced protein IAA9 | 5′UTR | |
| mTcCIR 358 | Storage protein (late embryogenesis abundant). | CDS | |
| mTcCIR 359 | Amia calva GARS-AIRS-GART | 3′UTR | |
| mTcCIR 360 | Phosphatidylserine synthase | 5′UTR | |
| mTcCIR 361 | Nac domain protein | 5′UTR | |
| mTcCIR 363 | Ubiquitin-conjugating enzyme | 5′UTR | |
| mTcCIR 364 | Importin beta | 5′UTR | |
| mTcCIR 365 | Cyclic nucleotide-gated calmodulin-binding ion channel | 3′UTR | |
| mTcCIR 366 | Calcium-dependent protein kinase | 5′UTR | |
| mTcCIR 367 | Gibberellin 3 beta-hydroxylase | 5′UTR | |
| mTcCIR 369 | NAC2-like protein | 5′UTR | |
| mTcCIR 373 | NAC domain protein | 3′UTR | |
| mTcCIR 374 | Heat shock protein binding | 5′UTR | |
| mTcCIR 375 | Immunophilin | 5′UTR | |
| mTcCIR 376 | ABC transporter family protein | 3′UTR | |
| mTcCIR 378 | Plastocyanin-like domain-containing protein | 3′UTR | |
| mTcCIR 379 | RING-H2 finger protein RHG1a | 5′UTR | |
| mTcCIR 380 | Glutathione reductase | 5′UTR | |
| mTcCIR 382 | Protein disulfide isomerase | 5′UTR | |
| mTcCIR 383 | Yippee-like protein | 5′UTR | |
| mTcCIR 384 | RAN binding protein | 5′UTR | |
| mTcCIR 387 | STI ATP binding DNA binding DNA-directed DNA polymerase | CDS | |
| mTcCIR 388 | 3-phosphoinositide-dependent protein kinase-1 | 5′UTR | |
| mTcCIR 390 | Villin 2 | CDS | |
| mTcCIR 391 | heat shock protein | CDS | |
| mTcCIR 392 | NHL repeat-containing | 5′UTR | |
| mTcCIR 393 | Inorganic pyrophosphatase | 5′UTR | |
| mTcCIR 394 | Plastocyanin-like domain-containing protein | 5′UTR | |
| mTcCIR 397 | Outer membrane OMP85 family protein | 5′UTR | |
| mTcCIR 398 | Monocarboxylic acid transporters | CDS | |
| mTcCIR 400 | CALM\_SPIOL calmodulin (CaM) | 3′UTR | |
| mTcCIR 402 | MADS-box protein BM5A | 3′UTR | |
| mTcCIR 403 | MADS-box interactor-like | CDS | |
| mTcCIR 404 | Transcription regulator | 3′UTR | |
| mTcCIR 405 | Zinc finger protein OBP4 | 5′UTR | |
| mTcCIR 406 | Rab GTPase activator | 3′UTR | |
| mTcCIR 408 | Zinc finger (C2H2 type) family protein | 3′UTR | |
| mTcCIR 409 | Nucleoid DNA-binding protein CND41 | 5′UTR | |
| mTcCIR 410 | N-rich protein | 5′UTR | |
| mTcCIR 411 | Somatic embryogenesis receptor kinase | 3′UTR | |
| mTcCIR 412 | Sm-D1 protein | 5′UTR | |
| mTcCIR 413 | Aldose 1-epimerase | 5′UTR | |
| mTcCIR 414 | CCCH-type zinc finger transcription factor | CDS | |
| mTcCIR 415 | Glycosyl hydrolase family 1 protein | 5′UTR | |
| mTcCIR 416 | AP2 domain containing protein | CDS | |
| mTcCIR 418 | Transcription factor | 3′UTR | |
| mTcCIR 419 | Branched-chain amino acid aminotransferase | 5′UTR | |
| mTcCIR 420 | Nucleic acid binding | 5′UTR | |
| mTcCIR 421 | Mitotic checkpoint protein | 5′UTR | |
| mTcCIR 422 | MYB transcription factor MYB92 | 5′UTR | |
