

A retrospective analysis of historical data from multi-environment trial evaluation for dry bean (*Phaseolus vulgaris*) in Michigan

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Last compiled on 28 March, 2023

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This is the supplemental material for the manuscript **A retrospective analysis of historical data from multi-environment trial evaluation for dry bean (*Phaseolus vulgaris*) in Michigan**.

It has six main sections: The first contains the Supplemental Tables; the second contains the Supplemental Figures; the third section contains the R code to reproduce the descriptive analysis and methods of this manuscript; section fourth contains the R code for reproducing the MET analysis (Multi Environmental Trials); section fifth contains the R code for reproducing the Multi-Trait Multi-Environmental analysis, while section sixth contains the references and literature cited in this manuscript.

introduce the metan (multienvironment trials analysis) R package reproducing the examples shown in the manuscript using the oat dataset.

1 Appendix A - Supplementary Tables

Supplementary Table S1: Code, commercial names, market class, release year, yield and maturity range observed in the trials of the dry beans cultivars used in the study.

| ComName | Code | MktCl | Source | RelYear | RangeYield | RangeMat |
|------------|------|-------|---------------|---------|-----------------|----------|
| 213SP | N1 | NB | Gentec | NA | 1327.08-3808.82 | 104 |
| ACE | B1 | BB | ADM | 2019 | 1602.9-4260.38 | 85 - 90 |
| ADAMS | B2 | BB | MSU | 2020 | 1483.23-5718.08 | 87 - 102 |
| ALPENA | N2 | NB | MSU | 2014 | 1598.2-3581.55 | NA |
| APEX | N3 | NB | AAFC-HARROW | 2011 | 1383.51-4483.24 | 87 - 104 |
| ARGOSY | N4 | NB | ACUG | 2016 | 1171.66-4475.56 | 87 - 102 |
| ARMADA | N5 | NB | ProVita Seeds | 2019 | 1286.15-4927.81 | 86 - 100 |
| PVT13505 | B3 | BB | ProVita Seeds | NA | 1355.15-4726.52 | NA |
| BL13SR1-1 | B4 | BB | Gentec | NA | 1695.75-4286.68 | 98 - 103 |
| BL1402-15 | B5 | BB | USDA-ARS | NA | 1708.5-5097.63 | 95 - 101 |
| BL15430 | B6 | BB | MSU | NA | 1912.4-4159.36 | NA |
| BL15442 | B7 | BB | MSU | NA | 2185.21-4289.16 | NA |
| BL15447 | B8 | BB | MSU | NA | 1593.92-4817.12 | NA |
| BL16501 | B9 | BB | MSU | NA | 2184.43-4459.89 | NA |
| BL16504 | B10 | BB | MSU | NA | 1704.39-5206.16 | NA |
| BL16506 | B11 | BB | MSU | NA | 1385.56-4254.7 | NA |
| BL16507 | B12 | BB | MSU | NA | 1937.44-4114.39 | NA |
| BL17220 | B13 | BB | MSU | NA | 1716.08-5010.39 | 96 - 102 |
| BL1726-2 | B14 | BB | USDA-ARS | NA | 1327.08-4677.09 | 85 - 92 |
| BL17536 | B15 | BB | MSU | NA | 2024.01-4909.58 | NA |
| BL17691 | B16 | BB | MSU | NA | 2195.96-4982.54 | NA |
| BL17922 | B17 | BB | MSU | NA | 1595.69-5468.59 | 99 - 101 |
| BL18094173 | B18 | BB | ADM | NA | 2333.06-4501.36 | 101 |
| BL18201 | B19 | BB | MSU | NA | 1891.45-5501.6 | 95 - 101 |
| BL18204 | B20 | BB | MSU | NA | 1424.79-5611.63 | 90 - 98 |
| BL19309 | B21 | BB | MSU | NA | 1507.6-4657.46 | 87 - 95 |
| BL19330 | B22 | BB | MSU | NA | 1952.66-4736.5 | 84 - 98 |
| BL19344 | B23 | BB | MSU | NA | 1893.22-5406.24 | 86 - 104 |
| BL20536 | B24 | BB | MSU | NA | 2486.05-3905.59 | 103 |
| BL20547 | B25 | BB | MSU | NA | 1355.45-4561.57 | 87 - 93 |
| BL20591 | B26 | BB | MSU | NA | 1586.82-4802.97 | 86 - 93 |
| BL20597 | B27 | BB | MSU | NA | 2380.71-4160.69 | 84 - 92 |
| BL20599 | B28 | BB | MSU | NA | 2616.34-4423.61 | 102 |
| BL21708 | B29 | BB | MSU | NA | 1771.54-4972.09 | 100 |
| BL21710 | B30 | BB | MSU | NA | 2590.07-4589.62 | 101 |
| BL21714 | B31 | BB | MSU | NA | 2217.06-3910.32 | 100 |
| BL3033350 | B32 | BB | ADM | NA | 1708.92-3438.01 | 97 |
| BL3035411 | B33 | BB | ADM | NA | 2912.65-3975.99 | 98 |
| BL3036368 | B34 | BB | ADM | NA | 1174.63-5310.16 | 93 - 100 |
| BL3036381 | B35 | BB | ADM | NA | 2068.64-5125.49 | 87 - 105 |
| BL5058320 | B36 | BB | ADM | NA | 1700.93-3758.7 | 98 |
| BL7071259 | B37 | BB | ADM | NA | 2402.93-4766.15 | 96 |

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|---------------|-----|----|---------------|-------|-----------------|----------|
| BL7072269 | B38 | BB | ADM | NA | 2030.03-4444.62 | 98 |
| BLACKBEAR | B39 | BB | ProVita Seeds | 2018 | 974.19-4937.31 | 90 - 105 |
| BLACKBEARD | B40 | BB | ProVita Seeds | 2019 | 1156.46-5436.5 | 90 - 101 |
| BLACKCAT | B41 | BB | ADM | 2014 | 1517.23-4965.22 | NA |
| BLACKTAILS | B42 | BB | ProVita Seeds | 2017 | 889.94-5179.46 | 87 - 102 |
| BLIZZARD | N6 | NB | ProVita Seeds | 2017 | 1065.87-4563.69 | 88 - 100 |
| BOUNTY | N7 | NB | ProVita Seeds | 2019 | 1009.56-4655.82 | 88 - 100 |
| CALDERA | R1 | SR | ProVita Seeds | 2018? | 1196.06-5385.04 | 97 - 101 |
| CAYENNE | R2 | SR | MSU | 2017 | 1545.11-4682.2 | 84 - 100 |
| CORAL | R3 | SR | MSU | NA | 854.25-4077.7 | 102 |
| DS105WO | N8 | NB | DOW | NA | 1946.32-4091.65 | NA |
| ECLIPSE | B43 | BB | NDSU | 2004 | 1277.47-4595.38 | 85 - 97 |
| EX1701 | N9 | NB | TVS | NA | 905.46-4163.67 | NA |
| EX1702 | N10 | NB | TVS | NA | 1153.41-4098.98 | 95 - 101 |
| EX1703 | N11 | NB | TVS | NA | 1656.7-4457.85 | NA |
| EX1708 | N12 | NB | TVS | NA | 670.86-4596.67 | 98 - 101 |
| EX1711 | N13 | NB | TVS | NA | 1020.8-5158.16 | 94 - 98 |
| EX1801 | N14 | NB | TVS | NA | 1760.95-4096.31 | 93 - 98 |
| EX1802 | N15 | NB | TVS | NA | 991.05-4569.08 | 85 - 96 |
| EX1803 | N16 | NB | TVS | NA | 1191.12-4448.04 | 85 - 102 |
| EX1804 | N17 | NB | TVS | NA | 1104.54-4184.9 | 85 - 98 |
| EX1914 | N18 | NB | TVS | NA | 1143.87-4970.85 | 95 - 100 |
| EX2109 | N19 | NB | TVS | NA | 1118.41-3627.57 | 97 |
| GTSOB-1723-03 | N20 | NB | Gentec | NA | 1748.11-3260.29 | NA |
| INDI | N21 | NB | ADM | 2010 | 1131.44-4030.38 | 90 - 95 |
| LIBERTY | N22 | NB | ProVita Seeds | 2021 | 1191.07-5322.3 | 87 - 100 |
| LORETO | B44 | BB | ProVita Seeds | 2007 | 1007.97-4569.47 | NA |
| MEDALIST | N23 | NB | ProVita Seeds | 2007 | 1478.68-4978.47 | 85 - 101 |
| MERLIN | N24 | NB | ProVita Seeds | 2010 | 998.54-4561.73 | 90 - 102 |
| MERLOT | R4 | SR | USDA/MSU | 2002 | 1356.14-4447.94 | NA |
| MIST | N25 | NB | Guelph | 2013 | 921.13-4301 | NA |
| NA14229 | N26 | NB | MSU | NA | 1334.35-4316.25 | NA |
| NA15341 | N27 | NB | MSU | NA | 2200.33-4256.5 | NA |
| NA16401 | N28 | NB | MSU | NA | 1270.06-3186.23 | NA |
| NA16405 | N29 | NB | MSU | NA | 1923-3834.66 | NA |
| NA17504 | N30 | NB | MSU | NA | 1864.97-4145.36 | NA |
| NA17506 | N31 | NB | MSU | NA | 1272.67-4366.3 | NA |
| NA18102 | N32 | NB | MSU | NA | 1096.13-3630.12 | NA |
| NA18103 | N33 | NB | MSU | NA | 1228.86-4517.17 | 86 - 95 |
| NA18109 | N34 | NB | MSU | NA | 1293.85-4939.4 | NA |
| NA19226 | N35 | NB | MSU | NA | 2086.6-4376.18 | 86 - 93 |
| NA19246 | N36 | NB | MSU | NA | 1447.5-4435.73 | 86 - 95 |
| NA19253 | N37 | NB | MSU | NA | 1520.92-4810.69 | 87 - 99 |
| NA19285 | N38 | NB | MSU | NA | 1241.64-4030.95 | 84 - 101 |
| NA20388 | N39 | NB | MSU | NA | 1682.97-4325.13 | 87 - 92 |
| NA20395 | N40 | NB | MSU | NA | 1241.55-4281.97 | 98 |
| NA20404 | N41 | NB | MSU | NA | 1536.18-4060.15 | 85 - 90 |
| NA21511 | N42 | NB | MSU | NA | 1147.41-3920.51 | 101 |
| NA21525 | N43 | NB | MSU | NA | 1152.87-4009.62 | 100 |
| NAUTICA | N44 | NB | AAFC-HARROW | 2004 | 1020.64-4230.28 | 86 - 102 |
| NDPOLAR | N45 | NB | NDSU | 2022 | 1465.99-3674.75 | 102 |
| NDTWILIGHT | B45 | BB | NDSU | 2020 | 1270.97-4140.56 | 84 - 95 |
| NIMBUS | B46 | BB | ProVita Seeds | 2021 | 1882.19-5708.71 | 89 - 103 |
| OACVortex | B47 | BB | NA | 2019 | 1539.75-4261.79 | 101 |
| PVT06063 | N46 | NB | ProVita Seeds | NA | 1848.4-3805.14 | NA |
| PVT12039 | N47 | NB | ProVita Seeds | NA | 904.55-5349.49 | 87 - 102 |
| PVT12062 | N48 | NB | ProVita Seeds | NA | 1352.32-5853.77 | NA |
| PVT12063 | N49 | NB | ProVita Seeds | NA | 1436.99-5235.81 | NA |
| PVT12064 | N50 | NB | ProVita Seeds | NA | 554.77-4168.64 | NA |
| PVT13049 | N51 | NB | ProVita Seeds | NA | 1739.78-3849.08 | NA |
| PVT13058 | N52 | NB | ProVita Seeds | NA | 988.66-4534.09 | NA |
| PVT13066 | N53 | NB | ProVita Seeds | NA | 1638.17-4497.35 | NA |
| PVT13490 | B48 | BB | ProVita Seeds | NA | 2128.87-4264.54 | NA |
| PVT13496 | B49 | BB | ProVita Seeds | NA | 1526.42-3442.4 | NA |
| PVT13503 | B50 | BB | ProVita Seeds | NA | 1104.68-3457.17 | NA |

| | | | | | | |
|----------|-----|----|--------------------|-------|-----------------|-----------|
| PVT14068 | N54 | NB | ProVita Seeds | NA | 1273.85-5141.5 | 87 - 103 |
| PVT14069 | N55 | NB | ProVita Seeds | NA | 2043-4228.37 | NA |
| PVT14075 | N56 | NB | ProVita Seeds | NA | 1692.95-3804.3 | 104 |
| PVT14078 | N57 | NB | ProVita Seeds | NA | 1622.35-4479.66 | 87 - 100 |
| PVT14080 | N58 | NB | ProVita Seeds | NA | 1078.05-4217.83 | 96 - 103 |
| PVT14081 | N59 | NB | ProVita Seeds | NA | 1954.85-3687.03 | NA |
| PVT14084 | N60 | NB | ProVita Seeds | NA | 921.7-4564.38 | 87 - 98 |
| PVT14089 | N61 | NB | ProVita Seeds | NA | 1673.84-4117.56 | 96 - 100 |
| PVT14496 | B51 | BB | ProVita Seeds | NA | 2017.05-5255.23 | NA |
| PVT14498 | B52 | BB | ProVita Seeds | NA | 1869.43-4938.29 | NA |
| PVT14504 | B53 | BB | ProVita Seeds | NA | 2059.98-5023.2 | NA |
| PVT14505 | B54 | BB | ProVita Seeds | NA | 2881.32-4994.5 | NA |
| PVT14510 | B55 | BB | ProVita Seeds | NA | 1477.68-3779.63 | NA |
| PVT14522 | B56 | BB | ProVita Seeds | NA | 1692.75-4231.31 | NA |
| PVT14531 | B57 | BB | ProVita Seeds | NA | 2196.46-3956.91 | 0 - 95 |
| PVT15610 | B58 | BB | ProVita Seeds | NA | 1369-5461.59 | 85 - 104 |
| PVT15619 | B59 | BB | ProVita Seeds | NA | 1374.37-5601.63 | 87 - 105 |
| PVT15629 | B60 | BB | ProVita Seeds | NA | 2890.2-4122.78 | 87 - 94 |
| PVT16113 | N62 | NB | ProVita Seeds | NA | 1327.08-4098.72 | 100 |
| PVT16590 | B61 | BB | ProVita Seeds | NA | 2232.82-4940.66 | 89 - 103 |
| PVT16598 | B62 | BB | ProVita Seeds | NA | 2441.91-4340.28 | 101 |
| PVT16648 | B63 | BB | ProVita Seeds | NA | 2016.09-4804.76 | 85 - 104 |
| PVT16686 | R5 | SR | ProVita Seeds | NA | 1307.27-5053.8 | 85 - 98 |
| PVT17704 | B64 | BB | ProVita Seeds | NA | 1750.84-4763.96 | 97 - 104 |
| PVT17708 | B65 | BB | ProVita Seeds | NA | 1726.98-4357.16 | 94 - 101 |
| PVT17715 | B66 | BB | ProVita Seeds | NA | 1988-6014.39 | 87 - 101 |
| PVT17724 | B67 | BB | ProVita Seeds | NA | 1982.1-4651.46 | 92 - 98 |
| PVT17751 | B68 | BB | ProVita Seeds | NA | 2465.45-5501.17 | 85 - 100 |
| PVT17822 | R6 | SR | ProVita Seeds | NA | 2360.38-4868.28 | 100 |
| PVT17835 | R7 | SR | ProVita Seeds | NA | 654.06-3876.72 | 100 - 101 |
| PVT17837 | R8 | SR | ProVita Seeds | NA | 1152.23-4547.04 | 88 - 101 |
| PVT17839 | R9 | SR | ProVita Seeds | NA | 1116.84-4342.43 | 88 - 101 |
| PVT17875 | R10 | SR | ProVita Seeds | NA | 1826.18-4885.76 | 84 - 92 |
| PVT19837 | R11 | SR | ProVita Seeds | NA | 2580.93-4075.81 | 97 |
| SR20627 | R12 | SR | MSU | NA | 1566.02-4226.28 | 87 - 103 |
| SR20667 | R13 | SR | MSU | NA | 1641.67-4772.77 | 102 |
| SR20669 | R14 | SR | MSU | NA | 2638.4-4766.99 | 104 |
| REXETER | N63 | NB | Guelph | 2011 | 1178.3-5089.48 | NA |
| ROGUE | N64 | NB | Guelph | 2020? | 1541.54-4112.92 | 0 - 92 |
| ROSETTA | R15 | SR | MSU | 2012 | 1458.75-4738.55 | 86 - 94 |
| RUBY | R16 | SR | ProVita Seeds | 2014 | 1088.14-5052.16 | 87 - 100 |
| SHANIA | B69 | BB | ADM | 2008 | 1629.88-3656.14 | NA |
| SHOCK | N65 | NB | ACUG | 2017 | 1548.47-4274.91 | 86 - 102 |
| SPECTRE | B70 | BB | ProVita Seeds | 2019 | 1445.67-5859.47 | 90 - 102 |
| SR16503 | R17 | SR | MSU | NA | 1419.17-4401.98 | NA |
| SR17603 | R18 | SR | MSU | NA | 1375.77-5617.34 | NA |
| SR17604 | R19 | SR | MSU | NA | 1189.34-4722.51 | 85 - 103 |
| SR17605 | R20 | SR | MSU | NA | 1326.57-4372.72 | NA |
| SV1893GH | N66 | NB | Seminis Seeds | 2015 | 1358.73-4918.82 | 87 - 104 |
| T9905 | N67 | NB | TVS/Bred by Hyland | NA | 1400.89-4338.23 | NA |
| VALIANT | N68 | NB | ProVita Seeds | 2019 | 1045.13-4751.38 | 86 - 98 |
| VICTORY | N69 | NB | ProVita Seeds | 2021 | 1238.93-4889.14 | 87 - 98 |
| VIGILANT | N70 | NB | ProVita Seeds | 2012 | 922.36-4562.16 | 86 - 98 |
| VIPER | R21 | SR | ProVita Seeds | 2015 | 1200.75-5624.94 | 19 - 102 |
| VISTA | N71 | NB | Gentec | 1991 | 1752.27-3372.03 | NA |
| ZENITH | B71 | BB | MSU | 2014 | 1172.34-4931.87 | 87 - 102 |
| ZORRO | B72 | BB | MSU | 2008 | 1157.27-5047.25 | 88 - 102 |

Supplementary Table S2: Summary of the results for random- and fixed-effects and overall means for each locations of the grain yield (GY: 2017 - 2022; GY2: only 2021), days to maturity (DM), plant height (PH) and lodging (LD) traits evaluated in the study.

| Market.Class | Parameters | GY | GY2 | DM | PH | LD |
|--------------|------------|----------------|----------------|-------------|-------------|------------|
| BB | LRTG | 12.0*** | 25.1*** | 30.2*** | 6.15* | 12.3*** |
| BB | LRTGE | 216*** | 3.95* | 9.7** | 0.4ns | 1.33ns |
| BB | E-MS | 1373806*** | 1637595*** | 152*** | 23.6** | 3.57*** |
| BB | E/B-MS | 1775719*** | 740206*** | 12.2*** | 16.9*** | 0.7** |
| BB | BA | 3004.17 | 2835 | 89.9 | 16.9 | 1.32 |
| BB | HU | 3461.59 | NA | NA | NA | NA |
| BB | SA | 3321.17 | 3362 | 91 | 18.4 | 1.96 |
| BB | TU | 3233.21 | 3402 | 94.4 | 19.1 | 1.91 |
| BB | Mean | 3255.05+-19.84 | 3199.25+-30.37 | 91.77+-0.19 | 18.14+-0.15 | 1.73+-0.04 |
| NB | LRTG | 17.2*** | 17.9*** | 25.4*** | 12.1*** | 36*** |
| NB | LRTGE | 83.4*** | 7.79** | 7.23** | 6.15* | 4.5* |
| NB | E-MS | 1944731*** | 1493686*** | 120*** | 41.2*** | 2.37*** |
| NB | E/B-MS | 1735124*** | 320888** | 12.7*** | 7.38* | 0.92*** |
| NB | BA | 2654.03 | 2732 | 90.6 | 17 | 1.46 |
| NB | HU | 3094 | NA | NA | NA | NA |
| NB | SA | 2978.02 | 3094 | 89.6 | 18.5 | 2.2 |
| NB | TU | 2970.59 | 3195 | 93.6 | 19.6 | 1.97 |
| NB | Mean | 2924+-17.22 | 3009.36+-26.04 | 91.28+-0.16 | 18.37+-0.15 | 1.87+-0.04 |
| SR | LRTG | 3.33* | 0 | 2.29ns | 8.13** | 11.3*** |
| SR | LRTGE | 46.3*** | 11.22*** | 2.58ns | 3.83ns | 0.76ns |
| SR | E-MS | 1299967*** | 1722395*** | 87.2*** | 13* | 1.24* |
| SR | E/B-MS | 353243** | 242390ns | 7.61* | 6.78ns | 1.49*** |
| SR | BA | 2732.2 | 2584 | 89.2 | 17.5 | 1.37 |
| SR | HU | 3267.9 | NA | NA | NA | NA |
| SR | SA | 3223.4 | 3335 | 89.9 | 17.6 | 2.01 |
| SR | TU | 3367.3 | 3546 | 93.5 | 19.6 | 2.24 |
| SR | Mean | 3147.37+-32.29 | 3157.34+-53.6 | 90.86+-0.25 | 18.23+-0.24 | 1.87+-0.07 |

Note:

* Significant at $P < 0.05$. ** Significant at $P < 0.01$. *** Significant at $P < 0.001$. ns, nonsignificant.

† LRTg and LRTge, Likelihood ratio tests for genotype and interaction gxe. ‡ Vg, Vge and Vr, variance components for genotype, interaction, and residuals, respectively. § E-MS and E/B-MS, mean squares for environment and and block-within-environment, respectively. ¶ Mean, grand mean; # Standart error

Supplementary Table S3: Estimated variance components and genetic parameters for grain yield (GY), days to maturity (DM), plant height (PH) and lodging (LD) for 37 Black, 37 Navy and 14 Red Small beans genotypes evaluated in BA, SA, and TU environments during 2021 growing season only.

Black Beans

| REML | GY2 | DM | PH | LD |
|------------------------------|--------------------------|--------------|--------------|---------------|
| $\hat{\sigma}_g^2$ | 68572 (32%) [‡] | 2.86 (39.5%) | 0.63 (10.5%) | 0.063 (17.6%) |
| $\hat{\sigma}_{ge}^2$ | 17115 (8%) | 0.8 (11%) | 0.18 (3.0%) | 0.02 (5.32%) |
| $\hat{\sigma}_\varepsilon^2$ | 128582 (60%) | 3.58 (49.5%) | 5.17 (86.4%) | 0.27 (77.1%) |
| $\hat{\sigma}_p^2$ | 214269 | 7.24 | 5.98 | 0.356 |
| h_g^2 | 0.32 | 0.395 | 0.105 | 0.176 |
| R_{gei}^2 | 0.08 | 0.11 | 0.0305 | 0.0532 |
| h_{gm}^2 | 0.81 | 0.835 | 0.561 | 0.682 |
| <i>Acc</i> | 0.90 | 0.914 | 0.749 | 0.826 |
| r_{ge} | 0.12 | 0.182 | 0.0341 | 0.0645 |
| <i>CVg</i> | 8.19 | 1.84 | 4.37 | 14.5 |
| <i>CVr</i> | 11.21 | 2.06 | 12.5 | 30.3 |
| <i>CVg/CVr</i> | 0.73 | 0.894 | 0.349 | 0.478 |

Navy Beans

| REML | GY2 | DM | PH | LD |
|------------------------------|-----------------------------|--------------|--------------|---------------|
| $\hat{\sigma}_g^2$ | 50195 (25.72%) [‡] | 1.97 (32%) | 1.36 (19.1%) | 0.195 (39.3%) |
| $\hat{\sigma}_{ge}^2$ | 22779 (11.67%) | 0.63 (10.2%) | 0.81 (11.4%) | 0.04 (7.19%) |
| $\hat{\sigma}_\varepsilon^2$ | 122206 (62.61%) | 3.56 (57.8%) | 4.95 (69.5%) | 0.27 (53.5%) |
| $\hat{\sigma}_p^2$ | 195181 | 6.17 | 7.12 | 0.496 |
| h_g^2 | 0.26 | 0.32 | 0.191 | 0.393 |
| R_{gei}^2 | 0.12 | 0.102 | 0.114 | 0.0719 |
| h_{gm}^2 | 0.74 | 0.796 | 0.666 | 0.851 |
| <i>Acc</i> | 0.86 | 0.892 | 0.816 | 0.923 |
| r_{ge} | 0.16 | 0.15 | 0.141 | 0.118 |
| <i>CVg</i> | 7.45 | 1.54 | 6.35 | 23.6 |
| <i>CVr</i> | 11.62 | 2.07 | 12.1 | 27.6 |
| <i>CVg/CVr</i> | 0.64 | 0.744 | 0.524 | 0.856 |

Red Beans

| REML [§] | GY2 | DM | PH | LD |
|------------------------------|--------------------------|--------------|--------------|--------------|
| $\hat{\sigma}_G^2$ | 0.1 (0.01%) [‡] | 0.61 (12.2%) | 1.81 (25.3%) | 0.18 (34.6%) |
| $\hat{\sigma}_{ge}^2$ | 75950 (31.4%) | 0.66 (13.2%) | 0.35 (4.9%) | 0.03 (5.0%) |
| $\hat{\sigma}_\varepsilon^2$ | 165822 (68.59%) | 3.72 (74.6%) | 4.99 (69.8%) | 0.32 (60.4%) |
| $\hat{\sigma}_P^2$ | 241772 | 4.98 | 7.142 | 0.53 |
| h_G^2 | 0.00 | 0.12 | 0.2531 | 0.35 |
| R_{gei}^2 | 0.31 | 0.13 | 0.04876 | 0.05 |
| h_{gm}^2 | 0.00 | 0.54 | 0.7728 | 0.84 |
| Acc | 0.00 | 0.73 | 0.8791 | 0.91 |
| r_{ge} | 0.31 | 0.15 | 0.06528 | 0.07 |
| CVg | 0.00 | 0.86 | 7.307 | 22.9 |
| CVr | 12.90 | 2.12 | 12.13 | 30.2 |
| CVg/CVr | 0.00 | 0.4 | 0.6022 | 0.76 |

$\hat{\sigma}_G^2$, genotypic variance; $\hat{\sigma}_{GE}^2$, variance of $G \times E$ interaction; $\hat{\sigma}_\varepsilon^2$ residual variance; $\hat{\sigma}_P^2$ phenotypic variance; h_G^2 broad-sense heritability; R_{gei}^2 coefficient of determination for the genotype-vs-environment interaction effects; h_{gm}^2 heritability of the genotypic mean; Acc accuracy of genotype selection; r_{GE} correlation between genotypic values across environments; CVg genotypic coefficient of variation; CVr residual coefficient of variation; CVg/CVr and is the ratio between genotypic and residual coefficient of variation.[‡] Parenthetical values indicate the percentage of the observed phenotypic variance $\hat{\sigma}_P^2$. The genetic parameters were estimated by $h_G^2 = \frac{\hat{\sigma}_G^2}{\hat{\sigma}_G^2 + \hat{\sigma}_{GE}^2 + \hat{\sigma}_\varepsilon^2}$; where $\hat{\sigma}_G^2$ is the genotypic variance; $\hat{\sigma}_{GE}^2$ is the genotype-by-environment interaction variance; and $\hat{\sigma}_\varepsilon^2$ is the residual variance. Coefficient of determination of the interaction effects: $R_{gei}^2 = \frac{\hat{\sigma}_{GE}^2}{\hat{\sigma}_G^2 + \hat{\sigma}_{GE}^2 + \hat{\sigma}_\varepsilon^2}$; heritability on the mean basis: $h_{gm}^2 = \frac{\hat{\sigma}_G^2}{[\hat{\sigma}_G^2 + \hat{\sigma}_{GE}^2/e + \hat{\sigma}_\varepsilon^2/(eb)]}$ where e and b are the number of environments and blocks, respectively; The accuracy of selection: $Acc = \sqrt{h_{GM}^2}$; genotype-environment correlation $r_{GE} = \frac{\hat{\sigma}_g^2}{\hat{\sigma}_G^2 + \hat{\sigma}_{GE}^2}$; genotypic coefficient of variation $CVg = \left(\sqrt{\hat{\sigma}_g^2/\mu} \right) \times 100$ residual coefficient of variation estimated: $CVr = \left(\sqrt{\hat{\sigma}_\varepsilon^2/\mu} \right) \times 100$ where μ is the grand mean; ratio between genotypic and residual coefficient of variation: CVg/CVr .

Supplementary Table S4: Selection differential of selected genotypes for mean performance and stability (WAASB index) at black beans. Selected genotypes: B14, B19, B21, B22, B25, B26, B51, B52, B53, B10, B17, B23, B61, B63, B66, B68, B2, B40, B46, B70, B24, B27, B30, B33, B60, B7.

| Geno | Mean performance | | | Stability (WAASB) | | |
|------|------------------|----------|--------|-------------------|----------|---------|
| | BLUPs | Overhall | SD (%) | WAASB | Overhall | SD (%) |
| B10 | 3391 | 3255 | 4.1787 | 0.2971 | 5.152 | -94.233 |
| B14 | 3283 | 3255 | 0.8469 | 2.7163 | 5.152 | -47.278 |
| B17 | 3281 | 3255 | 0.8017 | 5.4405 | 5.152 | 5.598 |
| B19 | 3316 | 3255 | 1.8723 | 3.6947 | 5.152 | -28.288 |
| B2 | 3401 | 3255 | 4.4717 | 3.1153 | 5.152 | -39.534 |
| B21 | 3458 | 3255 | 6.2395 | 3.3874 | 5.152 | -34.253 |
| B22 | 3285 | 3255 | 0.9310 | 3.1503 | 5.152 | -38.854 |
| B23 | 3433 | 3255 | 5.4621 | 2.9277 | 5.152 | -43.174 |
| B24 | 3336 | 3255 | 2.4965 | 2.9964 | 5.152 | -41.841 |
| B25 | 3398 | 3255 | 4.3767 | 4.8411 | 5.152 | -6.038 |
| B26 | 3448 | 3255 | 5.9262 | 1.8807 | 5.152 | -63.497 |
| B27 | 3346 | 3255 | 2.8048 | 2.6129 | 5.152 | -49.285 |
| B30 | 3373 | 3255 | 3.6317 | 5.7096 | 5.152 | 10.821 |
| B33 | 3344 | 3255 | 2.7175 | 5.7243 | 5.152 | 11.106 |
| B40 | 3377 | 3255 | 3.7361 | 1.5201 | 5.152 | -70.496 |
| B46 | 3526 | 3255 | 8.3099 | 3.2089 | 5.152 | -37.717 |
| B51 | 3397 | 3255 | 4.3524 | 1.7499 | 5.152 | -66.035 |
| B52 | 3359 | 3255 | 3.1927 | 3.1465 | 5.152 | -38.927 |
| B53 | 3382 | 3255 | 3.9096 | 2.8632 | 5.152 | -44.428 |
| B60 | 3338 | 3255 | 2.5341 | 2.7706 | 5.152 | -46.224 |
| B61 | 3381 | 3255 | 3.8636 | 2.4342 | 5.152 | -52.753 |
| B63 | 3362 | 3255 | 3.2767 | 2.9257 | 5.152 | -43.214 |
| B66 | 3348 | 3255 | 2.8490 | 1.0713 | 5.152 | -79.207 |
| B68 | 3523 | 3255 | 8.2229 | 2.7228 | 5.152 | -47.152 |
| B7 | 3282 | 3255 | 0.8249 | 3.7108 | 5.152 | -27.975 |
| B70 | 3372 | 3255 | 3.6026 | 1.2369 | 5.152 | -75.993 |

Supplementary Table S 5: Selection differential of selected genotypes for mean performance and stability (WAASB index) at navy beans. Selected genotypes: N37, N39, N41, N58, N64, N10, N21, N33, N3, N57, N68, N54, N69, N70, N23, N4, N44, N47, N5, N6, N60, N7, N27, N29, N59.

| Geno | Mean performance | | | Stability (WAASB) | | |
|------|------------------|----------|---------|-------------------|----------|---------|
| | BLUPs | Overhall | SD (%) | WAASB | Overhall | SD (%) |
| N10 | 2955 | 2924 | 1.0472 | 2.3226 | 3.912 | -40.628 |
| N21 | 2968 | 2924 | 1.5017 | 1.4534 | 3.912 | -62.846 |
| N23 | 3056 | 2924 | 4.5210 | 1.7097 | 3.912 | -56.294 |
| N27 | 3002 | 2924 | 2.6588 | 2.6325 | 3.912 | -32.706 |
| N29 | 2923 | 2924 | -0.0436 | 1.4228 | 3.912 | -63.629 |
| N3 | 3083 | 2924 | 5.4533 | 2.7463 | 3.912 | -29.794 |
| N33 | 2964 | 2924 | 1.3811 | 2.9489 | 3.912 | -24.618 |
| N37 | 3049 | 2924 | 4.2847 | 4.6672 | 3.912 | 19.310 |
| N39 | 2991 | 2924 | 2.3038 | 1.5480 | 3.912 | -60.428 |
| N4 | 3033 | 2924 | 3.7392 | 0.9353 | 3.912 | -76.092 |
| N41 | 3020 | 2924 | 3.2884 | 3.2316 | 3.912 | -17.391 |
| N44 | 2935 | 2924 | 0.3644 | 1.1779 | 3.912 | -69.890 |
| N47 | 3129 | 2924 | 7.0024 | 2.1505 | 3.912 | -45.026 |
| N5 | 3058 | 2924 | 4.5735 | 1.6651 | 3.912 | -57.435 |
| N54 | 3056 | 2924 | 4.5117 | 1.8380 | 3.912 | -53.015 |
| N57 | 3032 | 2924 | 3.6901 | 2.8651 | 3.912 | -26.758 |
| N58 | 2968 | 2924 | 1.4933 | 3.4484 | 3.912 | -11.849 |
| N59 | 2963 | 2924 | 1.3346 | 1.8183 | 3.912 | -53.518 |
| N6 | 2995 | 2924 | 2.4132 | 1.4008 | 3.912 | -64.192 |
| N60 | 3046 | 2924 | 4.1714 | 0.8606 | 3.912 | -78.000 |
| N64 | 3036 | 2924 | 3.8222 | 3.9567 | 3.912 | 1.146 |
| N68 | 2990 | 2924 | 2.2719 | 3.6703 | 3.912 | -6.176 |
| N69 | 3141 | 2924 | 7.4060 | 1.7844 | 3.912 | -54.386 |
| N7 | 3130 | 2924 | 7.0594 | 1.2604 | 3.912 | -67.779 |
| N70 | 2928 | 2924 | 0.1372 | 2.8340 | 3.912 | -27.555 |

Supplementary Table S6: Selection differential of selected genotypes for mean performance and stability (WAASB index) at red beans. Selected genotypes: R10, R13, R18, R1, R2, R21, R11.

| Geno | Mean performance | | | Stability (WAASB) | | |
|------|------------------|----------|--------|-------------------|----------|--------|
| | BLUPs | Overhall | SD (%) | WAASB | Overhall | SD (%) |
| R1 | 3251 | 3147 | 3.2992 | 3.110 | 6.065 | -48.72 |
| R10 | 3180 | 3147 | 1.0359 | 5.367 | 6.065 | -11.52 |
| R11 | 3174 | 3147 | 0.8525 | 7.646 | 6.065 | 26.06 |
| R13 | 3160 | 3147 | 0.3927 | 5.114 | 6.065 | -15.68 |
| R18 | 3278 | 3147 | 4.1476 | 3.705 | 6.065 | -38.92 |
| R2 | 3209 | 3147 | 1.9472 | 4.060 | 6.065 | -33.06 |
| R21 | 3313 | 3147 | 5.2734 | 3.143 | 6.065 | -48.19 |

Supplementary Table S7: BLUP-based indexes for selecting genotypes with performance and stability at black beans.

| GEN | Y | HMGV | HMGV_R | RPGV | RPGV_R | HMRPGV | HMRPGV_R | WAASB | WAASB_R | WAASBY | WAASBY_R |
|-----|------|------|--------|------|--------|--------|----------|-------|---------|--------|----------|
| B1 | 3122 | 3049 | 54 | 3083 | 55 | 3068 | 54 | 2.67 | 17 | 67.58 | 35 |
| B10 | 3300 | 3473 | 10 | 3489 | 10 | 3487 | 10 | 0.30 | 1 | 89.22 | 3 |
| B11 | 3369 | 2884 | 62 | 2987 | 61 | 2896 | 62 | 10.27 | 66 | 41.97 | 69 |
| B12 | 2985 | 3083 | 53 | 3121 | 54 | 3103 | 53 | 5.29 | 42 | 61.40 | 46 |
| B13 | 3666 | 3118 | 52 | 3136 | 52 | 3127 | 52 | 2.08 | 12 | 70.88 | 30 |
| B14 | 3305 | 3282 | 32 | 3296 | 35 | 3289 | 33 | 2.72 | 18 | 74.93 | 23 |
| B15 | 3539 | 3310 | 30 | 3419 | 23 | 3314 | 31 | 12.17 | 70 | 52.80 | 60 |
| B16 | 3644 | 3128 | 51 | 3228 | 40 | 3141 | 51 | 12.63 | 71 | 44.54 | 67 |
| B17 | 2775 | 3232 | 35 | 3278 | 37 | 3254 | 35 | 5.44 | 43 | 67.12 | 37 |
| B18 | 3537 | 3381 | 25 | 3431 | 21 | 3376 | 26 | 8.90 | 63 | 62.01 | 44 |
| B19 | 3459 | 3313 | 29 | 3351 | 31 | 3328 | 28 | 3.69 | 35 | 74.45 | 24 |
| B2 | 3507 | 3490 | 8 | 3509 | 8 | 3502 | 7 | 3.12 | 26 | 81.90 | 12 |
| B20 | 3526 | 2981 | 58 | 3006 | 59 | 2998 | 58 | 3.28 | 30 | 62.96 | 43 |
| B21 | 3296 | 3607 | 4 | 3619 | 4 | 3615 | 4 | 3.39 | 32 | 85.08 | 7 |
| B22 | 3613 | 3281 | 33 | 3301 | 34 | 3289 | 34 | 3.15 | 28 | 73.89 | 26 |
| B23 | 2969 | 3569 | 6 | 3581 | 6 | 3569 | 6 | 2.93 | 23 | 84.64 | 9 |
| B24 | 2865 | 3392 | 23 | 3403 | 29 | 3391 | 23 | 3.00 | 25 | 77.82 | 19 |
| B25 | 2939 | 3497 | 7 | 3515 | 7 | 3498 | 9 | 4.84 | 41 | 76.80 | 20 |
| B26 | 2620 | 3593 | 5 | 3602 | 5 | 3601 | 5 | 1.88 | 11 | 88.64 | 4 |
| B27 | 3504 | 3374 | 26 | 3405 | 27 | 3391 | 24 | 2.61 | 16 | 79.60 | 16 |
| B28 | 3464 | 3417 | 18 | 3459 | 16 | 3416 | 19 | 7.97 | 57 | 65.87 | 40 |
| B29 | 3435 | 3181 | 40 | 3233 | 39 | 3170 | 45 | 6.90 | 51 | 60.15 | 50 |
| B3 | 3800 | 2970 | 60 | 2994 | 60 | 2985 | 60 | 2.09 | 13 | 65.83 | 41 |
| B30 | 3072 | 3453 | 12 | 3471 | 14 | 3453 | 14 | 5.71 | 45 | 72.68 | 28 |
| B31 | 3025 | 3171 | 43 | 3226 | 41 | 3169 | 46 | 8.14 | 58 | 56.61 | 55 |
| B32 | 3225 | 2640 | 71 | 2690 | 70 | 2626 | 71 | 3.92 | 37 | 48.03 | 63 |
| B33 | 3546 | 3397 | 22 | 3418 | 24 | 3395 | 22 | 5.72 | 46 | 70.60 | 31 |
| B34 | 2857 | 2976 | 59 | 3133 | 53 | 2987 | 59 | 14.44 | 72 | 36.15 | 71 |
| B35 | 3182 | 3033 | 55 | 3047 | 57 | 3045 | 55 | 1.33 | 6 | 69.83 | 33 |
| B36 | 3190 | 2849 | 66 | 2906 | 63 | 2850 | 66 | 7.33 | 56 | 47.21 | 66 |
| B37 | 3496 | 3425 | 17 | 3475 | 12 | 3423 | 18 | 9.03 | 64 | 63.35 | 42 |
| B38 | 3143 | 3363 | 27 | 3410 | 26 | 3358 | 27 | 8.77 | 62 | 61.63 | 45 |
| B39 | 3806 | 3180 | 41 | 3196 | 46 | 3190 | 40 | 1.74 | 9 | 74.09 | 25 |
| B4 | 3487 | 2804 | 67 | 2828 | 67 | 2813 | 67 | 3.34 | 31 | 55.89 | 56 |
| B40 | 3171 | 3447 | 14 | 3464 | 15 | 3461 | 13 | 1.52 | 8 | 84.77 | 8 |
| B41 | 3006 | 2853 | 64 | 2898 | 64 | 2874 | 64 | 3.69 | 34 | 57.87 | 53 |
| B42 | 2948 | 3136 | 50 | 3152 | 51 | 3148 | 49 | 2.58 | 15 | 70.17 | 32 |
| B43 | 3110 | 2857 | 63 | 2892 | 65 | 2875 | 63 | 5.45 | 44 | 52.61 | 61 |
| B44 | 3440 | 2919 | 61 | 2961 | 62 | 2941 | 61 | 3.55 | 33 | 60.67 | 49 |
| B45 | 3228 | 2673 | 68 | 2695 | 69 | 2676 | 69 | 4.10 | 38 | 48.62 | 62 |
| B46 | 3439 | 3720 | 3 | 3739 | 3 | 3734 | 3 | 3.21 | 29 | 90.21 | 2 |
| B47 | 3411 | 3179 | 42 | 3214 | 45 | 3180 | 41 | 7.05 | 52 | 59.41 | 51 |
| B48 | 3432 | 3162 | 45 | 3193 | 47 | 3173 | 43 | 4.51 | 40 | 66.05 | 39 |
| B49 | 3476 | 2643 | 70 | 2685 | 71 | 2656 | 70 | 7.08 | 53 | 39.33 | 70 |
| B5 | 3210 | 3305 | 31 | 3366 | 30 | 3316 | 30 | 8.71 | 61 | 60.82 | 48 |
| B50 | 3489 | 2104 | 72 | 2192 | 72 | 2125 | 72 | 11.55 | 67 | 8.18 | 72 |
| B51 | 3209 | 3485 | 9 | 3501 | 9 | 3498 | 8 | 1.75 | 10 | 85.50 | 5 |
| B52 | 2586 | 3414 | 19 | 3432 | 20 | 3425 | 17 | 3.15 | 27 | 78.95 | 17 |
| B53 | 3426 | 3451 | 13 | 3473 | 13 | 3466 | 12 | 2.86 | 21 | 81.36 | 13 |
| B54 | 3129 | 3729 | 2 | 3765 | 1 | 3742 | 1 | 7.28 | 55 | 80.24 | 14 |
| B55 | 2854 | 2657 | 69 | 2723 | 68 | 2683 | 68 | 6.56 | 47 | 42.72 | 68 |
| B56 | 3491 | 3013 | 57 | 3066 | 56 | 3026 | 57 | 6.68 | 48 | 55.13 | 57 |
| B57 | 3415 | 3209 | 36 | 3222 | 42 | 3220 | 37 | 1.19 | 3 | 76.64 | 21 |
| B58 | 3201 | 3194 | 38 | 3221 | 43 | 3210 | 38 | 2.94 | 24 | 71.85 | 29 |
| B59 | 3184 | 3161 | 46 | 3187 | 48 | 3172 | 44 | 4.48 | 39 | 66.07 | 38 |
| B6 | 2594 | 3139 | 49 | 3177 | 50 | 3150 | 48 | 6.76 | 49 | 59.01 | 52 |
| B60 | 3386 | 3386 | 24 | 3404 | 28 | 3387 | 25 | 2.77 | 20 | 78.54 | 18 |
| B61 | 2031 | 3462 | 11 | 3477 | 11 | 3470 | 11 | 2.43 | 14 | 82.47 | 11 |
| B62 | 3853 | 3403 | 20 | 3438 | 19 | 3403 | 21 | 7.18 | 54 | 67.32 | 36 |
| B63 | 2652 | 3428 | 16 | 3441 | 18 | 3436 | 16 | 2.93 | 22 | 79.76 | 15 |
| B64 | 3039 | 3204 | 37 | 3282 | 36 | 3208 | 39 | 9.82 | 65 | 54.28 | 58 |
| B65 | 3221 | 3142 | 48 | 3252 | 38 | 3141 | 50 | 11.80 | 68 | 47.38 | 65 |
| B66 | 3164 | 3401 | 21 | 3414 | 25 | 3411 | 20 | 1.07 | 2 | 84.06 | 10 |
| B67 | 3414 | 3320 | 28 | 3427 | 22 | 3317 | 29 | 11.89 | 69 | 53.53 | 59 |
| B68 | 3452 | 3732 | 1 | 3742 | 2 | 3738 | 2 | 2.72 | 19 | 91.39 | 1 |
| B69 | 3283 | 2849 | 65 | 2889 | 66 | 2859 | 65 | 6.88 | 50 | 47.63 | 64 |
| B7 | 3244 | 3274 | 34 | 3302 | 33 | 3292 | 32 | 3.71 | 36 | 72.74 | 27 |
| B70 | 3438 | 3437 | 15 | 3455 | 17 | 3452 | 15 | 1.24 | 5 | 85.27 | 6 |
| B71 | 2828 | 3164 | 44 | 3177 | 49 | 3176 | 42 | 1.20 | 4 | 75.00 | 22 |
| B72 | 3319 | 3015 | 56 | 3029 | 58 | 3028 | 56 | 1.45 | 7 | 68.83 | 34 |
| B8 | 3348 | 3192 | 39 | 3321 | 32 | 3221 | 36 | 8.23 | 60 | 60.92 | 47 |
| B9 | 3219 | 3153 | 47 | 3218 | 44 | 3169 | 47 | 8.19 | 59 | 56.78 | 54 |

Supplementary Table S8: BLUP-based indexes for selecting genotypes with performance and stability at navy beans.

| GEN | Y | HMGV | HMGV_R | RPGV | RPGV_R | HMRPGV | HMRPGV_R | WAASB | WAASB_R | WAASBY | WAASBY_R |
|-----|------|------|--------|------|--------|--------|----------|-------|---------|--------|----------|
| N1 | 2469 | 2750 | 55 | 2765 | 55 | 2749 | 57 | 5.89 | 57 | 41.05 | 60 |
| N10 | 2809 | 2934 | 33 | 2954 | 32 | 2950 | 32 | 2.32 | 21 | 67.63 | 24 |
| N11 | 2734 | 2850 | 41 | 2905 | 39 | 2867 | 40 | 8.76 | 68 | 37.72 | 66 |
| N12 | 2661 | 2534 | 69 | 2545 | 69 | 2542 | 69 | 3.19 | 33 | 40.23 | 62 |
| N13 | 2849 | 2816 | 44 | 2827 | 46 | 2826 | 44 | 0.97 | 3 | 65.62 | 28 |
| N14 | 2723 | 2739 | 57 | 2761 | 57 | 2752 | 55 | 3.01 | 31 | 53.58 | 43 |
| N15 | 3302 | 2542 | 68 | 2567 | 68 | 2557 | 68 | 4.22 | 45 | 37.58 | 67 |
| N16 | 3144 | 2595 | 67 | 2606 | 67 | 2605 | 67 | 1.85 | 18 | 49.36 | 51 |
| N17 | 2677 | 2717 | 59 | 2731 | 59 | 2723 | 59 | 3.73 | 42 | 48.49 | 53 |
| N18 | 3037 | 2679 | 61 | 2700 | 61 | 2693 | 61 | 2.05 | 19 | 54.08 | 41 |
| N19 | 3090 | 2435 | 70 | 2456 | 70 | 2430 | 70 | 7.71 | 66 | 15.59 | 71 |
| N2 | 2802 | 2668 | 62 | 2686 | 62 | 2682 | 62 | 3.52 | 39 | 46.01 | 56 |
| N20 | 2913 | 2601 | 65 | 2613 | 66 | 2610 | 66 | 2.61 | 25 | 45.12 | 57 |
| N21 | 2993 | 2965 | 30 | 2979 | 30 | 2977 | 28 | 1.45 | 8 | 72.39 | 14 |
| N22 | 3119 | 3394 | 1 | 3417 | 1 | 3408 | 1 | 6.10 | 60 | 78.28 | 9 |
| N23 | 2903 | 3104 | 11 | 3116 | 12 | 3115 | 11 | 1.71 | 14 | 79.06 | 7 |
| N24 | 2852 | 2812 | 47 | 2824 | 47 | 2821 | 47 | 1.57 | 12 | 62.98 | 34 |
| N25 | 2803 | 2790 | 51 | 2816 | 50 | 2808 | 49 | 3.75 | 43 | 53.92 | 42 |
| N26 | 2969 | 2835 | 43 | 2855 | 43 | 2851 | 42 | 2.60 | 24 | 60.74 | 37 |
| N27 | 2994 | 3059 | 19 | 3072 | 20 | 3066 | 19 | 2.63 | 26 | 72.57 | 13 |
| N28 | 2805 | 2373 | 71 | 2401 | 71 | 2390 | 71 | 5.51 | 54 | 20.71 | 70 |
| N29 | 2987 | 2935 | 32 | 2947 | 33 | 2946 | 33 | 1.42 | 7 | 70.28 | 19 |
| N3 | 3337 | 3134 | 8 | 3152 | 8 | 3150 | 8 | 2.75 | 27 | 77.15 | 10 |
| N30 | 3257 | 2813 | 45 | 2850 | 44 | 2823 | 45 | 7.49 | 65 | 39.31 | 65 |
| N31 | 2632 | 2740 | 56 | 2755 | 58 | 2750 | 56 | 3.13 | 32 | 52.54 | 45 |
| N32 | 2919 | 2598 | 66 | 2661 | 65 | 2626 | 65 | 6.51 | 63 | 32.84 | 69 |
| N33 | 2630 | 2971 | 29 | 2981 | 29 | 2976 | 29 | 2.95 | 30 | 65.88 | 26 |
| N34 | 2503 | 2985 | 26 | 3068 | 21 | 3016 | 23 | 8.94 | 69 | 47.46 | 54 |
| N35 | 2544 | 3070 | 17 | 3115 | 13 | 3060 | 21 | 10.51 | 71 | 41.41 | 59 |
| N36 | 2690 | 3229 | 3 | 3243 | 3 | 3233 | 4 | 5.13 | 49 | 71.80 | 17 |
| N37 | 3207 | 3102 | 12 | 3116 | 11 | 3101 | 14 | 4.67 | 47 | 66.20 | 25 |
| N38 | 3112 | 2708 | 60 | 2730 | 60 | 2704 | 60 | 6.28 | 62 | 37.31 | 68 |
| N39 | 3035 | 3005 | 23 | 3016 | 25 | 3015 | 24 | 1.55 | 11 | 74.05 | 12 |
| N4 | 3523 | 3069 | 18 | 3081 | 18 | 3079 | 17 | 0.94 | 2 | 80.27 | 5 |
| N40 | 3156 | 3111 | 9 | 3125 | 10 | 3115 | 10 | 4.93 | 48 | 65.87 | 27 |
| N41 | 3020 | 3056 | 20 | 3066 | 22 | 3061 | 20 | 3.23 | 34 | 69.60 | 20 |
| N42 | 3312 | 2758 | 54 | 2769 | 54 | 2760 | 54 | 3.51 | 38 | 51.37 | 46 |
| N43 | 2920 | 2795 | 49 | 2811 | 52 | 2799 | 51 | 4.52 | 46 | 49.71 | 50 |
| N44 | 3156 | 2921 | 34 | 2931 | 35 | 2930 | 34 | 1.18 | 4 | 70.62 | 18 |
| N45 | 2805 | 2785 | 52 | 2821 | 49 | 2784 | 53 | 6.72 | 64 | 40.89 | 61 |
| N46 | 3114 | 2807 | 48 | 2832 | 45 | 2819 | 48 | 3.23 | 35 | 55.95 | 39 |
| N47 | 2933 | 3210 | 5 | 3225 | 6 | 3222 | 6 | 2.15 | 20 | 83.58 | 3 |
| N48 | 3290 | 3208 | 6 | 3252 | 2 | 3234 | 3 | 6.22 | 61 | 68.95 | 22 |
| N49 | 3159 | 3161 | 7 | 3190 | 7 | 3181 | 7 | 5.23 | 50 | 69.26 | 21 |
| N5 | 3043 | 3101 | 13 | 3115 | 14 | 3114 | 12 | 1.67 | 13 | 79.38 | 6 |
| N50 | 3138 | 2661 | 63 | 2679 | 63 | 2671 | 63 | 3.37 | 36 | 47.24 | 55 |
| N51 | 3293 | 2734 | 58 | 2761 | 56 | 2748 | 58 | 5.34 | 52 | 43.09 | 58 |
| N52 | 2721 | 2792 | 50 | 2814 | 51 | 2808 | 50 | 3.64 | 40 | 54.21 | 40 |
| N53 | 2901 | 2856 | 39 | 2901 | 40 | 2879 | 39 | 6.08 | 59 | 49.35 | 52 |
| N54 | 2344 | 3095 | 14 | 3112 | 15 | 3109 | 13 | 1.84 | 17 | 78.50 | 8 |
| N55 | 2619 | 3109 | 10 | 3136 | 9 | 3124 | 9 | 5.76 | 56 | 64.00 | 31 |
| N56 | 2521 | 2918 | 35 | 2939 | 34 | 2916 | 35 | 6.04 | 58 | 50.31 | 49 |
| N57 | 3100 | 3056 | 21 | 3074 | 19 | 3071 | 18 | 2.87 | 29 | 72.14 | 16 |
| N58 | 2261 | 2953 | 31 | 2975 | 31 | 2969 | 30 | 3.45 | 37 | 64.10 | 30 |
| N59 | 2947 | 2990 | 24 | 3006 | 28 | 3004 | 25 | 1.82 | 16 | 72.37 | 15 |
| N6 | 2824 | 3017 | 22 | 3025 | 23 | 3023 | 22 | 1.40 | 6 | 74.94 | 11 |
| N60 | 2602 | 3091 | 15 | 3101 | 16 | 3101 | 15 | 0.86 | 1 | 81.68 | 4 |
| N61 | 3122 | 2973 | 28 | 3018 | 24 | 2965 | 31 | 9.45 | 70 | 39.86 | 63 |
| N62 | 3132 | 2851 | 40 | 2883 | 41 | 2846 | 43 | 7.84 | 67 | 39.48 | 64 |
| N63 | 3160 | 2871 | 38 | 2907 | 38 | 2893 | 38 | 5.28 | 51 | 52.99 | 44 |
| N64 | 2731 | 3078 | 16 | 3090 | 17 | 3082 | 16 | 3.96 | 44 | 67.96 | 23 |
| N65 | 2784 | 2891 | 37 | 2912 | 37 | 2894 | 37 | 5.71 | 55 | 50.44 | 48 |
| N66 | 2790 | 2990 | 25 | 3008 | 27 | 2994 | 27 | 5.50 | 53 | 56.89 | 38 |
| N67 | 2803 | 2655 | 64 | 2675 | 64 | 2669 | 64 | 2.48 | 22 | 50.87 | 47 |
| N68 | 2716 | 2984 | 27 | 3008 | 26 | 3001 | 26 | 3.67 | 41 | 65.18 | 29 |
| N69 | 3192 | 3230 | 2 | 3243 | 4 | 3242 | 2 | 1.78 | 15 | 86.14 | 2 |
| N7 | 2930 | 3218 | 4 | 3229 | 5 | 3229 | 5 | 1.26 | 5 | 87.42 | 1 |
| N70 | 3025 | 2894 | 36 | 2914 | 36 | 2909 | 36 | 2.83 | 28 | 63.18 | 33 |
| N71 | 3007 | 2781 | 53 | 2795 | 53 | 2794 | 52 | 1.50 | 10 | 60.89 | 36 |
| N8 | 2859 | 2842 | 42 | 2860 | 42 | 2854 | 41 | 2.52 | 23 | 61.21 | 35 |
| N9 | 2755 | 2812 | 46 | 2823 | 48 | 2821 | 46 | 1.47 | 9 | 63.27 | 32 |

Supplementary Table S9: BLUP-based indexes for selecting genotypes with performance and stability at red beans.

| GEN | Y | HMGV | HMGV_R | RPGV | RPGV_R | HMRPGV | HMRPGV_R | WAASB | WAASB_R | WAASBY | WAASBY_R |
|-----|------|------|--------|------|--------|--------|----------|-------|---------|--------|----------|
| R1 | 3213 | 3307 | 5 | 3332 | 5 | 3331 | 5 | 3.11 | 3 | 70.44 | 3 |
| R10 | 2995 | 3174 | 8 | 3206 | 8 | 3193 | 7 | 5.37 | 10 | 54.74 | 7 |
| R11 | 3170 | 3181 | 7 | 3212 | 7 | 3183 | 8 | 7.65 | 16 | 47.05 | 11 |
| R12 | 3420 | 3005 | 13 | 3027 | 14 | 3014 | 14 | 5.44 | 12 | 41.75 | 14 |
| R13 | 3020 | 3155 | 9 | 3180 | 9 | 3163 | 9 | 5.11 | 9 | 53.00 | 8 |
| R14 | 2762 | 3681 | 1 | 3724 | 1 | 3679 | 1 | 11.37 | 19 | 69.93 | 4 |
| R15 | 3083 | 2990 | 15 | 3012 | 15 | 3001 | 16 | 5.42 | 11 | 40.95 | 16 |
| R16 | 2903 | 2987 | 16 | 3005 | 16 | 3003 | 15 | 1.54 | 1 | 52.65 | 9 |
| R17 | 3363 | 3006 | 12 | 3096 | 10 | 3014 | 13 | 14.62 | 21 | 18.25 | 20 |
| R18 | 2835 | 3323 | 4 | 3370 | 4 | 3360 | 4 | 3.70 | 6 | 71.93 | 2 |
| R19 | 3040 | 3030 | 10 | 3080 | 11 | 3063 | 10 | 5.49 | 13 | 46.71 | 12 |
| R2 | 2956 | 3233 | 6 | 3258 | 6 | 3251 | 6 | 4.06 | 7 | 62.28 | 6 |
| R20 | 2981 | 2819 | 20 | 2939 | 18 | 2873 | 19 | 12.06 | 20 | 17.67 | 21 |
| R21 | 3274 | 3420 | 3 | 3445 | 3 | 3444 | 3 | 3.14 | 4 | 78.03 | 1 |
| R3 | 2978 | 2850 | 19 | 2875 | 20 | 2872 | 20 | 3.50 | 5 | 38.31 | 17 |
| R4 | 3494 | 3018 | 11 | 3040 | 13 | 3036 | 11 | 2.56 | 2 | 52.00 | 10 |
| R5 | 3201 | 3003 | 14 | 3047 | 12 | 3031 | 12 | 6.31 | 14 | 41.72 | 15 |
| R6 | 3786 | 3474 | 2 | 3504 | 2 | 3482 | 2 | 8.32 | 18 | 65.20 | 5 |
| R7 | 3073 | 2722 | 21 | 2794 | 21 | 2765 | 21 | 7.67 | 17 | 21.26 | 19 |
| R8 | 2930 | 2933 | 17 | 2972 | 17 | 2965 | 17 | 4.22 | 8 | 43.20 | 13 |
| R9 | 3546 | 2860 | 18 | 2919 | 19 | 2900 | 18 | 6.72 | 15 | 32.45 | 18 |

Supplementary Table S10: Selection differential of the WAASBY index for 27 Black, 29 Navy and 12 Red beans.

Black Beans

| Factor | Trait | Xo [‡] | Xs [§] | SD (%) [¶] | Sense |
|--------|-------|-----------------|-----------------|---------------------|----------|
| FA 1 | GY | 3,201 | 3,258 | 57.92 (1.81) | Increase |
| FA 1 | LD | 1.73 | 1.63 | -0.1 (-5.556) | Decrease |
| FA 2 | DM | 91.78 | 91.90 | 0.12 (0.1324) | Decrease |
| FA 2 | PH | 18.15 | 18.34 | 0.19 (1.063) | Increase |

Navy Beans

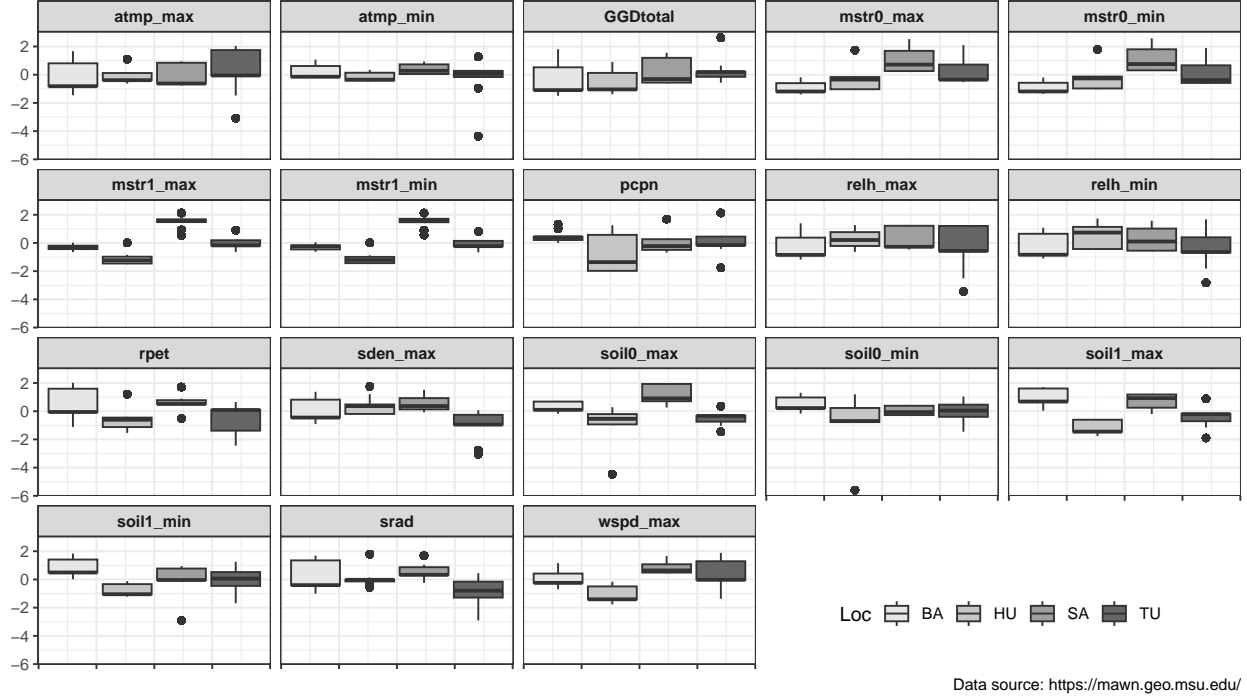
| Factor | Trait | Xo [‡] | Xs [§] | SD (%) [¶] | Sense |
|--------|-------|-----------------|-----------------|---------------------|----------|
| FA 1 | GY | 3,006 | 3,145 | 138.90 (4.619) | Increase |
| FA 1 | DM | 91.25 | 91.54 | 0.29 (0.3184) | Decrease |
| FA 1 | PH | 18.34 | 19.69 | 1.35 (7.371) | Increase |
| FA 1 | LD | 1.88 | 1.65 | -0.22 (-11.85) | Decrease |

Red Beans

| Factor | Trait | Xo [‡] | Xs [§] | SD (%) [¶] | Sense |
|--------|-------|-----------------|-----------------|---------------------|----------|
| FA 1 | PH | 18.25 | 20.07 | 1.82 (9.966) | Increase |
| FA 1 | LD | 1.87 | 1.91 | 0.04 (2.104) | Decrease |
| FA 2 | GY | 3,156 | 3,162 | 5.92 (0.1875) | Increase |
| FA 2 | DM | 90.85 | 90.88 | 0.03 (0.02776) | Decrease |

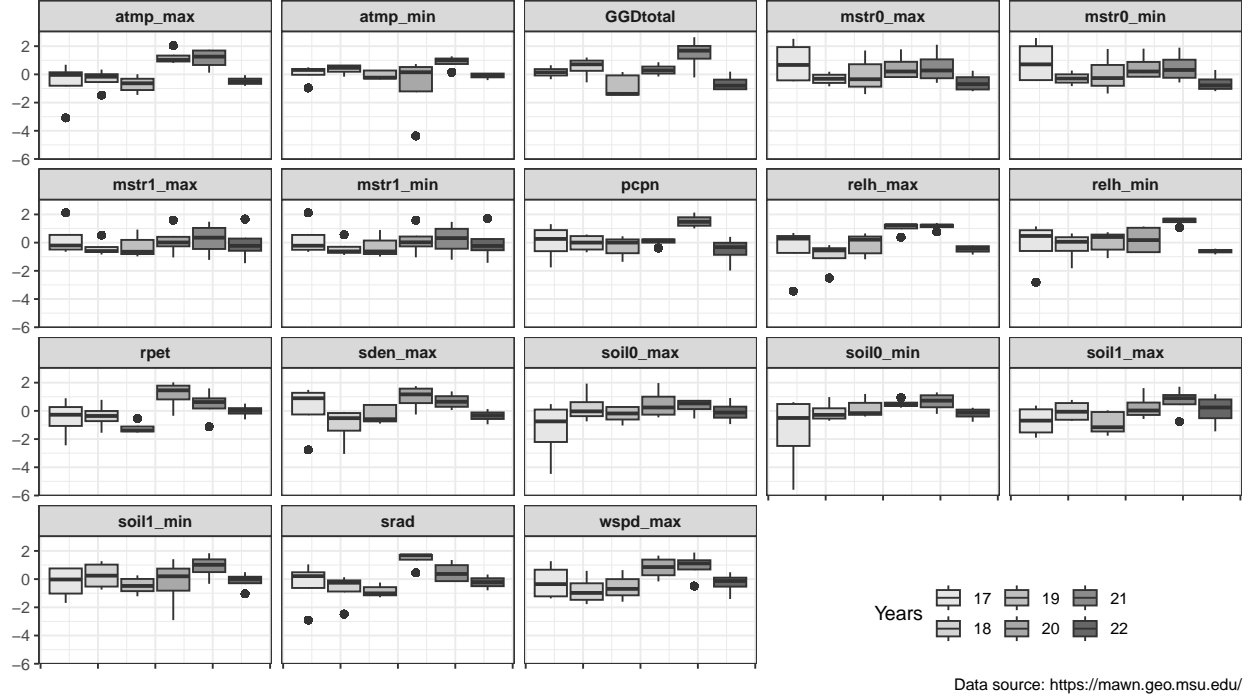
GY, grain yield; PH, plant height; DM, days to maturity; LD, lodging;[‡] Xo, mean for WAASBY index of the original population; [§] Xs, mean for WAASBY index of the selected genotypes (BB: B55, B1, B29, B20, B28; NB: N38, N6, N61, N35, N52, N22; SR: R2, R13); SD, Selection differential; [¶]% of SD in parenthesis.

2 Appendix B - Supplementary Figures



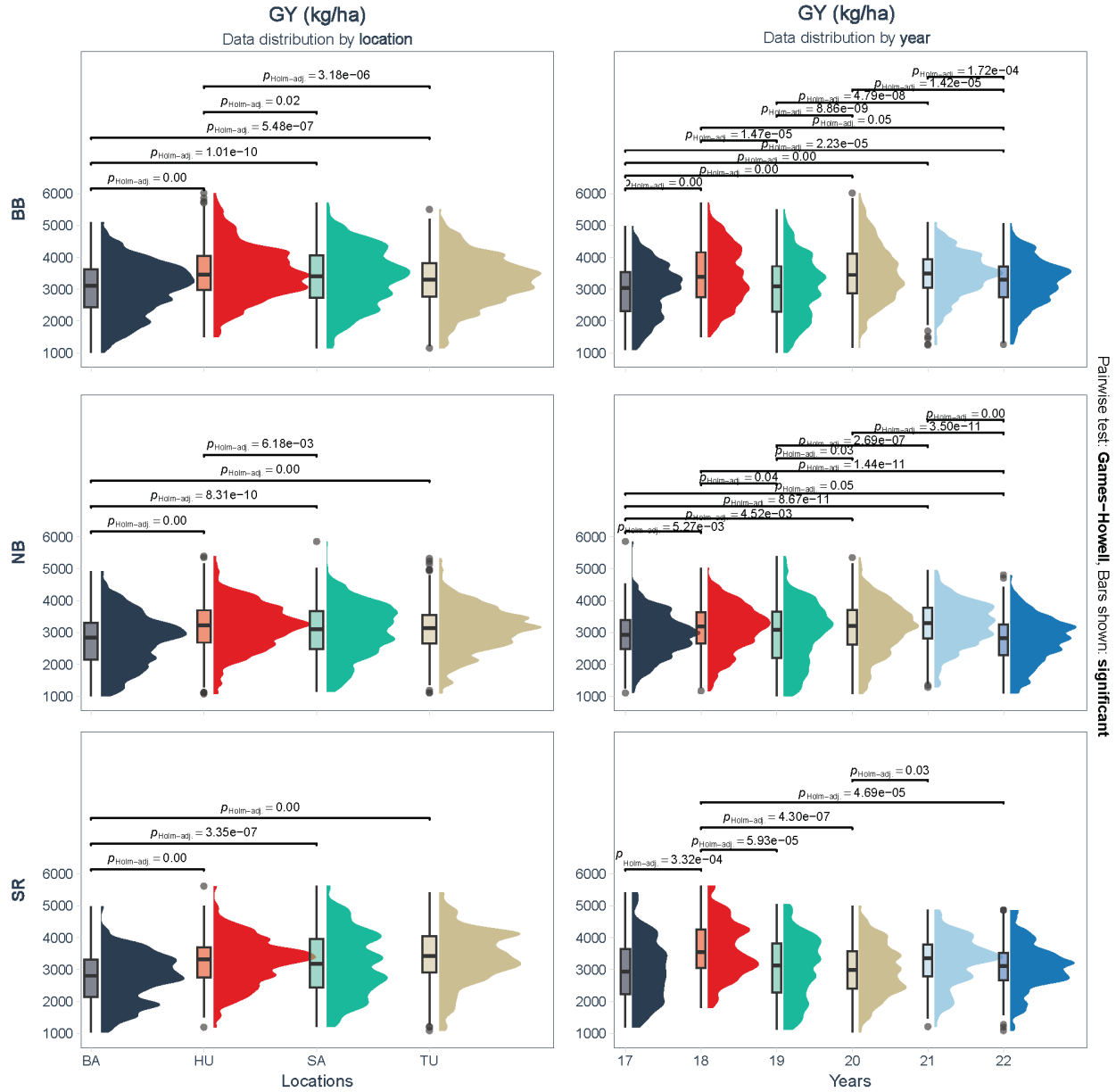
Supplementary Figure S1: Box plot distribution from the weather data collected by location from 2017 to 2022 cultivation years. Data were scaled to better plot visualization. Weather data obtained using daily average value from planting to harvesting.

atmp_max: Max Air Temperature (1.5m), atmp_min: Min Air Temperature (1.5m), mstr0_max: Max Soil Moisture (0-30cm), mstr0_min: Min Soil Moisture (0-30cm), mstr1_max: Max Soil Moisture (30-60cm), mstr1_min: Min Soil Moisture (30-60cm), pcpn: Precipitation, relh_max: Max Relative Humidity (1.5m), relh_min: Min Relative Humidity (1.5m), rpet: Reference Potential Evapotranspiration, sden_max: Max Solar Flux, soil0_max: Max Soil Temperature (5cm), soil0_min: Min Soil Temperature (5cm), soil1_max: Max Soil Temperature (10cm), soil1_min: Min Soil Temperature (10cm), srad: Total Solar Flux, wspd_max: Max Wind Speed (3m). GGDtotal: Growing Degree-Day Calculations in Celsius (C) given by: $(max - min)/2 - 10$

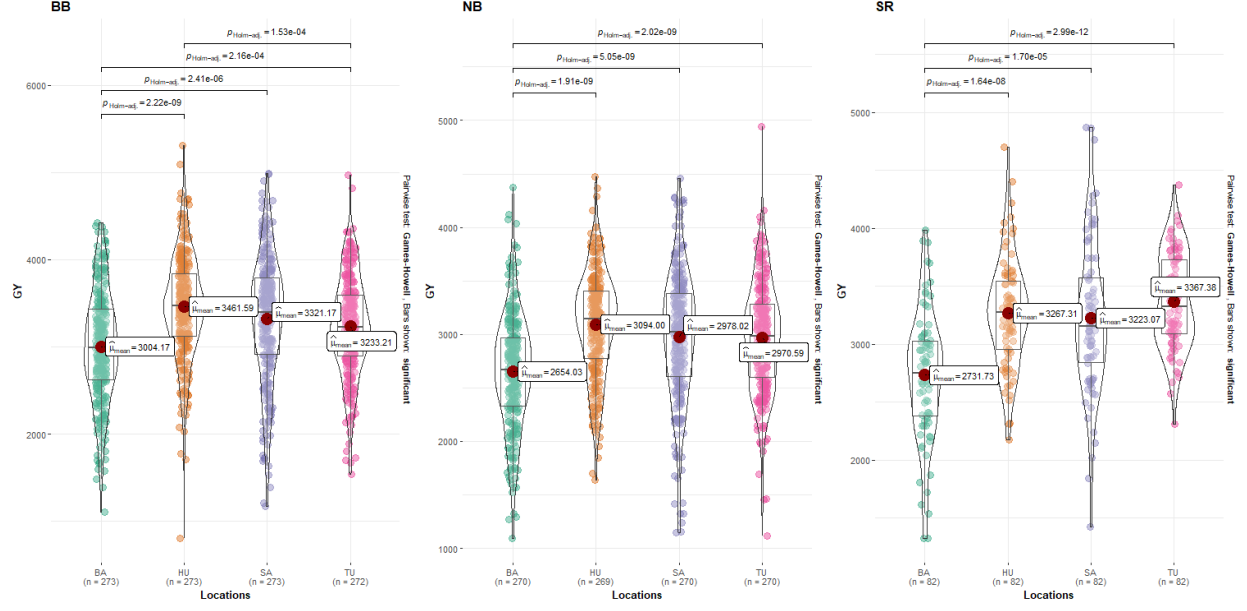


Supplementary Figure S2: Box plot distribution from the weather data collected by year from 2017 to 2022 cultivation locations. Data were scaled to better plot visualization. Weather data obtained using daily average value from planting to harvesting.

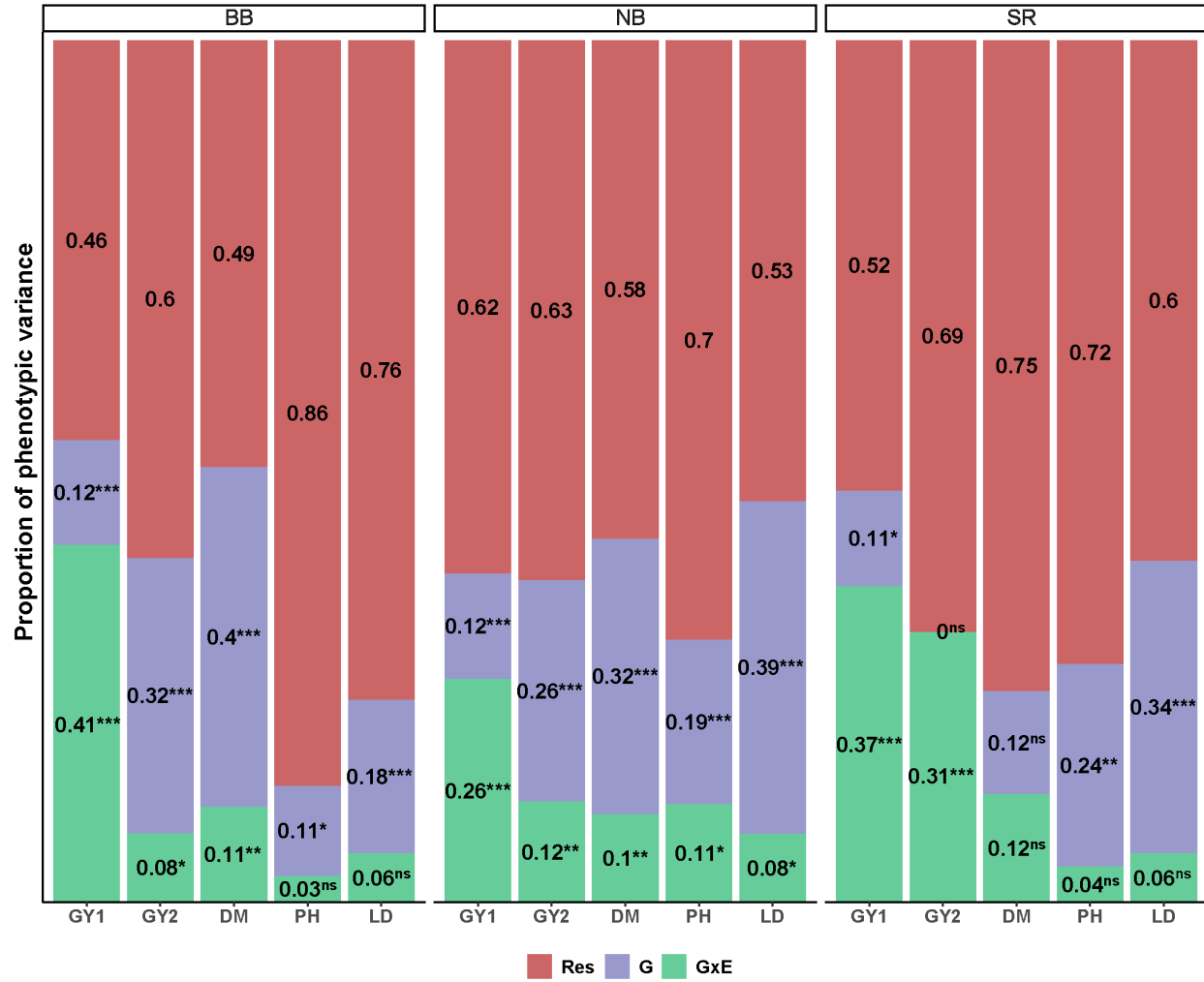
atmp_max: Max Air Temperature (1.5m), atmp_min: Min Air Temperature (1.5m), mstr0_max: Max Soil Moisture (0-30cm), mstr0_min: Min Soil Moisture (0-30cm), mstr1_max: Max Soil Moisture (30-60cm), mstr1_min: Min Soil Moisture (30-60cm), pcpn: Precipitation, relh_max: Max Relative Humidity (1.5m), relh_min: Min Relative Humidity (1.5m), rpet: Reference Potential Evapotranspiration, sden_max: Max Solar Flux, soil0_max: Max Soil Temperature (5cm), soil0_min: Min Soil Temperature (5cm), soil1_max: Max Soil Temperature (10cm), soil1_min: Min Soil Temperature (10cm), srad: Total Solar Flux, wspd_max: Max Wind Speed (3m). GGDtotal: Growing Degree-Day Calculations in Celsius (C) given by: $(max - min)/2 - 10$



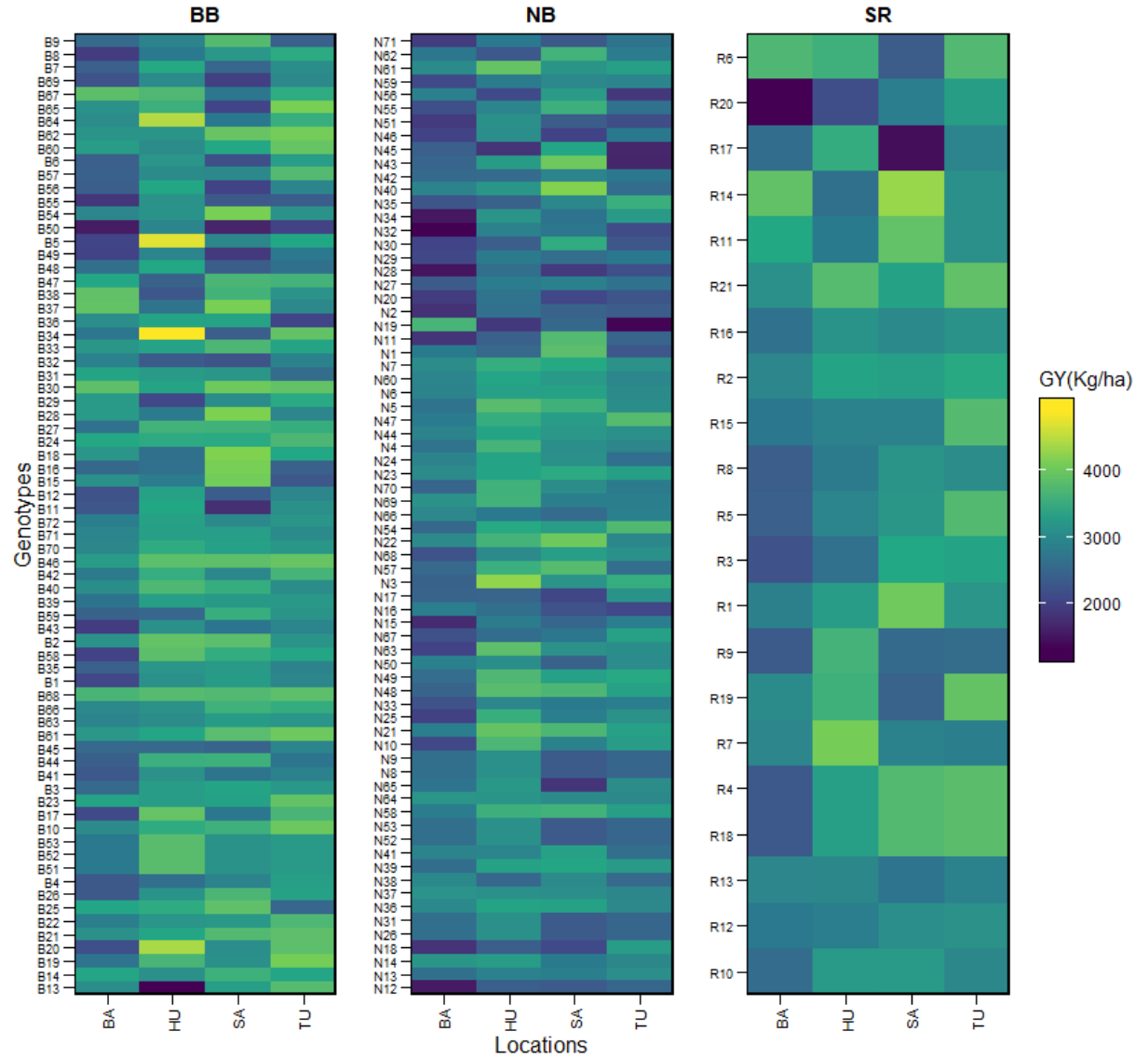
Supplementary Figure S3: Combination of box and density plots for between subjects comparisons by locations (left) and year (right) of grain yield (GY in Kg/ha) for black (BB), Navy (NB) and Red (SR) beans. BA: Bay, HU: Huron, SA:Sanilac, TU: Tuscola locations.



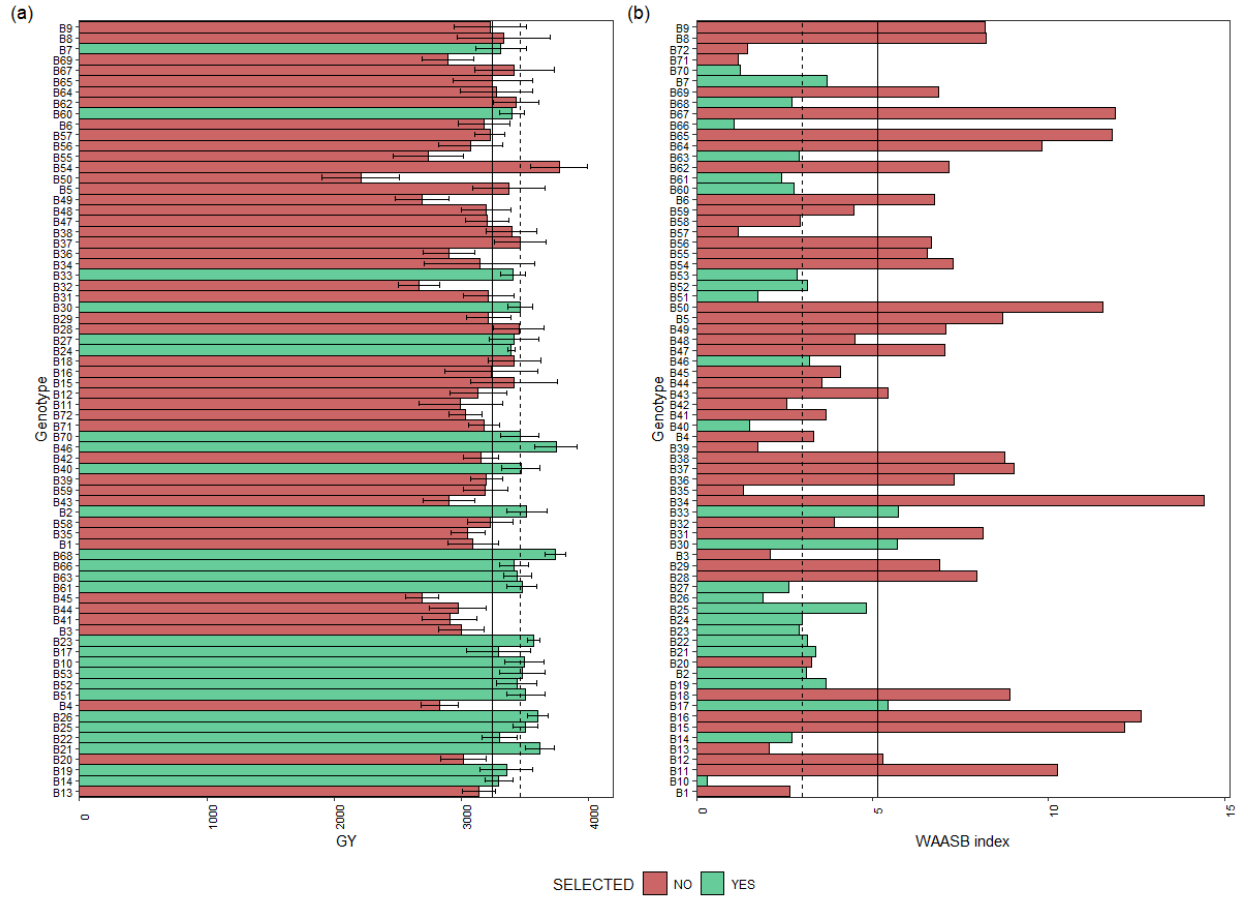
Supplementary Figure S4: Combination of box and violin plots along with jittered data points and grand mean values for between subjects comparisons by locations of grain yield (GY) for black (BB), Navy (NB) and Small Red (SR) beans. Pairwise Games-Howell test used. Comparisons showing only significant values. BA: Bay, HU: Huron, SA: Sanilac, TU: Tuscola. Pairwise Games-Howell test used. Comparisons showing only significant between the pairs of environments



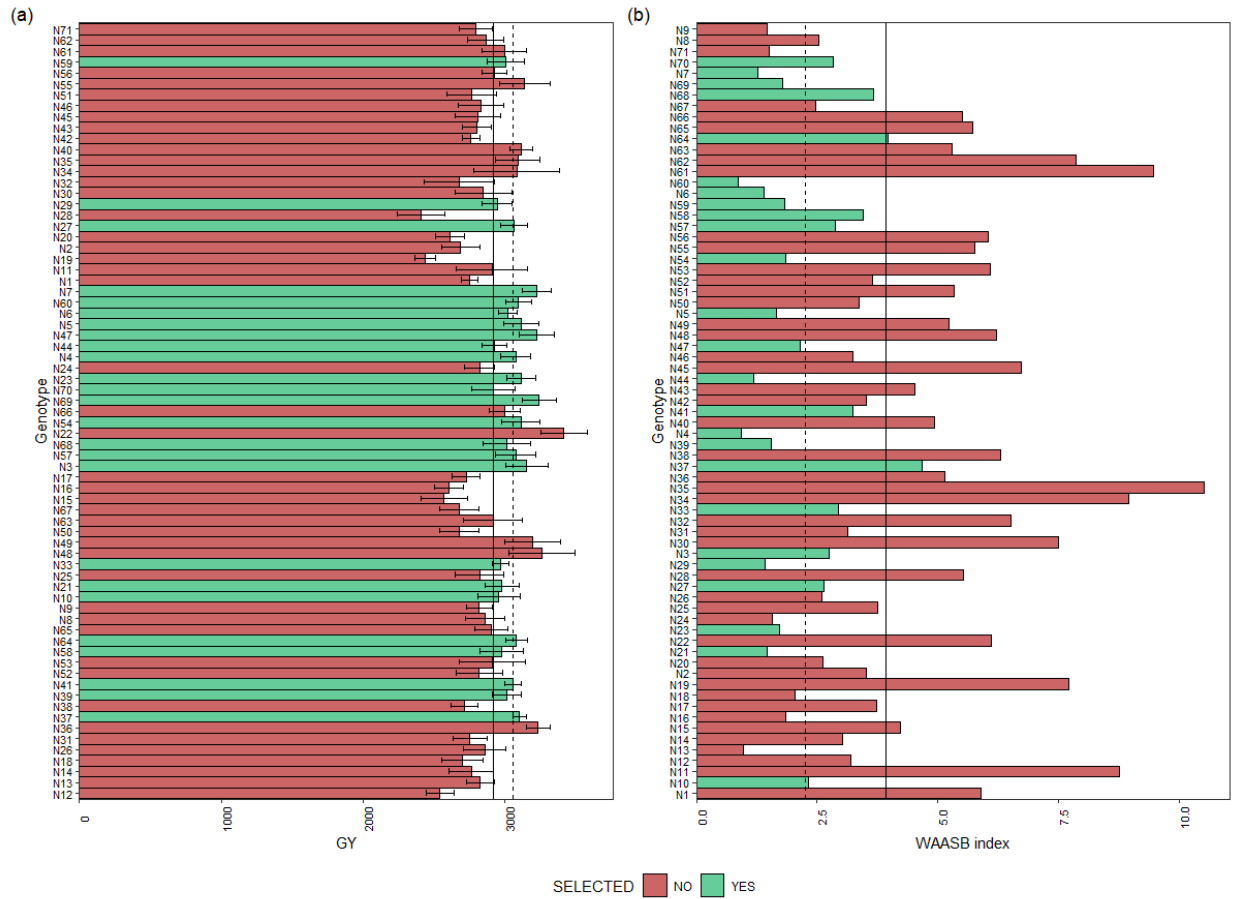
Supplementary Figure S5: Proportion of the phenotypic variance for 71 Black (BB), 72 Navy (NB), and 21 Red (SR) beans for grain yield in Kg/ha (GY: 2017 - 2022; GY2: only 2021) days to maturity (DM, days), plant height (PH, cm) and lodging (LD, scale) traits evaluated in the study. * Significant at $P < 0.05$. ** Significant at $P < 0.01$. *** Significant at $P < 0.001$. ^{ns}, nonsignificant.



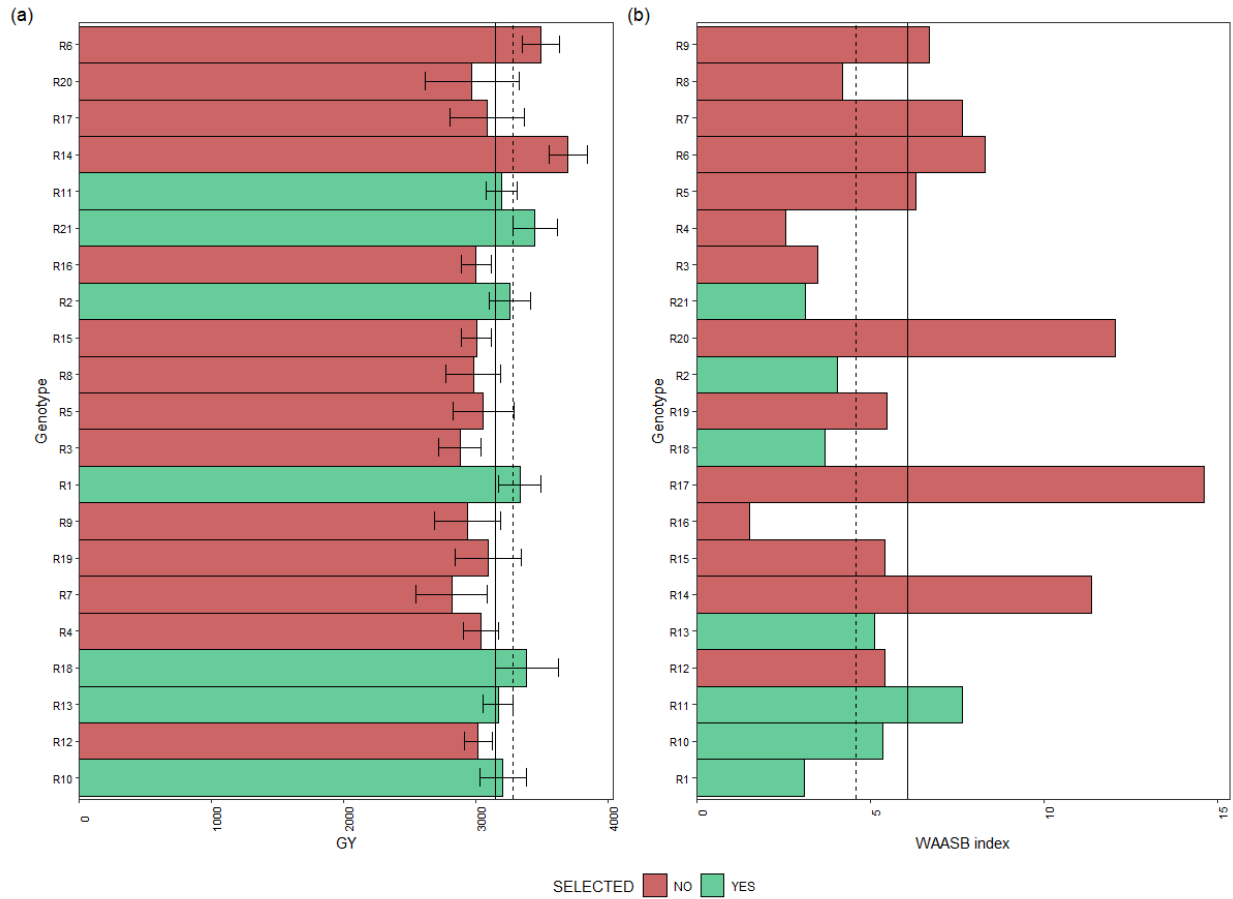
Supplementary Figure S6: Genotype's performance across the environments for Black (BB), Navy (NB), and Small Red (SR) beans using the estimated means (BLUEs) values. BA: Bay, HU: Huron, SA:Sanilac, TU: Tuscola locations



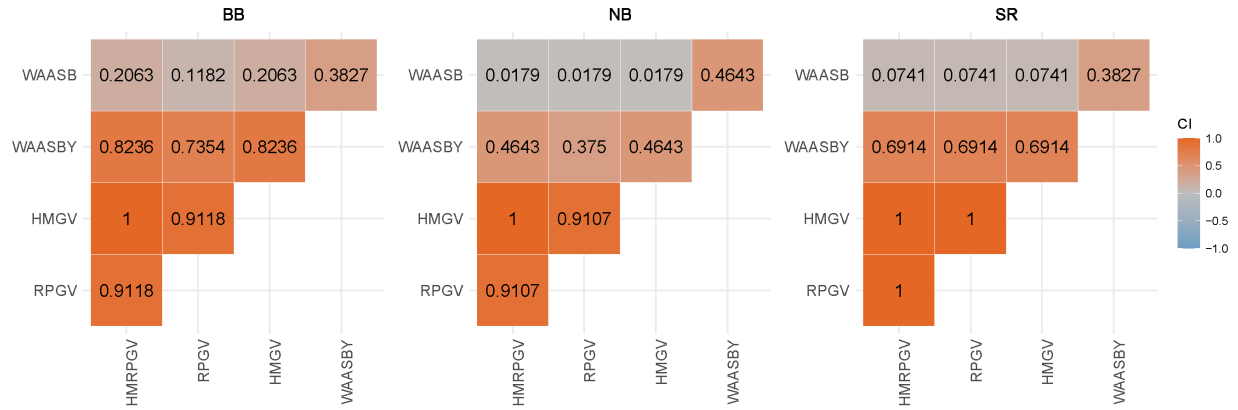
Supplementary Figure S7: Mean performance (a) and stability (b) for grain yield (GY) of 72 black beans genotypes. The vertical dashed and solid lines shows, respectively, the mean of the selected genotype and the overall mean for both mean performance and WAASB index.



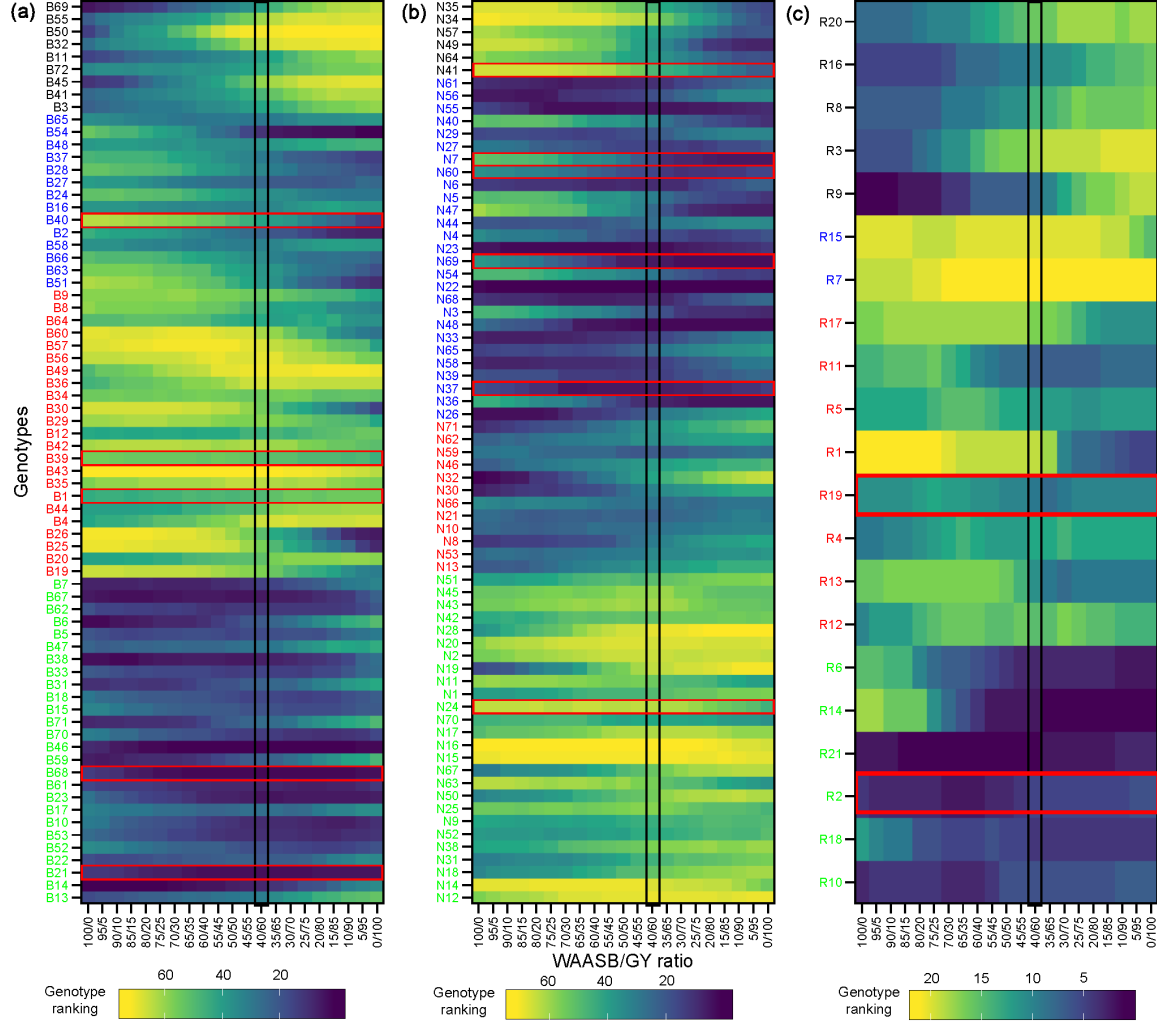
Supplementary Figure S8: Mean performance (a) and stability (b) for grain yield (GY) of 71 navy beans genotypes. The vertical dashed and solid lines shows, respectively, the mean of the selected genotype and the overall mean for both mean performance and WAASB index.



Supplementary Figure S9: Mean performance (a) and stability (b) for grain yield (GY) of 21 red beans genotypes. The vertical dashed and solid lines shows, respectively, the mean of the selected genotype and the overall mean for both mean performance and WAASB index.



Supplementary Figure S11: BLUP-based stability indexes coincidence index (CI) using selection intensity of 20 top genotypes. BB, black; NB, navy; SR, red beans.



Supplementary Figure S10: Ranks of dry beans genotypes (a: 72 black, b: 71 navys and c: 21 small red/pink) considering different weights for stability and yielding. The most-left ranks were obtained considering the stability only. The most right-ranks were obtained considering the grain yield only. Between the extremes, the ranks were obtained different weights for stability and yielding. The four clusters represent four classes of genotypes: (1) Poorly productive and unstable genotypes; (2) productive but unstable genotypes; (3) stable but poorly productive genotypes; and (4), highly productive and stable genotypes. The ranks highlighted by a black rectangle are the same from those BLUPs predicted to WAASBY index and the red rectangle box are the selected genotypes by the Multi-Trait Stability Index (MTSI).

3 Appendix C - R codes

Getting started

The present analysis aims to dissect the genotype by environment interaction study (aka GEI) using a data set from the Dry Beans breeding program at Michigan State University - MSU.

The trait in study is the grain yield (GY) per plot (lb/plot) adjusted to the international measurements (Kg/ha). A previous data analysis (not shown here) was done to perform the historical data mining and adjust of raw data. Besides the GY, plant height (PH), date of maturity (DM) and lodging (LD) were investigate using a subset from 2021, which contains the all the data available.

The main focus of this manuscript, as describe in the published paper, is to investigate the varieties performance of GY across four locations at different Michigan counties. However, the MTME (three locations and 4 traits) also was studied in this manuscript when available (only in 2021 in Bay, Tuscola and Sanilac sites). Thus, different types of analysis will be performed in order to study the GEI in the Multi-Environment-Trials (MET) data to provide better varieties recommendations to the Dry Beans breeding program, which:

- ☒ Multi-Environment Trials – Genotype x Environment Interaction to grain yield (GY)
- ☒ Mean performance and stability of multiple traits

3.1 Packages

This document was prepared on 2023-03-28.

The analysis was done using the R Statistical language (v4.2.2; R Core Team, 2022) on Windows 10 x64, using the packages rmarkdown (v2.19), ggpmisc (v0.5.1), ggpp (v0.5.0), gridExtra (v2.3), magrittr (v2.0.3), Matrix (v1.5.1), mapdata (v2.3.1), maps (v3.4.1), spData (v2.2.1), asremlPlus (v4.3.40), asreml (v4.1.0.160), tidyquant (v1.0.6), data.table (v1.14.4), flextable (v0.8.3), lubridate (v1.9.0), purrr (v0.3.5), raster (v3.6.3), ggcorrplot (v0.1.4), ggdist (v3.2.1), tibble (v3.1.8), rcartocolor (v2.0.0), metan (v1.17.0), ggstatsplot (v0.10.0), sf (v1.0.9), sp (v1.5.1), ggforce (v0.4.1), PerformanceAnalytics (v2.0.4), broom (v1.0.2), quantmod (v0.4.20), xts (v0.12.2), openxlsx (v4.2.5.1), timechange (v0.1.1), naniar (v0.6.1), TTR (v0.24.3), statgenGxE (v1.0.5), tigris (v2.0), plyr (v1.8.8), ggplot2 (v3.4.0), forcats (v0.5.2), stringr (v1.5.0), tidyverse (v1.3.2), dplyr (v1.0.10), tidyr (v1.2.1), readr (v2.1.3), cowplot (v1.1.1), nadiv (v2.17.2), DT (v0.26), zoo (v1.8.11) and kableExtra (v1.3.4).