| mTcCIR 423 | Receptor like protein | 3′UTR | |
| mTcCIR 424 | CGS1 mRNA stability 1 | 3′UTR | |
| mTcCIR 425 | Serrate transcription factor | 5′UTR | |
| mTcCIR 426 | ATP binding/ATP-dependent helicase | CDS | |
| mTcCIR 428 | Small heat shock protein | 3′UTR | |
| mTcCIR 429 | Dihydroflavonol reductase | 5′UTR | |
| mTcCIR 430 | Lipase-like protein | 3′UTR | |
| mTcCIR 431 | Protein kinase | 3′UTR | |
| mTcCIR 432 | Cytosolic factor | 5′UTR | |
| mTcCIR 433 | Pathogen-induced calmodulin-binding protein | 3′UTR | |
| mTcCIR 434 | Glyoxalase extradiol ring-cleavage dioxygenase | 5′UTR | |
| mTcCIR 436 | Translation initiation factor (eIF-4A) | 5′UTR | |
| mTcCIR 438 | Luminal binding protein | 5′UTR | |
| mTcCIR 439 | WRKY family transcription factor | 5′UTR | |
| mTcCIR 441 | Nitrilase-associated protein | 3′UTR | |
| mTcCIR 444 | Trypanothione-dependent peroxidase | 5′UTR | |
| mTcCIR 445 | GTP-binding protein RAB11 | 5′UTR | |
| mTcCIR 446 | Heterogeneous nuclearribonucleoprotein A2 | 5′UTR | |
| mTcCIR 447 | NPH4 transcription factor | 5′UTR | |
|  | EST-SSR | msEstTsh-1 | DNA polimerase related | ND | | NA | Clones  Sca-6  Catongo | Lima et al. 2010\* |
| msEstTsh-2 | Expressed protein | 5' UTR | |
| msEstTsh-3 | Protein F2D10.18 | ORF | |
| msEstTsh-4 | Expressed protein | ORF | |
| msEstTsh-5 | Unknown protein | ORF | |
| msEstTsh-6 | Unknown protein | ND | |
| msEstTsh-7 | Thyroid nuclear factor 1 | ND |  | |
|  | |
| msEstTsh-8 | Unknown protein | ORF | |  |
| msEstTsh-9 | Unknown protein | ND |  | |
|  | |
| msEstTsh-10 | Hypothetical protein | 5' UTR | |  |
| msEstTsh-11 | Casein kinase | 3' UTR | |
| msEstTsh-12 | Unknown protein | ORF | |
| SSR | mTcCIR12 | NA | NA | |
| mTcCIR26 |
| mTcCIR30 |
| mTcCIR37 |
| mTcCIR58 |
| mTcCIR157 |
| mTcCIR166 |
| mTcCIR215 |
| mTcCIR251 |
| SSR | mTcCIR35 | Resistance WBD | NA | | NA | F2 (Sca-6 x ICS-1) | Faleiro et al. 2006\* |
| MTcCIR24 |
| mTcCIR30 |
| RAPD | agcat.78 |
| AFLP | AV14.940 |
| SSR | mTcCIR91 | Resistance WBD | Cromossomo IV, V, VI, VIII e X | | NA | Acessos de cacau | Motilal et al. 2016\* |
| mTcCIR183 |
| TcSNP375 |
| TcSNP720 |
| TcSNP1230 |
| TcSNP1374 |
| *Theobroma grandiflorum* | EST-SSR | c2723 | Resistance WBD | ORF | | NA | Genótipos de cupuaçu | Dos Santos et al. 2016\* |
| c5718 | ORF | |
| c70 | 5' UTR | |
| c180 | 5' UTR | |
| c193B | ORF | |
| c203B | ORF | |
| c3202/3202B | ORF | |
| c733 | ORF | |
| c339 | ORF | |
| c733 | ORF | |
| c431B | 5' UTR | |
| SNP | 6M1252980 | Resistance WBD | Cromossomo VI | | 1.7 | Progênies (Clone 174 X Clone 1074) | Mournet et al. 2020\* |

NA: not assigned

\*References available at:<https://github.com/ArianaSantos/Santos-et-al.2022_systematic-review.git>