3.2 Data preparation

```
data_beans = read.csv("data/DataBean_MET_GYv2.csv",h=T, stringsAsFactors = T)

if (knitr::is_html_output()) {

  print_table(data_beans)

}else{

  flextable(head(data_beans)) %>%
    add_footer_lines(
      c("Varieties Dry Beans data set from 2017 to 2022",
        "Header data set showing the 6 first entry")) %>%
    autofit() %>%
```

```
add_header_lines("Dry Beans varieties trial") %>%
theme_design2()
}
```

Dry Beans varieties trial

| codename | name | repmkt | year_loc | loc | year | gy_kg_ha |
|----------|------|--------|----------|-----|------|----------|
| 213SP | N1 | 1NB | 17_BA | BA | 17 | |
| 213SP | N1 | 1NB | 17_HU | HU | 17 | |
| 213SP | N1 | 1NB | 17_SA | SA | 17 | |
| 213SP | N1 | 1NB | 17_TU | TU | 17 | |
| 213SP | N1 | 1NB | 18_BA | BA | 18 | |
| 213SP | N1 | 1NB | 18_HU | HU | 18 | |

Varieties Dry Beans data set from 2017 to 2022

Header data set showing the 6 first entry

```
# Data adjustment
# All the effect columns must be as a factor to run in ASReml-r.
cols <- c("rep", "name", "loc", "year", "mkt", "year_loc")
data_beans[cols] <- lapply(data_beans[cols], factor)
data_beans <- data.table(data_beans)
```

3.3 Descriptive Stats - Raw data

Data set distribution, checking data and locations of study.

```
data_beans = read.csv("data/DataBean_MET_GYv2.csv", h=T, stringsAsFactors = T)

# Data adjustment
# All the effect columns must be as a factor to run in ASReml-r.
cols <- c("rep", "name", "loc", "year", "mkt", "year_loc")
data_beans[cols] <- lapply(data_beans[cols], factor)
data_beans <- data.table(data_beans)
```

3.3.1 Box plot dist.

```
plotDM_stats_mkt_loc<- grouped_ggbetweenstats(data=data_beans, x= loc, y=gy_kg_ha, type =
  ↪ "parametric", bf.message = F, results.subtitle = F,
  ylab= "GY", xlab = "Locations",
  plot.type = "boxviolin", grouping.var = mkt )
```

```

#print(plotDM_stats_mkt_loc)

plotDM_stats_mkt_year<- grouped_ggbetweenstats(data=data_beans, x= year, y=gy_kg_ha, type
  ↪ = "parametric", bf.message = F, results.subtitle = F,
      ylab= "GY", xlab = "Years",
      plot.type = "boxviolin", grouping.var = mkt )

#print(plotDM_stats_mkt_year)

print(arrange_ggplot(plotDM_stats_mkt_loc,plotDM_stats_mkt_year))

a<- ggplot(data=data_beans, aes(x=reorder(loc, -gy_kg_ha), y=gy_kg_ha, fill=loc)) +
  ggdist::stat_halfeye(
    adjust = 0.5,
    justification = -0.1,
    .width = 0,
    point_colour = NA
  ) +

  geom_boxplot(
    width = .12,
    # outlier.color = NA,
    alpha = 0.5)+
  tidyquant::theme_tq()+
  facet_wrap("year")+
  facet_grid("mkt") +
  tidyquant::scale_fill_tq() +
  scale_x_discrete(expand = c(0.03,0)) +
  scale_y_continuous(limits = c(1000,6000), breaks = seq(1000, 6000, by = 1000)) +
  theme(axis.text.x=element_text(angle = 90),
    strip.text=element_blank(),
    legend.position = "none",
    panel.grid = element_blank())+
  labs(title="GY (kg/ha)",
    subtitle="Data distribution by location",
    caption=NULL, x=NULL, y=NULL)

b<- ggplot(data=data_beans, aes(x=reorder(year, -gy_kg_ha), y=gy_kg_ha, fill=year)) +
  ggdist::stat_halfeye(
    adjust = 0.5,
    justification = -0.1,
    .width = 0,
    point_colour = NA
  ) +

  geom_boxplot(
    width = .12,
    #outlier.color = NA,
    alpha = 0.5)+
  tidyquant::theme_tq()+
  facet_wrap("loc")+
  facet_grid("mkt") +
  tidyquant::scale_fill_tq() +
  scale_x_discrete(expand = c(0.03,0)) +

```

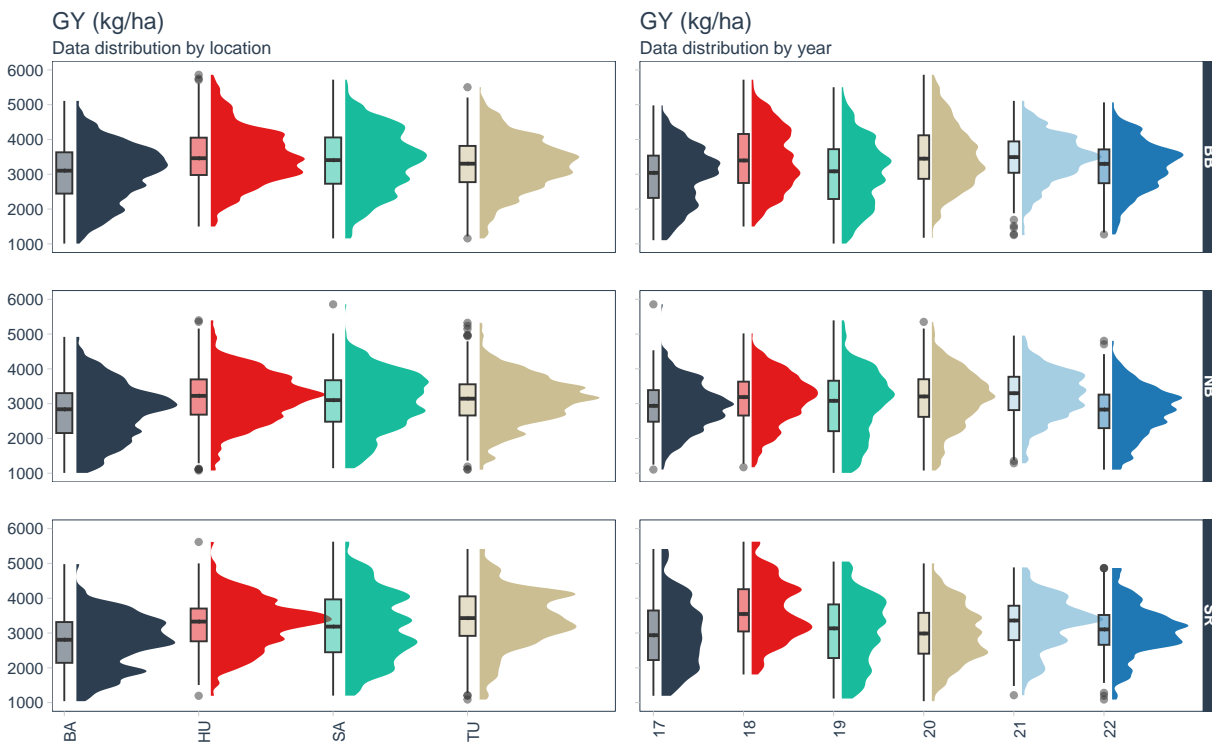


```

scale_y_continuous(limits = c(1000,6000), breaks = seq(1000, 6000, by = 1000)) +
theme(axis.text.x=element_text(angle = 90),
      strip.text=element_text(face="bold"),
      legend.position = "none",
      axis.text.y = element_blank(),
      panel.grid = element_blank())+
labs(title="GY (kg/ha)",
      subtitle="Data distribution by year",
      caption=NULL, x=NULL, y=NULL)

print(arrange_ggplot(a,b))

```



```

data_beans_plotBB<- droplevels(subset(data_beans, mkt=="BB"))

stats_results_BB<- ggbetweenstats(data=data_beans_plotBB, x= loc, y=gy_kg_ha) %>%
  ↪ extract_stats()
#print(stats_results_BB$pairwise_comparisons_data$p.value)

stats_results_BB2<- stats_results_BB$pairwise_comparisons_data %>%
dplyr::mutate(groups = purrr::pmap(.l = list(group1, group2), .f = c)) %>%
  dplyr::arrange(group1)%>%
  filter(p.value <= 0.05)

bb1<- ggplot(data=data_beans_plotBB, aes(x=reorder(loc, -gy_kg_ha), y=gy_kg_ha,
  ↪ fill=loc)) +

```

```

ggdist::stat_halfeye(
  adjust = 0.5,
  justification = -0.1,
  .width = 0,
  point_colour = NA
) +

geom_boxplot(
  width = .12,
  # outlier.color = NA,
  alpha = 0.5)+
tidyquant::theme_tq()+
#facet_grid("loc")+
tidyquant::scale_fill_tq() +
scale_x_discrete(expand = c(0.03,0)) +
scale_y_continuous(limits = c(1000,10000), breaks = seq(1000, 10000, by = 1000)) +
theme(axis.text.x=element_blank(),
      strip.text=element_blank(),
      legend.position = "none",
      panel.grid = element_blank())+
labs(title="GY (kg/ha)",
      subtitle="Data distribution by location",
      caption=NULL, x=NULL, y="BB")

bb1<-bb1 +
ggsignif::geom_signif(
  comparisons = stats_results_BB2$groups,
  map_signif_level = TRUE,
  tip_length = 0.01,
  textsize = 2.7,
  y_position = c(5900, 6700, 7500,8300, 9100),
  annotations = as.character(stats_results_BB2$expression),
  test = NULL,
  na.rm = TRUE,
  parse = TRUE
)

```

```

data_beans_plotBB<- droplevels(subset(data_beans, mkt=="BB"))

stats_results_BB<- ggbetweenstats(data=data_beans_plotBB, x= year, y=gy_kg_ha) %>%
  ↪ extract_stats()
#print(stats_results_BB$pairwise_comparisons_data$p.value)

stats_results_BB3<- stats_results_BB$pairwise_comparisons_data %>%
dplyr::mutate(groups = purrr::pmap(.l = list(group1, group2), .f = c)) %>%
  dplyr::arrange(group1) %>%
  filter(p.value <= 0.05)

bb2<- ggplot(data=data_beans_plotBB, aes(x=reorder(year, -gy_kg_ha), y=gy_kg_ha,
  ↪ fill=year)) +
  ggdist::stat_halfeye(
    adjust = 0.5,

```

```

      justification = -0.1,
      .width = 0,
      point_colour = NA
    ) +

    geom_boxplot(
      width = .12,
      # outlier.color = NA,
      alpha = 0.5)+
    tidyquant::theme_tq()+
    #facet_grid("loc")+
    tidyquant::scale_fill_tq() +
    scale_x_discrete(expand = c(0.03,0)) +
    scale_y_continuous(limits = c(1000,10000), breaks = seq(1000, 10000, by = 1000)) +
    theme(axis.text.x=element_blank(),
          strip.text=element_blank(),
          legend.position = "none",
          panel.grid = element_blank())+
    labs(title="GY (kg/ha)",
         subtitle="Data distribution by year",
         caption=NULL, x=NULL, y=NULL)

bb2<-bb2 +
  ggsignif::geom_signif(
    comparisons = stats_results_BB3$groups,
    map_signif_level = TRUE,
    tip_length = 0.01,
    textsize = 2.7,
    y_position = c(5900, 6300, 6700,7100, 7400, 7800,8200, 8600, 9000, 9400),
    annotations = as.character(stats_results_BB3$expression),
    test = NULL,
    na.rm = TRUE,
    parse = TRUE
  )

```

3.3.1.1 BB

```

data_beans_plotBB<- droplevels(subset(data_beans, mkt=="NB"))

stats_results_BB<- ggbetweenstats(data=data_beans_plotBB, x= loc, y=gy_kg_ha) %>%
  ↪ extract_stats()
#print(stats_results_BB$pairwise_comparisons_data$p.value)

stats_results_BB2<- stats_results_BB$pairwise_comparisons_data %>%
dplyr::mutate(groups = purrr::pmap(.l = list(group1, group2), .f = c)) %>%
  dplyr::arrange(group1)%>%
  filter(p.value <= 0.05)

nb1<- ggplot(data=data_beans_plotBB, aes(x=reorder(loc, -gy_kg_ha), y=gy_kg_ha,
  ↪ fill=loc)) +

```

```

ggdist::stat_halfeye(
  adjust = 0.5,
  justification = -0.1,
  .width = 0,
  point_colour = NA
) +

geom_boxplot(
  width = .12,
  # outlier.color = NA,
  alpha = 0.5)+
tidyquant::theme_tq()+
#facet_grid("loc")+
tidyquant::scale_fill_tq() +
scale_x_discrete(expand = c(0.03,0)) +
scale_y_continuous(limits = c(1000,10000), breaks = seq(1000, 10000, by = 1000)) +
theme(axis.text.x=element_blank(),
      strip.text=element_blank(),
      legend.position = "none",
      panel.grid = element_blank())+
labs(
  caption=NULL, x=NULL, y="NB")

nb1<-nb1 +
ggsignif::geom_signif(
  comparisons = stats_results_BB2$groups,
  map_signif_level = TRUE,
  tip_length = 0.01,
  textsize = 2.7,
  y_position = c(5900, 6700, 7500,8300, 9100),
  annotations = as.character(stats_results_BB2$expression),
  test = NULL,
  na.rm = TRUE,
  parse = TRUE
)

```

```

data_beans_plotBB<- droplevels(subset(data_beans, mkt=="NB"))

stats_results_BB<- ggbetweenstats(data=data_beans_plotBB, x= year, y=gy_kg_ha) %>%
  ↪ extract_stats()
#print(stats_results_BB$pairwise_comparisons_data$p.value)

stats_results_BB3<- stats_results_BB$pairwise_comparisons_data %>%
dplyr::mutate(groups = purrr::pmap(.l = list(group1, group2), .f = c)) %>%
  dplyr::arrange(group1) %>%
  filter(p.value <= 0.05)

nb2<- ggplot(data=data_beans_plotBB, aes(x=reorder(year, -gy_kg_ha), y=gy_kg_ha,
  ↪ fill=year)) +
  ggdist::stat_halfeye(
    adjust = 0.5,
    justification = -0.1,

```

```

    .width = 0,
    point_colour = NA
  ) +

  geom_boxplot(
    width = .12,
    # outlier.color = NA,
    alpha = 0.5)+
  tidyquant::theme_tq()+
  #facet_grid("loc")+
  tidyquant::scale_fill_tq() +
  scale_x_discrete(expand = c(0.03,0)) +
  scale_y_continuous(limits = c(1000,10000), breaks = seq(1000, 10000, by = 1000)) +
  theme(axis.text.x=element_blank(),
        strip.text=element_blank(),
        legend.position = "none",
        panel.grid = element_blank())+
  labs(
    caption=NULL, x=NULL, y=NULL)

nb2<-nb2 +
  ggsignif::geom_signif(
    comparisons = stats_results_BB3$groups,
    map_signif_level = TRUE,
    tip_length = 0.01,
    textsize = 2.7,
    y_position = c(5900, 6300, 6700,7100, 7400, 7800,8200, 8600, 9000, 9400),
    annotations = as.character(stats_results_BB3$expression),
    test = NULL,
    na.rm = TRUE,
    parse = TRUE
  )

```

3.3.1.2 NB

```

data_beans_plotBB<- droplevels(subset(data_beans, mkt=="SR"))

stats_results_BB<- ggbetweenstats(data=data_beans_plotBB, x= loc, y=gy_kg_ha) %>%
  ↪ extract_stats()
#print(stats_results_BB$pairwise_comparisons_data$p.value)

stats_results_BB2<- stats_results_BB$pairwise_comparisons_data %>%
dplyr::mutate(groups = purrr::pmap(.l = list(group1, group2), .f = c)) %>%
  dplyr::arrange(group1)%>%
  filter(p.value <= 0.05)

sr1<- ggplot(data=data_beans_plotBB, aes(x=reorder(loc, -gy_kg_ha), y=gy_kg_ha,
  ↪ fill=loc)) +
  ggdist::stat_halfeye(

```

```

    adjust = 0.5,
    justification = -0.1,
    .width = 0,
    point_colour = NA
  ) +

  geom_boxplot(
    width = .12,
    # outlier.color = NA,
    alpha = 0.5)+
  tidyquant::theme_tq()+
  #facet_grid("loc")+
  tidyquant::scale_fill_tq() +
  scale_x_discrete(expand = c(0.03,0)) +
  scale_y_continuous(limits = c(1000,10000), breaks = seq(1000, 10000, by = 1000)) +
  theme(
    strip.text=element_blank(),
    legend.position = "none",
    panel.grid = element_blank()+
  labs(
    caption=NULL, x="Locations", y="SR")

sr1<-sr1 +
  ggsignif::geom_signif(
    comparisons = stats_results_BB2$groups,
    map_signif_level = TRUE,
    tip_length = 0.01,
    textsize = 2.7,
    y_position = c(5900, 6700, 7500,8300, 9100),
    annotations = as.character(stats_results_BB2$expression),
    test = NULL,
    na.rm = TRUE,
    parse = TRUE
  )

```

```

data_beans_plotBB<- droplevels(subset(data_beans, mkt=="SR"))

stats_results_BB<- ggbetweenstats(data=data_beans_plotBB, x= year, y=gy_kg_ha) %>%
  ↪ extract_stats()
#print(stats_results_BB$pairwise_comparisons_data$p.value)

stats_results_BB3<- stats_results_BB$pairwise_comparisons_data %>%
dplyr::mutate(groups = purrr::pmap(.l = list(group1, group2), .f = c)) %>%
  dplyr::arrange(group1) %>%
  filter(p.value <= 0.05)

sr2<- ggplot(data=data_beans_plotBB, aes(x=reorder(year, -gy_kg_ha), y=gy_kg_ha,
  ↪ fill=year)) +
  ggdist::stat_halfeye(
    adjust = 0.5,
    justification = -0.1,
    .width = 0,

```

```

    point_colour = NA
  ) +

  geom_boxplot(
    width = .12,
    # outlier.color = NA,
    alpha = 0.5)+
  tidyquant::theme_tq()+
  #facet_grid("loc")+
  tidyquant::scale_fill_tq() +
  scale_x_discrete(expand = c(0.03,0)) +
  scale_y_continuous(limits = c(1000,10000), breaks = seq(1000, 10000, by = 1000)) +
  theme(
    strip.text=element_blank(),
    legend.position = "none",
    panel.grid = element_blank()+
  labs(
    caption=NULL, y=NULL, x="Years")

sr2<- sr2 +
  ggsignif::geom_signif(
    comparisons = stats_results_BB3$groups,
    map_signif_level = TRUE,
    tip_length = 0.01,
    textsize = 2.7,
    y_position = c(5900, 6500, 7200,8000, 8700, 9500),
    annotations = as.character(stats_results_BB3$expression),
    test = NULL,
    na.rm = TRUE,
    parse = TRUE
  )

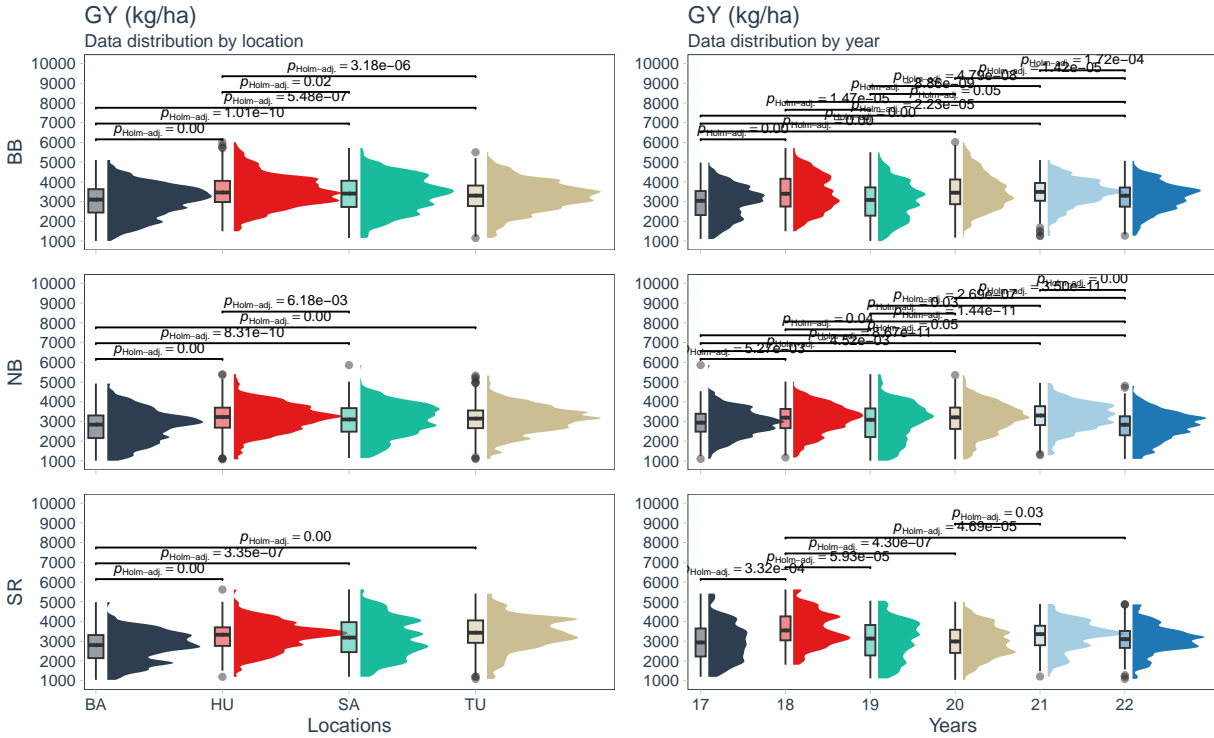
```

3.3.1.3 SR Box plot distribution for each market class in this study across years and locations.

```

print(arrange_ggplot(bb1,bb2,
                     nb1,nb2,
                     sr1,sr2,
                     nrow = 3,
                     ncol = 2))

```



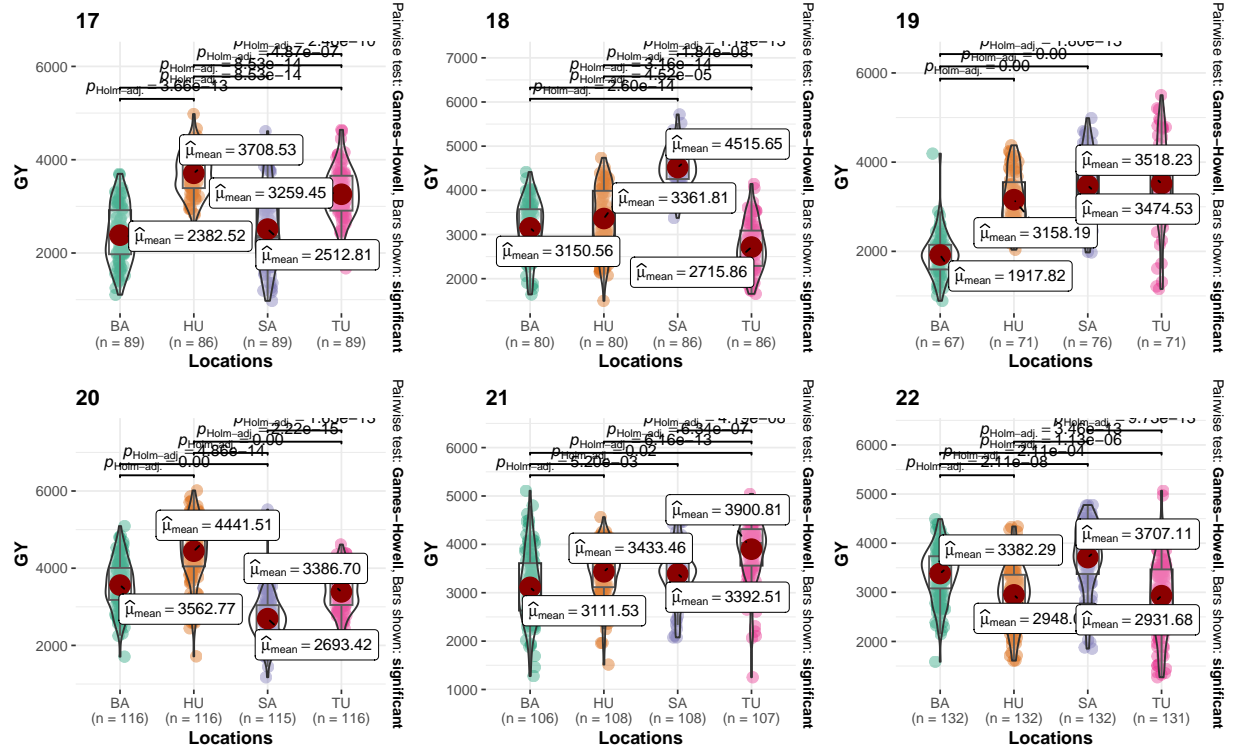
3.3.2 GEI Comparisons (loc:year) - BB

Box plots for between-subjects comparisons by locations using the R package `ggstatsplot`.

- Black beans (BB) **Pairwise Games-Howell test used. Comparisons showing only significant**

```
data_beans_plotBB<- droplevels(subset(data_beans, mkt=="BB"))

plotDM_stats_mkt_loc_BB<- grouped_ggbetweenstats(data=data_beans_plotBB, x= loc,
  ↪ y=gy_kg_ha, type = "parametric", bf.message = F, results.subtitle = F,
  ylab= "GY", xlab = "Locations",
  plot.type = "boxviolin", grouping.var = year )
print(plotDM_stats_mkt_loc_BB)
```

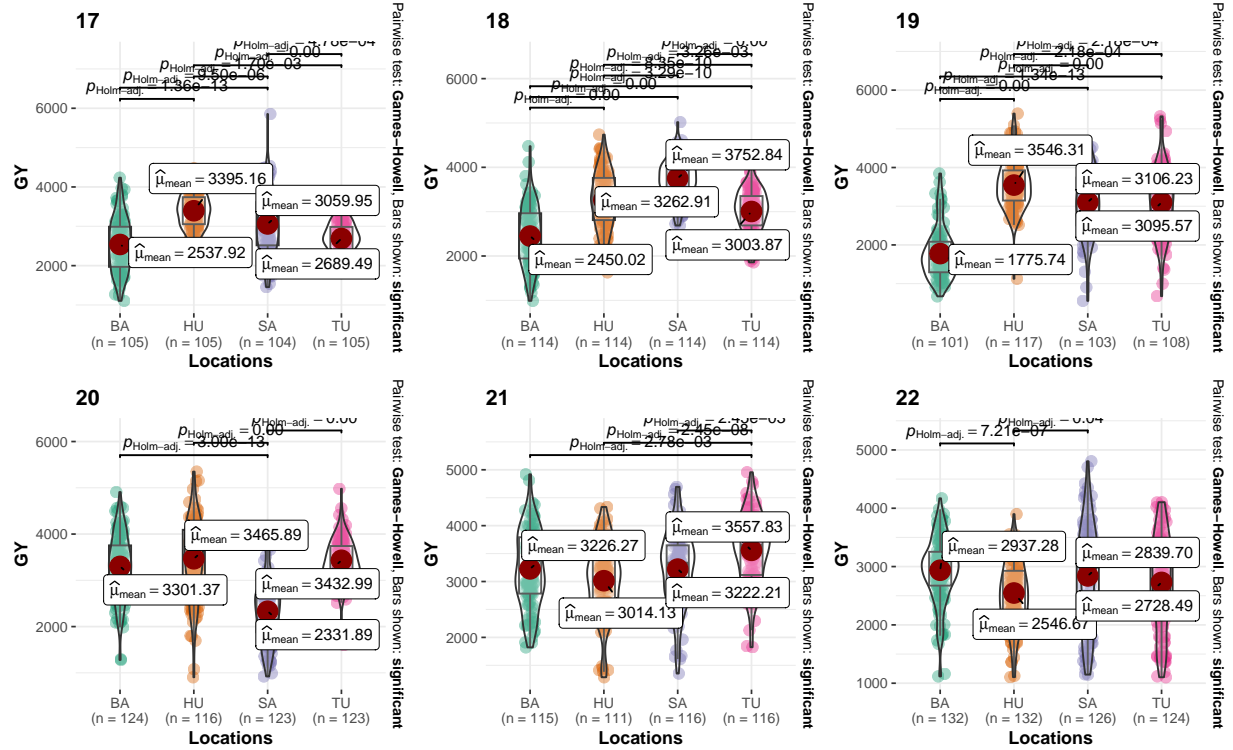
3.3.3 GEI Comparisons (loc:year) - NB

Box plots for between-subjects comparisons by locations using the R package `ggstatsplot`. - Navy beans (NB) **Pairwise Games-Howell test used. Comparisons showing only significant**

```
data_beans_plotNB<- droplevels(subset(data_beans, mkt=="NB"))

plotDM_stats_mkt_loc_NB<- grouped_ggbetweenstats(data=data_beans_plotNB, x= loc,
  ↪ y=gy_kg_ha, type = "parametric", bf.message = F, results.subtitle = F,
  ylab= "GY", xlab= "Locations",
  plot.type = "boxviolin", grouping.var = year )

print(plotDM_stats_mkt_loc_NB)
```



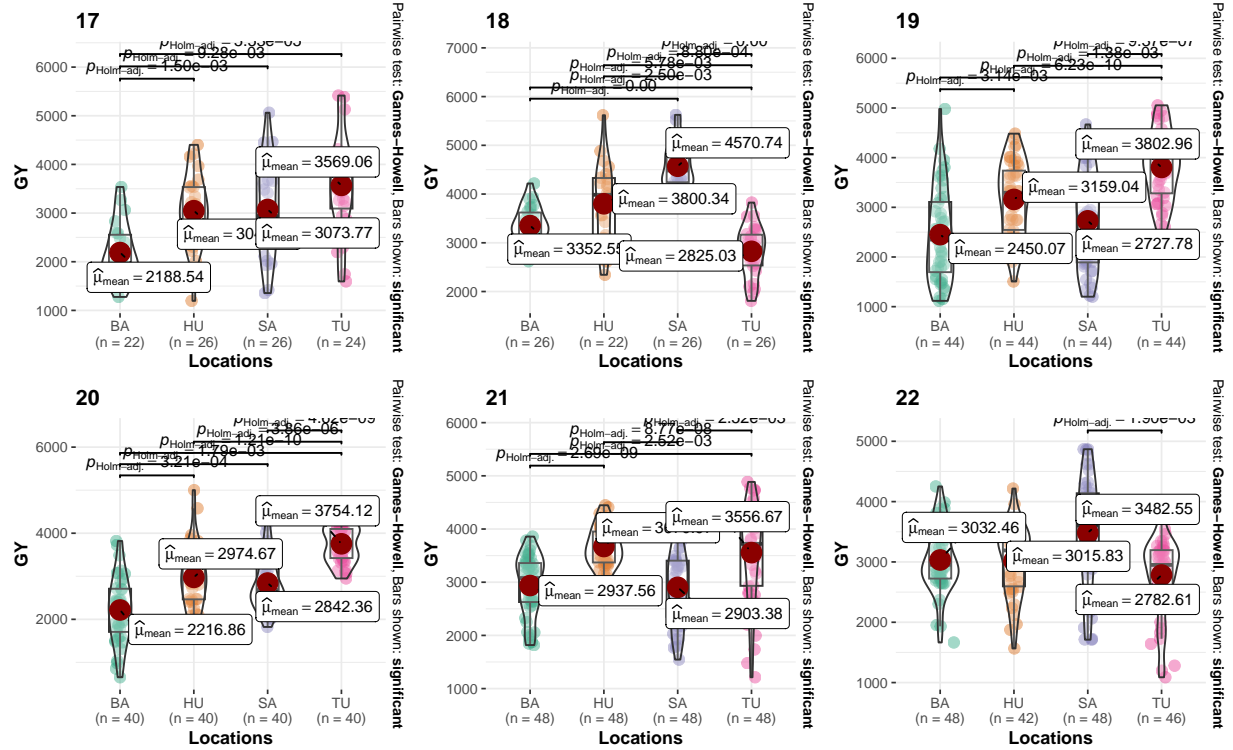
3.3.4 GEI Comparisons (loc:year) - SR

Box plots for between-subjects comparisons by locations using the R package `ggstatsplot`. - Black beans (SR) **Pairwise Games-Howell test used. Comparisons showing only significant**

```
data_beans_plotSR<- droplevels(subset(data_beans, mkt=="SR"))

plotDM_stats_mkt_loc_SR<- grouped_ggbetweenstats(data=data_beans_plotSR, x= loc,
  ↪ y=gy_kg_ha, type = "parametric", bf.message = F, results.subtitle = F,
  ylab= "GY", xlab = "Locations",
  plot.type = "boxviolin", grouping.var = year )

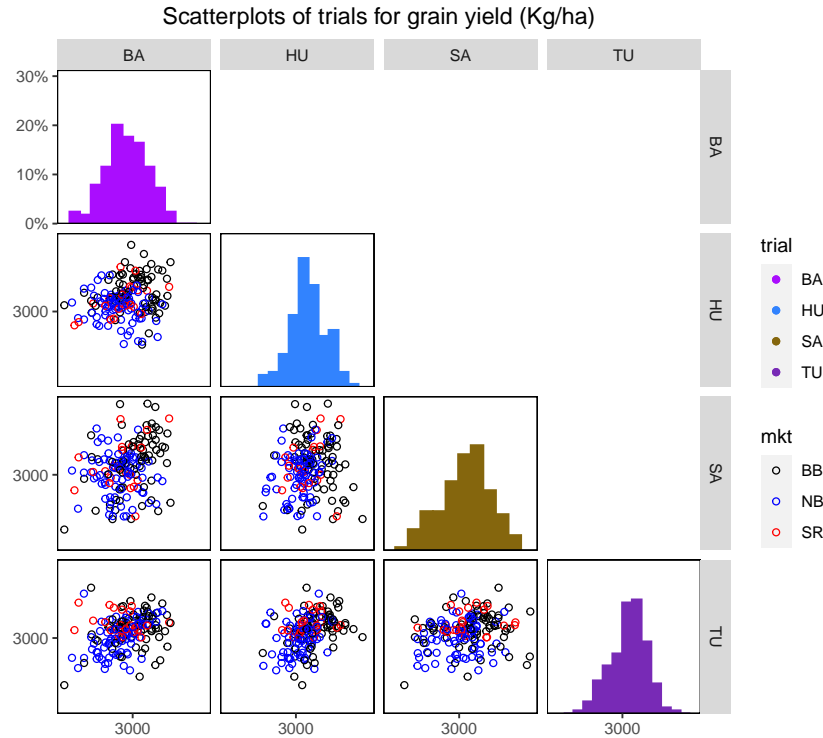
print(plotDM_stats_mkt_loc_SR)
```



3.3.5 Scatter plot

For further insight into the correlation structure between trials a scatter plot matrix can be made using the package `statgenGxE`

```
dropsTD <- statgenSTA::createTD(data = data_beans, genotype = "name", trial = "loc")
options("statgen.genoColors" = c("black", "blue", "red"))
plot(dropsTD, plotType = "scatter", traits = "gy_kg_ha", colorGenoBy = "mkt",
     colorTrialBy = "trial", title = "Scatterplots of trials for grain yield (Kg/ha) ")
```



3.3.6 Outliers

Check for common errors in multi-environment trial by market class data using the R package `metan`. However, the data set was cleaned before at a previous analysis not shown in this vignette using the criteria for GY:

- yield ≤ 0.5 | yield ≥ 7.5 (considering yield as Lb per plot)
- moisture ≥ 30 | moisture ≤ 5 (considering moisture in %)

At this point yield data will not be removed anymore, but we can check it out for further investigation, if it was needed.

```
out_beans<- find_outliers(data_beans, by=mkt, var = gy_kg_ha, plots = F)
```

Trait: gy_kg_ha Number of possible outliers: 9 Line(s): 1113 2052 4478 4522 4539 4620 4739 4740 4761
Proportion: 0.3% Mean of the outliers: 3320 Maximum of the outliers: 5854 | Line 4539 Minimum of the outliers: 554.8 | Line 4739 With outliers: mean = 3015 | CV = 26.27% Without outliers: mean = 3014 | CV = 25.93%

Trait: gy_kg_ha Number of possible outliers: 10 Line(s): 127 1910 3723 3993 4161 4358 5630 6302 6638 6710
Proportion: 0.4% Mean of the outliers: 4313 Maximum of the outliers: 6014 | Line 6302 Minimum of the outliers: 889.9 | Line 3993 With outliers: mean = 3298 | CV = 25.57% Without outliers: mean = 3294 | CV = 25.21%

Trait: gy_kg_ha Number of possible outliers: 4 Line(s): 533 1422 1951 1975 Proportion: 0.4% Mean of the outliers: 4355 Maximum of the outliers: 5625 | Line 1951 Minimum of the outliers: 654.1 | Line 533 With outliers: mean = 3139 | CV = 27.68% Without outliers: mean = 3134 | CV = 27.29%

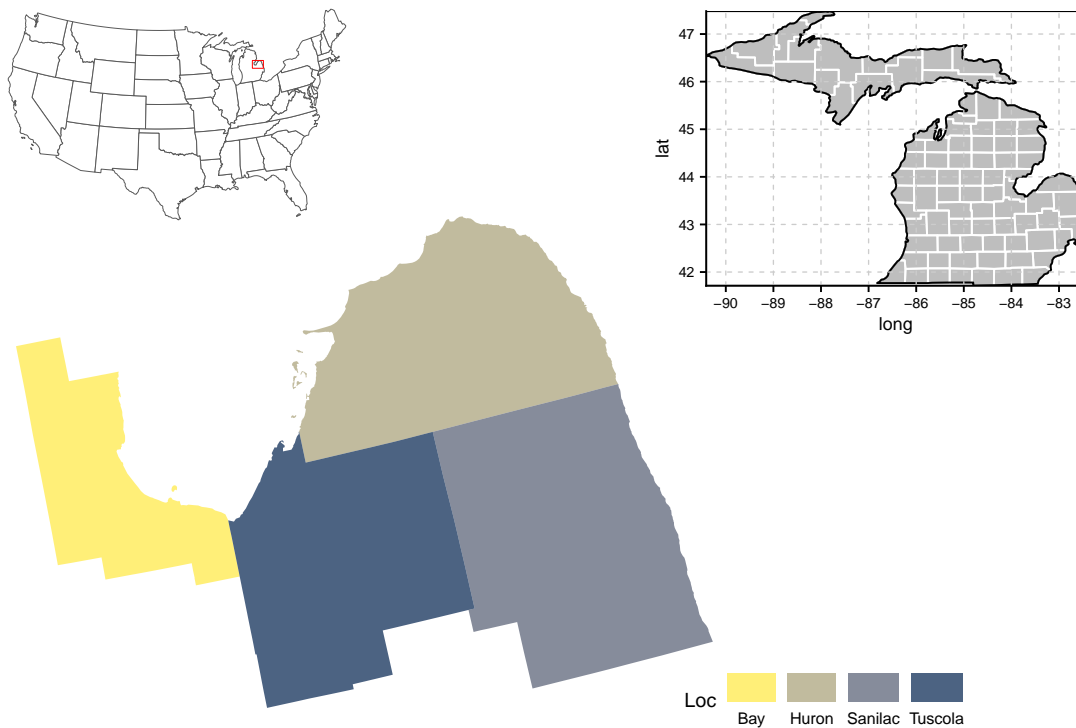
```
#out_beans
```

- No outliers removed after the data inspection based on the Breeder expertise.

3.3.7 Map of locations

This figure represent all counties locations evaluated in this study at Michigan, midwest in the USA.

```
source("utils/map.R")
print(MI_trials_beans_map)
```



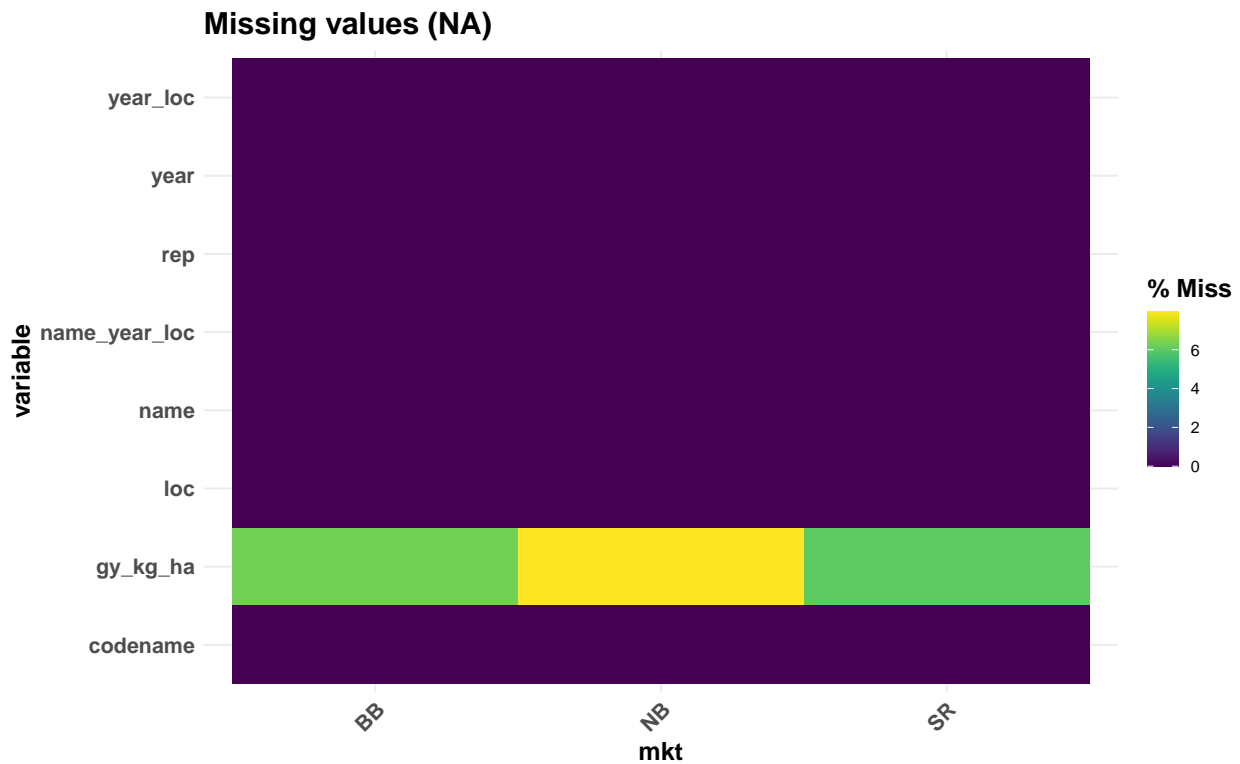
3.3.8 Missing values

```
data_beans.miss.f<- data_beans %>%
  unite(name_year_loc, c(name, year_loc), remove = F) %>%
  group_by(name_year_loc) %>%
  dplyr::summarise(Mean = mean(gy_kg_ha, na.rm = TRUE)) %>%
  filter(!is.na(Mean))

data_beans.miss<- data_beans %>%
  unite(name_year_loc, c(name, year_loc), remove = F)
```

```
data_beans.miss<- data_beans.miss%>%
  filter((name_year_loc %in% data_beans.miss.f$name_year_loc))

gg_miss_fct(data_beans.miss,fct = mkt)+ggtitle("Missing values (NA)") +
  theme(axis.text.x=element_text(face="bold", size = 12),
        axis.text.y = element_text(face = "bold",size = 12) ,
        title = element_text(face = "bold",size = 14))
```



Missing genotypes by market classes

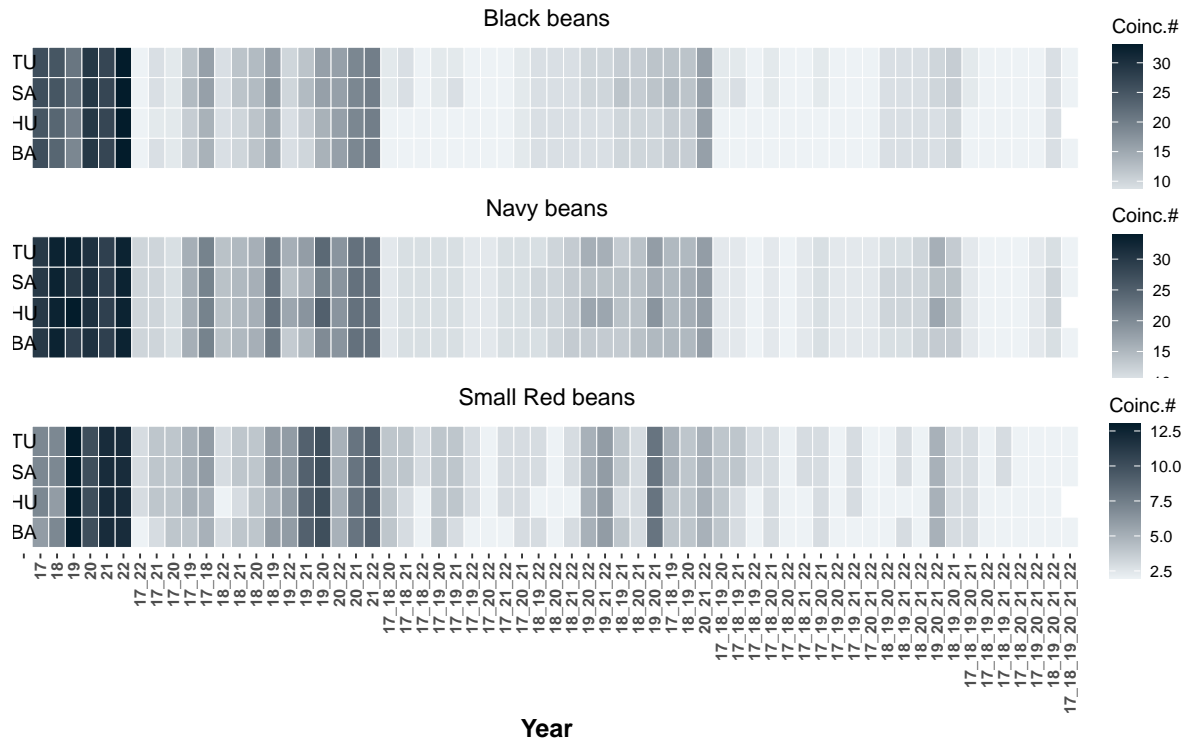
3.3.9 Coincidence Genotypes

Genotypes coincidentes across years combinations

```
source("utils/Coinc.R")
```

```
#> [1] "The coincidence file is present"
```

```
arrange_ggplot(plotB, plotN, plotSR,ncol = 1)
```



Coincidence genotypes per year and combinations of years across locations for each market class.

3.4 Predicted by year mixed model analysis

To predict the BLUPs per year and plot it versus year: BLUPs prediction for the vector of the variable GY in the *i*th genotype, and *j*th loc within year.

3.5 Data preparation

```
#setwd("G:/Shared
↳ drives/Bean_Lab/Volpato/GxE_Variety_trials_Scott/Manuscript/Suppl_mat/TemplateResults-main")
data_beans = read.csv("data/DataBean_MET_GYv2.csv",h=T, stringsAsFactors = T)

# Data adjustment
# All the effect columns must be as a factor to run in ASReml-r.
cols <- c("rep", "name", "loc","year", "mkt", "year_loc")
data_beans[cols] <- lapply(data_beans[cols], factor)
data_beans <- data.table(data_beans)
```

3.5.1 By year mixed model analysis

The BLUPS will be estimated using a mixed-effect model and these values obtained by year using a loop with ASReml and storage into the list.

The following mixed model was used to estimate the BLUPs of each genotype within year with one value per genotype per year (random effects are underlined in all equations):

$$Y_{ijl} = \mu + \underline{G_i} + E_l + \beta_{jl} + \underline{GE_{il}} + \underline{\varepsilon_{ijl}}$$

where Y_{ijl} is the response variable (e.g., grain yield) observed in the j th repetition of the i th genotype in the l th location ($i = 1, 2, \dots, g$; $j = 1, 2, \dots, b$; $l = 1, 2, \dots, e$); μ is the grand mean; $\underline{G_i}$ is the effect of the i th genotype; E_l is the effect of the l th location (env); β_{jl} is the effect of the j th rep with the l th location; $\underline{GE_{il}}$ is the interaction effect of the i th genotype nested within the l th location; and $\underline{\varepsilon_{ijl}}$ is the random error, in witch with $G_i \sim N(0, \sigma_G^2)$, $GE_{il} \sim N(0, \sigma_{GE}^2)$, and $\varepsilon_{ijl} \sim N(0, \sigma_\varepsilon^2)$, all independent, where G_G^2 is the genotype (name) variance, GS_{GE}^2 is the interaction genotype x environment variance, and σ_ε^2 is the mean error variance across experiments.

```
## Analysis per site and mkt class
mkt_n <- levels(data_beans$mkt)

Envs <- levels(data_beans$year)

stgI_list <- matrix(data=list(), nrow=length(Envs), ncol=1,
                    dimnames=list(Envs, c("BLUPS")))

mkt <- nlevels(data_beans$mkt)

for(k in 1:mkt){

  bk <- levels(data_beans$mkt)
  cj <- bk[k]
  #print(cj)

  data_beans_temp <- droplevels(subset(data_beans, mkt==cj))

  for (i in Envs){
    #i=Envs[1]
    Edat <- droplevels(subset(data_beans_temp, year==i))

    #print(i)

    mod.1 <- asreml(fixed      = gy_kg_ha ~ loc + loc:rep,
                   random     = ~ name + name:loc,
                   data       = Edat,
                   predict    = predict.asreml(classify = "name"),
                   trace      = F,
                   maxit      = 500)

    # print(summary.asreml(mod.1)$varcomp)
    # wald(mod.1)

    blup.1 <- data.table((mod.1$predictions$pvals[1:3]))
    names(blup.1) <- c("name", "yield", "se")
    blup.1$mkt <- cj

    stgI_list[[i, "BLUPS"]] <- blup.1 # put all the results of Stage 1 in the list

    # rm(Edat, mod.1, blue, blup.1)
```



```

}
  if(k==1){stgI_list.1<-stgI_list}else{stgI_list.1<-rbind(stgI_list.1, stgI_list)}
}

```

3.5.1.1 Preparing dataset Merging the original data to have all the factors in the final table with: name, year, and mkt

```

##### Unlist the results of Stage I and format as data.table #####
blups_stageI <- data.table(ldply(stgI_list.1[, "BLUPS"], data.frame, .id="year"))

blues_stage.I <- blups_stageI[order(blups_stageI$year,blups_stageI$mkt),]

# Change the order of columns
blues_stage.I <- blues_stage.I %>%
  dplyr::select(year, name, mkt, se, yield)

str(blues_stage.I)

```

Classes 'data.table' and 'data.frame': 984 obs. of 5 variables: \$ year : Factor w/ 6 levels "17","18","19",...: 1 1 1 1 1 1 1 1 1 1 ... \$ name : Factor w/ 164 levels "B1","B10","B11",...: 1 2 3 4 5 6 7 8 9 10 ... \$ mkt : chr "BB" "BB" "BB" "BB" ... \$ se : num 141.3 98.7 113.8 113.8 355.7 ... \$ yield: num 2727 3579 2947 3092 2959 ... - attr(*, "internal.selfref")=

3.5.2 Descriptive variance

```

if (knitr::is_html_output()) {

  print_table(blues_stage.I)

}else{

flextable(head(blues_stage.I)) %>%
  add_footer_lines(
    c("Beans data set by year",
      "Header data set showing the 6 first entry")) %>%
  autofit() %>%
  add_header_lines("Dry Beans varieties trial") %>%
  theme_design2()

}

```

3.5.2.1 Beans data set by year

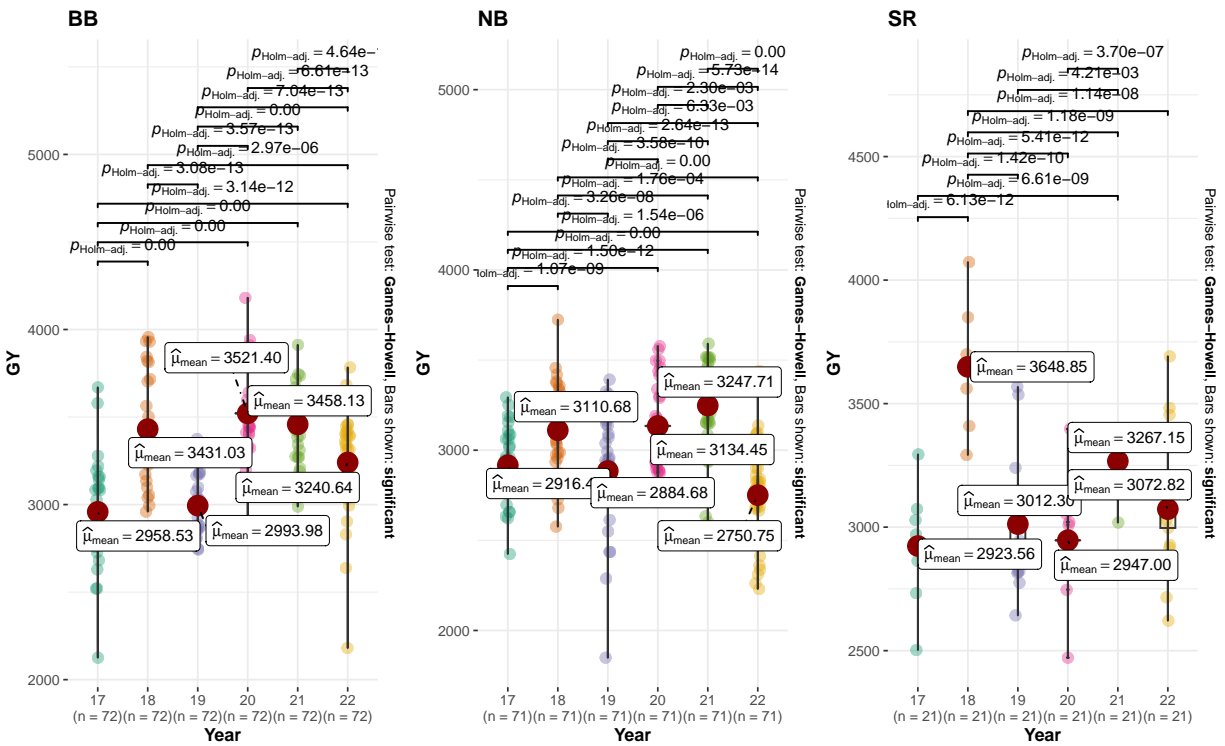
Dry Beans varieties trial

| year | name | mkt | se | yield |
|------|------|-----|--------|-------|
| 17 | B1 | BB | 141.29 | 2,727 |
| 17 | B10 | BB | 98.73 | 3,579 |
| 17 | B11 | BB | 113.83 | 2,947 |
| 17 | B12 | BB | 113.83 | 3,092 |
| 17 | B13 | BB | 355.72 | 2,959 |
| 17 | B14 | BB | 355.72 | 2,959 |

Beans data set by year

Header data set showing the 6 first entry

3.5.2.2 Box plot distribution Pairwise Games-Howell test used. Comparisons showing only significant



Combination of box and violin plots along with jittered data points for between subjects comparisons by years of grain yield (GY) for black (BB), Navy (NB) and Red (SR) beans. Pairwise Games-Howell test used. Comparisons showing only significant values.

```
str(blues_stage.I)
```

Classes 'data.table' and 'data.frame': 984 obs. of 5 variables: \$ year : Factor w/ 6 levels "17","18","19",...: 1 1 1 1 1 1 1 1 1 1 ... \$ name : Factor w/ 164 levels "B1","B10","B11",...: 1 2 3 4 5 6 7 8 9 10 ... \$ mkt : chr "BB" "BB" "BB" "BB" ... \$ se : num 141.3 98.7 113.8 113.8 355.7 ... \$ yield: num 2727 3579 2947 3092 2959 ... - attr(*, "internal.selfref")=

```
blues_stage.I$year <- as.numeric(blues_stage.I$year)
```

```
blues_stage.I$year[blues_stage.I$year == 1]<- 17
```

```
blues_stage.I$year[blues_stage.I$year == 2]<- 18
```

```
blues_stage.I$year[blues_stage.I$year == 3]<- 19
```

```
blues_stage.I$year[blues_stage.I$year == 4]<- 20
```

```
blues_stage.I$year[blues_stage.I$year == 5]<- 21
```

```
blues_stage.I$year[blues_stage.I$year == 6]<- 22
```

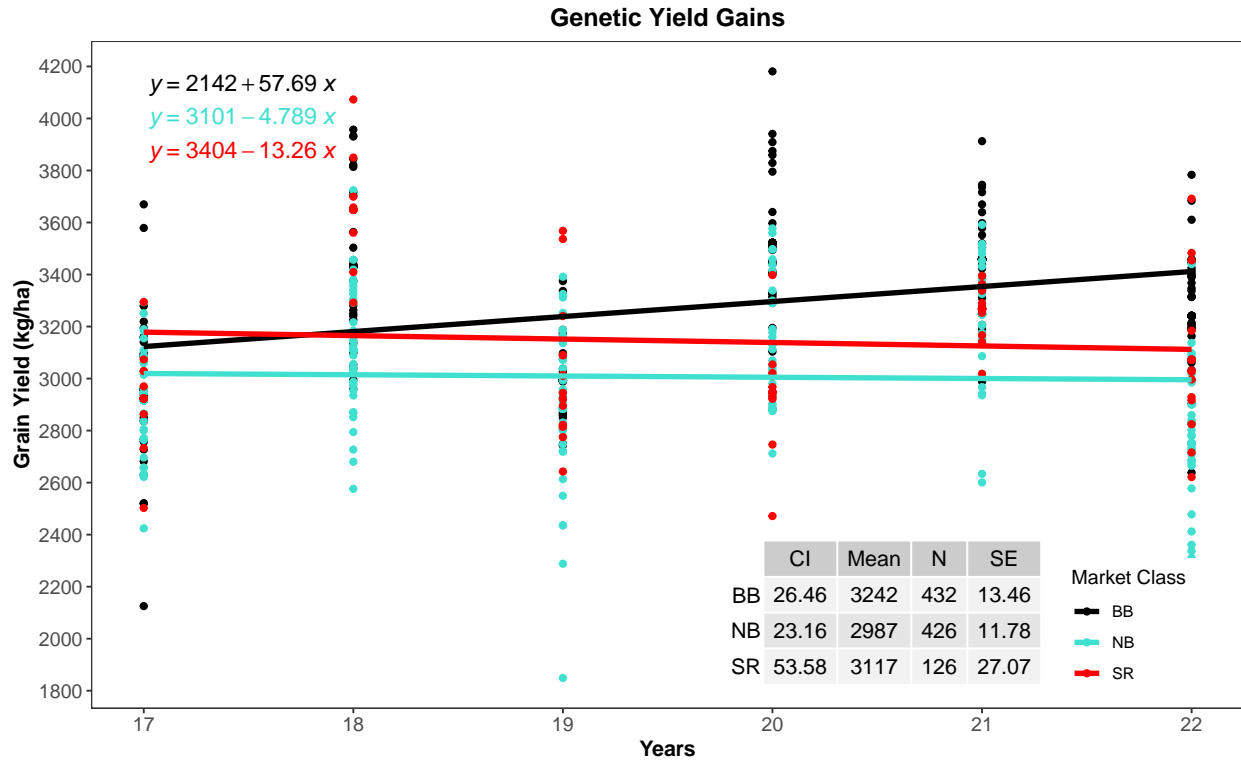
```
beans_desc <- desc_stat(blues_stage.I, yield, stats = ("ci.t, hmean, n, se"), by = mkt)
#print(beans_desc)
```

```
beans_desc<-beans_desc[-c(2)]
```

```
colnames(beans_desc)<- c("MKT","CI", "Mean", "N", "SE")
```

```
beans_desc<-data.frame(beans_desc, row.names =T)
```

```
#rownames(beans_desc) <- NULL
```



Combination of box and violin plots along with jittered data points for between subjects comparisons by years of grain yield (GY) for black (BB), Navy (NB) and Red (SR) beans. Pairwise Games-Howell test used. Comparisons showing only significant values.

3.6 Two Stage mixed model analysis

The following pipeline will be used: 1-Stage = BLUEs estimation for the vector of the variable GY in the *i*th genotype, and *j*th year within *loc*. Then the BLUEs from the 1-Stage (Y_{ik}) will be used to predict the BLUPs (Y_{ijl}) of the *i*th genotype in the *l*th location and *j*th rep in the 2-Stage in which this second model have *name* and *loc* effects as random.

3.6.1 1st Stage mixed model analysis

```
#rm(list=ls())
data_beans = read.csv("data/DataBean_MET_GYv2.csv",h=T, stringsAsFactors = T)
#str(data_beans)
# Data adjustment
# All the effect columns must be as a factor to run in ASReml-r.
cols <- c("rep", "name", "loc","year", "mkt", "year_loc")
data_beans[cols] <- lapply(data_beans[cols], factor)
data_beans <- data.table(data_beans)
```

The BLUEs will be estimated using a mixed-effect model. The BLUEs will be obtained by location using a loop with ASReml and storage into the list.

The following mixed model was used to estimate the BLUEs of each genotype within location with one value per genotype per experiment and rep, for the first step (random effects are underlined in all equations):

$$Y_{ik} = \mu + G_i + S_k + GS_{ik} + \varepsilon_{ik}$$

where Y_{ik} is the observed yield in the i th genotype and k th year, μ is the overall mean, G_i is the effect of the i th genotype, S_k is the effect of the k th year, GS_{ik} is the effect of the interaction between the i th genotype and the k th year, and ε_{ik} are the residual, with $S_k \sim N(0, \sigma_Y^2)$, $GS_{ik} \sim N(0, \sigma_Y^2)$, and $\varepsilon_{ik} \sim N(0, \sigma_\varepsilon^2)$, all independent, where σ_Y^2 is the year variance, and σ_ε^2 is the mean error variance across experiments.

```
#> `summarise()` has grouped output by 'name'. You can override using the `.groups` argument.
#> `summarise()` has grouped output by 'name'. You can override using the `.groups` argument.
#> `summarise()` has grouped output by 'name'. You can override using the `.groups` argument.
#> `summarise()` has grouped output by 'name'. You can override using the `.groups` argument.
#> `summarise()` has grouped output by 'name'. You can override using the `.groups` argument.
#> `summarise()` has grouped output by 'name'. You can override using the `.groups` argument.
#> `summarise()` has grouped output by 'name'. You can override using the `.groups` argument.
#> `summarise()` has grouped output by 'name'. You can override using the `.groups` argument.
#> `summarise()` has grouped output by 'name'. You can override using the `.groups` argument.
#> `summarise()` has grouped output by 'name'. You can override using the `.groups` argument.
```

```
## Loop to get the year effect corrected by year
## Only genotypes present in years

#str(data_beans)
data_beans$var_years <- as.factor(data_beans$var_years)
year <- nlevels(data_beans$var_years)
## Analysis per site and mkt class
#mkt_n <- levels(data_beans$mkt)

Envs <- levels(data_beans$loc)

stgI_list <- matrix(data=list(), nrow=length(Envs), ncol=1,
                    dimnames=list(Envs, c("BLUES")))

mkt <- nlevels(data_beans$mkt)

for (y in 1:year) {

  by <- levels(data_beans$var_years)
  cy <- by[y]

  data_beans_temp1 <- droplevels(subset(data_beans, var_years==cy))

  if(y == 1) {next
}else {

  for(k in 1:mkt){

    bk <- levels(data_beans_temp1$mkt)
    cj <- bk[k]
    #print(cj)
```

```

data_beans_temp2 <- droplevels(subset(data_beans_temp1, mkt==cj))

for (i in Envs){
  #i=Envs[1]
  Edat <- droplevels(subset(data_beans_temp2, loc==i))

  #print(i)

  mod.1 <- asreml(fixed      = gy_kg_ha ~ name:rep,
                  random    = ~ year + name:year ,
                  data       = Edat,
                  predict    = predict.asreml(classify = "name:rep",vcov=TRUE, aliased =
                    ↪ T),
                  trace      = F,
                  maxit      = 500)

  # print(summary.asreml(mod.1)$varcomp)
  # wald(mod.1)

  blue.1<- data.table((mod.1$predictions$pvals[1:4]))
  names(blue.1) <- c("name", "rep", "yield", "se")
  blue.1$mkt<- cj
  blue.1$var_years<- cy

  stgI_list[[i, "BLUES"]] <- blue.1 # put all the results of Stage 1 in the list

  rm(Edat,mod.1, blue, blue.1)

}
if(k==1){stgI_list.1<-stgI_list}else{stgI_list.1<-rbind(stgI_list.1, stgI_list)}
}
}
if(y==2){stgI_list.2<-stgI_list.1}else{stgI_list.2<-rbind(stgI_list.2, stgI_list.1)}
}

```

3.6.1.1 Preparing dataset of Stage I for Stage II Merging the original data to have all the factors in the final table with: name, loc, mkt, rep

```

##### Unlist the results of Stage I and format as data.table #####
blues_stageI <- data.table(ldply(stgI_list.2[, "BLUES"], data.frame, .id="loc"))

blues_stage.I <- blues_stageI[order(blues_stageI$loc,blues_stageI$name),]

blues_stage.I.SEmean <- blues_stage.I %>%
  dplyr::summarise(Mean_SE = mean(se, na.rm = TRUE))

print(blues_stage.I.SEmean)

```

Mean_SE 1 433.5

```
#str(blues_stage.I)
```

```
# Change the order of columns
blues_stage.I <- blues_stage.I %>%
  dplyr::select(loc, name, rep, mkt, yield)
```

3.6.2 2nd Stage mixed model analysis

The following linear mixed model with interaction effect will be used in the 2-Stage in order to investigate the multi-environment trials (MET) as follow:

$$Y_{ijl} = \mu + G_i + E_l + \beta_{jl} + GE_{il} + \varepsilon_{ijl}$$

where Y_{ijl} is the response variable (e.g., grain yield) observed in the j th repetition of the i th genotype in the l th location ($i = 1, 2, \dots, g$; $j = 1, 2, \dots, b$; $l = 1, 2, \dots, e$); μ is the grand mean; G_i is the effect of the i th genotype; E_l is the effect of the l th location (env); β_{jl} is the effect of the j th rep with the l th location; GE_{il} is the interaction effect of the i th genotype nested within the l th location; and ε_{ijl} is the random error, in witch with $G_i \sim N(0, \sigma_G^2)$, $GE_{il} \sim N(0, \sigma_{GE}^2)$, and $\varepsilon_{ijl} \sim N(0, \sigma_\varepsilon^2)$, all independent, where G_G^2 is the genotype (name) variance, GS_{GE}^2 is the interaction genotype x environment variance, and σ_ε^2 is the mean error variance across experiments.

3.6.3 By market classes

- Getting the files for the individually market classes

```
blues_stage.I_BB <- droplevels(subset(blues_stage.I, mkt=="BB"))
blues_stage.I_NB <- droplevels(subset(blues_stage.I, mkt=="NB"))
blues_stage.I_SR <- droplevels(subset(blues_stage.I, mkt=="SR"))
```

```
blues_stage.I_table1 <- blues_stage.I %>%
  group_by(loc, rep, mkt) %>%
  dplyr::summarise(count = length(name))

blues_stage.I_table1 <- blues_stage.I_table1[, 3:4]
blues_stage.I_table1 <- blues_stage.I_table1[1:3,]

blues_stage.I_table1
```

| mkt | count |
|--------|---------|
| factor | integer |
| BB | 72 |
| NB | 71 |
| SR | 21 |

```
str(blues_stage.I_BB)
```

Classes 'data.table' and 'data.frame': 1152 obs. of 5 variables: \$ loc : Factor w/ 4 levels "BA","HU","SA",...: 1 1 1 1 1 1 1 1 1 1 ... \$ name : Factor w/ 72 levels "B13","B14","B19",...: 1 1 1 1 2 2 2 2 3 3 ... \$ rep : Factor w/ 4 levels "1","2","3","4": 1 2 3 4 1 2 3 4 1 2 ... \$ mkt : Factor w/ 1 level "BB": 1 1 1 1 1 1 1 1 1 1 ... \$ yield: num 2626 2874 2391 3000 2851 ... - attr(*, ".internal.selfref")=

```
if (knitr::is_html_output()) {
  print_table(blues_stage.I_BB)
}else{
  flextable(head(blues_stage.I_BB)) %>%
    add_footer_lines(
      c("Black beans data set",
        "Header data set showing the 6 first entry")) %>%
    autofit() %>%
    add_header_lines("Dry Beans varieties trial") %>%
    theme_design2()
}
```

| Dry Beans varieties trial | | | | |
|---|------|-----|-----|-------|
| loc | name | rep | mkt | yield |
| BA | B13 | 1 | BB | 2,626 |
| BA | B13 | 2 | BB | 2,874 |
| BA | B13 | 3 | BB | 2,391 |
| BA | B13 | 4 | BB | 3,000 |
| BA | B14 | 1 | BB | 2,851 |
| BA | B14 | 2 | BB | 3,235 |
| Black beans data set | | | | |
| Header data set showing the 6 first entry | | | | |

```
if (knitr::is_html_output()) {
  print_table(blues_stage.I_NB)
}else{
  flextable(head(blues_stage.I_NB)) %>%
    add_footer_lines(
      c("Navy beans data set",
```



```

      "Header data set showing the 6 first entry")) %>%
autofit() %>%
add_header_lines("Dry Beans varieties trial") %>%
theme_design2()
}

```

| Dry Beans varieties trial | | | | |
|---|------|-----|-----|-------|
| loc | name | rep | mkt | yield |
| BA | N12 | 1 | NB | 2,505 |
| BA | N12 | 2 | NB | 2,642 |
| BA | N12 | 3 | NB | 2,862 |
| BA | N12 | 4 | NB | 1,323 |
| BA | N13 | 1 | NB | 2,451 |
| BA | N13 | 2 | NB | 2,673 |
| Navy beans data set | | | | |
| Header data set showing the 6 first entry | | | | |

```

if (knitr::is_html_output()) {

  print_table(blues_stage.I_SR)

}else{

flextable(head(blues_stage.I_SR)) %>%
  add_footer_lines(
    c("Red beans data set",
      "Header data set showing the 6 first entry")) %>%
  autofit() %>%
  add_header_lines("Dry Beans varieties trial") %>%
  theme_design2()
}

```

| Dry Beans varieties trial | | | | |
|---|------|-----|-----|-------|
| loc | name | rep | mkt | yield |
| BA | R10 | 1 | SR | 2,296 |
| BA | R10 | 2 | SR | 2,676 |
| Red beans data set | | | | |
| Header data set showing the 6 first entry | | | | |

Dry Beans varieties trial

| loc | name | rep | mkt | yield |
|-----|------|-----|-----|-------|
| BA | R10 | 3 | SR | 3,440 |
| BA | R10 | 4 | SR | 2,580 |
| BA | R12 | 1 | SR | 3,001 |
| BA | R12 | 2 | SR | 2,716 |

Red beans data set

Header data set showing the 6 first entry

3.6.4 Descriptive variance**3.6.4.1 Box plot distribution**

- Box plots for between-subjects comparisons by locations using the R package `ggstatsplot`.

Pairwise Games-Howell test used. Comparisons showing only significant

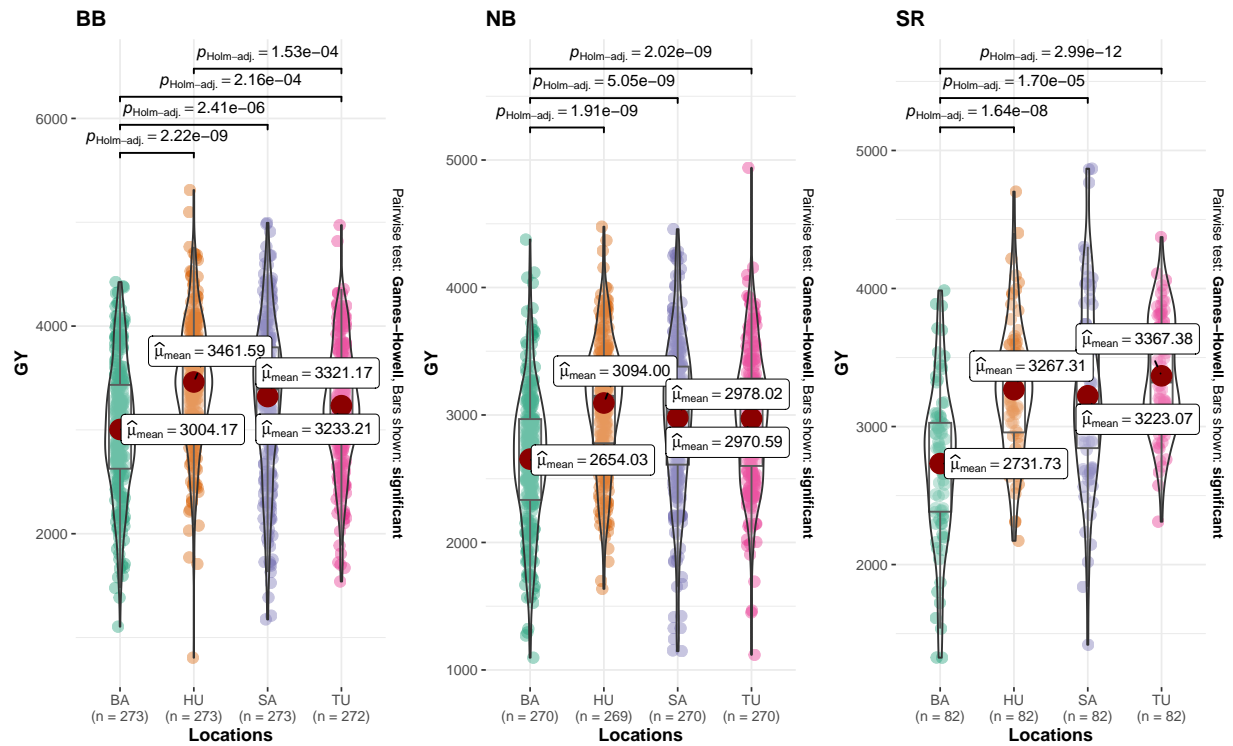


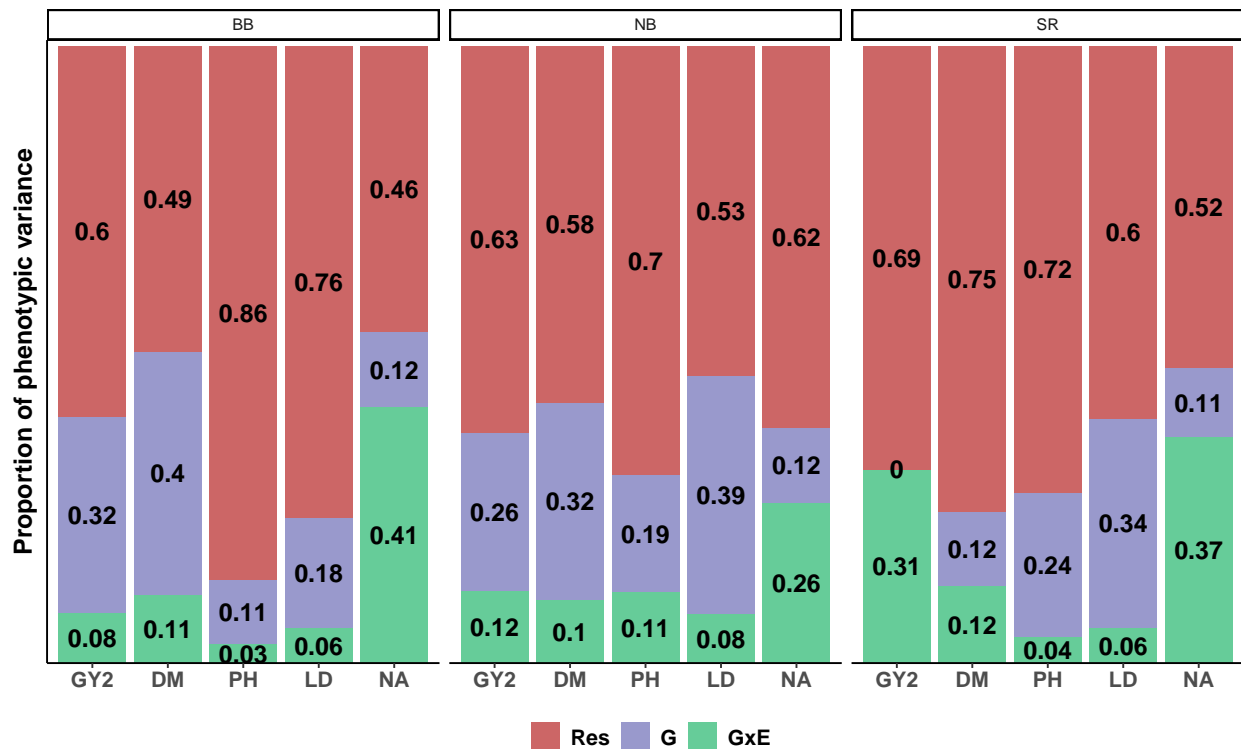
Figure S4: Combination of box and violin plots along with jittered data points for between subjects comparisons by locations of grain yield (GY) for black (BB), Navy (NB) and Red (SR) beans. Pairwise Games-Howell test used. Comparisons showing only significant values. BA: Bay, HU: Huron, SA: Sanilac, TU: Tuscola.

```

data_beans_var = read.csv("data/VarStack.csv",h=T, stringsAsFactors = T)
data_beans_var$trait <- factor(data_beans_var$trait, levels=c("GY1", "GY2", "DM", "PH",
  ↪ "LD"))

ggplot(data_beans_var, aes(x = trait, y = Freq, fill = Comp, label = Comp)) +
  geom_bar(stat = "identity") +
  #geom_text(size = 3, position = position_stack(vjust = 0.5)) +
  facet_wrap("mkt") +
  geom_text(aes(label = round(Freq, 2), x = trait, y = Freq), data = data_beans_var, size
  ↪ = 5, position = position_stack(vjust = 0.5), fontface = "bold") +
  labs(y = "Proportion of phenotypic variance", fill = "", x = NULL) +
  theme_classic() +
  #theme(strip.background = element_blank()) +
  scale_fill_manual(values=c("#CC6666", "#9999CC", "#66CC99"),
    labels = c("Res", "G", "GxE")) +
  theme(legend.position = "bottom",
    axis.text.x=element_text(face="bold", size = 12),
    axis.text.y=element_blank(),
    axis.ticks.y = element_blank(),
    axis.title.y=element_text(face="bold", size = 14) ,
    legend.text = element_text(size = 12, face="bold"), ) +
  scale_y_continuous(expand = expansion(mult = c(0, 0.01)))

```



Proportion of the phenotypic variance for three dry beans traits evaluated across three locations. GY1, grain yield from 2017 to 2021; GY2, grain yield only in 2021; DM, days to maturity; PH, plant height; LD, lodging.

3.6.4.2 Phenotypic variance components

```

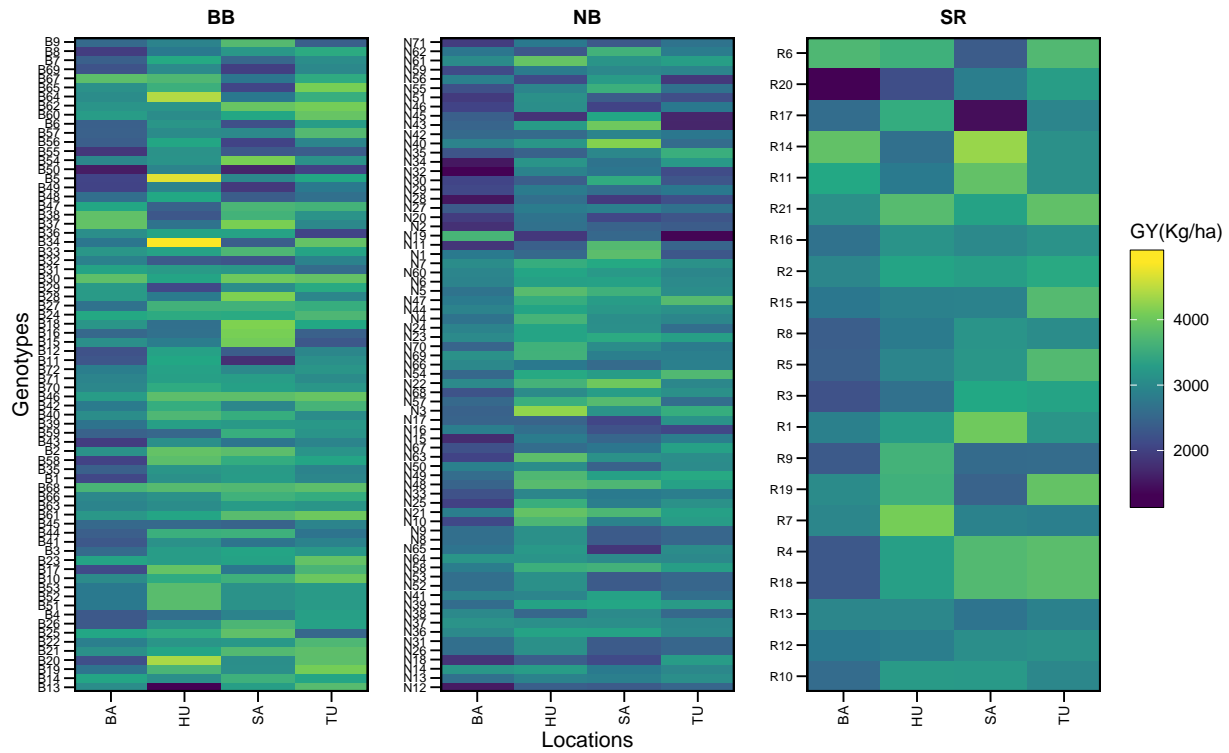
blues_stage.I_BB_ge<- na.omit(blues_stage.I_BB)
stab_bb <- ge_plot(blues_stage.I_BB_ge, type = 1,
  env = loc,
  gen = name,
  resp = yield) + xlab("") + ylab("Genotypes") +
theme(axis.text.x = element_text(size = 8, angle = 90, vjust = 0.5, hjust = 1),
  axis.text.y = element_text(size = 7, angle = 0, vjust = 0.5, hjust = 1),
  legend.position = "none", plot.title=element_text(hjust=0.5)) +
  labs(title = "BB")
#print (stab_bb)

blues_stage.I_NB_ge<- na.omit(blues_stage.I_NB)
stab_nb <- ge_plot(blues_stage.I_NB_ge, type = 1,
  env = loc,
  gen = name,
  resp = yield) + xlab("Locations") + ylab("") +
theme(axis.text.x = element_text(size = 8, angle = 90, vjust = 0.5, hjust = 1),
  axis.text.y = element_text(size = 7, angle = 0, vjust = 0.5, hjust = 1),
  legend.position = "none", plot.title=element_text(hjust=0.5)) +
  labs(title = "NB")
#print (stab_nb)

blues_stage.I_SR_ge<- na.omit(blues_stage.I_SR)
stab_sr <- ge_plot(blues_stage.I_SR_ge, type = 1,
  env = loc,
  gen = name,
  resp = yield) + xlab("") + ylab("") +
theme(axis.text.x = element_text(size = 8, angle = 90, vjust = 0.5, hjust = 1),
  axis.text.y = element_text(size = 7, angle = 0, vjust = 0.5, hjust = 1),
  legend.position = "right",
  plot.title=element_text(hjust=0.5)) +
  labs(fill="GY(Kg/ha)", title = "SR")
#print (stab_sr)

print(arrange_ggplot(stab_bb, stab_nb,stab_sr))

```



Genotype's performance across the environments for Black (BB), Navy (NB), and Small Red (SR) beans using the estimated means (BLUES) from the 1-stage mixed model analysis.

3.6.4.3 Genotyping performance

3.7 Descriptive MET

- Genetic correlations across environment using the Unstructured (US) variance-covariance structure.

This mixed model will be used only for genotype x environment correlations in order to investigate the GEI correlations.

```
mod.us.bb <- asreml(fixed = yield ~ loc + loc:rep ,
                    random  = ~ name:us(loc) ,
                    data     = blues_stage.I_BB,
                    predict  = predict.asreml(classify = "name"),
                    trace    = F,
                    maxit    = 500)

#print(wald(mod.us.bb))
#print(summary.asreml(mod.us.bb)$varcomp)

f=summary(mod.us.bb)$varcomp[1:10,1]
z=matrix(0, 4,4)
z[upper.tri(z)| row(z)==col(z)] <- f
corf=z/sqrt(diag(z)%*%t(diag(z)))
#corf
```

```

rownames(corf)=c(
"BA",
"HU",
"SA",
"JU")

colnames(corf)=rownames(corf)

plotBB<- ggcorrplot(corf, colors = c("#6D9EC1", "white", "#E46726"),
  title = "
      Black Beans",
  show.legend = F,
  legend.title = "rgg" ,lab_size=5,tl.srt = 90,type = c("upper"), lab = T,digits = 4,
  outline.color = "white",pch.col = "white", tl.col = "blue",show.diag = FALSE)
## genetic correlation: manual estimation
# corr.loc_BA_HU<-summary(mod.us.bb)$varcomp[2,1] /
#   sqrt(summary(mod.us.bb)$varcomp[1,1]*summary(mod.us.bb)$varcomp[3,1])

# print(plotBB)

mod.us.nb <- asreml(fixed = yield ~ loc + loc:rep ,
  random      = ~ name:us(loc) ,
  data        = blues_stage.I_NB,
  predict     = predict.asreml(classify = "name"),
  trace       = F,
  maxit       = 500)

#print(wald(mod.us.nb))
#print(summary.asreml(mod.us.nb)$varcomp)

f=summary(mod.us.nb)$varcomp[1:10,1]
z=matrix(0, 4,4)
z[upper.tri(z)| row(z)==col(z)] <- f
corf=z/sqrt(diag(z)%*%t(diag(z)))
#corf

rownames(corf)=c(
"BA",
"HU",
"SA",
"JU")

colnames(corf)=rownames(corf)

#corf<- as_tibble(corf,rownames=NA)

plotNB<-ggcorrplot(corf, colors = c("#6D9EC1", "white", "#E46726"),
  title = "
      Navy Beans",
  show.legend = F,
  legend.title = "r" ,lab_size=5,tl.srt = 90,type = c("upper"), lab = T,digits = 4,
  outline.color = "white",pch.col = "white", tl.col = "blue",show.diag = FALSE)
## genetic correlation: manual estimation
corr.loc<-summary(mod.us.nb)$varcomp[2,1] /

```

```

  sqrt(summary(mod.us.nb)$varcomp[1,1]*summary(mod.us.nb)$varcomp[3,1])
#print(plotNB)

mod.us.sr <- asreml(fixed = yield ~ loc + loc:rep ,
                  random  = ~ name:us(loc) ,
                  data     = blues_stage.I_SR,
                  predict  = predict.asreml(classify = "name"),
                  trace    = F,
                  maxit    = 50000)

#print(wald(mod.us.sr))
#print(summary.asreml(mod.us.sr)$varcomp)

f=summary(mod.us.sr)$varcomp[1:10,1]
z=matrix(0, 4,4)
z[upper.tri(z)| row(z)==col(z)] <- f
corf=z/sqrt(diag(z)%*%t(diag(z)))
#corf

rownames(corf)=c(
"BA",
"HU",
"SA",
"TI")

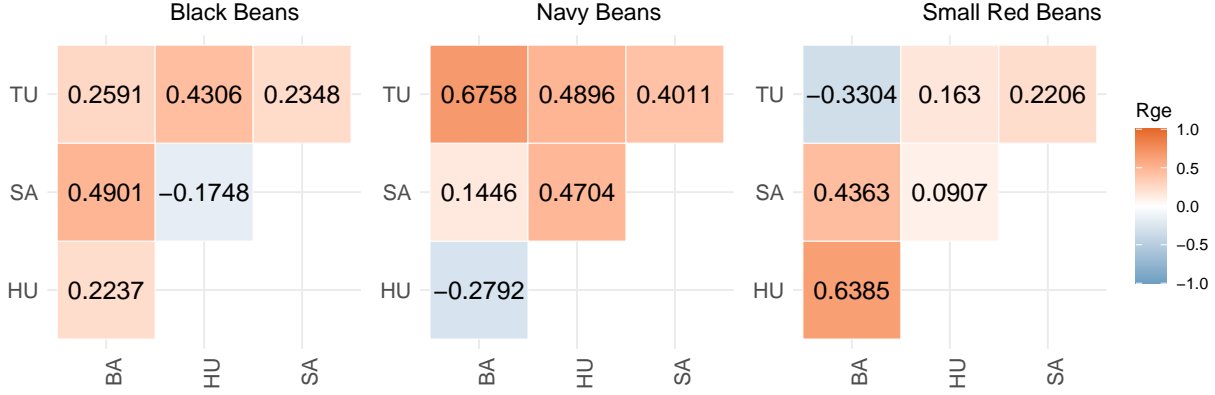
colnames(corf)=rownames(corf)

#corf<- as_tibble(corf,rownames=NA)

plotSR<- ggcorrplot(corf, colors = c("#6D9EC1", "white", "#E46726"),
                  title = "
                        Small Red Beans",
                  #show.legend = F,
                  legend.title = "Rge" ,lab_size=5,tl.srt = 90,type = c("upper"), lab = T,digits = 4,
                  outline.color = "white",pch.col = "white", tl.col = "blue",show.diag = FALSE)
## genetic correlation: manual estimation
corr.loc<-summary(mod.us.sr)$varcomp[2,1] /
  sqrt(summary(mod.us.sr)$varcomp[1,1]*summary(mod.us.sr)$varcomp[3,1])
#print(plotSR)

arrange_ggplot(plotBB,plotNB, plotSR,ncol = 3)

```



3.8 Analyzing MET - GGE

Genotype plus Genotype-vs-Environment interaction (GGE) model has been widely used to genotype evaluation and mega-environment identification in multi-environment trials (MET). This model considers a GGE (i.e., G + GE) biplot, which is constructed by the first two symmetrically scaled principal components (PC1 and PC2) derived from singular value decomposition of environment-centered MET data. The GGE biplot graphically displays G plus GE of a MET in a way that facilitates visual genotype evaluation and mega-environment identification Yan, Kang, Ma, Woods, & Cornelius (2007a).

3.8.1 GGE biplot model

The mean yield of genotype i in environment j is commonly described by a general linear model

$$\hat{y}_{ij} + \mu + \alpha_i + \beta_j + \phi_{ij}$$

where \hat{y}_{ij} is the mean yield of genotype i in environment j , $i = 1, \dots, g$; $j = 1, \dots, e$ being g and e the numbers of genotypes and environments, respectively; μ is the grand mean; α_i is the main effect of the genotype i ; β_j is the main effect of the environment j , and ϕ_{ij} is the interaction effect between genotype i and environment j . In the Genotype plus Genotype-vs-Environment interaction (GGE) model the α_i term is deleted from the above model and then the environment-centered data matrix, ϕ_{ij} , is subjected to SVD Yan & Kang (2003) and Yan et al. (2007a). Explicitly, we have

$$\phi_{ij} = \hat{y}_{ij} - \mu - \beta_j = \sum_{k=1}^p \xi_{ik}^* \eta_{jk}^*$$

where $\xi_{ik}^* = \lambda_k^\alpha \xi_{ik}$; $\eta_{jk}^* = \lambda_k^{1-\alpha} \eta_{jk}$ being λ_k the k th eigenvalue from the SVD ($k = 1, \dots, p$), with $p \leq \min(e, g)$; α is the singular value partition factor for the Principal Component (PC) k ; ξ_{ik}^* and η_{jk}^* are the PC scores for genotype i and environment j , respectively.

The function `gge()` from the R package `metan` Olivoto et al. (2019) according to Yan & Kang (2003) was deployed to produce the GGE model in this study.

3.9 WAASB index

The function `waasb()` function computes the Weighted Average of the Absolute Scores considering all possible IPCA from the Singular Value Decomposition of the BLUPs for genotype-vs-environment interaction effects obtained by an Linear Mixed-effect Model Olivoto et al. (2019), as follows:

$$WAASB_i = \sum_{k=1}^p |IPCA_{ik} \times EP_k| / \sum_{k=1}^p EP_k$$

where $WAASB_i$ is the weighted average of absolute scores of the i th genotype; $IPCA_{ik}$ is the scores of the i th genotype in the k th IPCA; and EP_k is the explained variance of the k th PCA for $k = 1, 2, \dots, p$, $p = \min(g - 1; e - 1)$.

3.10 WAASBY index

- Simultaneous selection for mean performance and stability

The `waasby` index is used for genotype ranking considering both the stability (`waasb`) and mean performance (`y`) based on the following model Olivoto et al. (2019).

$$waasby_i = \frac{(rY_i \times \theta_Y) + (rW_i \times \theta_W)}{\theta_Y + \theta_W}$$

where $waasby_i$ is the superiority index for the i -th genotype; rY_i and rW_i are the rescaled values (0-100) for the response variable (y) and the stability (WAAS or WAASB), respectively; θ_Y and θ_W are the weights for mean performance and stability, respectively.

4 Appendix D - R codes

4.1 MET analysis - Black beans

4.1.1 MET analysis - ASReml

Running MET using `ASReml` - only to comparison of variance components with `metan` outputs

```
mod.met.asreml.bb1 <- asreml(fixed      = yield ~ loc + loc:rep,
                             random    = ~ name + name:loc,
                             data      = blues_stage.I_BB,
                             predict   = predict.asreml(classify = "name"),
                             trace     = F,
                             maxit    = 500)

summFix.bb.met.asreml <- data.frame(wald(mod.met.asreml.bb1))
summFix.bb.met.asreml
```

| Df | Sum.of.Sq | Wald.statistic | Pr.Chisq. |
|---------|---------------|----------------|-----------|
| numeric | numeric | numeric | numeric |
| 1 | 1,368,373,852 | 7,427.1 | 0 |
| 3 | 7,396,784 | 40.1 | 0 |
| 12 | 21,308,617 | 115.7 | 0 |
| | 184,240 | | |

```
summ.bb.met.asreml<- data.frame(summary.asreml(mod.met.asreml.bb1)$varcomp)
summ.bb.met.asreml
```

| component | std.error | z.ratiobound | X.ch |
|-----------|-----------|------------------|---------|
| numeric | numeric | numericcharacter | numeric |
| 48,605.0 | 17,987.9 | 2.7P | 0 |
| 164,940.6 | 21,008.6 | 7.9P | 0 |
| 184,240.9 | 9,279.9 | 19.9P | 0 |

```
#print(summary.asreml(mod.met.asreml.bb1)$bic)
mod.met.asreml.bb<- data.table((mod.met.asreml.bb1$predictions$pvals[1:3]))
names(mod.met.asreml.bb) <- c("name", "yield_BLUPS_MET", "SE")

###
```

4.1.2 MET analysis - lme4

Running MET using **metan** R package Olivoto et al. (2019).

```
mixed_mod.bb<-
  gamem_met(blues_stage.I_BB,
    env = loc,
    gen = name,
    rep = rep,
    resp = yield,
    random = "gen", #Default
    verbose = TRUE) #Default
```

Evaluating trait yield |=====

100% 00:00:02

#> Method: REML/BLUP

#> Random effects: GEN, GEN:ENV

#> Fixed effects: ENV, REP(ENV)

```
#> Denominator DF: Satterthwaite's method
```

P-values for Likelihood Ratio Test of the analyzed traits

model yield COMPLETE NA GEN 5.40e-04 GEN:ENV 5.48e-49

All variables with significant ($p < 0.05$) genotype-vs-environment interaction

4.1.3 Printing the model outputs

4.1.3.1 Likelihood Ratio Tests The output LRT contains the Likelihood Ratio Tests for genotype and genotype-vs-environment random effects.

```
data_mod_bb_test <- get_model_data(mixed_mod.bb, "lrt")
```

```
#> Class of the model: waasb
```

```
#> Variable extracted: lrt
```

```
data_mod_bb_test
```

| VAR | model | npar | logLik | AIC | LRT | Df | Pr(>Chisq) |
|-----------|-----------|---------|----------|----------|---------|---------|------------|
| character | character | integer | numeric | numeric | numeric | numeric | numeric |
| yield | GEN | 18 | -8,314.1 | 16,664.3 | 12.0 | 1 | 0.0 |
| yield | GEN:ENV | 18 | -8,416.4 | 16,868.7 | 216.4 | 1 | 0.0 |

```
#customize the display of numbers and other data in a tibble
# old <- options(pillar.sigfig = 6)
#
# blues_stage.I_BB %>%
#   group_by(loc) %>%
#   dplyr::summarise(Mean = mean(yield, na.rm = TRUE))
```

```
data_mod_bb_det <- get_model_data(mixed_mod.bb, "details")
```

4.1.3.2 Detailed parameters

```
#> Class of the model: waasb
```

```
#> Variable extracted: details
```

```
data_mod_bb_det
```

| Parameters | yield |
|------------|---------------------|
| character | character |
| Mean | 3255.05 |
| SE | 19.84 |
| SD | 655 |
| CV | 20.13 |
| Min | 805.92 (B13 in HU) |
| Max | 5310.16 (B34 in HU) |
| MinENV | BA (3004.17) |
| MaxENV | HU (3461.59) |
| MinGEN | B50 (2031.07) |
| n: 12 | |

4.1.3.3 Random effects The output LRT contains the Likelihood Ratio Tests for genotype and genotype-vs-environment random effects.

```
#customize the display of numbers and other data in a tibble
old <- options(pillar.sigfig = 8)

data_mod_bb_var <- get_model_data(mixed_mod.bb, "vcomp")
```

```
#> Class of the model: waasb
```

```
#> Variable extracted: vcomp
```

```
data_mod_bb_var
```

| Group | yield |
|-----------|-----------|
| character | numeric |
| GEN | 48,616.4 |
| GEN:ENV | 164,935.3 |
| Residual | 184,240.5 |

```
old <- options(pillar.sigfig = 4)
data_mod_bb_comp <- get_model_data(mixed_mod.bb)
```

4.1.3.4 Variance components and genetic parameters

```
#> Class of the model: waasb
```

```
#> Variable extracted: genpar
```

```
data_mod_bb_comp
```

| Parameters | yield |
|-------------------------------|-----------|
| character | numeric |
| Phenotypic variance | 397,792.2 |
| Heritability | 0.1 |
| GEI _r ² | 0.4 |
| h ² _{mg} | 0.5 |
| Accuracy | 0.7 |
| r _{ge} | 0.5 |
| CV _g | 6.8 |
| CV _r | 13.2 |
| CV ratio | 0.5 |

4.1.4 MET - GGE biplot

Genotype plus Genotype-vs-Environment interaction (GGE). Mega-environment identification in multi-environment trials (MET) according to (**W?**). Yan et al. 2007

4.1.4.1 GGE ENV biplot GGE biplot done using:

- **sd**: each value is divided by the standard deviation of its corresponding environment.
- **environment**: environment-centered (G+GE)
- **environment**: singular value is entirely partitioned into the environment eigenvectors, also called column metric preserving

```
gge_model.bb <- gge(blues_stage.I_BB, loc, name, yield,
  centering = "environment", #2
  scaling = "sd", #2
  svp = "environment") #2

a <- plot(gge_model.bb, type=4,
```

```

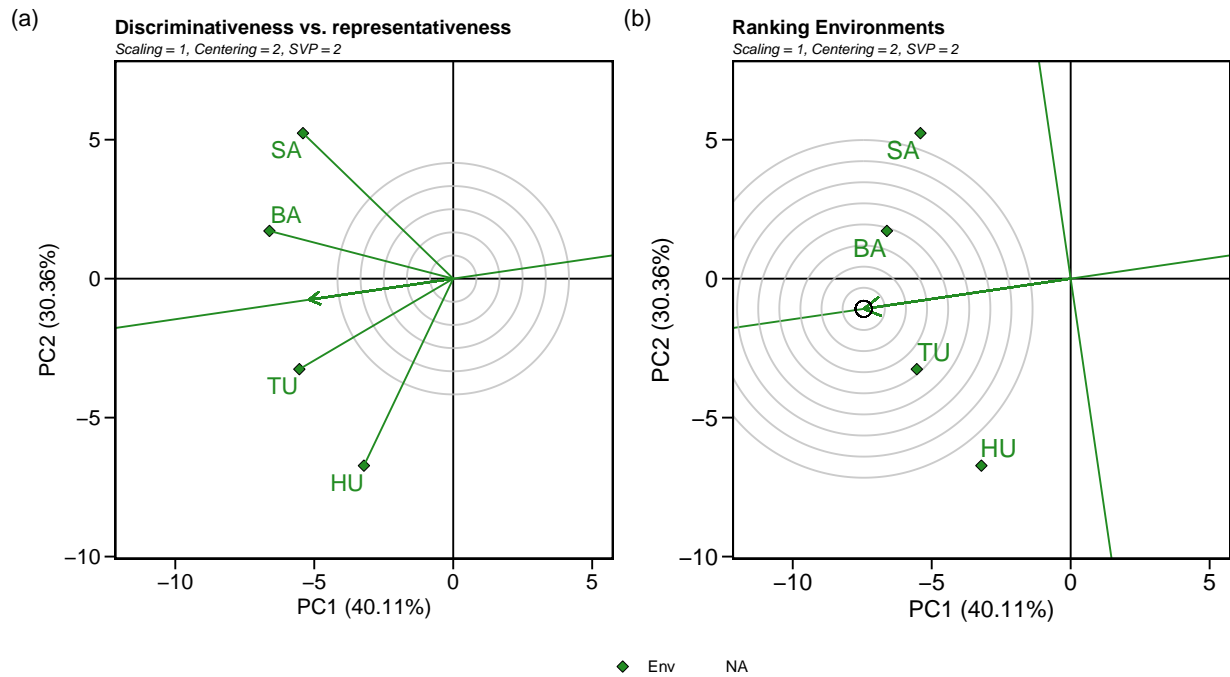
    size.text.env = 4.5,
    plot_theme = theme_metan(grid = "both",color.background =
      ↪ transparent_color()),
    axis_expand = 1.5,
    col.alpha.circle = 0.8,
    shape.gen = NA,
    col.gen = NA,
    size.text.lab = NA,
    size.text.gen = NA,
    leg.lab=c('Env'),
    #title = FALSE
  )

gge_model.bb <- gge(blues_stage.I_BB, loc, name, yield,
  centering = "environment", #1
  scaling = "sd", #2Y
  svp = "environment")#2)

b <- plot(gge_model.bb, type = 6,
  size.text.env = 5,
  plot_theme = theme_metan(grid = "both",color.background =
    ↪ transparent_color()),
  axis_expand = 1.5,
  # col.alpha.circle = 100,
  col.alpha.circle = 0.8,
  size.text.lab = 13,
  #title = FALSE
)

arrange_ggplot(a, b,
  guides = "collect",
  tag_levels = "a",
  tag_prefix = "(",
  tag_suffix = ")")

```



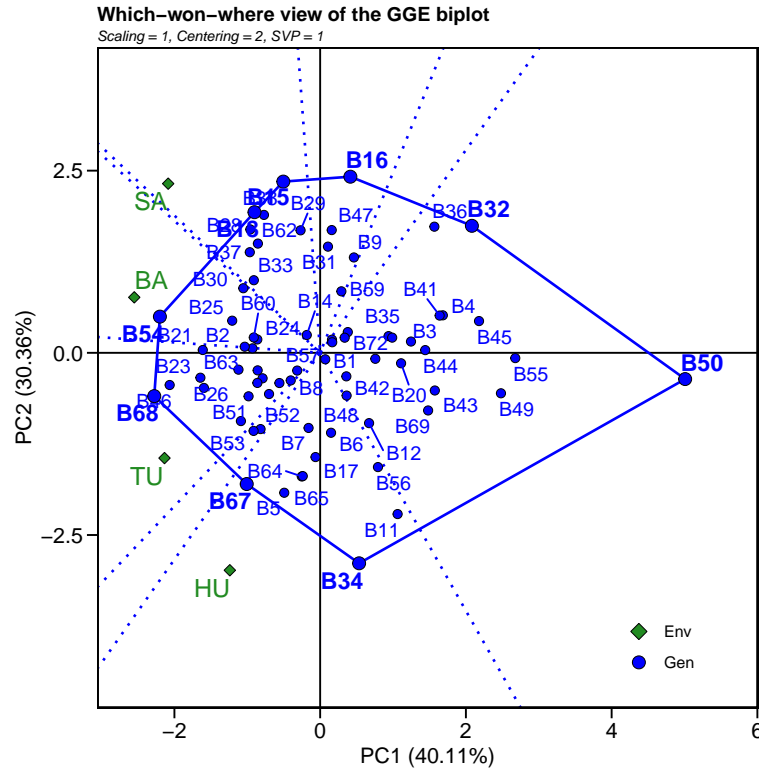
4.1.4.2 Biplot type 3: Which-won-where GGE biplot done using:

- **sd**: each value is divided by the standard deviation of its corresponding environment.
- **environment**: environment-centered (G+GE)
- **genotype**: singular value is entirely partitioned into the environment eigenvectors, also called column metric preserving

```
gge_model.bb <- gge(blues_stage.I_BB, loc, name, yield,
  centering = "environment", #2
  scaling = "sd", #1
  svp = "genotype")#2)

e <- plot(gge_model.bb, type = 3,
  size.text.env = 5,
  plot_theme = theme_metan(grid = "both", color.background =
    ↪ transparent_color()),
  axis_expand = 1.2,
  size.line = 0.7,
  size.text.gen = 4,
  size.text.win = 4.5
  #title = F
)

print(e)
```



4.1.5 Mean performance and stability analysis

WAASP index and BLUPs to estimate stability analysis.

```
#blues_stage.I_BB<- na.omit(blues_stage.I_BB)

waasb_model_bb <-
  waasb(blues_stage.I_BB,
    env = loc,
    gen = name,
    rep = rep,
    resp = yield,
    random = "gen", #Default
    verbose = TRUE,
    wresp = 60) #weight for response variable 60 and 40 for yielding and stability,
    ↪ respectively)
```

```
#> Evaluating trait yield |=====
#> -----
#> P-values for Likelihood Ratio Test of the analyzed traits
#> -----
#>      model      yield
#> COMPLETE      NA
#>      GEN 5.40e-04
#>      GEN:ENV 5.48e-49
#> -----
#> All variables with significant (p < 0.05) genotype-vs-environment interaction
```



```

waasb_model<- waasb_model_bb$yield$model

#waasb_ind <- gmd(waasb_model_bb, "WAASB")
#print_tbl(waasb_ind)

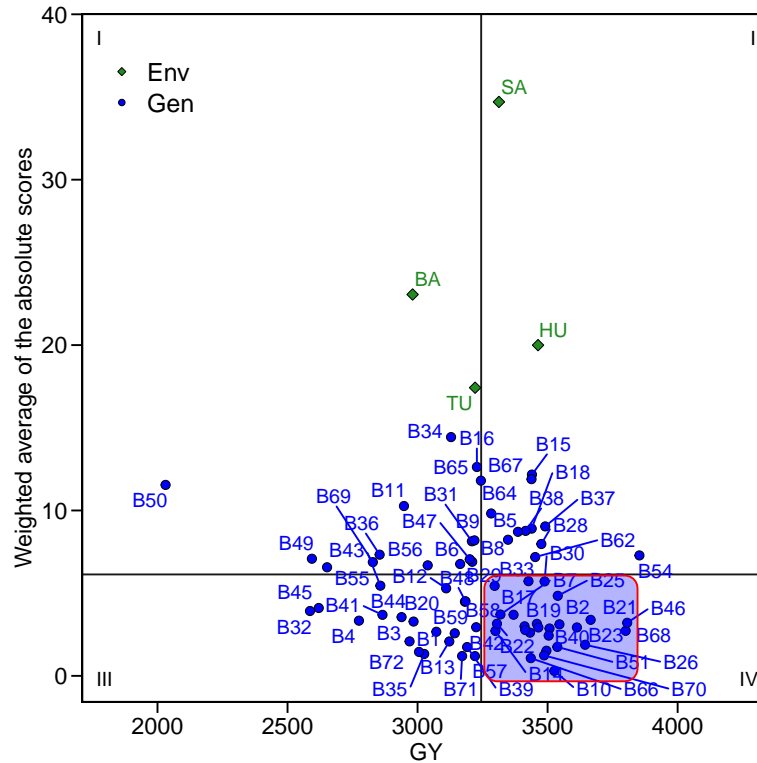
#desc <- c("Selected cultivar providing greater performance and stability for GY")

waasp_plot <- plot_scores(waasb_model_bb, type = 3,
  title = FALSE,
  size.tex.gen = 4,
  size.tex.env = 4,
  size.tex.lab = 13,
  # highlight = c("B55", "B1" , "B29", "B20" ,"B28"),
  plot_theme = theme_metan(grid = "both",color.background = transparent_color())
) +

  geom_mark_rect(aes(filter = Code %in% c("B17", "B46", "B10", "B14"),
    ),
    label.fontsize = 10,
    show.legend = F,
    con.cap = 0,
    con.colour = "red",
    color = "red",
    expand = 0.015,
    label.buffer = unit(10, "cm"))+
  #theme_gray()+
  theme(legend.position = c(0.1, 0.9),
    legend.background = element_blank(),
    legend.title = element_blank(),
    aspect.ratio = 1) +
  labs(x = "GY")

print(waasp_plot)

```



```

waasb_model_meanWaasb<-mean(waasb_model$WAASB)
waasb_model_meanY<-mean(waasb_model$Y)

selected <- waasb_model %>%
  dplyr::filter(Y >= waasb_model_meanY & WAASB <= waasb_model_meanWaasb)

selected_table <- selected

if (knitr::is_html_output()) {
  print_table(selected_table)
}else{
  selected_table[,1:8]
}

```

| type | Code | Y | PC1 | PC2 | PC3 | WAASB | PctResp |
|-----------|-----------|---------|---------|---------|---------|---------|---------|
| character | character | numeric | numeric | numeric | numeric | numeric | numeric |
| GEN | B14 | 3,299.5 | 1.7 | 4.6 | 3.1 | 2.7 | 69.6 |
| GEN | B19 | 3,369.1 | -0.5 | -8.0 | -7.6 | 3.7 | 73.4 |
| GEN | B21 | 3,665.5 | 5.0 | 0.9 | -1.8 | 3.4 | 89.7 |
| n: 26 | | | | | | | |

| type | Code | Y | PC1 | PC2 | PC3 | WAASB | PctResp |
|-----------|-----------|---------|---------|---------|---------|---------|---------|
| character | character | numeric | numeric | numeric | numeric | numeric | numeric |
| GEN | B22 | 3,305.2 | -2.3 | -2.2 | -7.5 | 3.2 | 69.9 |
| GEN | B25 | 3,539.1 | 4.7 | 8.2 | -0.2 | 4.8 | 82.8 |
| GEN | B26 | 3,644.3 | 0.9 | 3.2 | -3.1 | 1.9 | 88.5 |
| GEN | B51 | 3,537.4 | -2.4 | 1.3 | -0.3 | 1.7 | 82.7 |
| GEN | B52 | 3,458.7 | -4.3 | 2.3 | -0.5 | 3.1 | 78.4 |
| GEN | B53 | 3,507.4 | -3.4 | 2.1 | 2.3 | 2.9 | 81.0 |
| n: 26 | | | | | | | |

```
#selected$Code
```

```
#Create a data frame with BLUPS - selected and non-selected
blups_sel <-
  gmd(waasb_model_bb, "blupge") %>%
  add_cols(SELECTED = ifelse(GEN %in% selected$Code, "yes", "no")) %>%
  dplyr::rename(BLUPs_sel = yield) %>%
  droplevels()

blups_sel_mean<-
  gmd(waasb_model_bb, "blupge") %>%
  add_cols(SELECTED = ifelse(GEN %in% selected$Code, "yes", "no")) %>%
  filter(SELECTED == "yes") %>%
  dplyr::summarise(mean_GY = mean(yield,na.rm = TRUE), n = n())

# Create a data frame with the waasb index - selected and non-selected
waasb_sel <-
  gmd(waasb_model_bb, "WAASB") %>%
  add_cols(SELECTED = ifelse(GEN %in% selected$Code, "yes", "no")) %>%
  dplyr::rename(WAASB_sel = yield) %>%
  droplevels()
#str(waasb_sel)

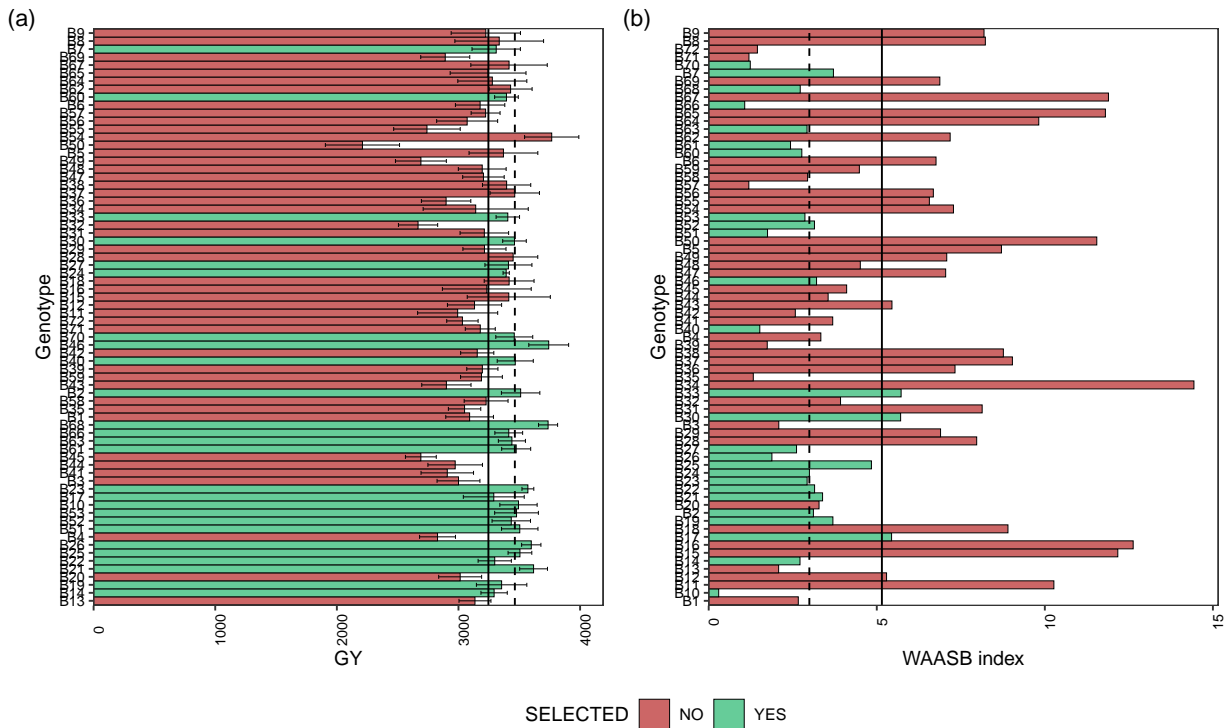
waasb_sel_mean<-
  gmd(waasb_model_bb, "WAASB") %>%
  add_cols(SELECTED = ifelse(GEN %in% selected$Code, "yes", "no")) %>%
  filter(SELECTED == "yes") %>%
  dplyr::summarise(mean_GY = mean(yield,na.rm = TRUE), n = n())

p1<- plot_selected(blups_sel, GEN, BLUPs_sel, mean_sel = blups_sel_mean$mean_GY) +
  labs(y = "GY")

p3<- plot_selected(waasb_sel, GEN, WAASB_sel, mean_sel = waasb_sel_mean$mean_GY) +
```

```
labs(y = "WAASB index")

arrange_ggplot(p1, p3,
  guides = "collect",
  tag_levels = "a",
  tag_prefix = "(",
  tag_suffix = ")")
```



Mean performance (a) and stability (b) for grain yield (GY) of 72 Black beans genotypes. The vertical dashed and solid lines shows, respectively, the mean of the selected genotype and the overall mean for both mean performance and WAASB index

4.1.5.1 Selection differentials Percentage (SD_gain in %) gain from the selected genotypes compared to the general mean.

```
blups_sel2 <-
  gmd(waasb_model_bb, "blupg") %>%
  add_cols(SELECTED = ifelse(GEN %in% selected$Code, "yes", "no")) %>%
  dplyr::rename(BLUPs_sel = yield) %>%
  droplevels()
```

```
#> Class of the model: waasb
```

```
#> Variable extracted: blupg
```

```

blups_sel_mean2<-
  gmd(waasb_model_bb, "blupg") %>%
  add_cols(SELECTED = ifelse(GEN %in% selected$Code, "yes", "no")) %>%
  filter(SELECTED == "yes") %>%
  dplyr::summarise(mean_GY = mean(yield,na.rm = TRUE), n = n())

#> Class of the model: waasb
#> Variable extracted: blupg

SD_blups<- as_tibble((blups_sel_mean2$mean_GY/mean(blups_sel2$BLUPs_sel, na.rm = T))
  ↪ -1)*100
SD_WAASP<- as_tibble((waasb_sel_mean$mean_GY /mean(waasb_sel$WAASB_sel, na.rm = T))
  ↪ -1)*100

SD_comb<- full_join(SD_blups, SD_WAASP, by = "value") %>%
  dplyr::rename(SD_gain = value) %>%
  tibble::add_column(Comp_name = c('BLUPs', 'WAASB')) %>%
  relocate(Comp_name)

SD_comb$n_selected<- blups_sel_mean2$n
SD_comb

```

| Comp_name | SD_gain | n_selected |
|-----------|---------|------------|
| character | numeric | integer |
| BLUPs | 3.7 | 26 |
| WAASB | -41.9 | 26 |

```

blups_sel2$mean_blup <- mean(blups_sel2$BLUPs_sel, na.rm = T)
waasb_sel$mean_waasb <- mean(waasb_sel$WAASB_sel, na.rm = T)

#str(waasb_sel)
data_comb<- merge(blups_sel2, waasb_sel, by = c("GEN", "SELECTED"))
#names(data_comb)
## SD for each genotype
data_sel_perc <- data_comb %>%
  rowwise %>%
  mutate(Perc_blup_gain = ((BLUPs_sel/mean_blup)*100)-100) %>%
  mutate(Perc_WAASB_gain = ((WAASB_sel/mean_waasb)*100)-100) %>%
  as_tibble()

# data_sel_perc_mean <- data_sel_perc %>%
#   dplyr::filter(SELECTED == "yes")
#
# mean(data_sel_perc_mean$Perc_blup_gain)

if (knitr::is_html_output()) {
  print_table(data_sel_perc)
}

```

```

}else{

data_sel_perc[,1:7]
}

```

| GEN | SELECTED | BLUPs_sel | mean_blup | WAASB_sel | mean_waasb | Perc_blup_gain |
|-----------|-----------|-----------|-----------|-----------|------------|----------------|
| character | character | numeric | numeric | numeric | numeric | numeric |
| B1 | no | 3,173.6 | 3,255.1 | 2.7 | 5.2 | -2.5 |
| B10 | yes | 3,391.1 | 3,255.1 | 0.3 | 5.2 | 4.2 |
| B11 | no | 3,110.5 | 3,255.1 | 10.3 | 5.2 | -4.4 |
| B12 | no | 3,185.4 | 3,255.1 | 5.3 | 5.2 | -2.1 |
| B13 | no | 3,197.5 | 3,255.1 | 2.1 | 5.2 | -1.8 |
| B14 | yes | 3,282.6 | 3,255.1 | 2.7 | 5.2 | 0.8 |
| B15 | no | 3,337.8 | 3,255.1 | 12.2 | 5.2 | 2.5 |
| B16 | no | 3,240.1 | 3,255.1 | 12.6 | 5.2 | -0.5 |
| B17 | yes | 3,281.1 | 3,255.1 | 5.4 | 5.2 | 0.8 |

n: 72

```

data_sel_perc<- data_sel_perc %>%
  dplyr::relocate(GEN,SELECTED,BLUPs_sel,mean_blup,Perc_blup_gain,
                  WAASB_sel,mean_waasb ,Perc_WAASB_gain)

#write.xlsx(data_sel_perc, "./data/sel_SD_bb_2.xlsx")

data_sel_perc2 <- data_sel_perc %>%
  dplyr::select(GEN,SELECTED, BLUPs_sel, WAASB_sel, Perc_blup_gain, Perc_WAASB_gain)

data_sel_perc2

```

| GEN | SELECTED | BLUPs_sel | WAASB_sel | Perc_blup_gain | Perc_WAASB_gain |
|-----------|-----------|-----------|-----------|----------------|-----------------|
| character | character | numeric | numeric | numeric | numeric |
| B1 | no | 3,173.6 | 2.7 | -2.5 | -48.3 |
| B10 | yes | 3,391.1 | 0.3 | 4.2 | -94.2 |
| B11 | no | 3,110.5 | 10.3 | -4.4 | 99.3 |
| B12 | no | 3,185.4 | 5.3 | -2.1 | 2.7 |

n: 72

| GEN | SELECTED | BLUPs_sel | WAASB_sel | Perc_blup_gain | Perc_WAASB_gain |
|-----------|-----------|-----------|-----------|----------------|-----------------|
| character | character | numeric | numeric | numeric | numeric |
| B13 | no | 3,197.5 | 2.1 | -1.8 | -59.6 |
| B14 | yes | 3,282.6 | 2.7 | 0.8 | -47.3 |
| B15 | no | 3,337.8 | 12.2 | 2.5 | 136.2 |
| B16 | no | 3,240.1 | 12.6 | -0.5 | 145.1 |
| B17 | yes | 3,281.1 | 5.4 | 0.8 | 5.6 |
| n: 72 | | | | | |

```
##BLUPs indexes
stab_blups_bb<- blup_indexes(waasb_model_bb)
stab_blups_bb<- as_tibble(stab_blups_bb$yield)

data_waasby <- waasb_model_bb$yield$model %>%
  dplyr::filter(type != "ENV") %>%
  dplyr::select("Code", "WAASBY", "OrWAASBY") %>%
  dplyr::rename(GEN = Code)

stab_blups_bb<- stab_blups_bb %>%
  full_join(data_waasby, by = "GEN")

if (knitr::is_html_output()) {
  print_table(stab_blups_bb)
}else{
  stab_blups_bb[,1:8]
}
```

| GEN | Y | HMGV | HMGV_R | RPGV | RPGV_Y | RPGV_R | HMRPGV |
|-----------|---------|---------|---------|---------|---------|---------|---------|
| character | numeric | numeric | numeric | numeric | numeric | numeric | numeric |
| B1 | 3,122.0 | 3,048.9 | 54 | 1.0 | 3,083.2 | 55 | 0.9 |
| B10 | 3,299.5 | 3,473.1 | 10 | 1.1 | 3,489.4 | 10 | 1.1 |
| B11 | 3,369.1 | 2,884.2 | 62 | 0.9 | 2,986.8 | 61 | 0.9 |
| B12 | 2,984.7 | 3,083.1 | 53 | 1.0 | 3,121.1 | 54 | 1.0 |
| B13 | 3,665.5 | 3,118.1 | 52 | 1.0 | 3,136.3 | 52 | 1.0 |
| B14 | 3,305.2 | 3,282.3 | 32 | 1.0 | 3,295.9 | 35 | 1.0 |
| B15 | 3,539.1 | 3,310.4 | 30 | 1.1 | 3,419.2 | 23 | 1.0 |
| n: 72 | | | | | | | |

| GEN | Y | HMGV | HMGV_R | RPGV | RPGV_Y | RPGV_R | HMRPGV |
|-----------|---------|---------|---------|---------|---------|---------|---------|
| character | numeric | numeric | numeric | numeric | numeric | numeric | numeric |
| B16 | 3,644.3 | 3,128.3 | 51 | 1.0 | 3,228.3 | 40 | 1.0 |
| B17 | 2,774.6 | 3,232.1 | 35 | 1.0 | 3,278.4 | 37 | 1.0 |
| n: 72 | | | | | | | |

```
# library(openxlsx)
# write.xlsx(stab_blups_bb, "../data/blups_bb_2.xlsx")
```

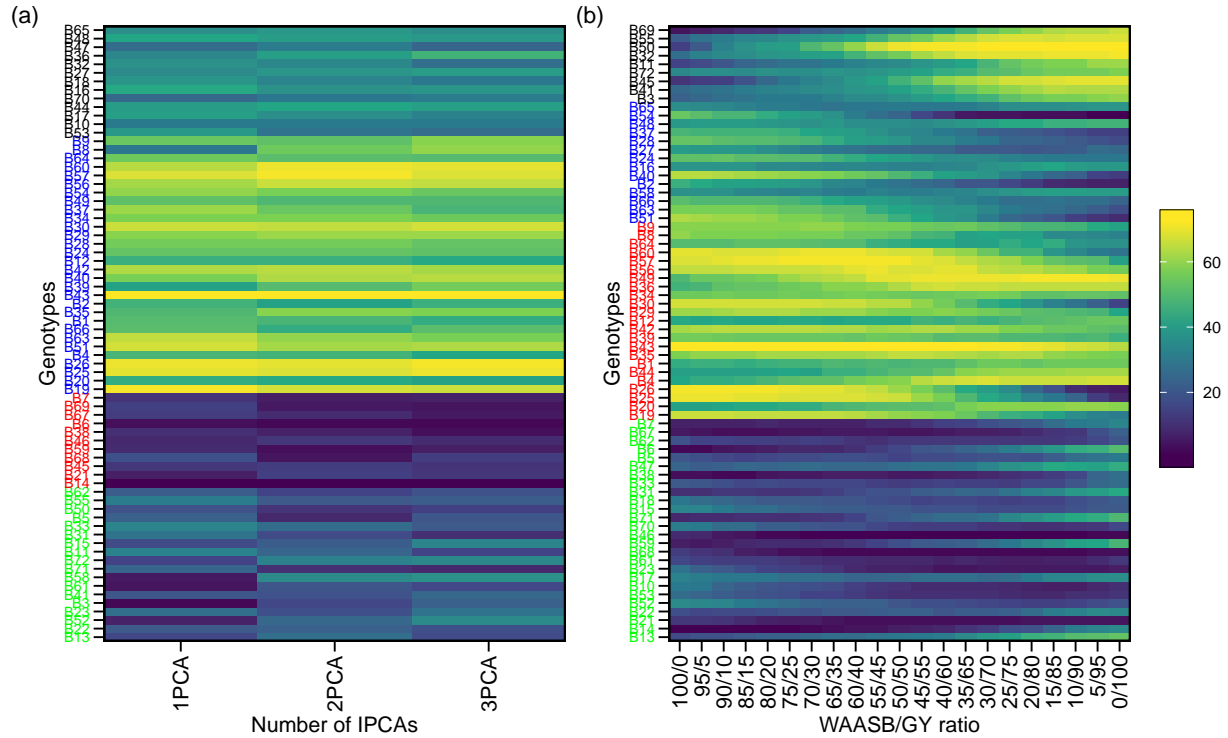
4.1.5.2 Scenarios of waasby estimation Planning different scenarios of waasby estimation by changing the weights assigned to the stability and the mean performance according to Olivoto et al. (2019)

```
scenarios <- wsmpt(waasb_model_bb, progbar = F)

scen1<- plot(scenarios, type = 1) +
  theme(axis.text.y = element_text(size=8))

scen2<-plot(scenarios, type = 2) +
  theme(axis.text.y = element_text(size=8))

arrange_ggplot(scen1, scen2,
  guides = "collect",
  legend.position = "right",
  tag_levels = "a",
  tag_prefix = "(",
  tag_suffix = ")")
```

4.1.5.3 Coincidence index of genotype selection Computes the coincidence index (Hamblin and Zimmermann, 1986) as follows:

$$CI = \frac{A - C}{M - C} \times 100$$

where A is the number of selected genotypes common to different methods; C is the number of expected genotypes selected by chance; and M is the number of genotypes selected according to the selection intensity.

```
coinc_1 <- stab_blups_bb %>% dplyr::select(GEN,HMRPGV_R) %>% arrange(HMRPGV_R)
coinc_2 <- stab_blups_bb %>% dplyr::select(GEN,RPGV_R) %>% arrange(RPGV_R)
coinc_3 <- stab_blups_bb %>% dplyr::select(GEN,HMGV_R) %>% arrange(HMGV_R)
coinc_4 <- stab_blups_bb %>% dplyr::select(GEN,OrWAASBY) %>% arrange(OrWAASBY)
coinc_5 <- stab_blups_bb %>% dplyr::select(GEN,WAASB_R) %>% arrange(WAASB_R)

selc_perc<- round(nrow(stab_blups_bb)*0.2)

coinc_1.1 <-1
coinc_1.2 <- coincidence_index(sel1 = coinc_1$GEN[1:selc_perc],
                              sel2 = coinc_2$GEN[1:selc_perc],
                              total = 72)/100
coinc_1.3 <- coincidence_index(sel1 = coinc_1$GEN[1:selc_perc],
                              sel2 = coinc_3$GEN[1:selc_perc],
                              total = 72)/100
coinc_1.4 <- coincidence_index(sel1 = coinc_1$GEN[1:selc_perc],
                              sel2 = coinc_4$GEN[1:selc_perc],
                              total = 72)/100
coinc_1.5 <- coincidence_index(sel1 = coinc_1$GEN[1:selc_perc],
```

```

                                sel2 = coinc_5$GEN[1:selc_perc],
                                total = 72)/100
coinc_2.2 <-1
coinc_2.3 <- coincidence_index(sel1 = coinc_2$GEN[1:selc_perc],
                                sel2 = coinc_3$GEN[1:selc_perc],
                                total = 72)/100
coinc_2.4 <- coincidence_index(sel1 = coinc_2$GEN[1:selc_perc],
                                sel2 = coinc_4$GEN[1:selc_perc],
                                total = 72)/100
coinc_2.5 <- coincidence_index(sel1 = coinc_2$GEN[1:selc_perc],
                                sel2 = coinc_5$GEN[1:selc_perc],
                                total = 72)/100

coinc_3.3<- 1
coinc_3.4 <- coincidence_index(sel1 = coinc_3$GEN[1:selc_perc],
                                sel2 = coinc_4$GEN[1:selc_perc],
                                total = 72)/100
coinc_3.5 <- coincidence_index(sel1 = coinc_3$GEN[1:selc_perc],
                                sel2 = coinc_5$GEN[1:selc_perc],
                                total = 72)/100

coinc_4.4 <- 1
coinc_4.5 <- coincidence_index(sel1 = coinc_4$GEN[1:selc_perc],
                                sel2 = coinc_5$GEN[1:selc_perc],
                                total = 72)/100

coinc_5.5 <- 1

coinc<- c(coinc_1.1,coinc_1.2,coinc_2.2,coinc_1.3,coinc_2.3,
          coinc_3.3,coinc_1.4, coinc_2.4, coinc_3.4,
          coinc_4.4, coinc_1.5, coinc_2.5,
          coinc_3.5, coinc_4.5,
          coinc_5.5)

z=matrix(0,5,5)
z[upper.tri(z)| row(z)==col(z)] <- coinc

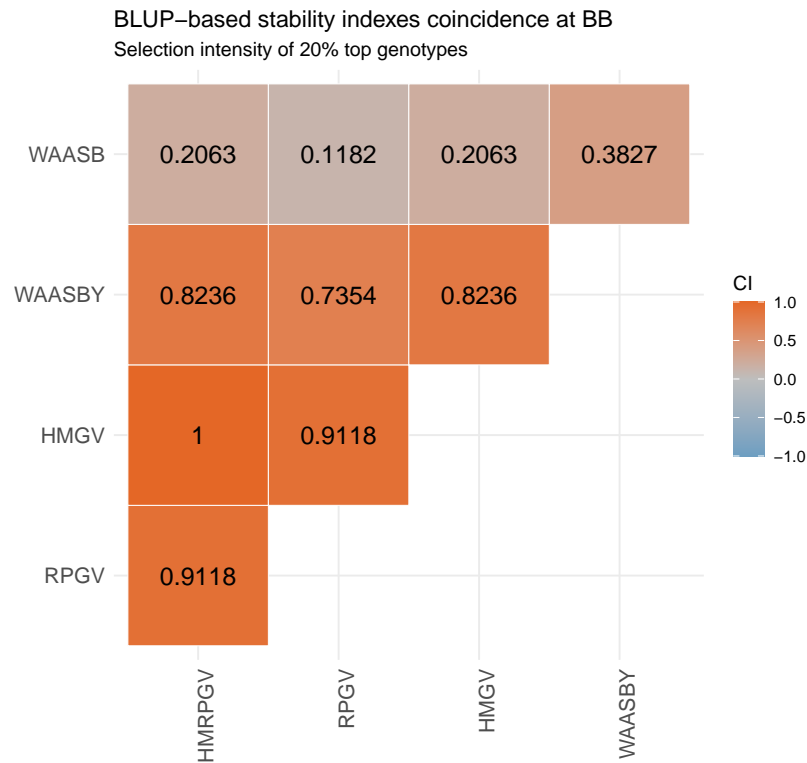
rownames(z)=c(
"HMRPGV",
"RPGV",
'HMGV',
'WAASBY',
'WAASB')

colnames(z)=rownames(z)

plotBB<- ggcorrplot(z, colors = c("#6D9EC1", "gray", "#E46726"),
                    show.legend = T,
                    legend.title = "CI", lab_size=5,tl.srt = 90,type = c("upper"), lab = T,digits = 4,
                    outline.color = "white",pch.col = "white", tl.col = "blue",show.diag = F) +
  labs(title = "BLUP-based stability indexes coincidence at BB",
        subtitle = "Selection intensity of 20% top genotypes")

print(plotBB)

```



4.2 MET analysis - Navy beans

4.2.1 MET analysis - ASReml

Running MET using ASReml - only to comparison of variance components with metan outputs

```
mod.met.asreml.nb1 <- asreml(fixed      = yield ~ loc + loc:rep,
  random      = ~ name + name:loc,
  data        = blues_stage.I_NB,
  predict     = predict.asreml(classify = "name"),
  trace       = F,
  maxit       = 500)

summFix.nb.met.asreml <- data.frame(wald(mod.met.asreml.nb1))
summFix.nb.met.asreml
```

| Df | Sum.of.Sq | Wald.statistic | Pr.Chisq. |
|---------|---------------|----------------|-----------|
| numeric | numeric | numeric | numeric |
| 1 | 1,636,916,005 | 9,420.3 | 0 |
| 3 | 11,631,057 | 66.9 | 0 |
| 12 | 20,821,488 | 119.8 | 0 |
| | 173,765 | | |

```
summ.nb.met.asreml<- data.frame(summary.asreml(mod.met.asreml.nb1)$varcomp)
summ.nb.met.asreml
```

| component | std.error | z.ratiobound | X.ch |
|-----------|-----------|------------------|---------|
| numeric | numeric | numericcharacter | numeric |
| 34,501.8 | 11,258.8 | 3.1P | 0 |
| 72,760.9 | 11,918.4 | 6.1P | 0 |
| 173,765.2 | 8,797.2 | 19.8P | 0 |

```
#print(summary.asreml(mod.met.asreml.nb1)$bic)
mod.met.asreml.nb<- data.table((mod.met.asreml.nb1$predictions$pvals[1:3]))
names(mod.met.asreml.nb) <- c("name", "yield_BLUPS_MET", "SE")

###
```

4.2.2 MET analysis - lme4

Running MET using metan R package Olivoto et al. (2019).

```
#str(blues_stage.I_NB)
mixed_mod.nb<-
  gamem_met(blues_stage.I_NB,
    env = loc,
    gen = name,
    rep = rep,
    resp = yield,
    random = "gen", #Default
    verbose = TRUE) #Default
```

Evaluating trait yield |=====

100% 00:00:04

#> Method: REML/BLUP

#> Random effects: GEN, GEN:ENV

#> Fixed effects: ENV, REP(ENV)

#> Denominator DF: Satterthwaite's method

P-values for Likelihood Ratio Test of the analyzed traits

model yield COMPLETE NA GEN 3.41e-05 GEN:ENV 6.69e-20

All variables with significant ($p < 0.05$) genotype-vs-environment interaction

4.2.3 Printing the model outputs

4.2.3.1 Likelihood Ratio Tests The output LRT contains the Likelihood Ratio Tests for genotype and genotype-vs-environment random effects.

```
data_mod_nb_test <- get_model_data(mixed_mod.nb, "lrt")
```

```
#> Class of the model: waasb
```

```
#> Variable extracted: lrt
```

```
data_mod_nb_test
```

| VAR | model | npar | logLik | AIC | LRT | Df | Pr(>Chisq) |
|-----------|-----------|---------|----------|----------|---------|---------|------------|
| character | character | integer | numeric | numeric | numeric | numeric | numeric |
| yield | GEN | 18 | -8,123.2 | 16,282.4 | 17.2 | 1 | 0.0 |
| yield | GEN:ENV | 18 | -8,156.3 | 16,348.7 | 83.4 | 1 | 0.0 |

```
#customize the display of numbers and other data in a tibble
# old <- options(pillar.sigfig = 6)
#
# blues_stage.I_NB %>%
#   group_by(loc) %>%
#   dplyr::summarise(Mean = mean(yield, na.rm = TRUE))
```

```
data_mod_nb_det <- get_model_data(mixed_mod.nb, "details")
```

4.2.3.2 Detailed parameters

```
#> Class of the model: waasb
```

```
#> Variable extracted: details
```

```
data_mod_nb_det
```

| Parameters | yield |
|------------|-----------|
| character | character |
| Mean | 2924 |
| n: 12 | |

| Parameters | yield |
|------------|---------------------|
| character | character |
| SE | 17.22 |
| SD | 565.35 |
| CV | 19.34 |
| Min | 1096.13 (N32 in BA) |
| Max | 4939.4 (N34 in TU) |
| MinENV | BA (2654.03) |
| MaxENV | HU (3094) |
| MinGEN | N28 (2260.58) |
| n: 12 | |

4.2.3.3 Random effects The output LRT contains the Likelihood Ratio Tests for genotype and genotype-vs-environment random effects.

```
old <- options(pillar.sigfig = 8)
data_mod_nb_var <- get_model_data(mixed_mod.nb, "vcomp")
```

```
#> Class of the model: waasb
```

```
#> Variable extracted: vcomp
```

```
data_mod_nb_var
```

| Group | yield |
|-----------|-----------|
| character | numeric |
| GEN | 34,502.1 |
| GEN:ENV | 72,760.9 |
| Residual | 173,765.0 |

```
old <- options(pillar.sigfig = 4)
data_mod_nb_comp <- get_model_data(mixed_mod.nb)
```

4.2.3.4 Variance components and genetic parameters

```
#> Class of the model: waasb
```

```
#> Variable extracted: genpar
```

```
data_mod_nb_comp
```

| Parameters | yield |
|---------------------|-----------|
| character | numeric |
| Phenotypic variance | 281,028.0 |
| Heritability | 0.1 |
| GEIr2 | 0.3 |
| h2mg | 0.5 |
| Accuracy | 0.7 |
| rge | 0.3 |
| CVg | 6.4 |
| CVr | 14.3 |
| CV ratio | 0.4 |

4.2.4 MET - GGE biplot

Genotype plus Genotype-vs-Environment interaction (GGE). Mega-environment identification in multi-environment trials (MET) according to (**W?**). Yan et al. 2007

4.2.4.1 GGE ENV biplot GGE biplot done using:

- **sd**: each value is divided by the standard deviation of its corresponding environment.
- **environment**: environment-centered (G+GE)
- **environment**: singular value is entirely partitioned into the environment eigenvectors, also called column metric preserving

```
gge_model.nb <- gge(blues_stage.I_NB, loc, name, yield,
  centering = "environment", #1
  scaling = "sd", #2
  svp = "environment")#2

a <- plot(gge_model.nb, type=4,
  size.text.env = 4.5,
  plot_theme = theme_metan(grid = "both", color.background =
    ↪ transparent_color()),
  axis_expand = 1.5,
  col.alpha.circle = 0.8,
  shape.gen = NA,
  col.gen = NA,
  size.text.lab = NA,
```

```

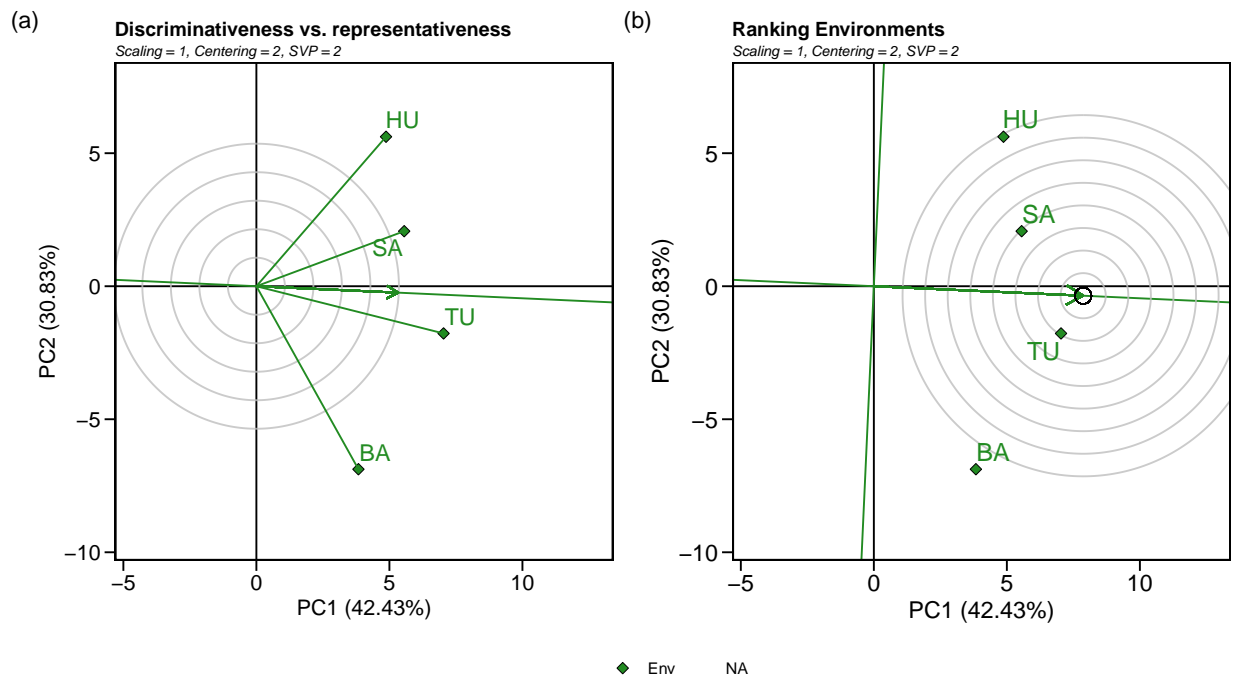
size.text.gen = NA,
leg.lab=c('Env')
#title = FALSE
)

gge_model.nb <- gge(blues_stage.I_NB, loc, name, yield,
  centering = "environment", #1
  scaling = "sd", #2Y
  svp = "environment")#2)

b <- plot(gge_model.nb, type = 6,
  size.text.env = 5,
  plot_theme = theme_metan(grid = "both", color.background =
    transparent_color()),
  axis_expand = 1.5,
  # col.alpha.circle = 100,
  col.alpha.circle = 0.8,
  size.text.lab = 13
  #title = FALSE
)

arrange_ggplot(a, b,
  guides = "collect",
  tag_levels = "a",
  tag_prefix = "(",
  tag_suffix = ")")

```



4.2.4.2 Biplot type 3: Which-won-where GGE biplot done using:

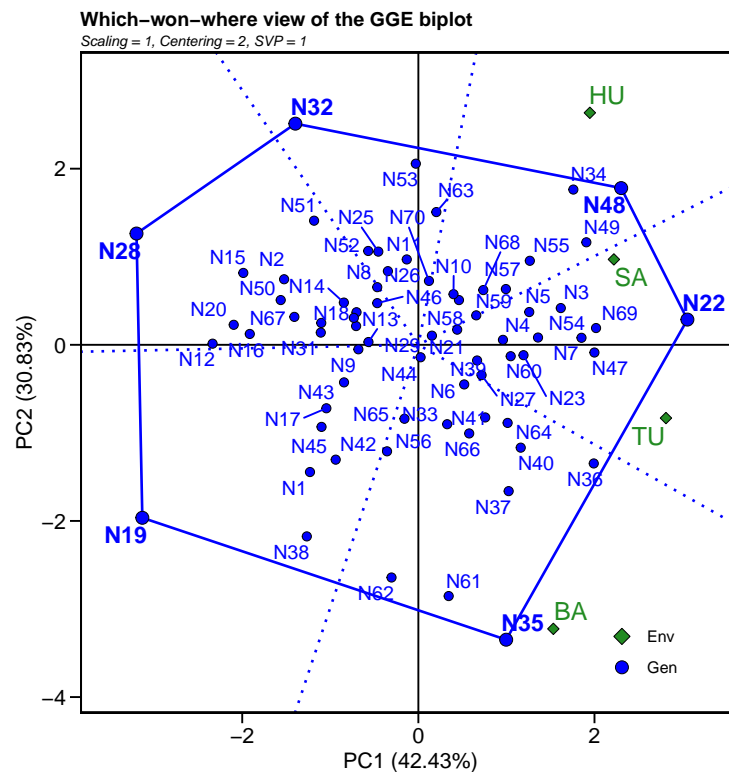
- **sd**: each value is divided by the standard deviation of its corresponding environment.
- **environment**: environment-centered (G+GE)
- **genotype**: singular value is entirely partitioned into the environment eigenvectors, also called column metric preserving

```
gge_model.nb <- gge(blues_stage.I_NB, loc, name, yield,
  centering = "environment", #2
  scaling = "sd", #1
  svp = "genotype")#2)

e <- plot(gge_model.nb, type = 3,
  size.text.env = 5,
  plot_theme = theme_metan(grid = "both", color.background =
    ↪ transparent_color()),
  axis_expand = 1.2,
  size.line = 0.7,
  size.text.gen = 4,
  size.text.win = 4.5
  #title = FALSE

)

print(e)
```



4.2.5 Mean performance and stability analysis

WAASP index and BLUPs to estimate stability analysis.

```

waasb_model_nb <-
  waasb(blues_stage.I_NB,
        env = loc,
        gen = name,
        rep = rep,
        resp = yield,
        random = "gen", #Default
        verbose = TRUE,
        wresp = 60) #weight for response variable 60 and 40 for yielding and stability,
        ↪ respectively)

```

```

#> Evaluating trait yield |=====
#> -----
#> P-values for Likelihood Ratio Test of the analyzed traits
#> -----
#>      model      yield
#> COMPLETE      NA
#>      GEN 3.41e-05
#>      GEN:ENV 6.69e-20
#> -----
#> All variables with significant (p < 0.05) genotype-vs-environment interaction

```

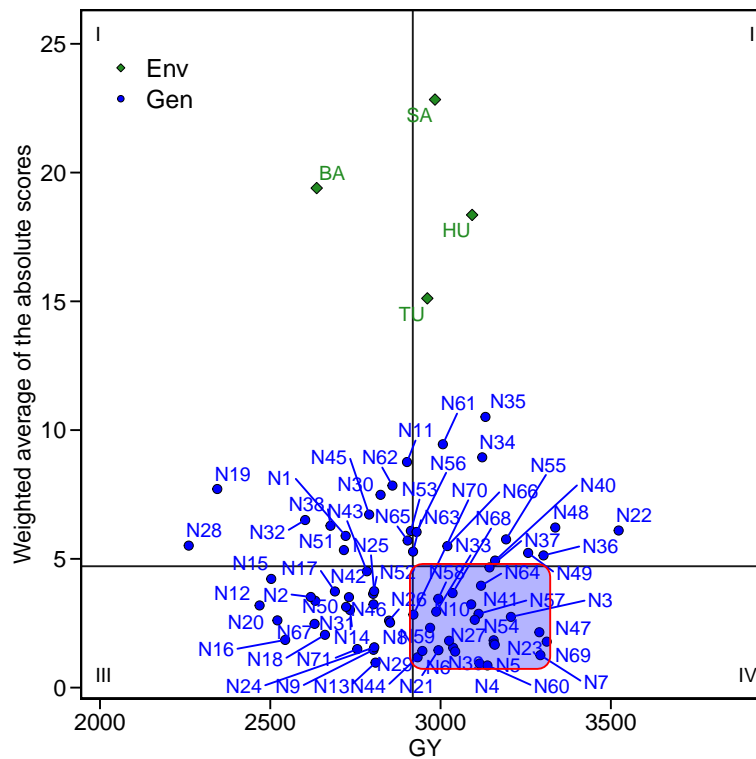
```

waasb_model<- waasb_model_nb$yield$model

waasp_plot <- plot_scores(waasb_model_nb, type = 3,
  title = FALSE,
  size.tex.gen = 4,
  size.tex.env = 4,
  size.tex.lab = 13,
  # highlight = c("N38", "N6" , "N61", "N35" ,"N52", "N22"),
  plot_theme = theme_metan(grid = "both",color.background = transparent_color())
) +

  geom_mark_rect(aes(filter = Code %in% c("N70", "N37", "N69", "N60"),
    ),
    label.fontsize = 10,
    show.legend = F,
    con.cap = 0,
    con.colour = "red",
    color = "red",
    expand = 0.005,
    label.buffer = unit(10, "cm"))+
  #theme_gray()+
  theme(legend.position = c(0.1, 0.9),
    legend.background = element_blank(),
    legend.title = element_blank(),
    aspect.ratio = 1) +
  labs(x = "GY")
print(waasp_plot)

```



```

waasb_model_meanWaasb<-mean(waasb_model$WAASB)
waasb_model_meanY<-mean(waasb_model$Y)

selected <- waasb_model %>%
  dplyr::filter(Y >= waasb_model_meanY & WAASB <= waasb_model_meanWaasb)

selected_table <- selected

if (knitr::is_html_output()) {
  print_table(selected_table)
}else{
selected_table[,1:8]
}

```

| type | Code | Y | PC1 | PC2 | PC3 | WAASB | PctResp |
|-----------|-----------|---------|---------|---------|---------|---------|---------|
| character | character | numeric | numeric | numeric | numeric | numeric | numeric |
| GEN | N37 | 3,143.7 | -8.6 | 0.3 | 1.9 | 4.7 | 70.0 |
| GEN | N39 | 3,037.0 | -1.1 | -1.3 | 3.0 | 1.5 | 61.5 |
| GEN | N41 | 3,090.0 | -3.0 | 4.8 | 1.4 | 3.2 | 65.7 |
| n: 25 | | | | | | | |

| type | Code | Y | PC1 | PC2 | PC3 | WAASB | PctResp |
|-----------|-----------|---------|---------|---------|---------|---------|---------|
| character | character | numeric | numeric | numeric | numeric | numeric | numeric |
| GEN | N58 | 2,993.3 | 3.7 | 3.3 | 3.1 | 3.4 | 58.0 |
| GEN | N64 | 3,118.8 | -5.3 | -2.7 | 2.7 | 4.0 | 68.0 |
| GEN | N10 | 2,969.3 | 3.1 | -0.3 | 3.4 | 2.3 | 56.1 |
| GEN | N21 | 2,993.8 | -0.1 | -3.8 | 1.3 | 1.5 | 58.1 |
| GEN | N33 | 2,987.3 | -4.9 | -0.9 | 1.3 | 2.9 | 57.6 |
| GEN | N3 | 3,206.6 | 2.1 | -1.5 | 6.2 | 2.7 | 74.9 |
| n: 25 | | | | | | | |

```
#selected$Code
```

```
#Create a data frame with BLUPS - selected and non-selected
blups_sel <-
  gmd(waasb_model_nb, "blupge") %>%
  add_cols(SELECTED = ifelse(GEN %in% selected$Code, "yes", "no")) %>%
  dplyr::rename(BLUPs_sel = yield) %>%
  droplevels()

blups_sel_mean<-
  gmd(waasb_model_nb, "blupge") %>%
  add_cols(SELECTED = ifelse(GEN %in% selected$Code, "yes", "no")) %>%
  filter(SELECTED == "yes") %>%
  dplyr::summarise(mean_GY = mean(yield,na.rm = TRUE), n = n())

# Create a data frame with the waasb index - selected and non-selected
waasb_sel <-
  gmd(waasb_model_nb, "WAASB") %>%
  add_cols(SELECTED = ifelse(GEN %in% selected$Code, "yes", "no")) %>%
  dplyr::rename(WAASB_sel = yield) %>%
  droplevels()
#str(waasb_sel)

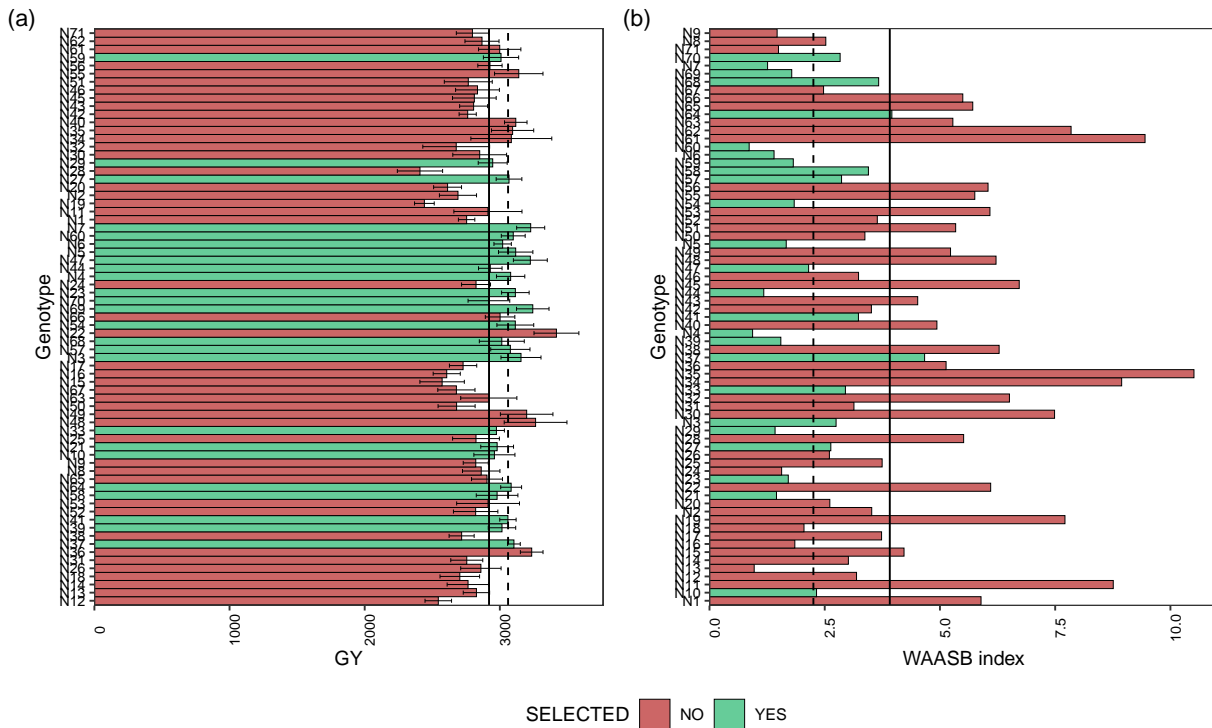
waasb_sel_mean<-
  gmd(waasb_model_nb, "WAASB") %>%
  add_cols(SELECTED = ifelse(GEN %in% selected$Code, "yes", "no")) %>%
  filter(SELECTED == "yes") %>%
  dplyr::summarise(mean_GY = mean(yield,na.rm = TRUE), n = n())

p1<- plot_selected(blups_sel, GEN, BLUPs_sel, mean_sel = blups_sel_mean$mean_GY) +
  labs(y = "GY")

p3<- plot_selected(waasb_sel, GEN, WAASB_sel, mean_sel = waasb_sel_mean$mean_GY) +
```

```
labs(y = "WAASB index")

arrange_ggplot(p1, p3,
  guides = "collect",
  tag_levels = "a",
  tag_prefix = "(",
  tag_suffix = ")")
```



Mean performance (a) and stability (b) for grain yield (GY) of 71 Navy beans genotypes. The vertical dashed and solid lines shows, respectively, the mean of the selected genotype and the overall mean for both mean performance and WAASB index

4.2.5.1 Selection differentials Percentage (SD_gain in %) gain from the selected genotypes compared to the general mean.

```
blups_sel2 <-
  gmd(waasb_model_nb, "blupg") %>%
  add_cols(SELECTED = ifelse(GEN %in% selected$Code, "yes", "no")) %>%
  dplyr::rename(BLUPs_sel = yield) %>%
  droplevels()
```

```
#> Class of the model: waasb
```

```
#> Variable extracted: blupg
```

```

blups_sel_mean2<-
  gmd(waasb_model_nb, "blupg") %>%
  add_cols(SELECTED = ifelse(GEN %in% selected$Code, "yes", "no")) %>%
  filter(SELECTED == "yes") %>%
  dplyr::summarise(mean_GY = mean(yield, na.rm = TRUE), n = n())

#> Class of the model: waasb
#> Variable extracted: blupg

SD_blups<- as_tibble((blups_sel_mean2$mean_GY/mean(blups_sel2$BLUPs_sel, na.rm = T))
  ↪ -1)*100
SD_WAASP<- as_tibble((waasb_sel_mean$mean_GY /mean(waasb_sel$WAASB_sel, na.rm = T))
  ↪ -1)*100

SD_comb<- full_join(SD_blups, SD_WAASP, by = "value") %>%
  dplyr::rename(SD_gain = value) %>%
  tibble::add_column(Comp_name = c('BLUPs', 'WAASB')) %>%
  relocate(Comp_name)

SD_comb$n_selected<- blups_sel_mean2$n
SD_comb

```

| Comp_name | SD_gain | n_selected |
|-----------|---------|------------|
| character | numeric | integer |
| BLUPs | 3.2 | 25 |
| WAASB | -42.4 | 25 |

```

blups_sel2$mean_blup <- mean(blups_sel2$BLUPs_sel, na.rm = T)
waasb_sel$mean_waasb <- mean(waasb_sel$WAASB_sel, na.rm = T)

#str(waasb_sel)
data_comb<- merge(blups_sel2, waasb_sel, by = c("GEN", "SELECTED"))
#names(data_comb)
## SD for each genotype
data_sel_perc <- data_comb %>%
  rowwise %>%
  mutate(Perc_blup_gain = ((BLUPs_sel/mean_blup)*100)-100) %>%
  mutate(Perc_WAASB_gain = ((WAASB_sel/mean_waasb)*100)-100) %>%
  as_tibble()

# data_sel_perc_mean <- data_sel_perc %>%
#   dplyr::filter(SELECTED == "yes")
#
# mean(data_sel_perc_mean$Perc_blup_gain)

if (knitr::is_html_output()) {
  print_table(data_sel_perc)
}

```

```

}else{

data_sel_perc[,1:7]
}

```

| GEN | SELECTED | BLUPs_sel | mean_blup | WAASB_sel | mean_waasb | Perc_blup_gain |
|-----------|-----------|-----------|-----------|-----------|------------|----------------|
| character | character | numeric | numeric | numeric | numeric | numeric |
| N1 | no | 2,820.0 | 2,924.0 | 5.9 | 3.9 | -3.6 |
| N10 | yes | 2,954.6 | 2,924.0 | 2.3 | 3.9 | 1.0 |
| N11 | no | 2,899.6 | 2,924.0 | 8.8 | 3.9 | -0.8 |
| N12 | no | 2,682.8 | 2,924.0 | 3.2 | 3.9 | -8.2 |
| N13 | no | 2,867.6 | 2,924.0 | 1.0 | 3.9 | -1.9 |
| N14 | no | 2,826.9 | 2,924.0 | 3.0 | 3.9 | -3.3 |
| N15 | no | 2,701.3 | 2,924.0 | 4.2 | 3.9 | -7.6 |
| N16 | no | 2,723.6 | 2,924.0 | 1.9 | 3.9 | -6.9 |
| N17 | no | 2,802.9 | 2,924.0 | 3.7 | 3.9 | -4.1 |

n: 71

```

data_sel_perc<- data_sel_perc %>%
  dplyr::relocate(GEN,SELECTED,BLUPs_sel,mean_blup,Perc_blup_gain,
                  WAASB_sel,mean_waasb ,Perc_WAASB_gain)

#write.xlsx(data_sel_perc, "./data/sel_SD_nb_2.xlsx")

data_sel_perc2 <- data_sel_perc %>%
  dplyr::select(GEN,SELECTED, BLUPs_sel, WAASB_sel, Perc_blup_gain, Perc_WAASB_gain)

data_sel_perc2

```

| GEN | SELECTED | BLUPs_sel | WAASB_sel | Perc_blup_gain | Perc_WAASB_gain |
|-----------|-----------|-----------|-----------|----------------|-----------------|
| character | character | numeric | numeric | numeric | numeric |
| N1 | no | 2,820.0 | 5.9 | -3.6 | 50.6 |
| N10 | yes | 2,954.6 | 2.3 | 1.0 | -40.6 |
| N11 | no | 2,899.6 | 8.8 | -0.8 | 123.9 |
| N12 | no | 2,682.8 | 3.2 | -8.2 | -18.4 |

n: 71

| GEN | SELECTED | BLUPs_sel | WAASB_sel | Perc_blup_gain | Perc_WAASB_gain |
|-----------|-----------|-----------|-----------|----------------|-----------------|
| character | character | numeric | numeric | numeric | numeric |
| N13 | no | 2,867.6 | 1.0 | -1.9 | -75.2 |
| N14 | no | 2,826.9 | 3.0 | -3.3 | -23.0 |
| N15 | no | 2,701.3 | 4.2 | -7.6 | 7.9 |
| N16 | no | 2,723.6 | 1.9 | -6.9 | -52.7 |
| N17 | no | 2,802.9 | 3.7 | -4.1 | -4.6 |
| n: 71 | | | | | |

```
##BLUPs indexes
stab_blups_nb<- blup_indexes(waasb_model_nb)
stab_blups_nb<- as_tibble(stab_blups_nb$yield)

data_waasby <- waasb_model_nb$yield$model %>%
  dplyr::filter(type != "ENV") %>%
  dplyr::select("Code", "WAASBY", "OrWAASBY") %>%
  dplyr::rename(GEN = Code)

stab_blups_nb<- stab_blups_nb %>%
  full_join(data_waasby, by = "GEN")

if (knitr::is_html_output()) {
  print_table(stab_blups_nb)
}else{
stab_blups_nb[,1:8]
}
```

| GEN | Y | HMGV | HMGV_R | RPGV | RPGV_Y | RPGV_R | HMRPGV |
|-----------|---------|---------|---------|---------|---------|---------|---------|
| character | numeric | numeric | numeric | numeric | numeric | numeric | numeric |
| N1 | 2,468.6 | 2,750.2 | 55 | 0.9 | 2,764.8 | 55 | 0.9 |
| N10 | 2,809.0 | 2,933.7 | 33 | 1.0 | 2,954.2 | 32 | 1.0 |
| N11 | 2,734.1 | 2,849.5 | 41 | 1.0 | 2,905.1 | 39 | 1.0 |
| N12 | 2,660.6 | 2,533.6 | 69 | 0.9 | 2,545.2 | 69 | 0.9 |
| N13 | 2,848.7 | 2,816.4 | 44 | 1.0 | 2,826.8 | 46 | 1.0 |
| N14 | 2,722.7 | 2,739.4 | 57 | 0.9 | 2,761.4 | 57 | 0.9 |
| N15 | 3,302.2 | 2,541.6 | 68 | 0.9 | 2,566.7 | 68 | 0.9 |
| n: 71 | | | | | | | |

| GEN | Y | HMGV | HMGV_R | RPGV | RPGV_Y | RPGV_R | HMRPGV |
|-----------|---------|---------|---------|---------|---------|---------|---------|
| character | numeric | numeric | numeric | numeric | numeric | numeric | numeric |
| N16 | 3,143.7 | 2,595.2 | 67 | 0.9 | 2,606.1 | 67 | 0.9 |
| N17 | 2,676.8 | 2,716.8 | 59 | 0.9 | 2,730.8 | 59 | 0.9 |
| n: 71 | | | | | | | |

```
# library(openxlsx)
# write.xlsx(stab_blups_nb, "../data/blups_nb_2.xlsx")
```

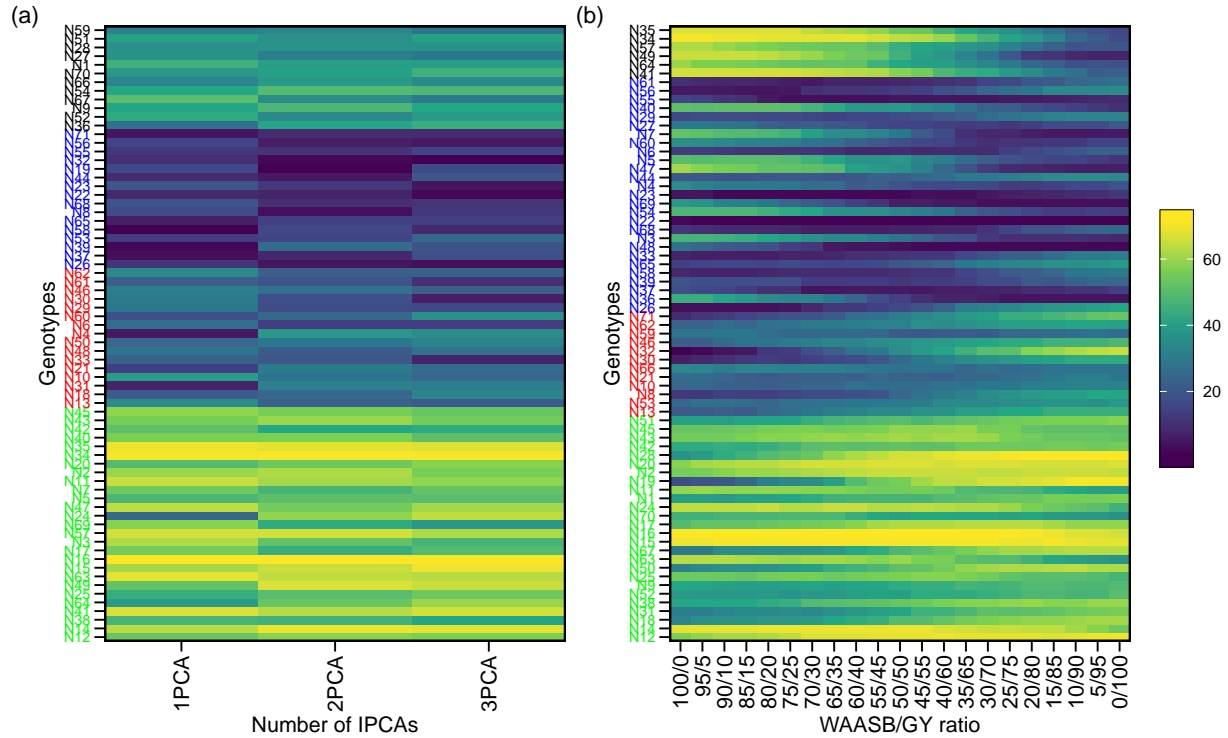
4.2.5.2 Scenarios of waasby estimation Planning different scenarios of waasby estimation by changing the weights assigned to the stability and the mean performance according to Olivoto et al. (2019).

```
scenarios <- wsmpt(waasb_model_nb, progbar = F)

scen1<- plot(scenarios, type = 1) +
  theme(axis.text.y = element_text(size=8))

scen2<-plot(scenarios, type = 2) +
  theme(axis.text.y = element_text(size=8))

arrange_ggplot(scen1, scen2,
  guides = "collect",
  legend.position = "right",
  tag_levels = "a",
  tag_prefix = "(",
  tag_suffix = ")")
```



4.2.5.3 Coincidence index of genotype selection Computes the coincidence index (Hamblin and Zimmermann, 1986) as follows:

$$CI = \frac{A - C}{M - C} \times 100$$

where A is the number of selected genotypes common to different methods; C is the number of expected genotypes selected by chance; and M is the number of genotypes selected according to the selection intensity.

```
coinc_1 <- stab_blups_nb %>% dplyr::select(GEN,HMRPGV_R) %>% arrange(HMRPGV_R)
coinc_2 <- stab_blups_nb %>% dplyr::select(GEN,RPGV_R) %>% arrange(RPGV_R)
coinc_3 <- stab_blups_nb %>% dplyr::select(GEN,HMGV_R) %>% arrange(HMGV_R)
coinc_4 <- stab_blups_nb %>% dplyr::select(GEN,OrWAASBY) %>% arrange(OrWAASBY)
coinc_5 <- stab_blups_nb %>% dplyr::select(GEN,WAASB_R) %>% arrange(WAASB_R)

selc_perc<- round(nrow(stab_blups_nb)*0.2)

coinc_1.1 <-1
coinc_1.2 <- coincidence_index(sel1 = coinc_1$GEN[1:selc_perc],
                              sel2 = coinc_2$GEN[1:selc_perc],
                              total = 71)/100
coinc_1.3 <- coincidence_index(sel1 = coinc_1$GEN[1:selc_perc],
                              sel2 = coinc_3$GEN[1:selc_perc],
                              total = 71)/100
coinc_1.4 <- coincidence_index(sel1 = coinc_1$GEN[1:selc_perc],
                              sel2 = coinc_4$GEN[1:selc_perc],
                              total = 71)/100
coinc_1.5 <- coincidence_index(sel1 = coinc_1$GEN[1:selc_perc],
```

```

                                sel2 = coinc_5$GEN[1:selc_perc],
                                total = 71)/100
coinc_2.2 <-1
coinc_2.3 <- coincidence_index(sel1 = coinc_2$GEN[1:selc_perc],
                                sel2 = coinc_3$GEN[1:selc_perc],
                                total = 71)/100
coinc_2.4 <- coincidence_index(sel1 = coinc_2$GEN[1:selc_perc],
                                sel2 = coinc_4$GEN[1:selc_perc],
                                total = 71)/100
coinc_2.5 <- coincidence_index(sel1 = coinc_2$GEN[1:selc_perc],
                                sel2 = coinc_5$GEN[1:selc_perc],
                                total = 71)/100

coinc_3.3<- 1
coinc_3.4 <- coincidence_index(sel1 = coinc_3$GEN[1:selc_perc],
                                sel2 = coinc_4$GEN[1:selc_perc],
                                total = 71)/100
coinc_3.5 <- coincidence_index(sel1 = coinc_3$GEN[1:selc_perc],
                                sel2 = coinc_5$GEN[1:selc_perc],
                                total = 71)/100

coinc_4.4 <- 1
coinc_4.5 <- coincidence_index(sel1 = coinc_4$GEN[1:selc_perc],
                                sel2 = coinc_5$GEN[1:selc_perc],
                                total = 71)/100

coinc_5.5 <- 1

coinc<- c(coinc_1.1,coinc_1.2,coinc_2.2,coinc_1.3,coinc_2.3,
          coinc_3.3,coinc_1.4, coinc_2.4, coinc_3.4,
          coinc_4.4, coinc_1.5, coinc_2.5,
          coinc_3.5, coinc_4.5,
          coinc_5.5)

z=matrix(0,5,5)
z[upper.tri(z)| row(z)==col(z)] <- coinc

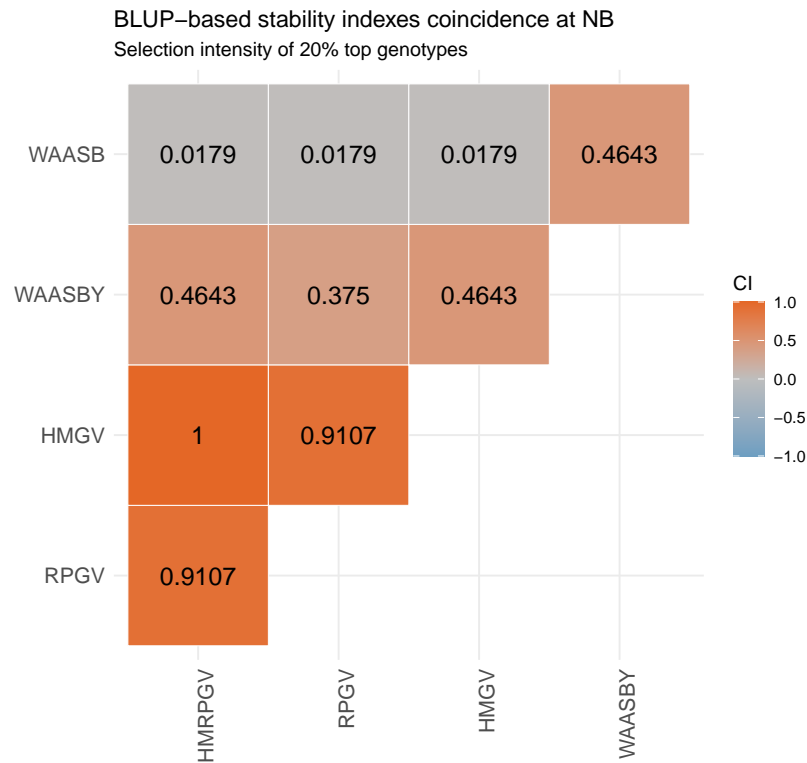
rownames(z)=c(
"HMRPGV",
"RPGV",
'HMGV',
'WAASBY',
'WAASB')

colnames(z)=rownames(z)

plotNB<- ggcorrplot(z, colors = c("#6D9EC1", "gray", "#E46726"),
                    show.legend = T,
                    legend.title = "CI" ,lab_size=5,tl.srt = 90,type = c("upper"), lab = T,digits = 4,
                    outline.color = "white",pch.col = "white", tl.col = "blue",show.diag = F) +
  labs(title = "BLUP-based stability indexes coincidence at NB",
        subtitle = "Selection intensity of 20% top genotypes")

print(plotNB)

```



4.3 MET analysis - Red beans

4.3.1 MET analysis - ASReml

Running MET using ASReml - only to comparison of variance components with metan outputs

```
mod.met.asreml.sr1 <- asreml(fixed      = yield ~ loc + loc:rep,
  random      = ~ name + name:loc,
  data        = blues_stage.I_SR,
  predict     = predict.asreml(classify = "name"),
  trace       = F,
  maxit       = 500)

summFix.sr.met.asreml <- data.frame(wald(mod.met.asreml.sr1))
summFix.sr.met.asreml
```

| Df | Sum.of.Sq | Wald.statistic | Pr.Chisq. |
|---------|-------------|----------------|-----------|
| numeric | numeric | numeric | numeric |
| 1 | 457,238,258 | 3,083.4 | 0.0 |
| 3 | 5,392,039 | 36.4 | 0.0 |
| 12 | 4,238,922 | 28.6 | 0.0 |
| | 148,291 | | |

```
summ.sr.met.asreml<- data.frame(summary.asreml(mod.met.asreml.sr1)$varcomp)
summ.sr.met.asreml
```

| component | std.error | z.ratiobound | X.ch |
|-----------|-----------|------------------|---------|
| numeric | numeric | numericcharacter | numeric |
| 31,775.8 | 22,260.3 | 1.4P | 0 |
| 104,069.5 | 26,514.2 | 3.9P | 0 |
| 148,291.7 | 13,802.9 | 10.7P | 0 |

```
#print(summary.asreml(mod.met.asreml.sr1)$bic)
mod.met.asreml.sr<- data.table((mod.met.asreml.sr1$predictions$pvals[1:3]))
names(mod.met.asreml.sr) <- c("name", "yield_BLUPS_MET", "SE")

###
```

4.3.2 MET analysis - lme4

Running MET using metan R package Olivoto et al. (2019).

```
mixed_mod.sr<-
  gamem_met(blues_stage.I_SR,
    env = loc,
    gen = name,
    rep = rep,
    resp = yield,
    random = "gen", #Default
    verbose = TRUE) #Default
```

Evaluating trait yield |=====

100% 00:00:00

#> Method: REML/BLUP

#> Random effects: GEN, GEN:ENV

#> Fixed effects: ENV, REP(ENV)

#> Denominador DF: Satterthwaite's method

P-values for Likelihood Ratio Test of the analyzed traits

model yield COMPLETE NA GEN 6.80e-02 GEN:ENV 9.94e-12

All variables with significant ($p < 0.05$) genotype-vs-environment interaction

4.3.3 Printing the model outputs

4.3.3.1 Likelihood Ratio Tests The output LRT contains the Likelihood Ratio Tests for genotype and genotype-vs-environment random effects.

```
data_mod_sr_test <- get_model_data(mixed_mod.sr, "lrt")
```

```
#> Class of the model: waasb
```

```
#> Variable extracted: lrt
```

```
data_mod_sr_test
```

| VAR | model | npar | logLik | AIC | LRT | Df | Pr(>Chisq) |
|-----------|-----------|---------|----------|---------|---------|---------|------------|
| character | character | integer | numeric | numeric | numeric | numeric | numeric |
| yield | GEN | 18 | -2,385.1 | 4,806.1 | 3.3 | 1 | 0.1 |
| yield | GEN:ENV | 18 | -2,406.6 | 4,849.1 | 46.3 | 1 | 0.0 |

```
#customize the display of numbers and other data in a tibble
# old <- options(pillar.sigfig = 6)
#
# blues_stage.I_SR %>%
#   group_by(loc) %>%
#   dplyr::summarise(Mean = mean(yield, na.rm = TRUE))
```

```
data_mod_sr_det <- get_model_data(mixed_mod.sr, "details")
```

4.3.3.2 Detailed parameters

```
#> Class of the model: waasb
```

```
#> Variable extracted: details
```

```
data_mod_sr_det
```

| Parameters | yield |
|------------|-----------|
| character | character |
| Mean | 3147.37 |
| n: 12 | |

| Parameters | yield |
|------------|--------------------|
| character | character |
| SE | 32.29 |
| SD | 583.92 |
| CV | 18.58 |
| Min | 1325.5 (R7 in BA) |
| Max | 4868.28 (R6 in SA) |
| MinENV | BA (2731.73) |
| MaxENV | TU (3367.38) |
| MinGEN | R7 (2761.81) |
| n: 12 | |

4.3.3.3 Random effects The output LRT contains the Likelihood Ratio Tests for genotype and genotype-vs-environment random effects.

```
old <- options(pillar.sigfig = 8)
data_mod_sr_var <- get_model_data(mixed_mod.sr, "vcomp")
```

```
#> Class of the model: waasb
```

```
#> Variable extracted: vcomp
```

```
data_mod_sr_var
```

| Group | yield |
|-----------|-----------|
| character | numeric |
| GEN | 31,774.8 |
| GEN:ENV | 104,069.3 |
| Residual | 148,290.9 |

```
old <- options(pillar.sigfig = 4)
data_mod_sr_comp <- get_model_data(mixed_mod.sr)
```

4.3.3.4 Variance components and genetic parameters

```
#> Class of the model: waasb
```

```
#> Variable extracted: genpar
```

```
data_mod_sr_comp
```

| Parameters | yield |
|---------------------|-----------|
| character | numeric |
| Phenotypic variance | 284,135.1 |
| Heritability | 0.1 |
| GEIr2 | 0.4 |
| h2mg | 0.5 |
| Accuracy | 0.7 |
| rge | 0.4 |
| CVg | 5.7 |
| CVr | 12.2 |
| CV ratio | 0.5 |

4.3.4 MET - GGE biplot

Genotype plus Genotype-vs-Environment interaction (GGE). Mega-environment identification in multi-environment trials (MET) according to (**W?**). Yan et al. 2007

4.3.4.1 GGE ENV biplot GGE biplot done using:

- **sd**: each value is divided by the standard deviation of its corresponding environment.
- **environment**: environment-centered (G+GE)
- **environment**: singular value is entirely partitioned into the environment eigenvectors, also called column metric preserving

```
gge_model.sr <- gge(blues_stage.I_SR, loc, name, yield,
  centering = "environment", #1
  scaling = "sd", #2
  svp = "environment")#2

a <- plot(gge_model.sr, type=4,
  size.text.env = 4.5,
  plot_theme = theme_metan(grid = "both",color.background =
    ↪ transparent_color()),
  axis_expand = 1.5,
  col.alpha.circle = 0.8,
  shape.gen = NA,
  col.gen = NA,
  size.text.lab = NA,
```



```

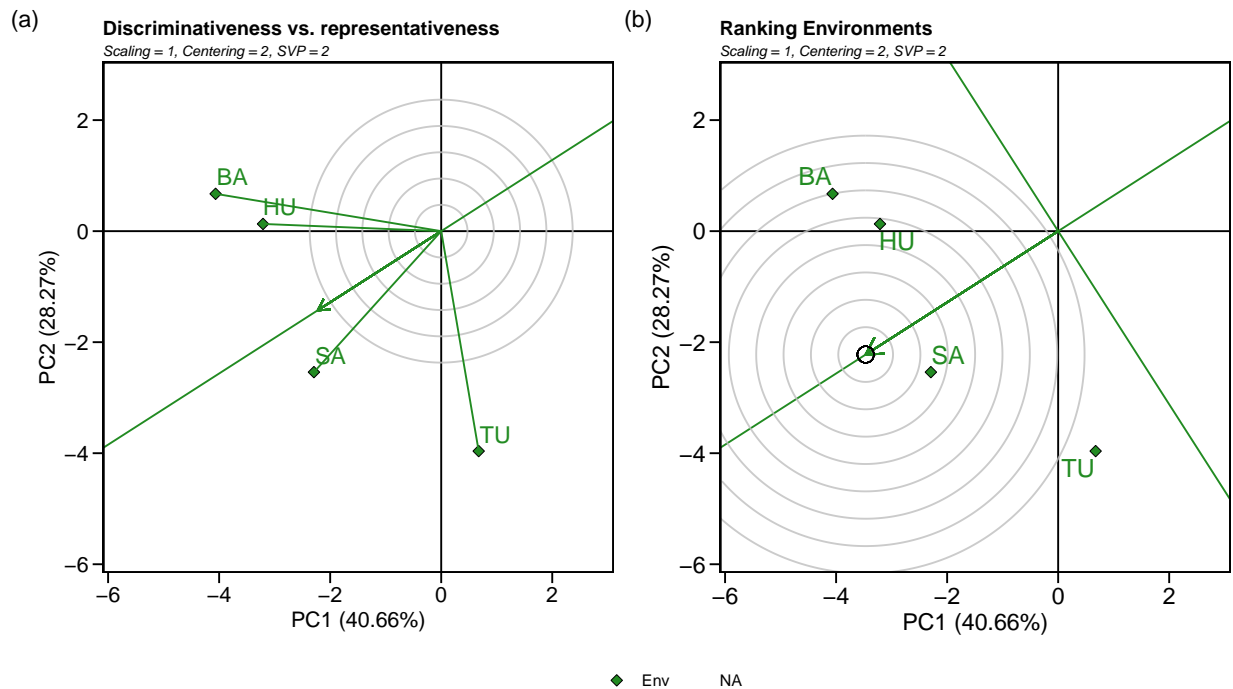
size.text.gen = NA,
leg.lab=c('Env'),
#title = FALSE
)

gge_model.sr <- gge(blues_stage.I_SR, loc, name, yield,
  centering = "environment", #1
  scaling = "sd", #2Y
  svp = "environment")#2)

b <- plot(gge_model.sr, type = 6,
  size.text.env = 5,
  plot_theme = theme_metan(grid = "both", color.background =
    ↪ transparent_color()),
  axis_expand = 1.5,
  # col.alpha.circle = 100,
  col.alpha.circle = 0.8,
  size.text.lab = 13,
  #title = FALSE
)

arrange_ggplot(a, b,
  guides = "collect",
  tag_levels = "a",
  tag_prefix = "(",
  tag_suffix = ")")

```



4.3.4.2 Biplot type 3: Which-won-where GGE biplot done using:

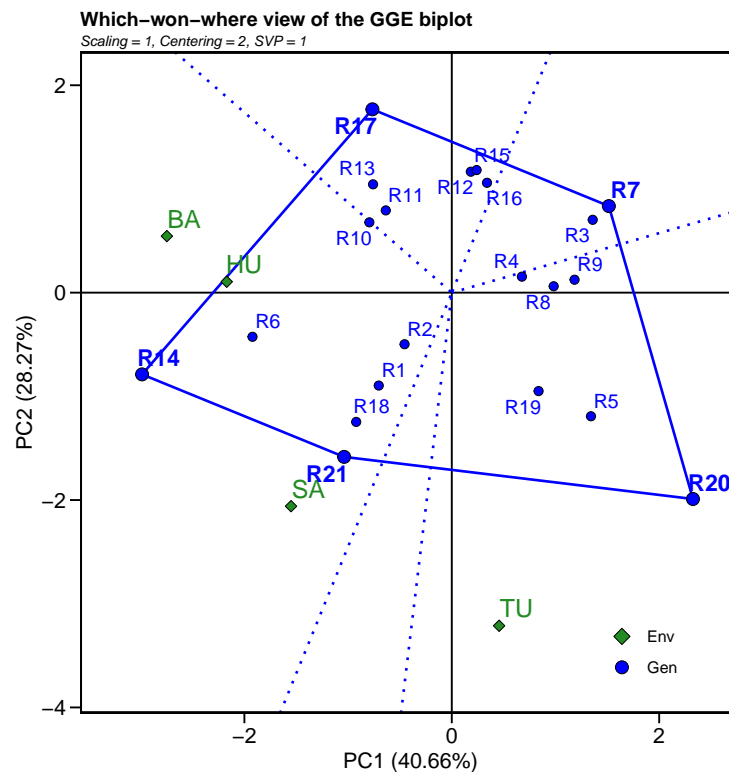
- **sd**: each value is divided by the standard deviation of its corresponding environment.
- **environment**: environment-centered (G+GE)
- **genotype**: singular value is entirely partitioned into the environment eigenvectors, also called column metric preserving

```
gge_model.sr <- gge(blues_stage.I_SR, loc, name, yield,
  centering = "environment", #2
  scaling = "sd", #1
  svp = "genotype")#2)

e <- plot(gge_model.sr, type = 3,
  size.text.env = 5,
  plot_theme = theme_metan(grid = "both", color.background =
    ↪ transparent_color()),
  axis_expand = 1.2,
  size.line = 0.7,
  size.text.gen = 4,
  size.text.win = 4.5
  #title = FALSE

)

print(e)
```



4.3.5 Mean performance and stability analysis

WAASP index and BLUPs to estimate stability analysis.

```

waasb_model_sr <-
  waasb(blues_stage.I_SR,
        env = loc,
        gen = name,
        rep = rep,
        resp = yield,
        random = "gen", #Default
        verbose = TRUE,
        wresp = 60) #weight for response variable 60 and 40 for yielding and stability,
        ↪ respectively)

```

```

#> Evaluating trait yield |=====
#> -----
#> P-values for Likelihood Ratio Test of the analyzed traits
#> -----
#>      model      yield
#> COMPLETE      NA
#>      GEN 6.80e-02
#>      GEN:ENV 9.94e-12
#> -----
#> All variables with significant (p < 0.05) genotype-vs-environment interaction

```

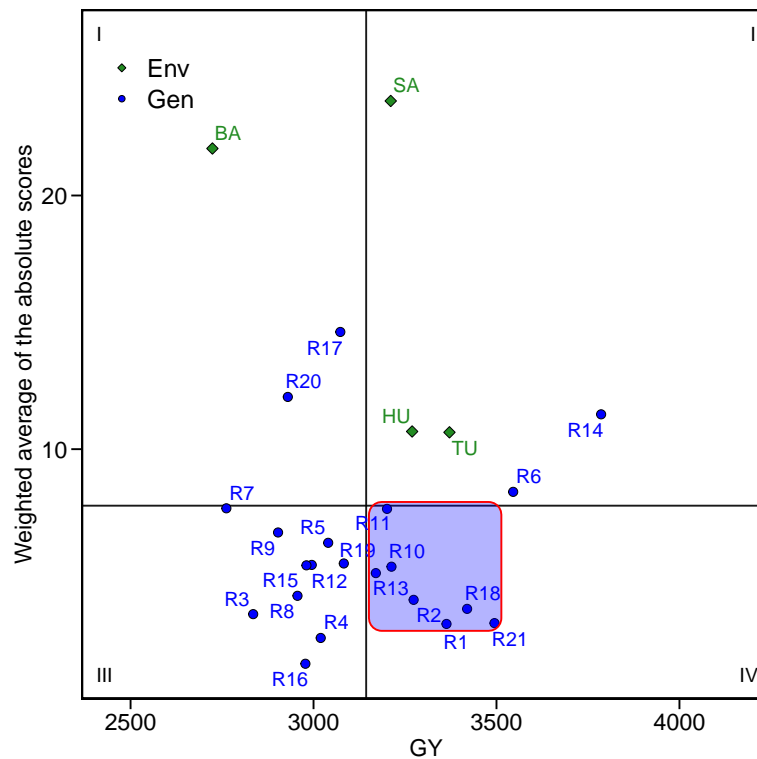
```

waasb_model<- waasb_model_sr$yield$model

waasp_plot <- plot_scores(waasb_model_sr, type = 3,
  title = FALSE,
  size.tex.gen = 4,
  size.tex.env = 4,
  size.tex.lab = 13,
  #highlight = c('R13','R2'),
  plot_theme = theme_metan(grid = "both",color.background = transparent_color())
) +

  geom_mark_rect(aes(filter = Code %in% c("R13", "R11", "R21", "R1"),
    ),
    label.fontsize = 10,
    show.legend = F,
    con.cap = 0,
    con.colour = "red",
    color = "red",
    expand = 0.01,
    label.buffer = unit(10, "cm"))+
#theme_gray()+
theme(legend.position = c(0.1, 0.9),
  legend.background = element_blank(),
  legend.title = element_blank(),
  aspect.ratio = 1) +
  labs(x = "GY")
print(waasp_plot)

```



```

waasb_model_meanWaasb<-mean(waasb_model$WAASB)
waasb_model_meanY<-mean(waasb_model$Y)

selected <- waasb_model %>%
  dplyr::filter(Y >= waasb_model_meanY & WAASB <= waasb_model_meanWaasb)

selected_table <- selected

if (knitr::is_html_output()) {
  print_table(selected_table)
}else{
selected_table[,1:8]
}

```

| type | Code | Y | PC1 | PC2 | PC3 | WAASB | PctResp |
|-----------|-----------|---------|---------|---------|---------|---------|---------|
| character | character | numeric | numeric | numeric | numeric | numeric | numeric |
| GEN | R10 | 3,213.0 | -7.5 | -2.3 | 7.0 | 5.4 | 44.1 |
| GEN | R13 | 3,170.3 | -0.8 | 11.6 | -0.3 | 5.1 | 39.9 |
| GEN | R18 | 3,419.7 | 1.3 | -3.4 | 14.3 | 3.7 | 64.2 |
| GEN | R1 | 3,363.4 | -3.2 | -2.7 | 4.2 | 3.1 | 58.7 |

| type | Code | Y | PC1 | PC2 | PC3 | WAASB | PctResp |
|-----------|-----------|---------|---------|---------|---------|---------|---------|
| character | character | numeric | numeric | numeric | numeric | numeric | numeric |
| GEN | R2 | 3,273.6 | 3.2 | 6.0 | 0.9 | 4.1 | 50.0 |
| GEN | R21 | 3,494.5 | -3.0 | -2.6 | 5.4 | 3.1 | 71.5 |
| GEN | R11 | 3,200.8 | -13.6 | -0.6 | -7.8 | 7.6 | 42.9 |

```
#selected$Code
```

```
#Create a data frame with BLUPS - selected and non-selected
blups_sel <-
  gmd(waasb_model_sr, "blupge") %>%
  add_cols(SELECTED = ifelse(GEN %in% selected$Code, "yes", "no")) %>%
  dplyr::rename(BLUPs_sel = yield) %>%
  droplevels()

blups_sel_mean<-
  gmd(waasb_model_sr, "blupge") %>%
  add_cols(SELECTED = ifelse(GEN %in% selected$Code, "yes", "no")) %>%
  filter(SELECTED == "yes") %>%
  dplyr::summarise(mean_GY = mean(yield, na.rm = TRUE), n = n())

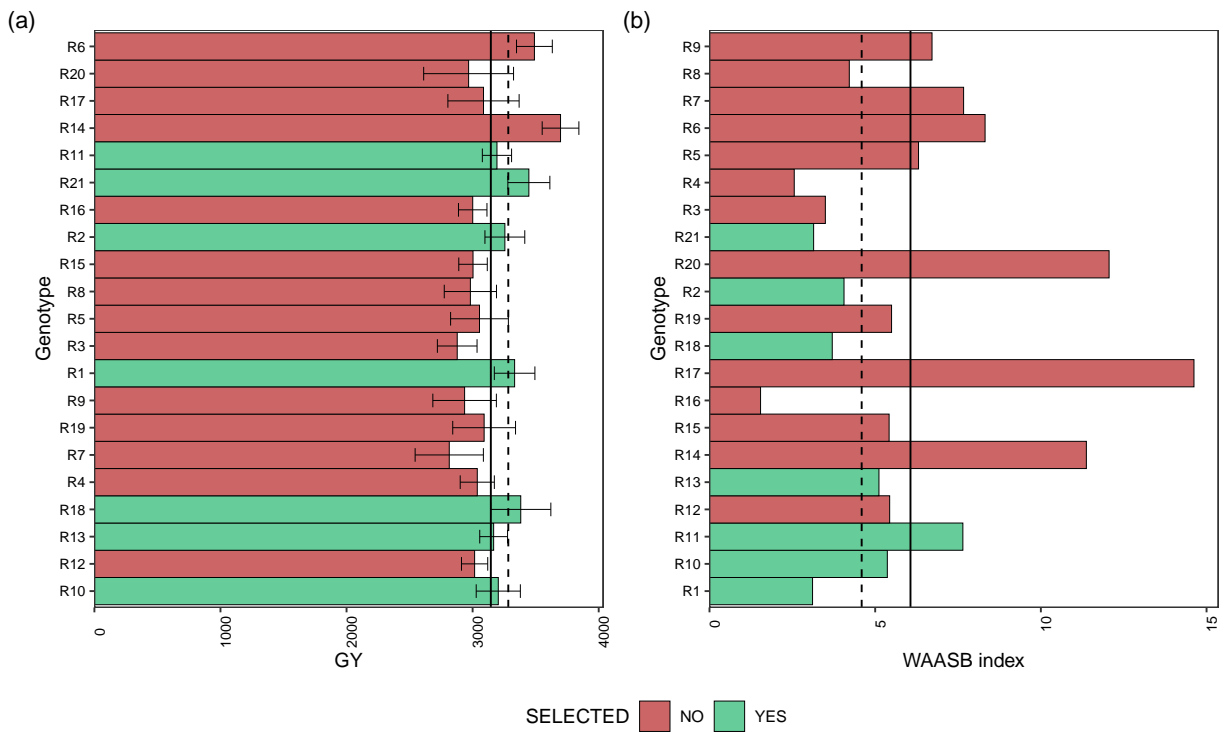
# Create a data frame with the waasb index - selected and non-selected
waasb_sel <-
  gmd(waasb_model_sr, "WAASB") %>%
  add_cols(SELECTED = ifelse(GEN %in% selected$Code, "yes", "no")) %>%
  dplyr::rename(WAASB_sel = yield) %>%
  droplevels()
#str(waasb_sel)

waasb_sel_mean<-
  gmd(waasb_model_sr, "WAASB") %>%
  add_cols(SELECTED = ifelse(GEN %in% selected$Code, "yes", "no")) %>%
  filter(SELECTED == "yes") %>%
  dplyr::summarise(mean_GY = mean(yield, na.rm = TRUE), n = n())

p1<- plot_selected(blups_sel, GEN, BLUPs_sel, mean_sel = blups_sel_mean$mean_GY) +
  labs(y = "GY")

p3<- plot_selected(waasb_sel, GEN, WAASB_sel, mean_sel = waasb_sel_mean$mean_GY) +
  labs(y = "WAASB index")

arrange_ggplot(p1, p3,
  guides = "collect",
  tag_levels = "a",
  tag_prefix = "(",
  tag_suffix = ")")
```



Mean performance (a) and stability (b) for grain yield (GY) of 24 Small Red beans genotypes. The vertical dashed and solid lines shows, respectively, the mean of the selected genotype and the overall mean for both mean performance and WAASB index

4.3.5.1 Selection differentials Percentage (SD_gain in %) gain from the selected genotypes compared to the general mean.

```
blups_sel2 <-
  gmd(waasb_model_sr, "blupg") %>%
  add_cols(SELECTED = ifelse(GEN %in% selected$Code, "yes", "no")) %>%
  dplyr::rename(BLUPs_sel = yield) %>%
  droplevels()
```

```
#> Class of the model: waasb
```

```
#> Variable extracted: blupg
```

```
blups_sel_mean2<-
  gmd(waasb_model_sr, "blupg") %>%
  add_cols(SELECTED = ifelse(GEN %in% selected$Code, "yes", "no")) %>%
  filter(SELECTED == "yes") %>%
  dplyr::summarise(mean_GY = mean(yield, na.rm = TRUE), n = n())
```

```
#> Class of the model: waasb
```

```
#> Variable extracted: blupg
```

```
SD_blups<- as_tibble((blups_sel_mean2$mean_GY/mean(blups_sel2$BLUPs_sel, na.rm = T))
  ↪ -1)*100
SD_WAASP<- as_tibble((waasb_sel_mean$mean_GY /mean(waasb_sel$WAASB_sel, na.rm = T))
  ↪ -1)*100

SD_comb<- full_join(SD_blups, SD_WAASP, by = "value") %>%
  dplyr::rename(SD_gain = value) %>%
  tibble::add_column(Comp_name = c('BLUPs', 'WAASB')) %>%
  relocate(Comp_name)

SD_comb$n_selected<- blups_sel_mean2$n
SD_comb
```

| Comp_name | SD_gain | n_selected |
|-----------|---------|------------|
| character | numeric | integer |
| BLUPs | 2.4 | 7 |
| WAASB | -24.3 | 7 |

```
blups_sel2$mean_blup <- mean(blups_sel2$BLUPs_sel, na.rm = T)
waasb_sel$mean_waasb <- mean(waasb_sel$WAASB_sel, na.rm = T)

#str(waasb_sel)
data_comb<- merge(blups_sel2, waasb_sel, by = c("GEN", "SELECTED"))
#names(data_comb)
## SD for each genotype
```

```

data_sel_perc <- data_comb %>%
  rowwise %>%
  mutate(Perc_blup_gain = ((BLUPs_sel/mean_blup)*100)-100) %>%
  mutate(Perc_WAASB_gain = ((WAASB_sel/mean_waasb)*100)-100) %>%
  as_tibble()

# data_sel_perc_mean <- data_sel_perc %>%
#   dplyr::filter(SELECTED == "yes")
#
# mean(data_sel_perc_mean$Perc_blup_gain)

if (knitr::is_html_output()) {
  print_table(data_sel_perc)
}else{
data_sel_perc[,1:7]
}

```

| GEN | SELECTED | BLUPs_sel | mean_blup | WAASB_sel | mean_waasb | Perc_blup_gain |
|-----------|-----------|-----------|-----------|-----------|------------|----------------|
| character | character | numeric | numeric | numeric | numeric | numeric |
| R1 | yes | 3,251.2 | 3,147.4 | 3.1 | 6.1 | 3.3 |
| R10 | yes | 3,180.0 | 3,147.4 | 5.4 | 6.1 | 1.0 |
| R11 | yes | 3,174.2 | 3,147.4 | 7.6 | 6.1 | 0.9 |
| R12 | no | 3,076.7 | 3,147.4 | 5.4 | 6.1 | -2.2 |
| R13 | yes | 3,159.7 | 3,147.4 | 5.1 | 6.1 | 0.4 |
| R14 | no | 3,451.4 | 3,147.4 | 11.4 | 6.1 | 9.7 |
| R15 | no | 3,069.8 | 3,147.4 | 5.4 | 6.1 | -2.5 |
| R16 | no | 3,068.5 | 3,147.4 | 1.5 | 6.1 | -2.5 |
| R17 | no | 3,113.8 | 3,147.4 | 14.6 | 6.1 | -1.1 |

n: 21

```

data_sel_perc<- data_sel_perc %>%
  dplyr::relocate(GEN,SELECTED,BLUPs_sel,mean_blup,Perc_blup_gain,
    WAASB_sel,mean_waasb ,Perc_WAASB_gain)

#write.xlsx(data_sel_perc, "./data/sel_SD_sr_2.xlsx")

data_sel_perc2 <- data_sel_perc %>%
  dplyr::select(GEN,SELECTED, BLUPs_sel, WAASB_sel, Perc_blup_gain, Perc_WAASB_gain)

data_sel_perc2

```


| GEN | SELECTED | BLUPs_sel | WAASB_sel | Perc_blup_gain | Perc_WAASB_gain |
|-----------|-----------|-----------|-----------|----------------|-----------------|
| character | character | numeric | numeric | numeric | numeric |
| R1 | yes | 3,251.2 | 3.1 | 3.3 | -48.7 |
| R10 | yes | 3,180.0 | 5.4 | 1.0 | -11.5 |
| R11 | yes | 3,174.2 | 7.6 | 0.9 | 26.1 |
| R12 | no | 3,076.7 | 5.4 | -2.2 | -10.4 |
| R13 | yes | 3,159.7 | 5.1 | 0.4 | -15.7 |
| R14 | no | 3,451.4 | 11.4 | 9.7 | 87.5 |
| R15 | no | 3,069.8 | 5.4 | -2.5 | -10.6 |
| R16 | no | 3,068.5 | 1.5 | -2.5 | -74.6 |
| R17 | no | 3,113.8 | 14.6 | -1.1 | 141.0 |
| n: 21 | | | | | |

```
##BLUPs indexes
stab_blups_sr<- blup_indexes(waasb_model_sr)
stab_blups_sr<- as_tibble(stab_blups_sr$yield)

data_waasby <- waasb_model_sr$yield$model %>%
  dplyr::filter(type != "ENV") %>%
  dplyr::select("Code", "WAASBY", "OrWAASBY") %>%
  dplyr::rename(GEN = Code)

stab_blups_sr<- stab_blups_sr %>%
  full_join(data_waasby, by = "GEN")

if (knitr::is_html_output()) {
  print_table(stab_blups_sr)
}else{
  stab_blups_sr[,1:8]
}
```

| GEN | Y | HMGV | HMGV_R | RPGV | RPGV_Y | RPGV_R | HMRPGV |
|-----------|---------|---------|---------|---------|---------|---------|---------|
| character | numeric | numeric | numeric | numeric | numeric | numeric | numeric |
| R1 | 3,213.0 | 3,307.4 | 5 | 1.1 | 3,332.3 | 5 | 1.1 |
| R10 | 2,995.1 | 3,173.5 | 8 | 1.0 | 3,205.9 | 8 | 1.0 |
| n: 21 | | | | | | | |

| GEN | Y | HMGV | HMGV_R | RPGV | RPGV_Y | RPGV_R | HMRPGV |
|-----------|---------|---------|---------|---------|---------|---------|---------|
| character | numeric | numeric | numeric | numeric | numeric | numeric | numeric |
| R11 | 3,170.3 | 3,181.2 | 7 | 1.0 | 3,211.9 | 7 | 1.0 |
| R12 | 3,419.7 | 3,005.0 | 13 | 1.0 | 3,027.2 | 14 | 1.0 |
| R13 | 3,019.6 | 3,155.4 | 9 | 1.0 | 3,179.9 | 9 | 1.0 |
| R14 | 2,761.8 | 3,681.0 | 1 | 1.2 | 3,723.7 | 1 | 1.2 |
| R15 | 3,082.8 | 2,990.4 | 15 | 1.0 | 3,012.4 | 15 | 1.0 |
| R16 | 2,903.1 | 2,987.0 | 16 | 1.0 | 3,005.0 | 16 | 1.0 |
| R17 | 3,363.4 | 3,005.7 | 12 | 1.0 | 3,095.9 | 10 | 1.0 |
| n: 21 | | | | | | | |

```
# library(openxlsx)
# write.xlsx(stab_blups_sr, "../data/blups_sr_2.xlsx")
```

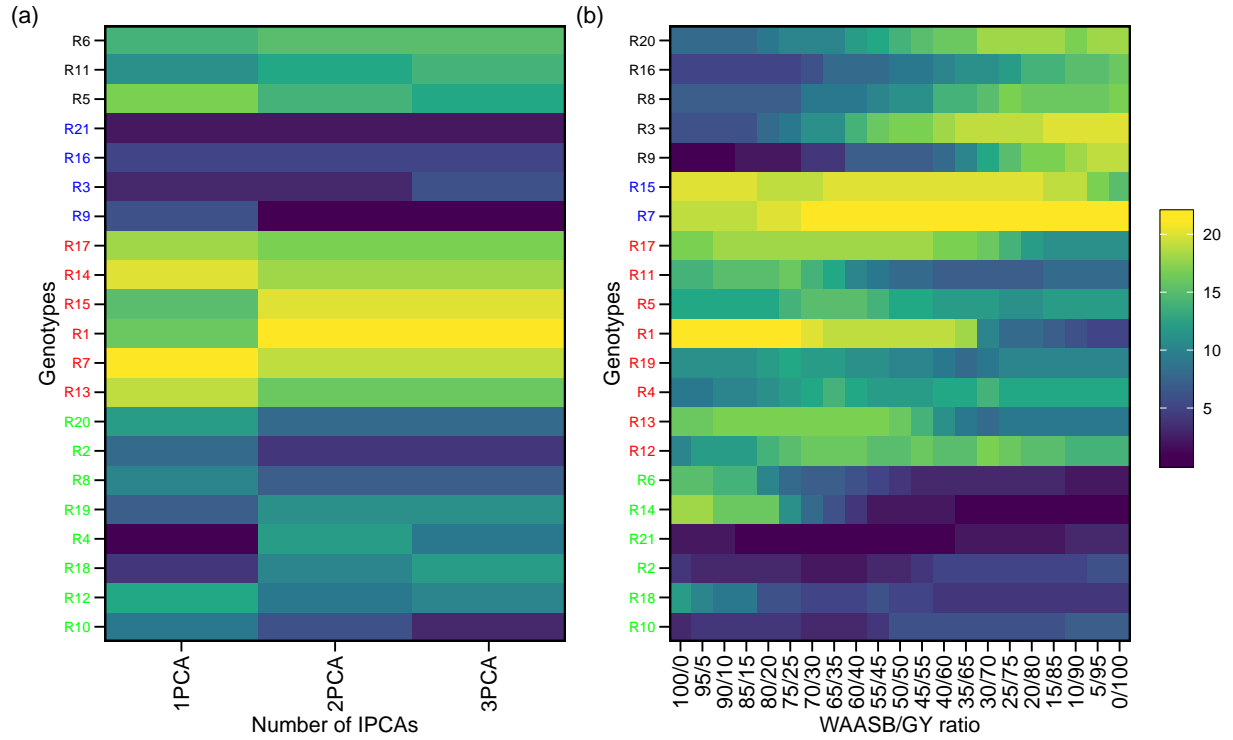
4.3.5.2 Scenarios of waasby estimation Planning different scenarios of waasby estimation by changing the weights assigned to the stability and the mean performance according to Olivoto et al. (2019).

```
scenarios <- wsmpt(waasb_model_sr, progbar = F)

scen1<- plot(scenarios, type = 1) +
  theme(axis.text.y = element_text(size=8))

scen2<-plot(scenarios, type = 2) +
  theme(axis.text.y = element_text(size=8))

arrange_ggplot(scen1, scen2,
  guides = "collect",
  legend.position = "right",
  tag_levels = "a",
  tag_prefix = "(",
  tag_suffix = ")")
```



```
#plot_eigen(waasb_model_sr, size.lab = 14, size.tex.lab = 14)
```

4.3.5.3 Coincidence index of genotype selection Computes the coincidence index (Hamblin and Zimmermann, 1986) as follows:

$$CI = \frac{A - C}{M - C} \times 100$$

where A is the number of selected genotypes common to different methods; C is the number of expected genotypes selected by chance; and M is the number of genotypes selected according to the selection intensity.

```
coinc_1 <- stab_blups_sr %>% dplyr::select(GEN,HMRPGV_R) %>% arrange(HMRPGV_R)
coinc_2 <- stab_blups_sr %>% dplyr::select(GEN,RPGV_R) %>% arrange(RPGV_R)
coinc_3 <- stab_blups_sr %>% dplyr::select(GEN,HMGV_R) %>% arrange(HMGV_R)
coinc_4 <- stab_blups_sr %>% dplyr::select(GEN,OrWAASBY) %>% arrange(OrWAASBY)
coinc_5 <- stab_blups_sr %>% dplyr::select(GEN,WAASB_R) %>% arrange(WAASB_R)

selc_perc<- round(nrow(stab_blups_sr)*0.2)

coinc_1.1 <-1
coinc_1.2 <- coincidence_index(sel1 = coinc_1$GEN[1:selc_perc],
                              sel2 = coinc_2$GEN[1:selc_perc],
                              total = 21)/100
coinc_1.3 <- coincidence_index(sel1 = coinc_1$GEN[1:selc_perc],
                              sel2 = coinc_3$GEN[1:selc_perc],
                              total = 21)/100
coinc_1.4 <- coincidence_index(sel1 = coinc_1$GEN[1:selc_perc],
```

```

                                sel2 = coinc_4$GEN[1:selc_perc],
                                total = 21)/100
coinc_1.5 <- coincidence_index(sel1 = coinc_1$GEN[1:selc_perc],
                                sel2 = coinc_5$GEN[1:selc_perc],
                                total = 21)/100

coinc_2.2 <- 1
coinc_2.3 <- coincidence_index(sel1 = coinc_2$GEN[1:selc_perc],
                                sel2 = coinc_3$GEN[1:selc_perc],
                                total = 21)/100

coinc_2.4 <- coincidence_index(sel1 = coinc_2$GEN[1:selc_perc],
                                sel2 = coinc_4$GEN[1:selc_perc],
                                total = 21)/100

coinc_2.5 <- coincidence_index(sel1 = coinc_2$GEN[1:selc_perc],
                                sel2 = coinc_5$GEN[1:selc_perc],
                                total = 21)/100

coinc_3.3 <- 1
coinc_3.4 <- coincidence_index(sel1 = coinc_3$GEN[1:selc_perc],
                                sel2 = coinc_4$GEN[1:selc_perc],
                                total = 21)/100

coinc_3.5 <- coincidence_index(sel1 = coinc_3$GEN[1:selc_perc],
                                sel2 = coinc_5$GEN[1:selc_perc],
                                total = 21)/100

coinc_4.4 <- 1
coinc_4.5 <- coincidence_index(sel1 = coinc_4$GEN[1:selc_perc],
                                sel2 = coinc_5$GEN[1:selc_perc],
                                total = 21)/100

coinc_5.5 <- 1

coinc <- c(coinc_1.1,coinc_1.2,coinc_2.2,coinc_1.3,coinc_2.3,
           coinc_3.3,coinc_1.4, coinc_2.4, coinc_3.4,
           coinc_4.4, coinc_1.5, coinc_2.5,
           coinc_3.5, coinc_4.5,
           coinc_5.5)

z=matrix(0,5,5)
z[upper.tri(z)| row(z)==col(z)] <- coinc

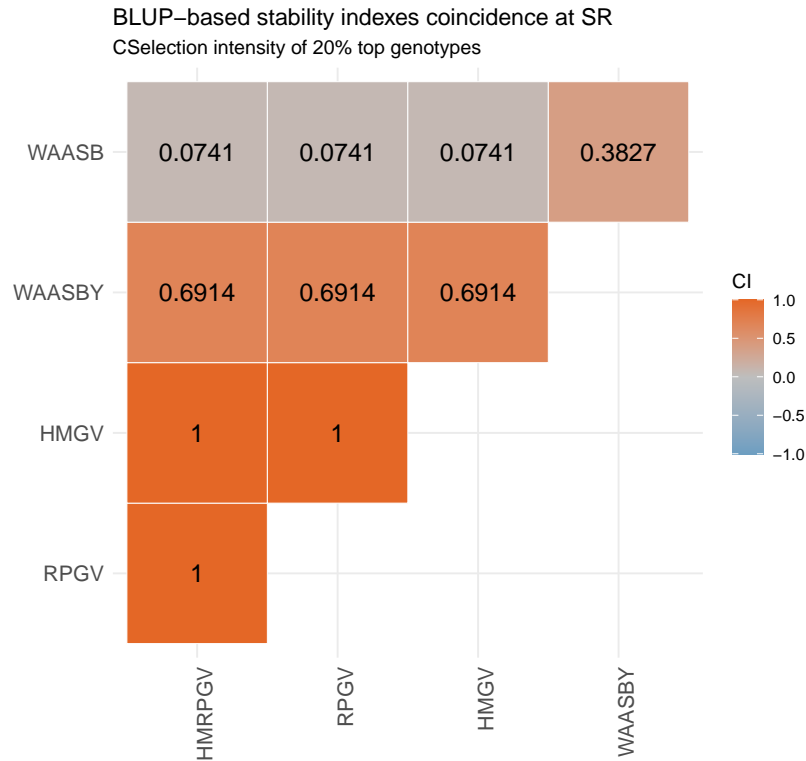
rownames(z)=c(
  "HMRPGV",
  "RPGV",
  'HMGV',
  'WAASBY',
  'WAASB')

colnames(z)=rownames(z)

plotSR<- ggcorrplot(z, colors = c("#6D9EC1", "gray", "#E46726"),
                    show.legend = T,
                    legend.title = "CI" ,lab_size=5,tl.srt = 90,type = c("upper"), lab = T,digits = 4,
                    outline.color = "white",pch.col = "white", tl.col = "blue",show.diag = F) +
  labs(title = "BLUP-based stability indexes coincidence at SR",
        subtitle = "CSelection intensity of 20% top genotypes")

```

```
print(plotSR)
```



5 Appendix E - R codes

5.1 Multi-trait Multi-env analysis

5.2 Descriptive Stats - Multi-trait data

- GY data set: were obtained from the adjusted data in the 2nd-stage mixed models analysis.
- PH, PM, and LD were obtained from the coincident locations (TU, BA and SA) in 2021 only.

5.2.1 Data set

```
data_beans_compl = read.csv("data/data_beans_Multi-trait.csv",h=T, stringsAsFactors = T)
data_beans_compl<- data_beans_compl[,-c(1:2)]
colnames(data_beans_compl)<- c('name', 'loc', 'mkt', 'rep', 'GY', 'DM', 'PH', "LD")
#str(data_beans_compl)

# Data adjustment
# All the effect columns must be as a factor to run in ASReml-r.
cols <- c("rep", "name", "loc", "mkt")
data_beans_compl[cols] <- lapply(data_beans_compl[cols], factor)
```

```
data_beans_compl <- data.table(data_beans_compl)
```

```
data_beans_compl
```

| name | loc | mkt | rep | GY | DM | PH | LD |
|---------|--------|--------|--------|---------|---------|---------|---------|
| factor | factor | factor | factor | numeric | numeric | numeric | numeric |
| B1 | BA | BB | 1 | 2,481.7 | 89 | 16 | 1 |
| B1 | BA | BB | 2 | 3,279.0 | 90 | 18 | 1 |
| B1 | BA | BB | 3 | 2,479.2 | 90 | 14 | 1 |
| B1 | BA | BB | 4 | 1,911.4 | 89 | 15 | 1 |
| B2 | BA | BB | 1 | 3,159.8 | 90 | 20 | 2 |
| B2 | BA | BB | 2 | 3,424.3 | 89 | 19 | 1 |
| B2 | BA | BB | 3 | 2,655.0 | 91 | 15 | 2 |
| B2 | BA | BB | 4 | 2,923.2 | 92 | 18 | 2 |
| B4 | BA | BB | 1 | 2,565.5 | | | |
| n: 1056 | | | | | | | |

Number of genotype per market class:

```
data_beans_compl_count <- data_beans_compl %>%
  means_by(name, mkt, na.rm = TRUE) %>%
  group_by(mkt) %>%
  dplyr::summarise(n = n())
```

```
data_beans_compl_count
```

| mkt | n |
|--------|---------|
| factor | integer |
| BB | 37 |
| NB | 37 |
| SR | 14 |

5.2.2 Box plot distribution

```
## Data visualization
```

```

#print(c)
a<- ggplot(data=data_beans_compl, aes(x=reorder(loc, -DM), y=DM, fill=loc)) +
  geom_boxplot()+
  facet_grid("mkt")+
  theme_bw()+
  theme(axis.text.x=element_text(angle = 90),
        strip.text=element_text(face="bold"), legend.position = "none")+
  labs(title="Days to Plant DM in days (DPM)",
        caption=NULL, x=NULL, y=NULL)

#print(a)

b<- ggplot(data=data_beans_compl, aes(x=reorder(loc, -PH), y=PH, fill=loc)) +
  geom_boxplot()+
  facet_grid("mkt")+
  theme_bw()+
  theme(axis.text.x=element_text(angle = 90),
        strip.text=element_text(face="bold"), legend.position = "none")+
  labs(title="Plant PH in cm (PH)",
        caption=NULL, x=NULL, y=NULL)

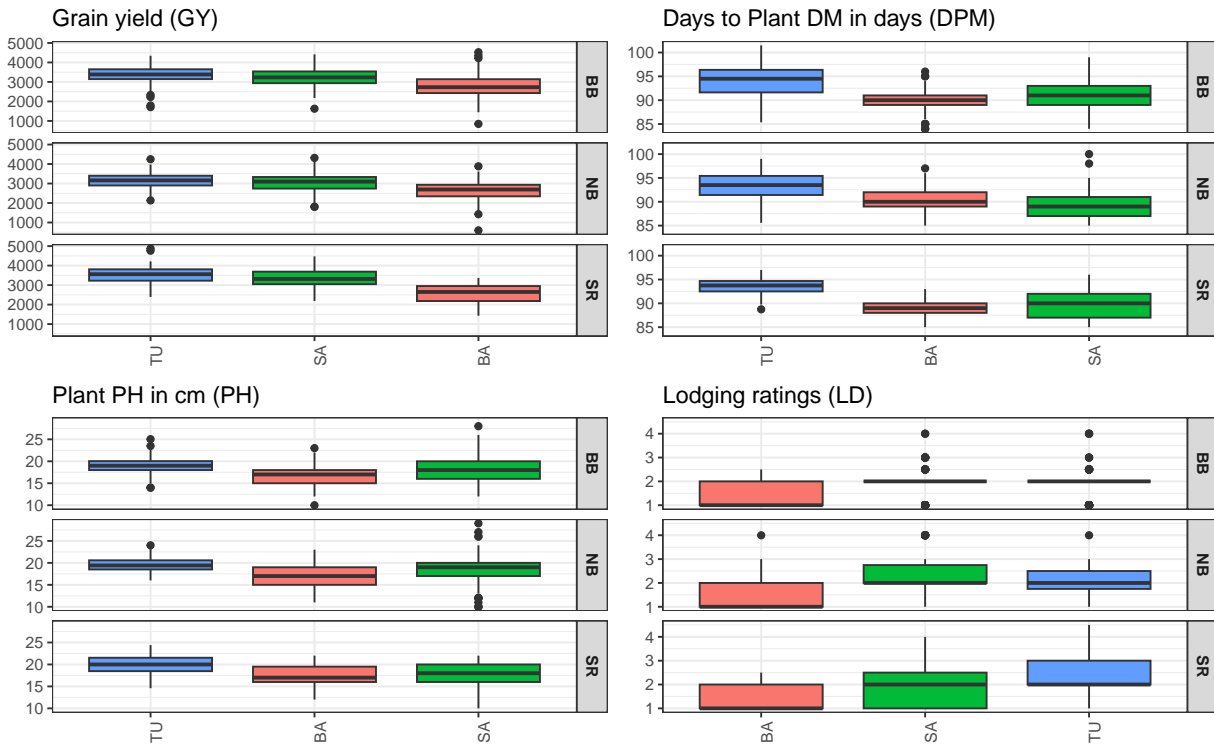
d<- ggplot(data=data_beans_compl, aes(x=reorder(loc, -LD), y=LD , fill=loc)) +
  geom_boxplot()+
  facet_grid("mkt")+
  theme_bw()+
  theme(axis.text.x=element_text(angle = 90),
        strip.text=element_text(face="bold"), legend.position = "none")+
  labs(title="Lodging ratings (LD)",
        caption=NULL, x=NULL, y=NULL)

c<- ggplot(data=data_beans_compl, aes(x=reorder(loc, -GY), y=GY , fill=loc)) +
  geom_boxplot()+
  facet_grid("mkt")+
  theme_bw()+
  theme(axis.text.x=element_text(angle = 90),
        strip.text=element_text(face="bold"), legend.position = "none")+
  labs(title="Grain yield (GY)",
        caption=NULL, x=NULL, y=NULL)

#print(a)

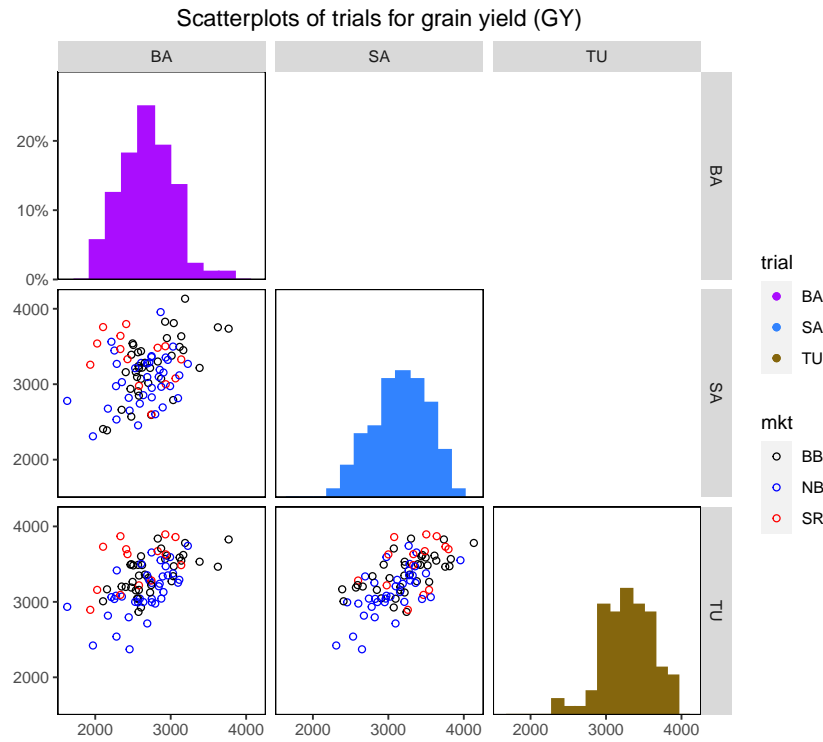
arrange_ggplot(c,a,b,d)

```



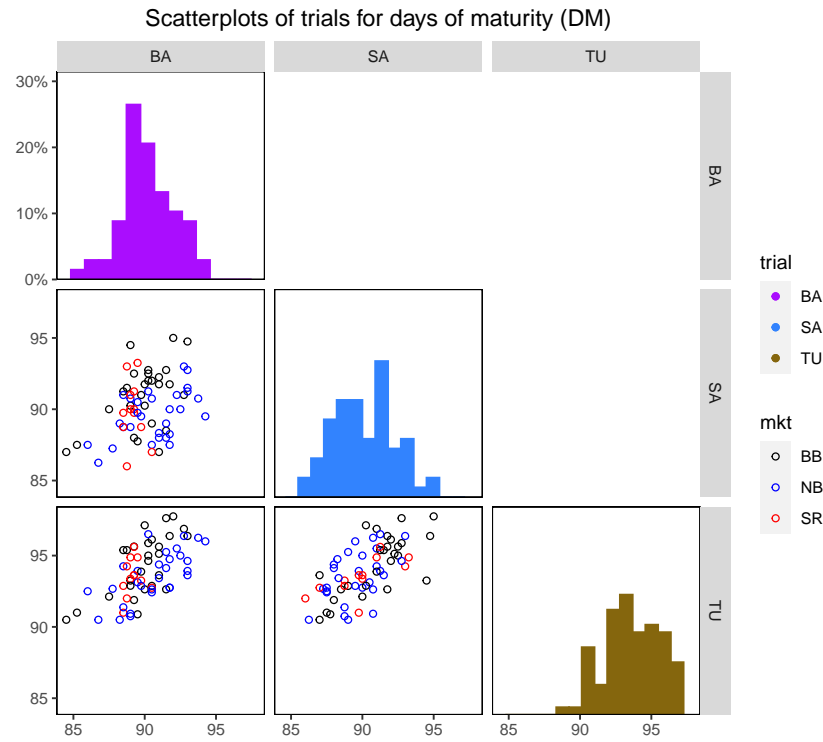
Box Plot for grain yield (GY), date of maturity (DM), Plant height (PH), and Lodging (LD) across environment

5.2.3 Scatter plot distribution GY



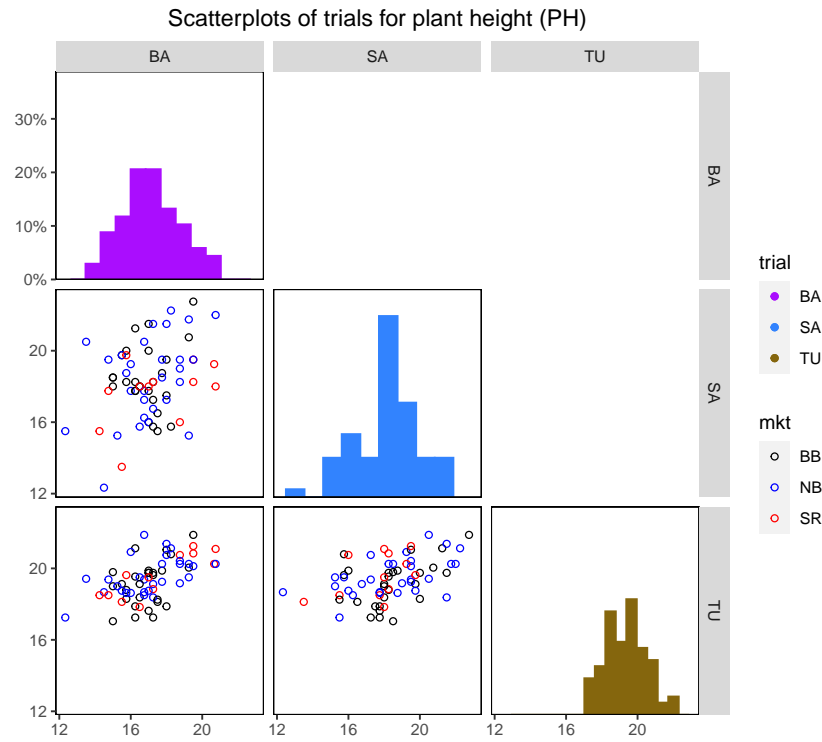
Scatterplot matrix of trials for grain yield (GY). The diagonal shows the distribution and the bottom left shows the scatter points for DM in each location.

5.2.4 Scatter plot distribution DM



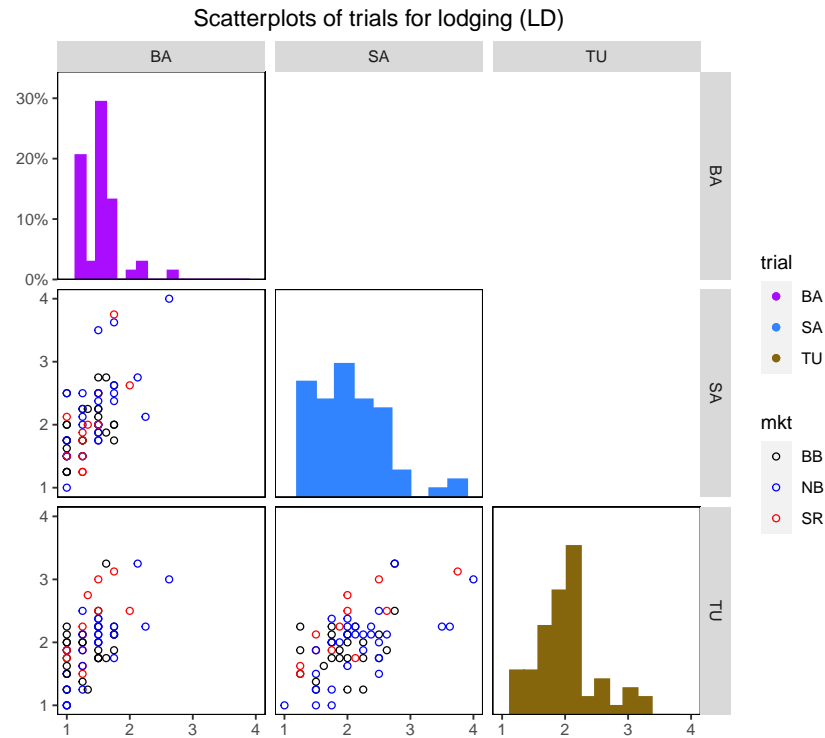
Scatterplot matrix of trials for days of maturity (DM). The diagonal shows the distribution and the bottom left shows the scatter points for DM in each location.

5.2.5 Scatter plot distribution PH



Scatterplot matrix of trials for plant height (PH). The diagonal shows the distribution and the bottom left shows the scatter points for PH in each location.

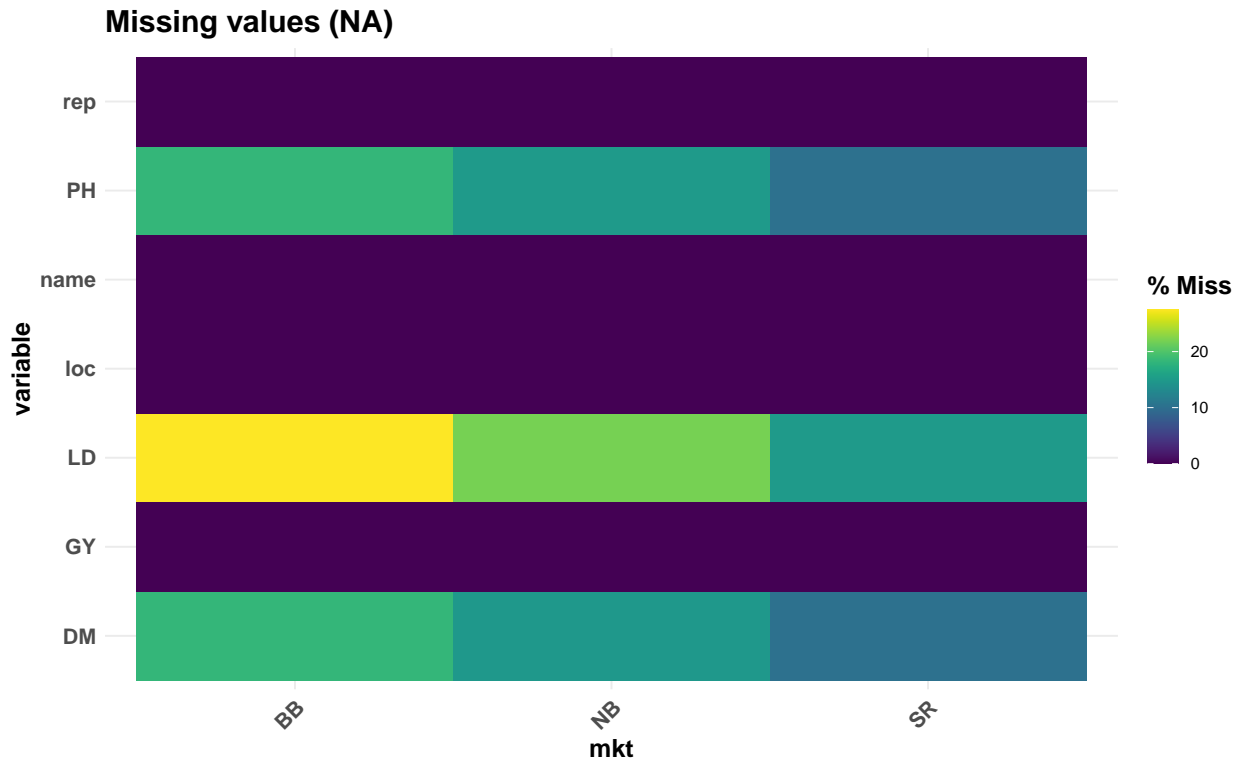
5.2.6 Scatter plot distribution LD



Scatterplot matrix of trials for lodging (LD). The diagonal shows the distribution and the bottom left shows the scatter points for LD in each location.

5.2.7 Missing values

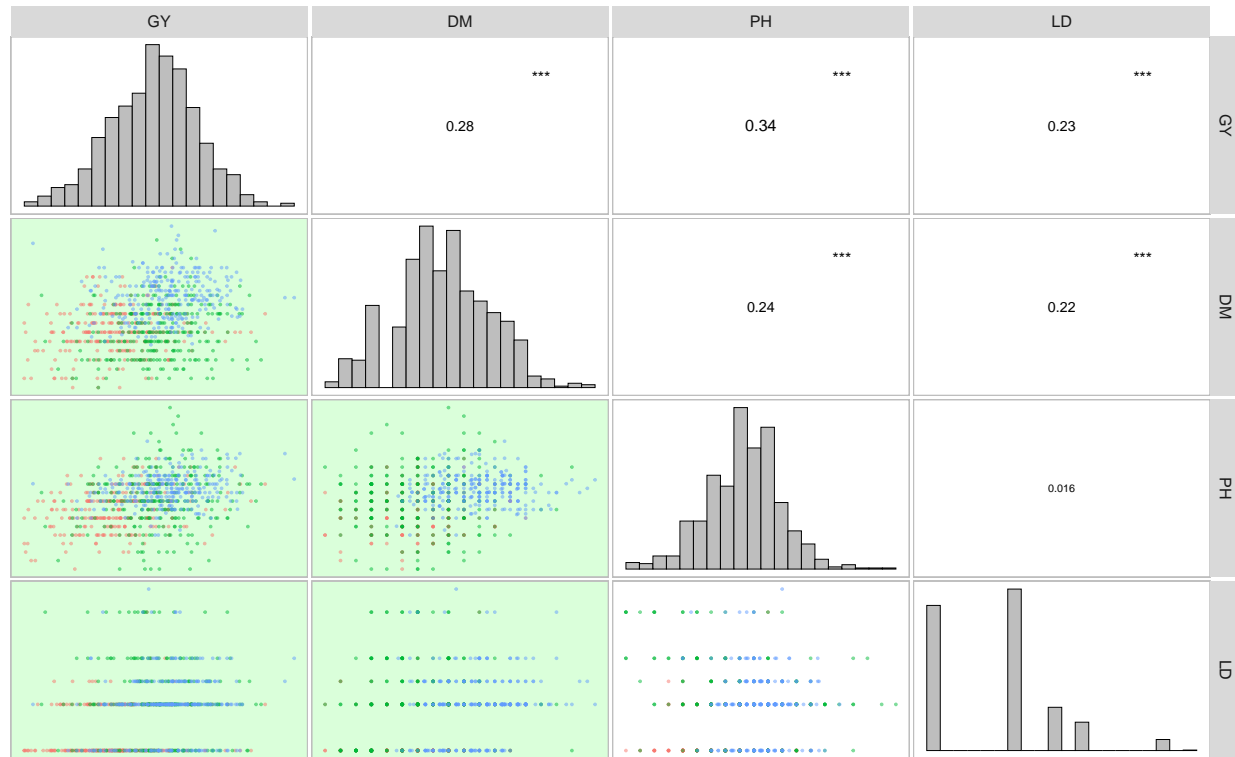
```
#str(data_beans_compl)
gg_miss_fct(data_beans_compl, fct = mkt) + ggtitle("Missing values (NA)") +
  theme(axis.text.x = element_text(face = "bold", size = 12),
        axis.text.y = element_text(face = "bold", size = 12),
        title = element_text(face = "bold", size = 14))
```



Missing genotypes by market classes

5.2.8 Linear phenotypic correlation

```
corr_plot(data_beans_compl,
  col.by = loc, # Different color for each level of ENV
  alpha.point = 0.5, # Color transparency of the points
  size.point = 0.3, # Size of the point
  size.line = 0.1) # The size of the line
```



Pearson's linear correlation between the studied traits. The lower diagonal shows the scatter plot where the environments are mapped with different point colors (BA = green, SA = salmon, TU = cyan)

5.3 Multi-trait stability index and selection gains

- For this study, the goal to response variables GY, DM, PH and LD are:
 - GY: higher (increase)
 - DM: smaller (decrease)
 - PH: higher (increase)
 - LD: smaller (decrease)
- The weights for the response variable are:
 - GY: 60 (60 yielding and 40 stability)
 - DM: 40 (40 maturity and 60 stability)
 - PH: 40 (40 height and 60 stability)
 - LD: 40 (40 lodging and 60 stability)
- Selection intensity (SI) of 20%

5.4 Black beans

```
data_beans_BB <- droplevels(subset(data_beans_compl, mkt == "BB"))

data_beans_BB <- droplevels(na.omit(data_beans_BB))
#str(data_beans_BB)
```

5.4.1 Multi-trait index selection

```

waasb_model_bb.1 <- waasb(data_beans_BB,
  env = loc,
  gen = name,
  rep = rep,
  resp = everything(),
  random = "gen", #Default
  verbose = F,
  wresp = c(60, 40, 40, 40),
  mresp = c("h,l,h,l") ) #'GY', 'DM', 'PH', LD
  #weight for response variable 60 and 40 for yielding and stability,
  ↪ respectively)

options(digits = 3)
mtsi1 = mtsi(waasb_model_bb.1, index = "waasby", SI = 20, mineval = 1, verbose = F)

Sel_waasb <- sel_gen(mtsi1)

mtsi1_resul<- mtsi1$sel_dif_trait

if (knitr::is_html_output()) {

  print_table(mtsi1_resul[,1:6])

}else{

mtsi1_resul[,1:6]
}

```

| VAR | Factor | Xo | Xs | SD | SDperc |
|-----------|-----------|---------|---------|---------|---------|
| character | character | numeric | numeric | numeric | numeric |
| GY | FA 1 | 3,200.6 | 3,258.5 | 57.9 | 1.8 |
| LD | FA 1 | 1.7 | 1.6 | -0.1 | -5.6 |
| DM | FA 2 | 91.8 | 91.9 | 0.1 | 0.1 |
| PH | FA 2 | 18.1 | 18.3 | 0.2 | 1.1 |

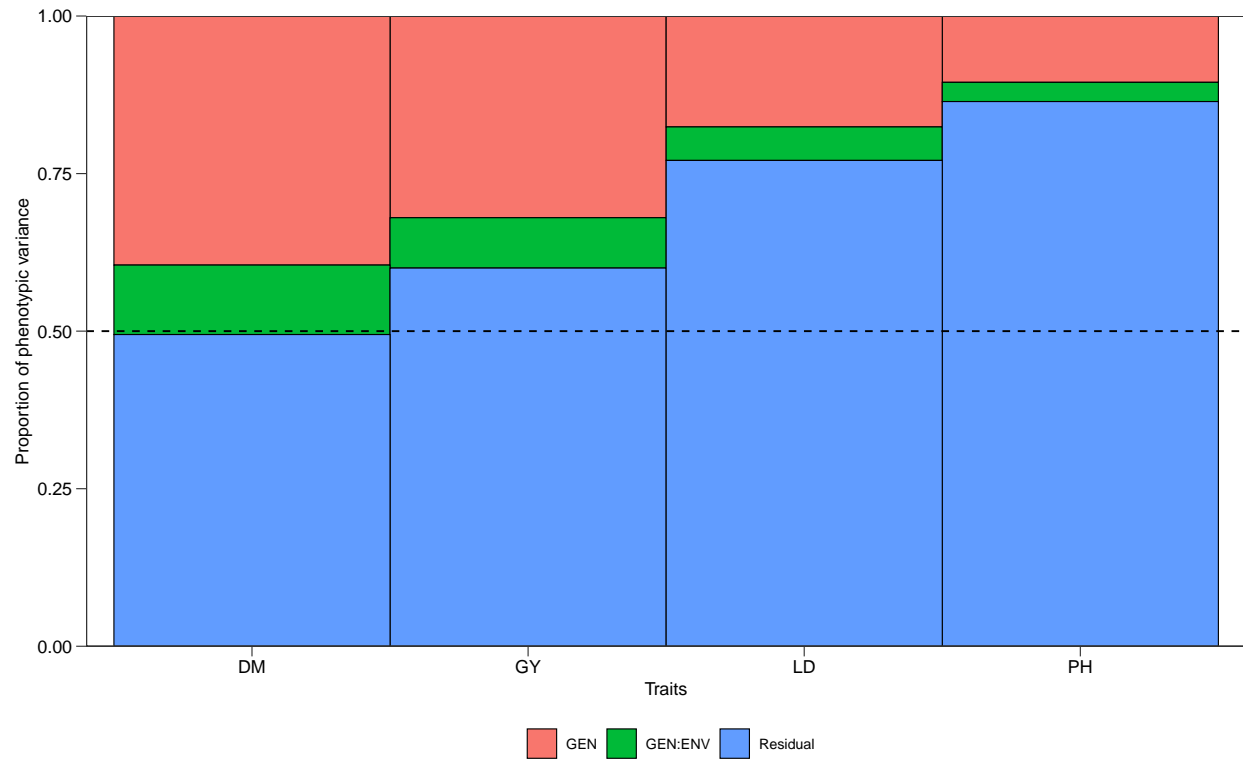
5.4.2 Model outputs

```

plot(waasb_model_bb.1,
  type = "vcomp", # Chose the type of plot.
  width.bar = 1, # No spaces between the bars
  size.line = 0.3) + # Controls the size of the line
  geom_hline(yintercept = 0.5, linetype = 2) # Add the dashed line

```

5.4.2.1 Variance plot



```
get_model_data(waasb_model_bb.1, "lrt")
```

5.4.2.2 Likelihood-ratio test

```
#> Class of the model: waasb
```

```
#> Variable extracted: lrt
```

| VAR | model | npar | logLik | AIC | LRT | Df | Pr(>Chisq) |
|-----------|-----------|---------|----------|---------|---------|---------|------------|
| character | character | integer | numeric | numeric | numeric | numeric | numeric |
| GY | GEN | 14 | -2,333.5 | 4,695.1 | 25.1 | 1 | 0.0 |
| GY | GEN:ENV | 14 | -2,322.9 | 4,673.9 | 4.0 | 1 | 0.0 |
| DM | GEN | 14 | -720.5 | 1,469.0 | 30.2 | 1 | 0.0 |
| DM | GEN:ENV | 14 | -710.2 | 1,448.5 | 9.7 | 1 | 0.0 |
| PH | GEN | 14 | -733.1 | 1,494.3 | 6.1 | 1 | 0.0 |
| PH | GEN:ENV | 14 | -730.3 | 1,488.5 | 0.4 | 1 | 0.5 |
| LD | GEN | 14 | -289.8 | 607.5 | 12.3 | 1 | 0.0 |
| LD | GEN:ENV | 14 | -284.3 | 596.6 | 1.3 | 1 | 0.2 |

| VAR | model | npar | logLik | AIC | LRT | Df | Pr(>Chisq) |
|-----------|-----------|---------|---------|---------|---------|---------|------------|
| character | character | integer | numeric | numeric | numeric | numeric | numeric |

```
get_model_data(waasb_model_bb.1, "vcomp")
```

5.4.2.3 Variance components

```
#> Class of the model: waasb
```

```
#> Variable extracted: vcomp
```

| Group | GY | DM | PH | LD |
|-----------|-----------|---------|---------|---------|
| character | numeric | numeric | numeric | numeric |
| GEN | 68,571.6 | 2.9 | 0.6 | 0.1 |
| GEN:ENV | 17,115.1 | 0.8 | 0.2 | 0.0 |
| Residual | 128,582.1 | 3.6 | 5.2 | 0.3 |

```
get_model_data(waasb_model_bb.1, "genpar")
```

5.4.2.4 Genetic parameters

```
#> Class of the model: waasb
```

```
#> Variable extracted: genpar
```

| Parameters | GY | DM | PH | LD |
|------------------------------|-----------|---------|---------|---------|
| character | numeric | numeric | numeric | numeric |
| Phenotypic variance | 214,268.9 | 7.2 | 6.0 | 0.4 |
| Heritability | 0.3 | 0.4 | 0.1 | 0.2 |
| GEI _{r2} | 0.1 | 0.1 | 0.0 | 0.1 |
| h ² _{mg} | 0.8 | 0.8 | 0.6 | 0.7 |
| Accuracy | 0.9 | 0.9 | 0.7 | 0.8 |
| r _{ge} | 0.1 | 0.2 | 0.0 | 0.1 |
| CV _g | 8.2 | 1.8 | 4.4 | 14.5 |

| Parameters | GY | DM | PH | LD |
|------------|---------|---------|---------|---------|
| character | numeric | numeric | numeric | numeric |
| CVr | 11.2 | 2.1 | 12.5 | 30.3 |
| CV ratio | 0.7 | 0.9 | 0.3 | 0.5 |

```
get_model_data(waasb_model_bb.1, "details")
```

5.4.2.5 Models details

```
#> Class of the model: waasb
```

```
#> Variable extracted: details
```

| Parameters | GY | DM | PH | LD |
|------------|---------------------|-------------------|----------------|---------------|
| character | character | character | character | character |
| Mean | 3199.25 | 91.77 | 18.14 | 1.73 |
| SE | 30.37 | 0.19 | 0.15 | 0.04 |
| SD | 544.12 | 3.32 | 2.67 | 0.67 |
| CV | 17.03 | 3.63 | 14.75 | 38.72 |
| Min | 1601.88 (B43 in BA) | 84 (B22 in BA) | 10 (B27 in BA) | 1 (B1 in BA) |
| Max | 4524.05 (B26 in BA) | 101.5 (B61 in TU) | 28 (B40 in SA) | 4 (B25 in SA) |
| MinENV | BA (2828.83) | BA (89.91) | BA (16.86) | BA (1.32) |
| MaxENV | TU (3405.26) | TU (94.44) | TU (19.13) | SA (1.96) |
| MinGEN | B45 (2570.2) | B45 (87.33) | B60 (16.85) | B14 (1.25) |
| n: 14 | | | | |

```
get_model_data(waasb_model_bb.1, "fixed")
```

5.4.2.6 Fixed effects

```
#> Class of the model: waasb
```

```
#> Variable extracted: fixed
```

| VAR | SOURCE | Sum Sq | Mean Sq | NumDF | DenDF | F value | Pr(>F) |
|-----------|-----------|-------------|-------------|---------|---------|---------|---------|
| character | character | numeric | numeric | integer | numeric | numeric | numeric |
| GY | ENV | 3,275,190.1 | 1,637,595.1 | 2 | 243.1 | 12.7 | 0.0 |
| GY | ENV:REP | 6,661,855.0 | 740,206.1 | 9 | 229.8 | 5.8 | 0.0 |
| DM | ENV | 303.7 | 151.9 | 2 | 221.8 | 42.4 | 0.0 |
| DM | ENV:REP | 110.2 | 12.2 | 9 | 232.4 | 3.4 | 0.0 |
| PH | ENV | 47.2 | 23.6 | 2 | 267.7 | 4.6 | 0.0 |
| PH | ENV:REP | 152.1 | 16.9 | 9 | 233.3 | 3.3 | 0.0 |
| LD | ENV | 7.1 | 3.6 | 2 | 260.5 | 13.0 | 0.0 |
| LD | ENV:REP | 6.1 | 0.7 | 9 | 233.1 | 2.5 | 0.0 |

```
get_model_data(waasb_model_bb.1, "blupge") %>%
  means_by(ENV)
```

5.4.2.7 Enviroment means

```
#> Class of the model: waasb
```

```
#> Variable extracted: blupge
```

| ENV | GY | DM | PH | LD |
|--------|---------|---------|---------|---------|
| factor | numeric | numeric | numeric | numeric |
| BA | 2,835.2 | 89.9 | 16.9 | 1.3 |
| SA | 3,362.1 | 91.0 | 18.4 | 2.0 |
| TU | 3,401.9 | 94.4 | 19.1 | 1.9 |

5.4.3 Selection Description

5.4.3.1 Genotype ranking

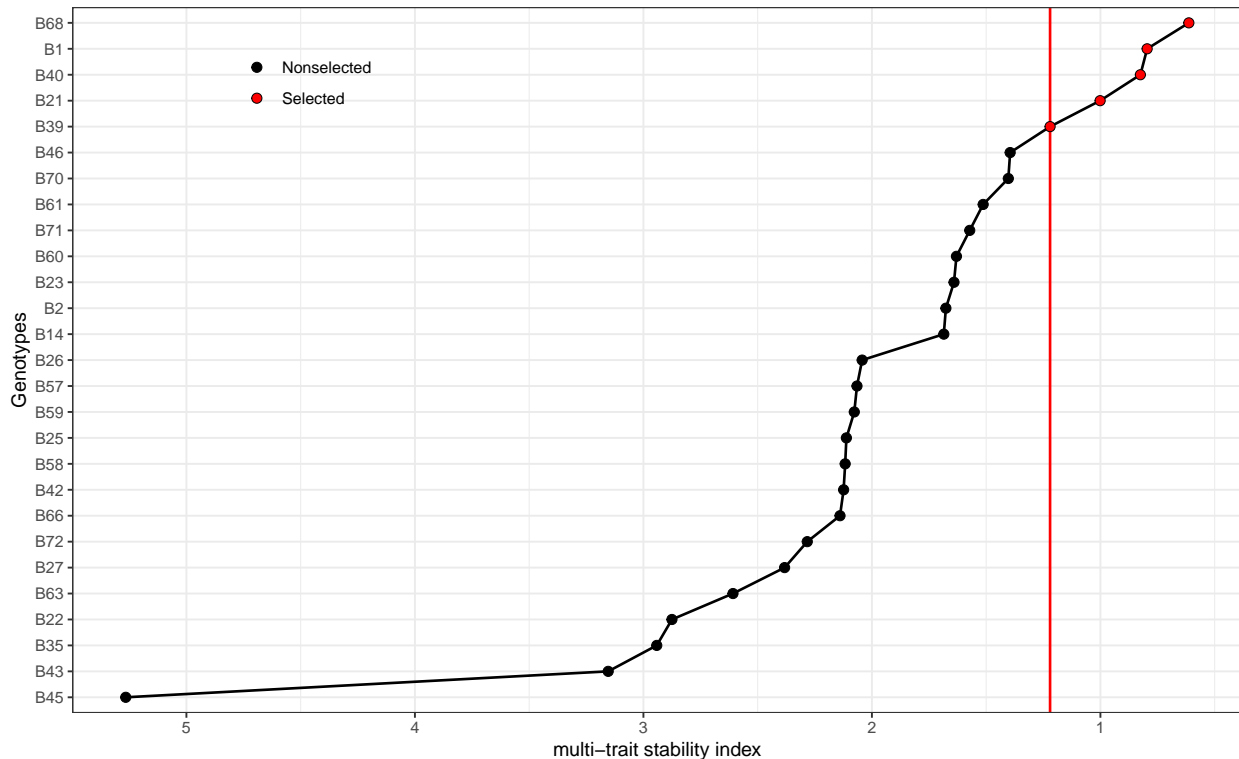
- Varieties ranking based on the multi-trait stability index. Selected varieties are highlighted in red.

```
# Get the random effects
#get_model_data(waasb_model_bb.1, what = "ranef")

mtsi1_value<- mtsi1$MTSI

#plot(mtsi1, arrange.label = TRUE)
```

```
p2 = plot(mtsi1, SI = 20, radar = FALSE) +
  coord_flip() +
  theme_bw() +
  labs(x = "Genotypes", y = "multi-trait stability index") +
  theme(legend.position = c(0.2, 0.9),
        legend.background = element_blank(),
        legend.key = element_blank(),
        legend.title = element_blank())
print(p2)
```



Cultivars ranking based on the multi-trait stability index. Selected cultivars are highlighted in red.

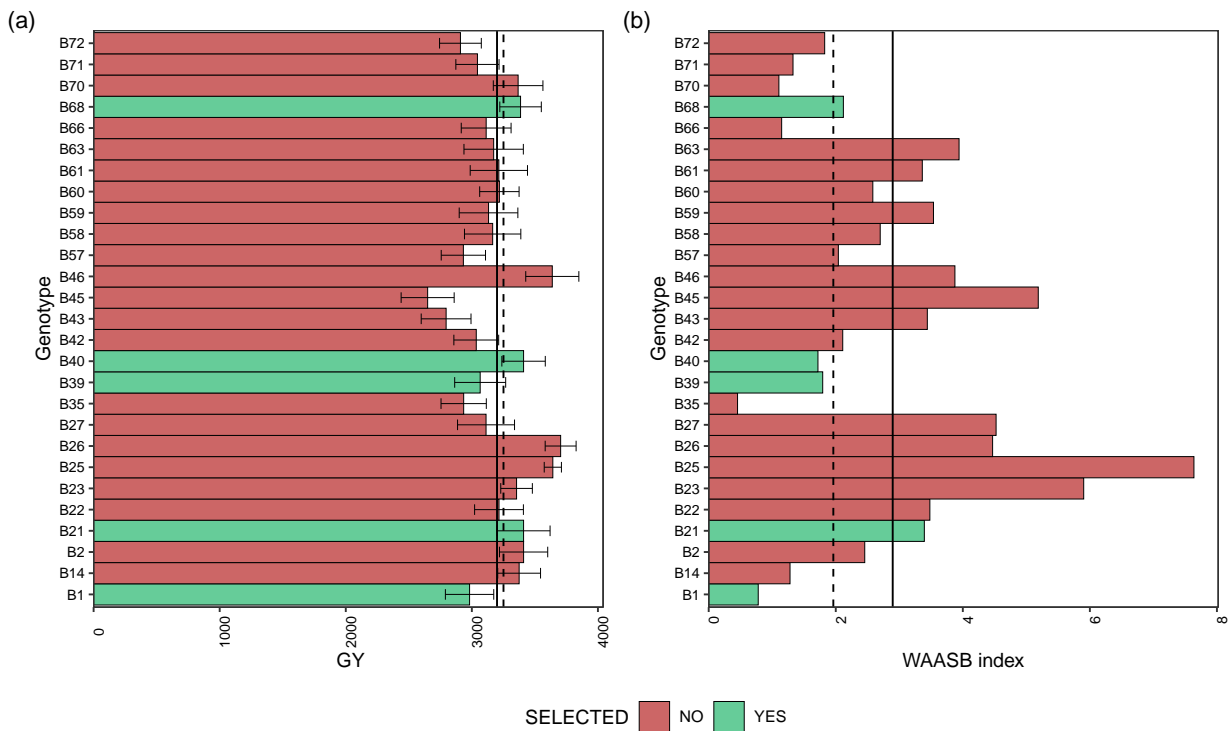
```
Sel_waasb
```

```
#> [1] "B68" "B1" "B40" "B21" "B39"
```

```
p1<- plot_selected(blups_sel, GEN, GY, blups_sel_mean_GY$mean_GY)
p2<- plot_selected(waasb_sel, GEN, GY, waasb_sel_mean_GY$mean_GY) + labs(y = "WAASB
  ↪ index")

arrange_ggplot(p1, p2,
  guides = "collect",
  tag_levels = "a",
```

```
tag_prefix = "(",
tag_suffix = ")")
```

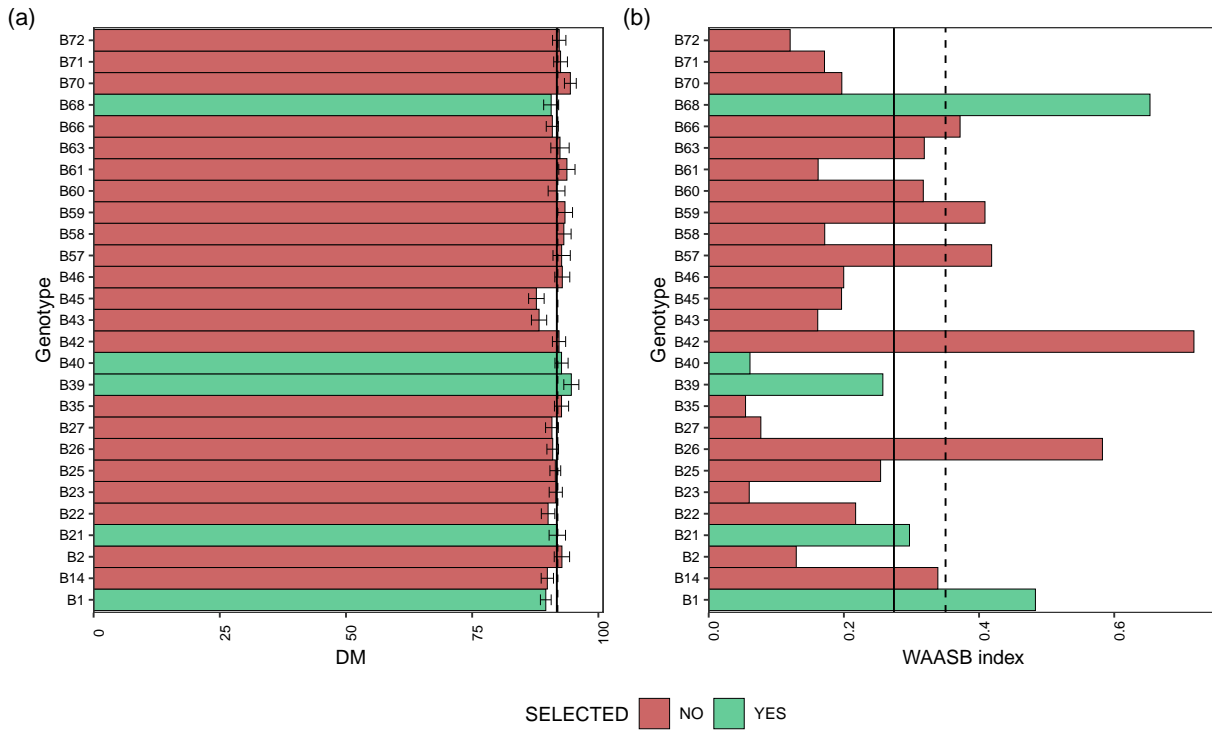


Mean performance (a) and stability (b) for grain yield (GY) of 27 black beans genotypes. The vertical dashed and solid lines shows, respectively, the mean of the selected genotype and the overall mean for both mean performance and WAASB index

5.4.3.2 Mean performance and stability for GY

```
p1<- plot_selected(blups_sel, GEN, DM, blups_sel_mean_DM$mean_DM)
p2<- plot_selected(waasb_sel, GEN, DM, waasb_sel_mean_DM$mean_DM) + labs(y = "WAASB
  ↪ index")

arrange_ggplot(p1, p2,
  guides = "collect",
  tag_levels = "a",
  tag_prefix = "(",
  tag_suffix = ")")
```

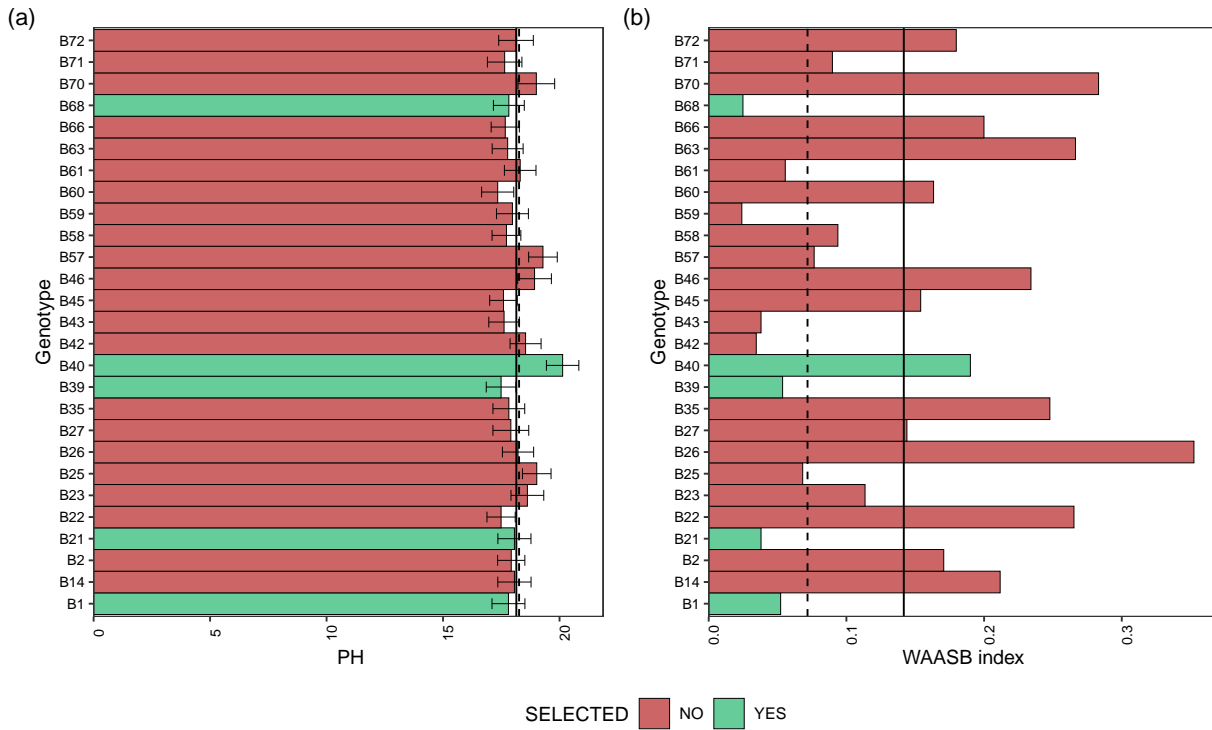


Mean performance (a) and stability (b) for days of maturity (DM) of 27 black beans genotypes. The vertical dashed and solid lines shows, respectively, the mean of the selected genotype and the overall mean for both mean performance and WAASB index

5.4.3.3 Mean performance and stability for DM

```
p1<- plot_selected(blups_sel, GEN, PH, blups_sel_mean_PH$mean_PH)
p2<- plot_selected(waasb_sel, GEN, PH, waasb_sel_mean_PH$mean_PH) + labs(y = "WAASB
  ↪ index")

arrange_ggplot(p1, p2,
  guides = "collect",
  tag_levels = "a",
  tag_prefix = "(",
  tag_suffix = ")")
```

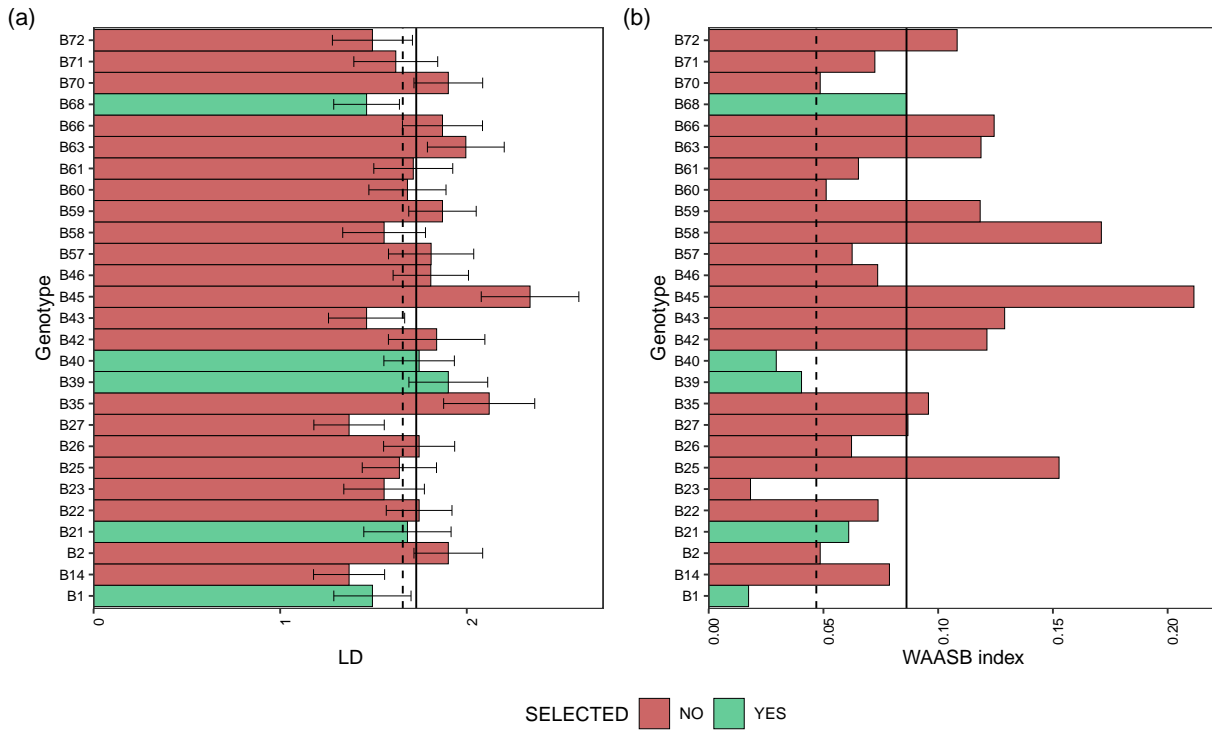


Mean performance (a) and stability (b) for plant height (PH) of 27 black beans genotypes. The vertical dashed and solid lines shows, respectively, the mean of the selected genotype and the overall mean for both mean performance and WAASB index

5.4.3.4 Mean performance and stability for PH

```
p1<- plot_selected(blups_sel, GEN, LD, blups_sel_mean_LD$mean_LD)
p2<- plot_selected(waasb_sel, GEN, LD, waasb_sel_mean_LD$mean_LD) + labs(y = "WAASB
  ↪ index")

arrange_ggplot(p1, p2,
  guides = "collect",
  tag_levels = "a",
  tag_prefix = "(",
  tag_suffix = ")")
```



Mean performance (a) and stability (b) for lodging (LD) of 27 black beans genotypes. The vertical dashed and solid lines shows, respectively, the mean of the selected genotype and the overall mean for both mean performance and WAASB index

5.4.3.5 Mean performance and stability for LD

5.5 Navy beans

```
data_beans_NB <- droplevels(subset(data_beans_compl, mkt == "NB"))
data_beans_NB <- droplevels(na.omit(data_beans_NB))
#str(data_beans_NB)
```

5.5.1 Multi-trait index selection

```
waasb_model_nb.1 <- waasb(data_beans_NB,
  env = loc,
  gen = name,
  rep = rep,
  resp = everything(),
  random = "gen", #Default
  verbose = F,
  wresp = c(60, 40, 40, 40),
```



```

mresp = c("h, l,h, l") ) #'GY', 'DM', 'PH', LD
#weight for response variable 60 and 40 for yielding and stability,
↪ respectively)

options(digits = 3)
mtsi1 = mtsi(waasb_model_nb.1, index = "waasby", SI = 20, mineval = 1, verbose = F)

mtsi1_resul<- mtsi1$sel_dif_trait

Sel_waasb <- sel_gen(mtsi1)

if (knitr::is_html_output()) {

  print_table(mtsi1_resul[,1:6])

}else{

mtsi1_resul[,1:6]
}

```

| VAR | Factor | Xo | Xs | SD | SDperc |
|-----------|-----------|---------|---------|---------|---------|
| character | character | numeric | numeric | numeric | numeric |
| GY | FA 1 | 3,006.1 | 3,145.0 | 138.9 | 4.6 |
| DM | FA 1 | 91.3 | 91.5 | 0.3 | 0.3 |
| PH | FA 1 | 18.3 | 19.7 | 1.4 | 7.4 |
| LD | FA 1 | 1.9 | 1.7 | -0.2 | -11.9 |

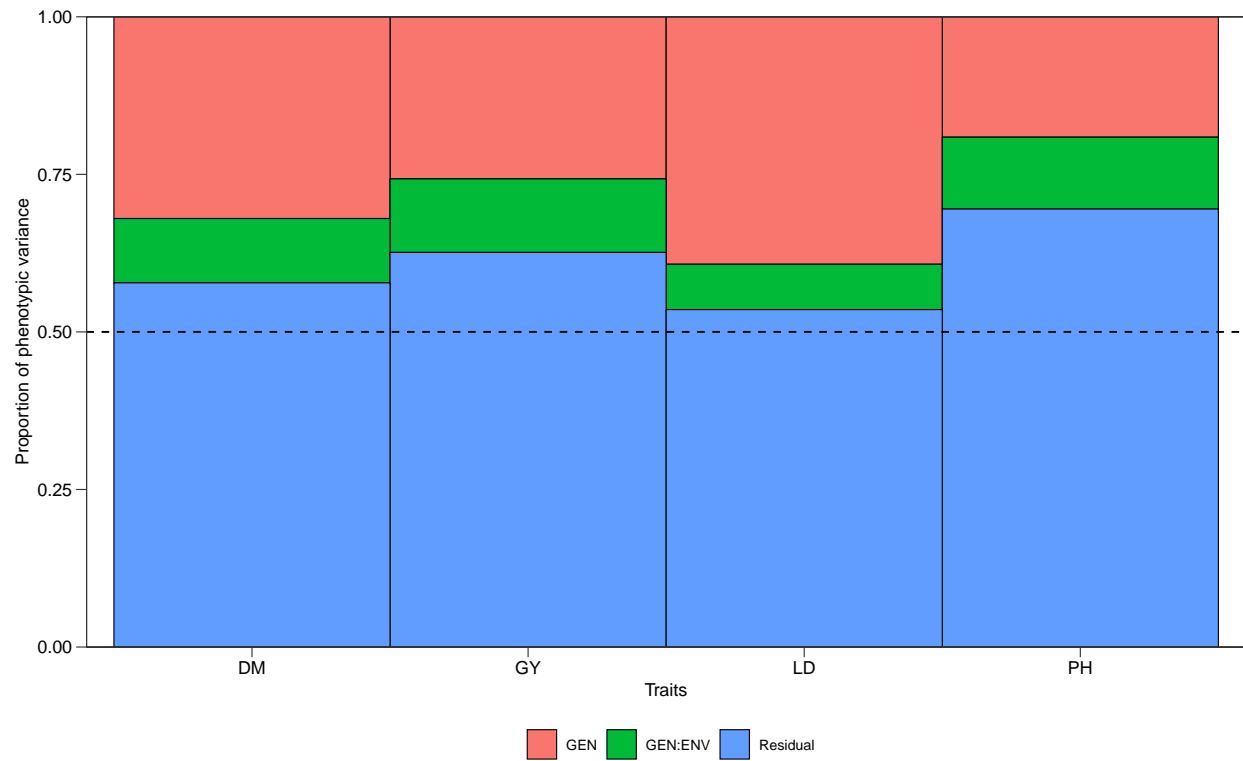
5.5.2 Model outputs

```

plot(waasb_model_nb.1,
type = "vcomp", # Chose the type of plot.
width.bar = 1, # No spaces between the bars
size.line = 0.3) + # Controls the size of the line
geom_hline(yintercept = 0.5, linetype = 2) # Add the dashed line

```

5.5.2.1 Variance plot



```
get_model_data(waasb_model_nb.1, "lrt")
```

5.5.2.2 Likelihood-ratio test

```
#> Class of the model: waasb
```

```
#> Variable extracted: lrt
```

| VAR | model | npar | logLik | AIC | LRT | Df | Pr(>Chisq) |
|-----------|-----------|---------|----------|---------|---------|---------|------------|
| character | character | integer | numeric | numeric | numeric | numeric | numeric |
| GY | GEN | 14 | -2,501.2 | 5,030.4 | 17.9 | 1 | 0.0 |
| GY | GEN:ENV | 14 | -2,496.2 | 5,020.3 | 7.8 | 1 | 0.0 |
| DM | GEN | 14 | -763.5 | 1,555.0 | 25.4 | 1 | 0.0 |
| DM | GEN:ENV | 14 | -754.4 | 1,536.8 | 7.2 | 1 | 0.0 |
| PH | GEN | 14 | -803.6 | 1,635.2 | 12.1 | 1 | 0.0 |
| PH | GEN:ENV | 14 | -800.6 | 1,629.3 | 6.1 | 1 | 0.0 |
| LD | GEN | 14 | -335.4 | 698.9 | 36.0 | 1 | 0.0 |
| LD | GEN:ENV | 14 | -319.7 | 667.4 | 4.5 | 1 | 0.0 |

```
get_model_data(waasb_model_nb.1, "vcomp")
```

5.5.2.3 Variance components

```
#> Class of the model: waasb
```

```
#> Variable extracted: vcomp
```

| Group | GY | DM | PH | LD |
|--------------|-----------|-----------|-----------|-----------|
| character | numeric | numeric | numeric | numeric |
| GEN | 50,195.5 | 2.0 | 1.4 | 0.2 |
| GEN:ENV | 22,779.4 | 0.6 | 0.8 | 0.0 |
| Residual | 122,206.2 | 3.6 | 4.9 | 0.3 |

```
get_model_data(waasb_model_nb.1, "genpar")
```

5.5.2.4 Genetic parameters

```
#> Class of the model: waasb
```

```
#> Variable extracted: genpar
```

| Parameters | GY | DM | PH | LD |
|------------------------------|-----------|-----------|-----------|-----------|
| character | numeric | numeric | numeric | numeric |
| Phenotypic variance | 195,181.1 | 6.2 | 7.1 | 0.5 |
| Heritability | 0.3 | 0.3 | 0.2 | 0.4 |
| GEI _{r2} | 0.1 | 0.1 | 0.1 | 0.1 |
| h ² _{mg} | 0.7 | 0.8 | 0.7 | 0.9 |
| Accuracy | 0.9 | 0.9 | 0.8 | 0.9 |
| r _{ge} | 0.2 | 0.2 | 0.1 | 0.1 |
| CV _g | 7.4 | 1.5 | 6.3 | 23.6 |
| CV _r | 11.6 | 2.1 | 12.1 | 27.6 |
| CV ratio | 0.6 | 0.7 | 0.5 | 0.9 |

```
get_model_data(waasb_model_nb.1, "details")
```

5.5.2.5 Models details

```
#> Class of the model: waasb
```

```
#> Variable extracted: details
```

| Parameters | GY | DM | PH | LD |
|------------|---------------------|-----------------|----------------|---------------|
| character | character | character | character | character |
| Mean | 3009.36 | 91.28 | 18.37 | 1.87 |
| SE | 26.04 | 0.16 | 0.15 | 0.04 |
| SD | 483.58 | 3.02 | 2.84 | 0.77 |
| CV | 16.09 | 3.31 | 15.46 | 41.04 |
| Min | 1618.91 (N35 in BA) | 85 (N15 in BA) | 10 (N38 in SA) | 1 (N3 in BA) |
| Max | 4313.9 (N36 in SA) | 100 (N57 in SA) | 29 (N23 in SA) | 4 (N47 in BA) |
| MinENV | BA (2737.08) | SA (89.57) | BA (17.05) | BA (1.46) |
| MaxENV | TU (3195.31) | TU (93.57) | TU (19.57) | SA (2.19) |
| MinGEN | N15 (2272.31) | N15 (87.82) | N15 (15.27) | N15 (1) |
| n: 14 | | | | |

```
get_model_data(waasb_model_nb.1, "fixed")
```

5.5.2.6 Fixed effects

```
#> Class of the model: waasb
```

```
#> Variable extracted: fixed
```

| VAR | SOURCE | Sum Sq | Mean Sq | NumDF | DenDF | F value | Pr(>F) |
|-----------|-----------|-------------|-------------|---------|---------|---------|---------|
| character | character | numeric | numeric | integer | numeric | numeric | numeric |
| GY | ENV | 2,987,371.0 | 1,493,685.5 | 2 | 247.7 | 12.2 | 0.0 |
| GY | ENV:REP | 2,887,992.3 | 320,888.0 | 9 | 250.1 | 2.6 | 0.0 |
| DM | ENV | 240.1 | 120.0 | 2 | 251.3 | 33.7 | 0.0 |

| VAR | SOURCE | Sum Sq | Mean Sq | NumDF | DenDF | F value | Pr(>F) |
|-----------|-----------|---------|---------|---------|---------|---------|---------|
| character | character | numeric | numeric | integer | numeric | numeric | numeric |
| DM | ENV:REP | 114.4 | 12.7 | 9 | 250.3 | 3.6 | 0.0 |
| PH | ENV | 82.4 | 41.2 | 2 | 254.2 | 8.3 | 0.0 |
| PH | ENV:REP | 66.4 | 7.4 | 9 | 247.6 | 1.5 | 0.2 |
| LD | ENV | 4.7 | 2.4 | 2 | 262.2 | 8.9 | 0.0 |
| LD | ENV:REP | 8.3 | 0.9 | 9 | 249.5 | 3.5 | 0.0 |

```
get_model_data(waasb_model_nb.1, "blupge") %>%
  means_by(ENV)
```

5.5.2.7 Enviroment means

```
#> Class of the model: waasb
```

```
#> Variable extracted: blupge
```

| ENV | GY | DM | PH | LD |
|--------|---------|---------|---------|---------|
| factor | numeric | numeric | numeric | numeric |
| BA | 2,732.0 | 90.6 | 17.0 | 1.5 |
| SA | 3,094.1 | 89.6 | 18.5 | 2.2 |
| TU | 3,195.3 | 93.6 | 19.6 | 2.0 |

5.5.3 Selection Description

5.5.3.1 Genotype ranking

- Varieties ranking based on the multi-trait stability index. Selected varieties are highlighted in red.

```
# Get the random effects
#get_model_data(waasb_model_nb.1, what = "ranef")

mtsi1_value<- mtsi1$MTSI

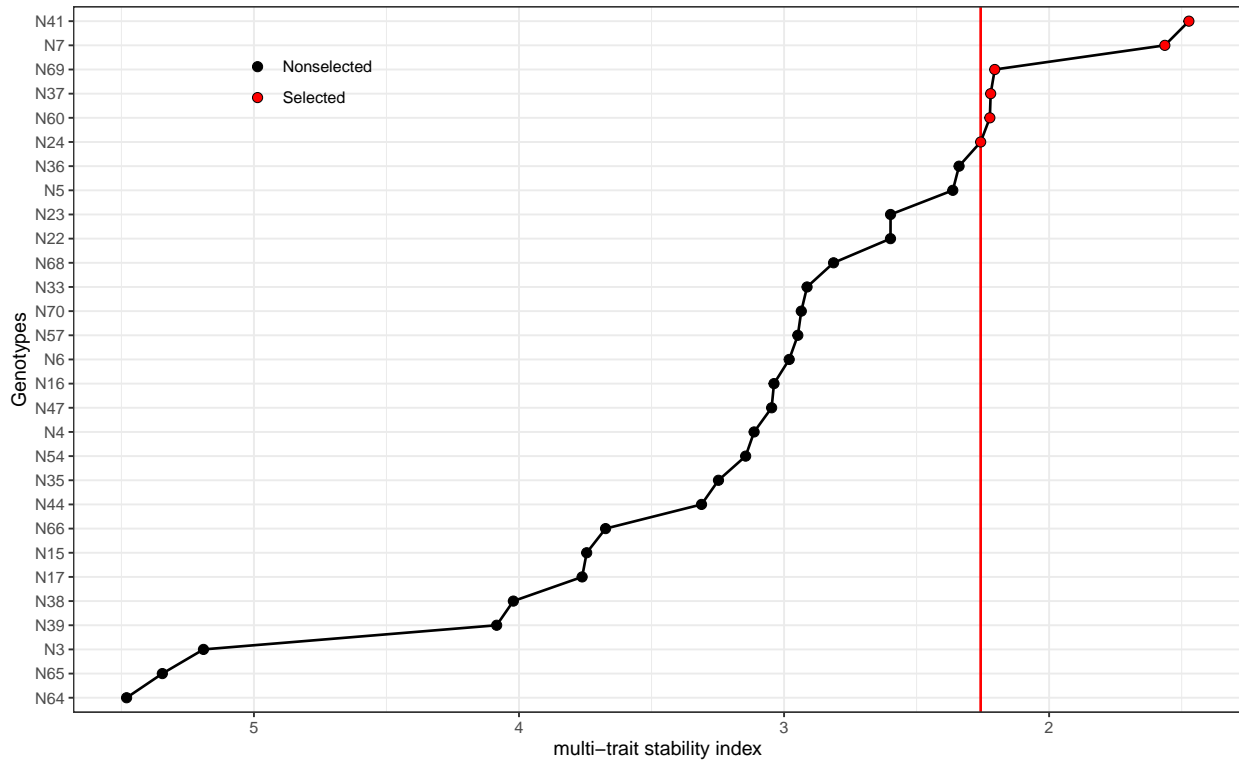
#plot(mtsi1, arrange.label = TRUE)

p2 = plot(mtsi1, SI = 20, radar = FALSE) +
  coord_flip() +
  theme_bw() +
  labs(x = "Genotypes", y = "multi-trait stability index") +
  theme(legend.position = c(0.2, 0.9),
```

```

legend.background = element_blank(),
legend.key = element_blank(),
legend.title = element_blank()
print(p2)

```



Cultivars ranking based on the multi-trait stability index. Selected cultivars are highlighted in red.

```
Sel_waasb
```

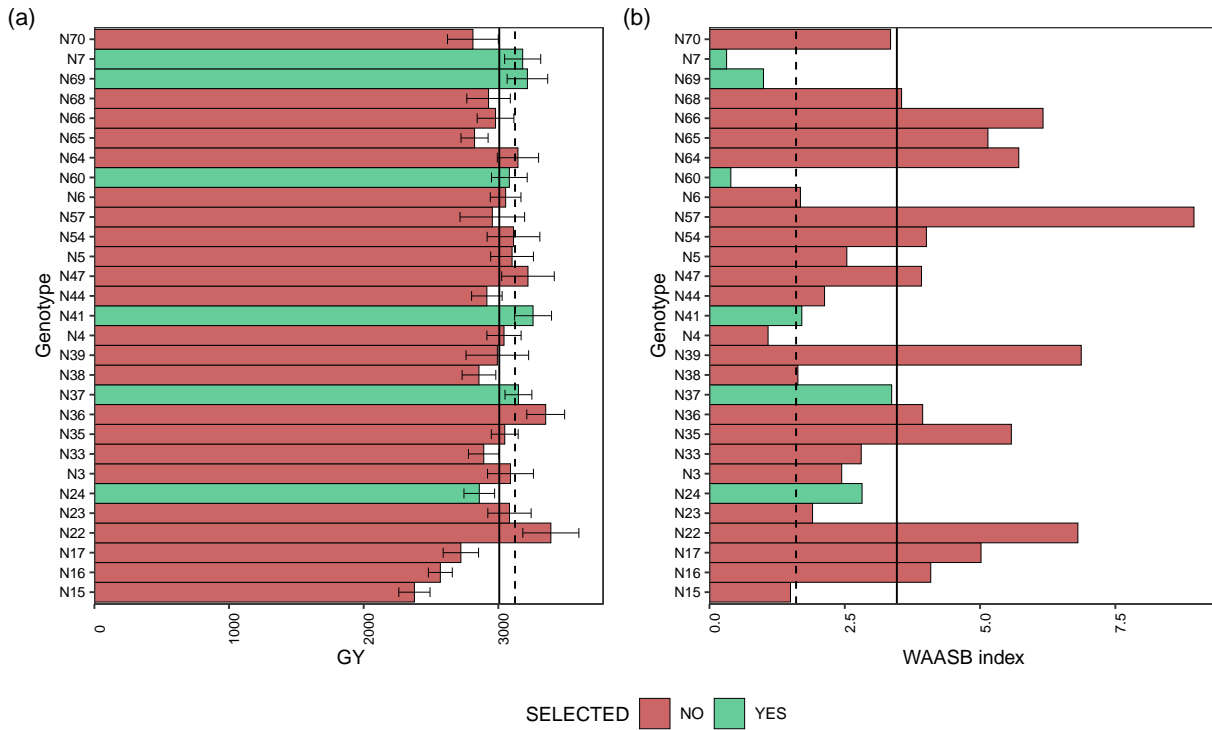
```
#> [1] "N41" "N7" "N69" "N37" "N60" "N24"
```

```

p1<- plot_selected(blups_sel, GEN, GY, blups_sel_mean_GY$mean_GY)
p2<- plot_selected(waasb_sel, GEN, GY, waasb_sel_mean_GY$mean_GY) + labs(y = "WAASB
  ↪ index")

arrange_ggplot(p1, p2,
  guides = "collect",
  tag_levels = "a",
  tag_prefix = "(",
  tag_suffix = ")")

```

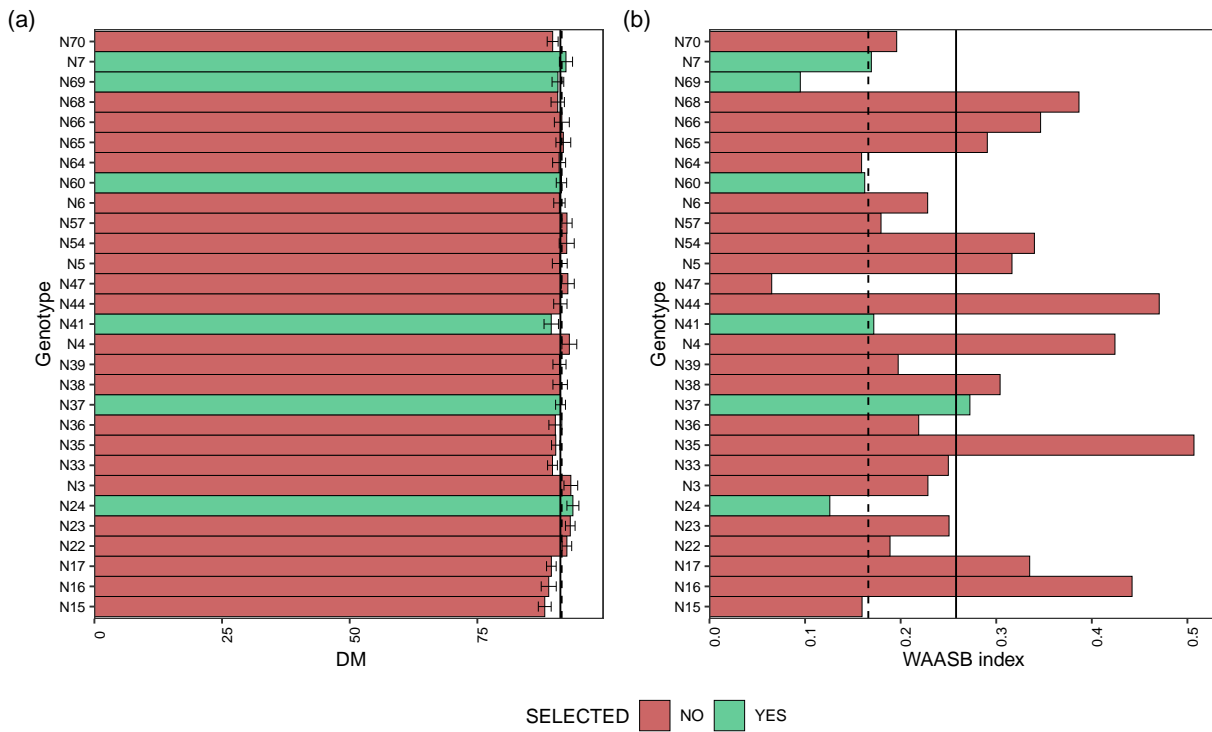


Mean performance (a) and stability (b) for grain yield (GY) of 29 navy beans genotypes. The vertical dashed and solid lines shows, respectively, the mean of the selected genotype and the overall mean for both mean performance and WAASB index

5.5.3.2 Mean performance and stability for GY

```
p1<- plot_selected(blups_sel, GEN, DM, blups_sel_mean_DM$mean_DM)
p2<- plot_selected(waasb_sel, GEN, DM, waasb_sel_mean_DM$mean_DM) + labs(y = "WAASB
  ↪ index")

arrange_ggplot(p1, p2,
  guides = "collect",
  tag_levels = "a",
  tag_prefix = "(",
  tag_suffix = ")")
```

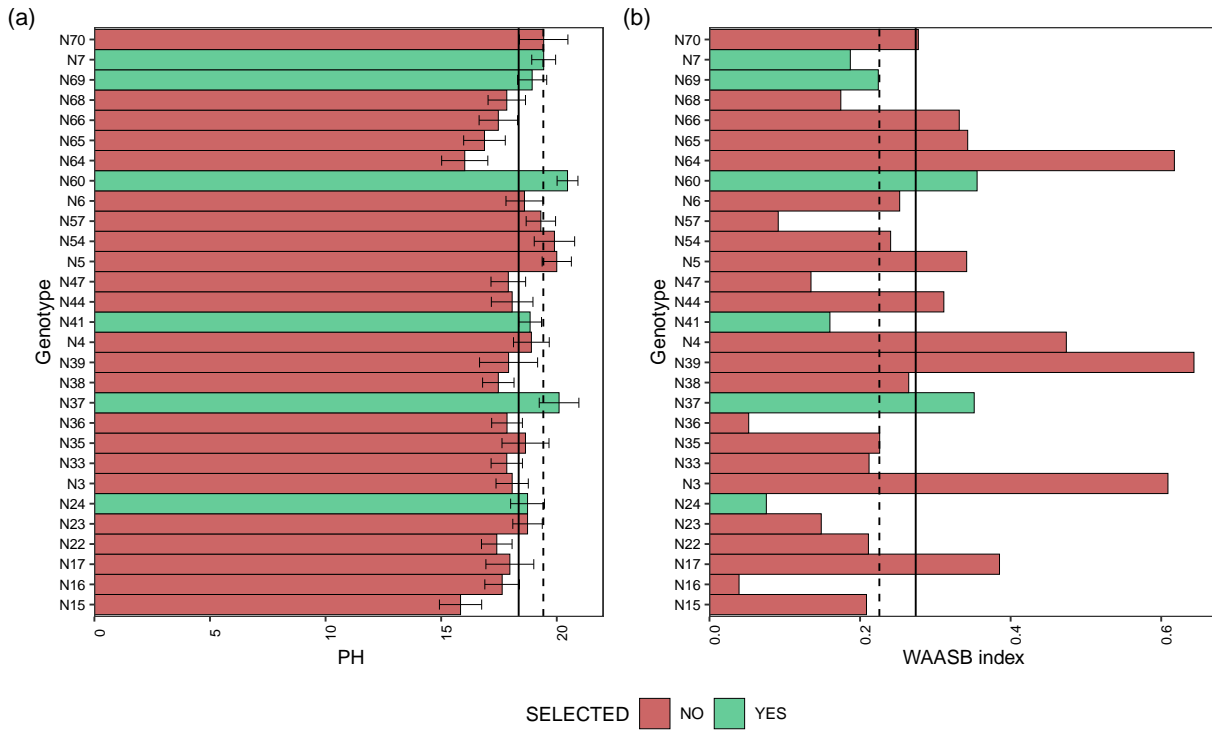


Mean performance (a) and stability (b) for days of maturity (DM) of 29 navy beans genotypes. The vertical dashed and solid lines shows, respectively, the mean of the selected genotype and the overall mean for both mean performance and WAASB index

5.5.3.3 Mean performance and stability for DM

```
p1<- plot_selected(blups_sel, GEN, PH, blups_sel_mean_PH$mean_PH)
p2<- plot_selected(waasb_sel, GEN, PH, waasb_sel_mean_PH$mean_PH) + labs(y = "WAASB
  ↪ index")

arrange_ggplot(p1, p2,
  guides = "collect",
  tag_levels = "a",
  tag_prefix = "(",
  tag_suffix = ")")
```

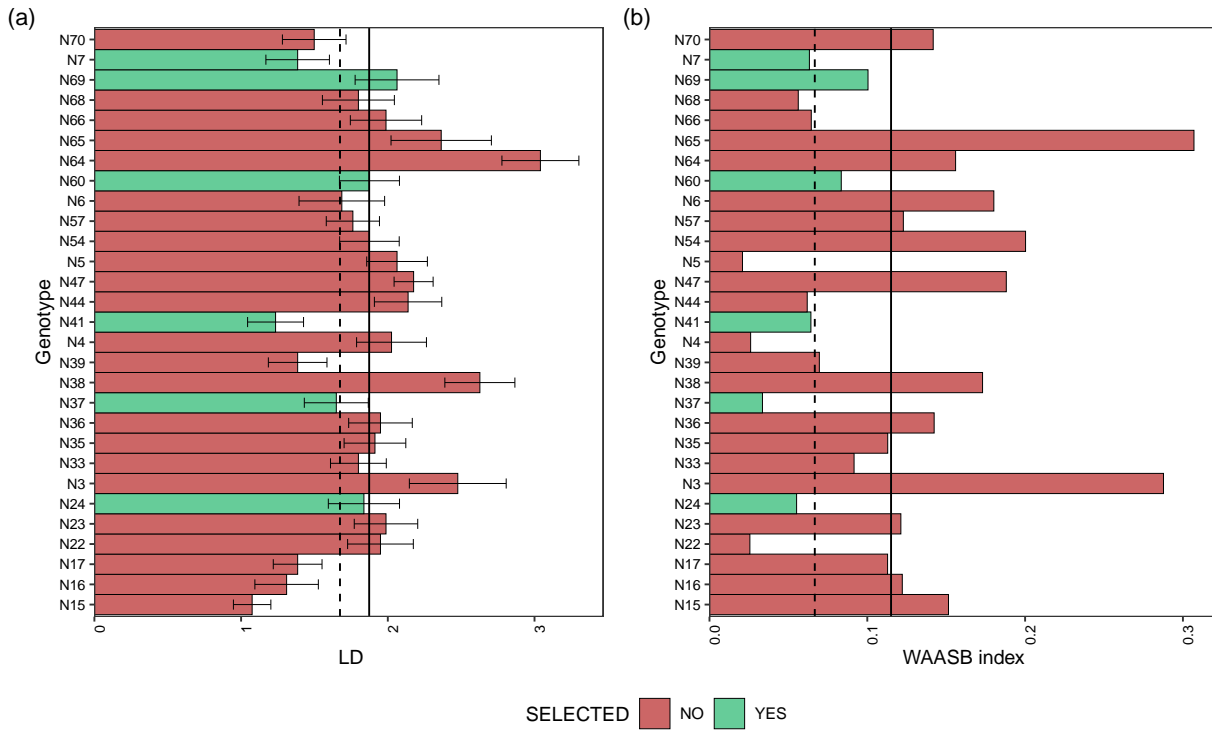



Mean performance (a) and stability (b) for plant height (PH) of 29 navy beans genotypes. The vertical dashed and solid lines shows, respectively, the mean of the selected genotype and the overall mean for both mean performance and WAASB index

5.5.3.4 Mean performance and stability for PH

```
p1<- plot_selected(blups_sel, GEN, LD, blups_sel_mean_LD$mean_LD)
p2<- plot_selected(waasb_sel, GEN, LD, waasb_sel_mean_LD$mean_LD) + labs(y = "WAASB
  ↪ index")

arrange_ggplot(p1, p2,
  guides = "collect",
  tag_levels = "a",
  tag_prefix = "(",
  tag_suffix = ")")
```



Mean performance (a) and stability (b) for lodging (LD) of 29 navy beans genotypes. The vertical dashed and solid lines show, respectively, the mean of the selected genotype and the overall mean for both mean performance and WAASB index

5.5.3.5 Mean performance and stability for LD

5.6 Red beans

```
data_beans_SR <- droplevels(subset(data_beans_compl, mkt == "SR"))

data_beans_SR <- droplevels(na.omit(data_beans_SR))
#str(data_beans_SR)
```

5.6.1 Multi-trait index selection

```
waasb_model_sr.1 <- waasb(data_beans_SR,
  env = loc,
  gen = name,
  rep = rep,
  resp = everything(),
  random = "gen", #Default
  verbose = F,
  wresp = c(60, 40, 40, 40),
  mresp = c("h, l, h, l") ) #'GY', 'DM', 'PH', LD
```

```

#weight for response variable 60 and 40 for yielding and stability,
↪ respectively)

options(digits = 3)
mtsi1 = mtsi(waasb_model_sr.1, index = "waasby", SI = 20, mineval = 1, verbose = F)

mtsi1_resul<- mtsi1$sel_dif_trait

Sel_waasb <- sel_gen(mtsi1)

if (knitr::is_html_output()) {

  print_table(mtsi1_resul[,1:6])

}else{

mtsi1_resul[,1:6]
}

```

| VAR | Factor | Xo | Xs | SD | SDperc |
|-----------|-----------|---------|---------|---------|---------|
| character | character | numeric | numeric | numeric | numeric |
| PH | FA 1 | 18.3 | 20.1 | 1.8 | 10.0 |
| LD | FA 1 | 1.9 | 1.9 | 0.0 | 2.1 |
| GY | FA 2 | 3,155.9 | 3,161.8 | 5.9 | 0.2 |
| DM | FA 2 | 90.8 | 90.9 | 0.0 | 0.0 |

```
#print_table(mtsi1_resul[,1:6])
```

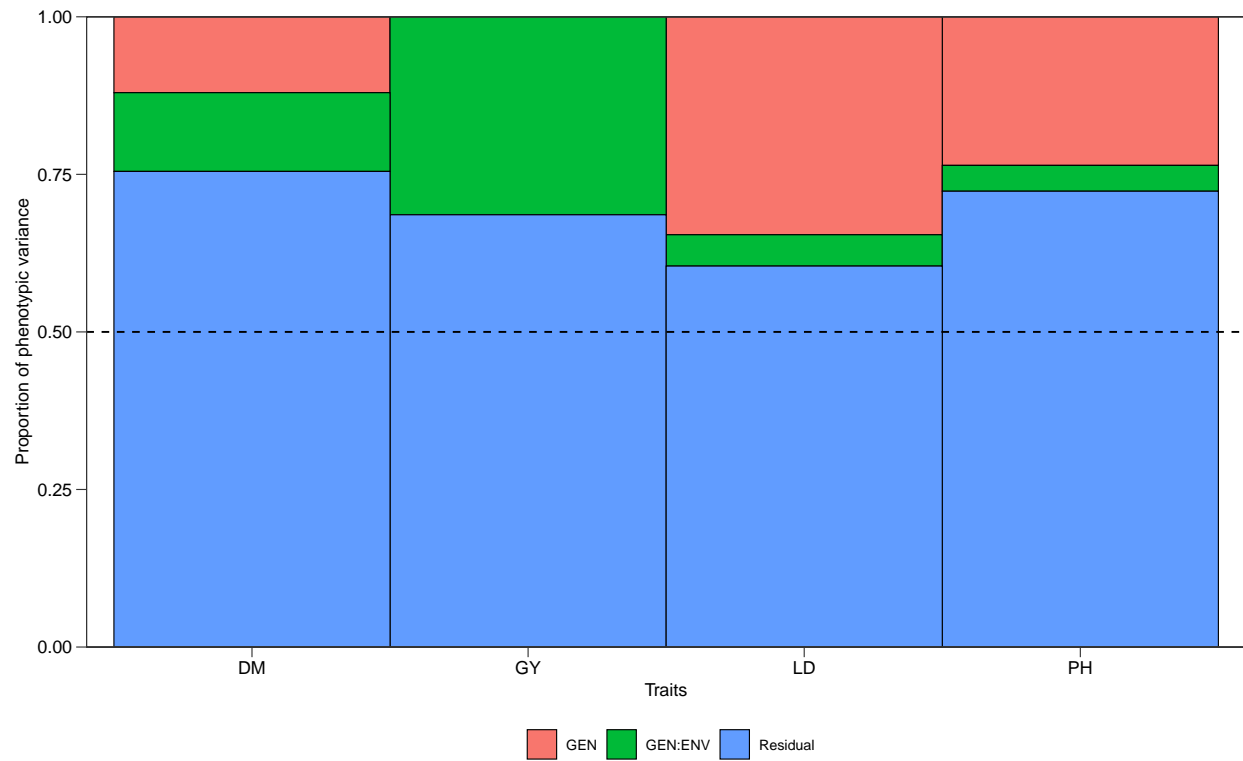
5.6.2 Model outputs

```

plot(waasb_model_sr.1,
type = "vcomp", # Chose the type of plot.
width.bar = 1, # No spaces between the bars
size.line = 0.3) + # Controls the size of the line
geom_hline(yintercept = 0.5, linetype = 2) # Add the dashed line

```

5.6.2.1 Variance plot



```
get_model_data(waasb_model_sr.1, "lrt")
```

5.6.2.2 Likelihood-ratio test

```
#> Class of the model: waasb
```

```
#> Variable extracted: lrt
```

| VAR | model | npar | logLik | AIC | LRT | Df | Pr(>Chisq) |
|-----------|-----------|---------|----------|---------|---------|---------|------------|
| character | character | integer | numeric | numeric | numeric | numeric | numeric |
| GY | GEN | 14 | -1,005.1 | 2,038.1 | -0.0 | 1 | 1.0 |
| GY | GEN:ENV | 14 | -1,011.2 | 2,050.3 | 12.2 | 1 | 0.0 |
| DM | GEN | 14 | -302.1 | 632.2 | 2.3 | 1 | 0.1 |
| DM | GEN:ENV | 14 | -302.3 | 632.5 | 2.6 | 1 | 0.1 |
| PH | GEN | 14 | -323.0 | 674.0 | 8.1 | 1 | 0.0 |
| PH | GEN:ENV | 14 | -319.1 | 666.2 | 0.4 | 1 | 0.5 |
| LD | GEN | 14 | -147.4 | 322.7 | 13.0 | 1 | 0.0 |
| LD | GEN:ENV | 14 | -141.3 | 310.5 | 0.8 | 1 | 0.4 |

```
get_model_data(waasb_model_sr.1, "vcomp")
```

5.6.2.3 Variance components

```
#> Class of the model: waasb
```

```
#> Variable extracted: vcomp
```

| Group | GY | DM | PH | LD |
|--------------|-----------|-----------|-----------|-----------|
| character | numeric | numeric | numeric | numeric |
| GEN | 0.0 | 0.6 | 1.7 | 0.2 |
| GEN:ENV | 75,950.2 | 0.6 | 0.3 | 0.0 |
| Residual | 165,821.6 | 3.8 | 5.1 | 0.3 |

```
get_model_data(waasb_model_sr.1, "genpar")
```

5.6.2.4 Genetic parameters

```
#> Class of the model: waasb
```

```
#> Variable extracted: genpar
```

| Parameters | GY | DM | PH | LD |
|-------------------------------|-----------|-----------|-----------|-----------|
| character | numeric | numeric | numeric | numeric |
| Phenotypic variance | 241,771.8 | 5.1 | 7.1 | 0.5 |
| Heritability | 0.0 | 0.1 | 0.2 | 0.3 |
| GEI _r ² | 0.3 | 0.1 | 0.0 | 0.0 |
| h ² _{mg} | 0.0 | 0.5 | 0.8 | 0.8 |
| Accuracy | 0.0 | 0.7 | 0.9 | 0.9 |
| r _{ge} | 0.3 | 0.1 | 0.1 | 0.1 |
| CV _g | 0.0 | 0.9 | 7.1 | 22.9 |
| CV _r | 12.9 | 2.1 | 12.4 | 30.2 |
| CV ratio | 0.0 | 0.4 | 0.6 | 0.8 |

```
get_model_data(waasb_model_sr.1, "details")
```

5.6.2.5 Models details

```
#> Class of the model: waasb
```

```
#> Variable extracted: details
```

| Parameters | GY | DM | PH | LD |
|------------|---------------------|---------------|-------------------|-----------------|
| character | character | character | character | character |
| Mean | 3157.34 | 90.86 | 18.23 | 1.87 |
| SE | 53.6 | 0.25 | 0.24 | 0.07 |
| SD | 638.78 | 2.95 | 2.8 | 0.85 |
| CV | 20.3 | 3.26 | 15.42 | 45.39 |
| Min | 1643.85 (R10 in BA) | 85 (R5 in BA) | 10 (R5 in SA) | 1 (R2 in BA) |
| Max | 4876.34 (R10 in TU) | 97 (R9 in TU) | 23.59 (R12 in TU) | 4.5 (R16 in TU) |
| MinENV | BA (2579) | BA (89.17) | BA (17.45) | BA (1.36) |
| MaxENV | TU (3546.13) | TU (93.51) | TU (19.59) | TU (2.24) |
| MinGEN | R15 (2875.55) | R13 (88.92) | R16 (15.71) | R12 (1.33) |
| n: 14 | | | | |

```
get_model_data(waasb_model_sr.1, "fixed")
```

5.6.2.6 Fixed effects

```
#> Class of the model: waasb
```

```
#> Variable extracted: fixed
```

| VAR | SOURCE | Sum Sq | Mean Sq | NumDF | DenDF | F value | Pr(>F) |
|-----------|-----------|-------------|-------------|---------|---------|---------|---------|
| character | character | numeric | numeric | integer | numeric | numeric | numeric |
| GY | ENV | 3,444,789.9 | 1,722,394.9 | 2 | 101.3 | 10.4 | 0.0 |
| GY | ENV:REP | 2,181,509.9 | 242,390.0 | 9 | 98.2 | 1.5 | 0.2 |
| DM | ENV | 174.4 | 87.2 | 2 | 99.8 | 22.9 | 0.0 |

| VAR | SOURCE | Sum Sq | Mean Sq | NumDF | DenDF | F value | Pr(>F) |
|-----------|-----------|---------|---------|---------|---------|---------|---------|
| character | character | numeric | numeric | integer | numeric | numeric | numeric |
| DM | ENV:REP | 68.4 | 7.6 | 9 | 98.5 | 2.0 | 0.0 |
| PH | ENV | 26.0 | 13.0 | 2 | 111.3 | 2.5 | 0.1 |
| PH | ENV:REP | 61.0 | 6.8 | 9 | 97.9 | 1.3 | 0.2 |
| LD | ENV | 2.5 | 1.2 | 2 | 108.6 | 3.9 | 0.0 |
| LD | ENV:REP | 13.4 | 1.5 | 9 | 98.4 | 4.6 | 0.0 |

```
get_model_data(waasb_model_sr.1, "blupge") %>%
  means_by(ENV)
```

5.6.2.7 Enviroment means

```
#> Class of the model: waasb
```

```
#> Variable extracted: blupge
```

| ENV | GY | DM | PH | LD |
|--------|---------|---------|---------|---------|
| factor | numeric | numeric | numeric | numeric |
| BA | 2,583.6 | 89.2 | 17.5 | 1.4 |
| SA | 3,334.8 | 89.9 | 17.6 | 2.0 |
| TU | 3,546.1 | 93.5 | 19.6 | 2.2 |

5.6.3 Selection Description

5.6.3.1 Genotype ranking

- Varieties ranking based on the multi-trait stability index. Selected varieties are highlighted in red.

```
# Get the random effects
#get_model_data(waasb_model_sr.1, what = "ranef")

mtsi1_value<- mtsi1$MTSI

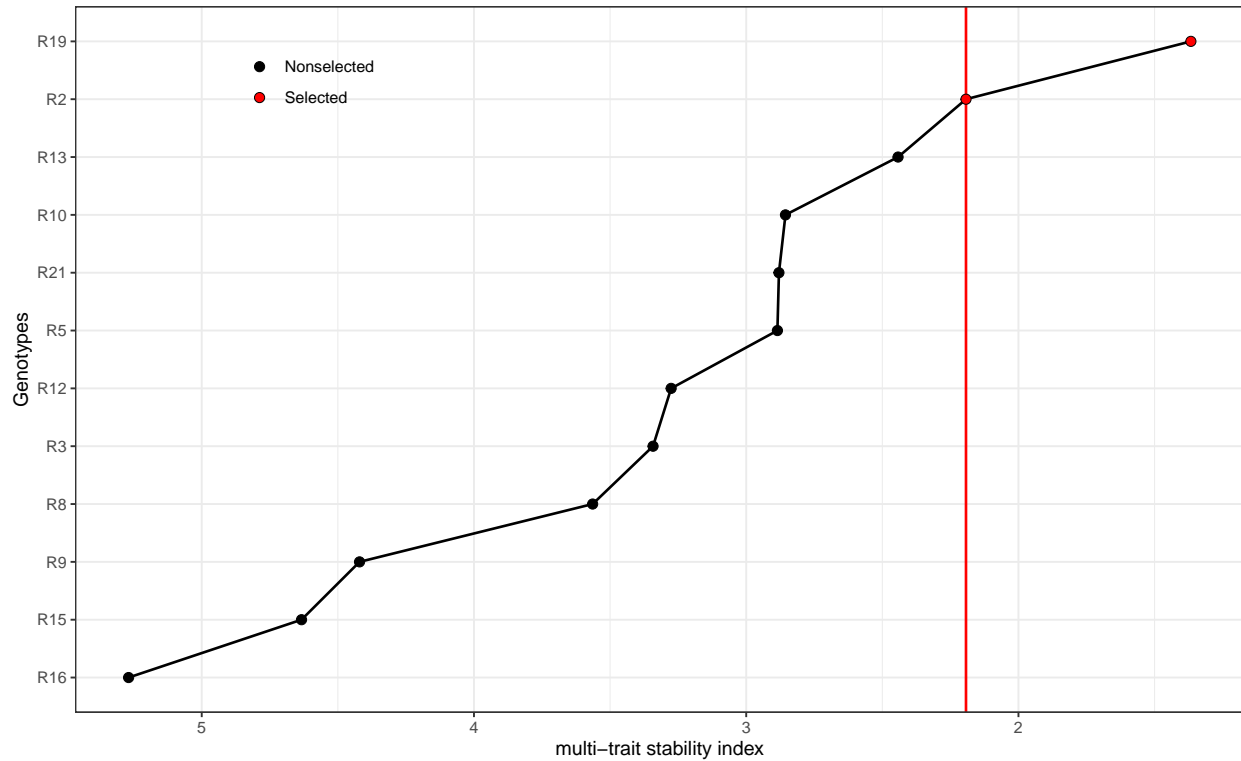
#plot(mtsi1, arrange.label = TRUE)

p2 = plot(mtsi1, SI = 20, radar = FALSE) +
  coord_flip() +
  theme_bw() +
  labs(x = "Genotypes", y = "multi-trait stability index") +
  theme(legend.position = c(0.2, 0.9),
```

```

legend.background = element_blank(),
legend.key = element_blank(),
legend.title = element_blank()
print(p2)

```



Cultivars ranking based on the multi-trait stability index. Selected cultivars are highlighted in red.

```
Sel_waasb
```

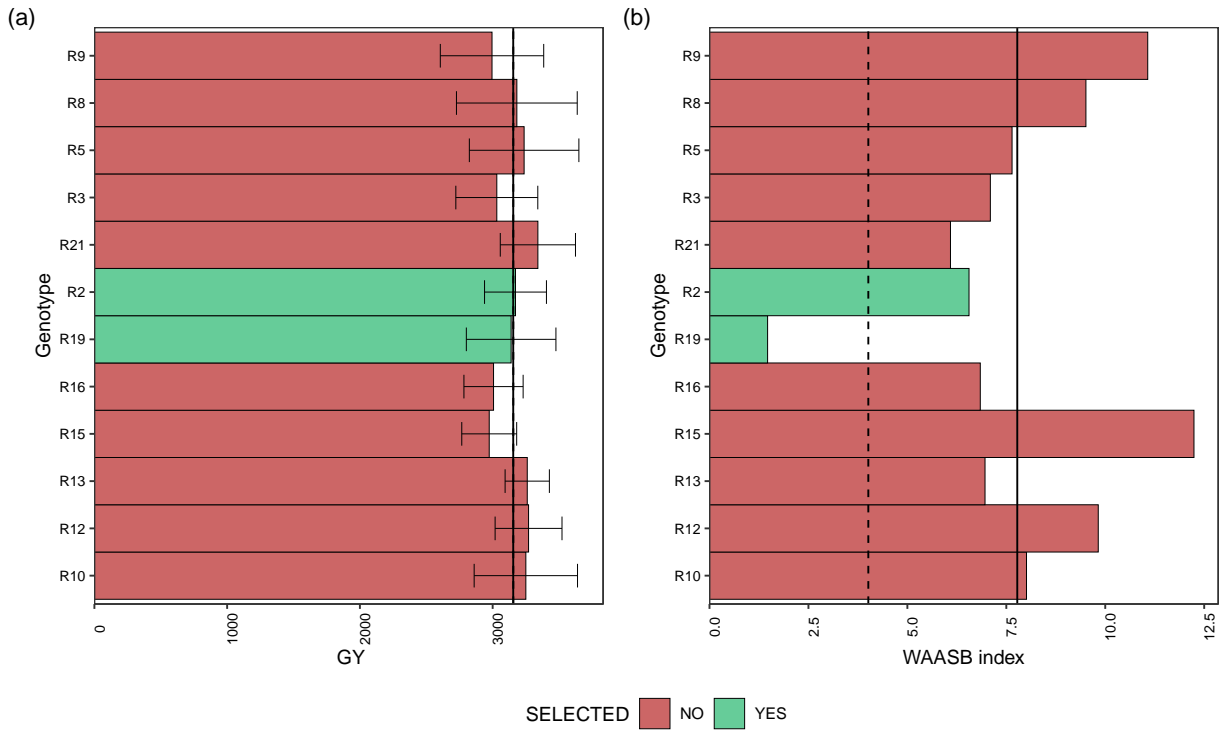
```
#> [1] "R19" "R2"
```

```

p1<- plot_selected(blups_sel, GEN, GY, blups_sel_mean_GY$mean_GY)
p2<- plot_selected(waasb_sel, GEN, GY, waasb_sel_mean_GY$mean_GY) + labs(y = "WAASB
  ↪ index")

arrange_ggplot(p1, p2,
  guides = "collect",
  tag_levels = "a",
  tag_prefix = "(",
  tag_suffix = ")")

```

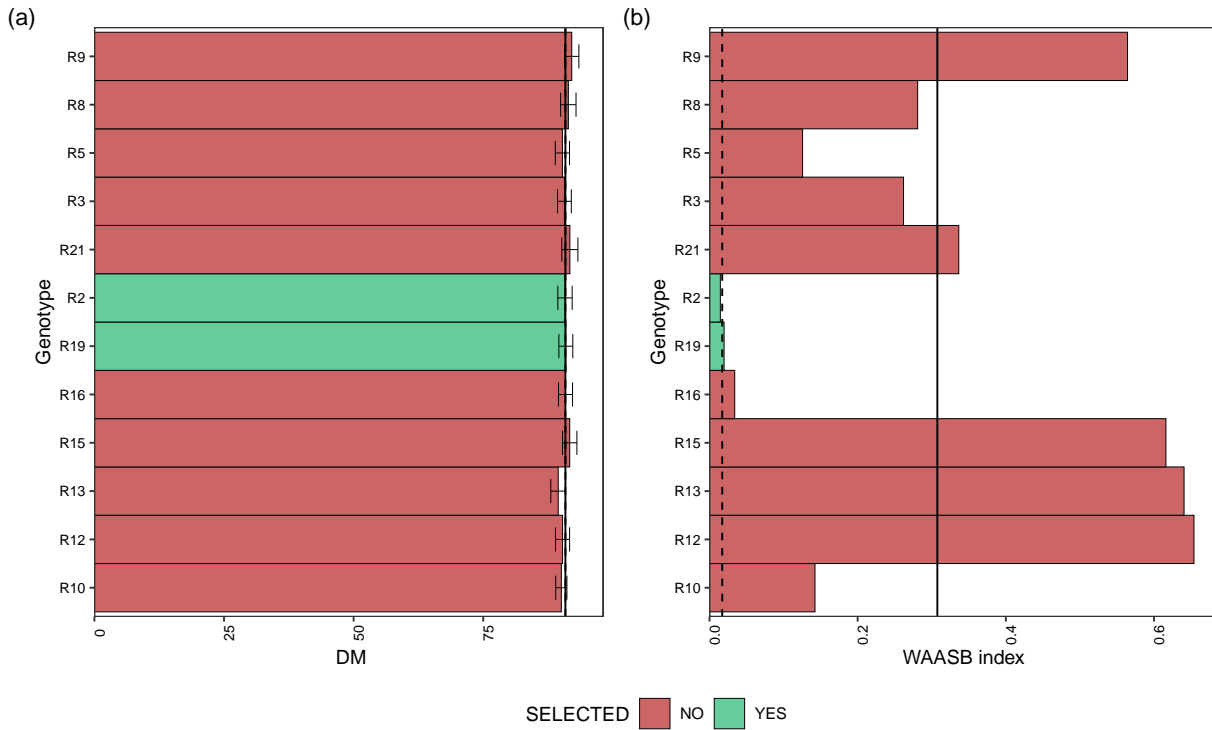



Mean performance (a) and stability (b) for grain yield (GY) of 12 red beans genotypes. The vertical dashed and solid lines shows, respectively, the mean of the selected genotype and the overall mean for both mean performance and WAASB index

5.6.3.2 Mean performance and stability for GY

```
p1<- plot_selected(blups_sel, GEN, DM, blups_sel_mean_DM$mean_DM)
p2<- plot_selected(waasb_sel, GEN, DM, waasb_sel_mean_DM$mean_DM) + labs(y = "WAASB
  ↪ index")

arrange_ggplot(p1, p2,
  guides = "collect",
  tag_levels = "a",
  tag_prefix = "(",
  tag_suffix = ")")
```

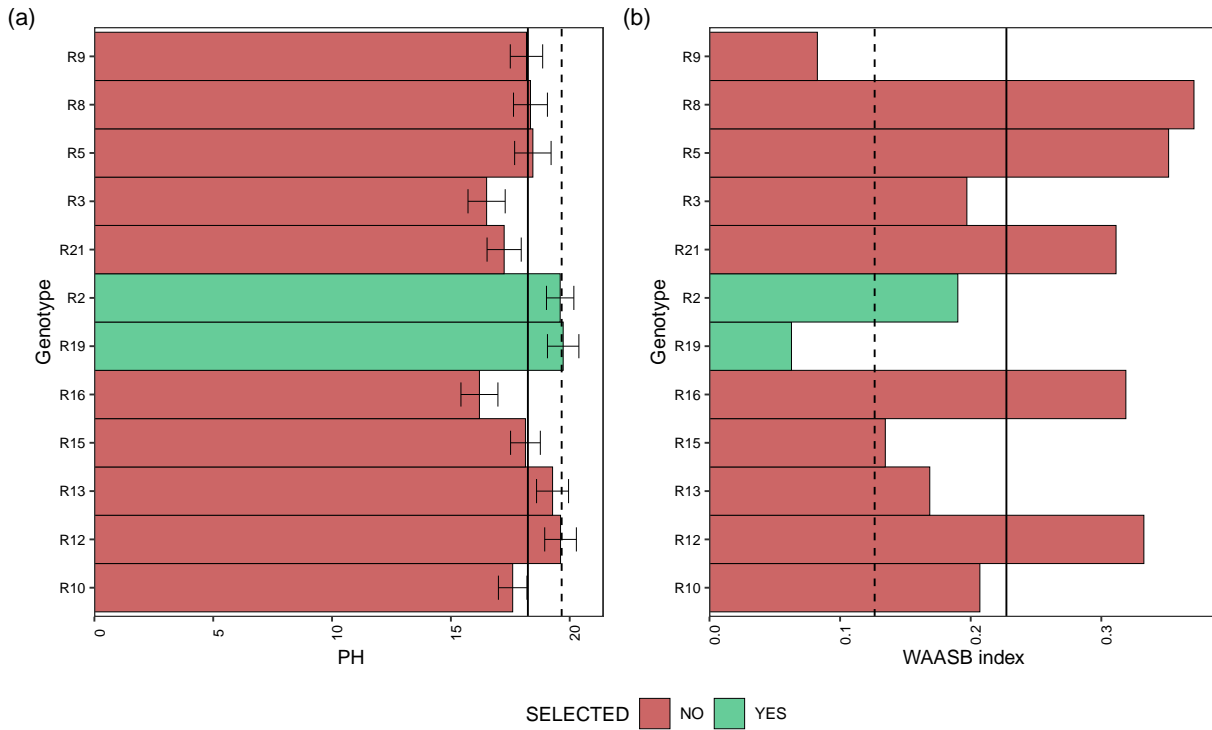


Mean performance (a) and stability (b) for days of maturity (DM) of 12 red beans genotypes. The vertical dashed and solid lines shows, respectively, the mean of the selected genotype and the overall mean for both mean performance and WAASB index

5.6.3.3 Mean performance and stability for DM

```
p1<- plot_selected(blups_sel, GEN, PH, blups_sel_mean_PH$mean_PH)
p2<- plot_selected(waasb_sel, GEN, PH, waasb_sel_mean_PH$mean_PH) + labs(y = "WAASB
  ↪ index")

arrange_ggplot(p1, p2,
  guides = "collect",
  tag_levels = "a",
  tag_prefix = "(",
  tag_suffix = ")")
```

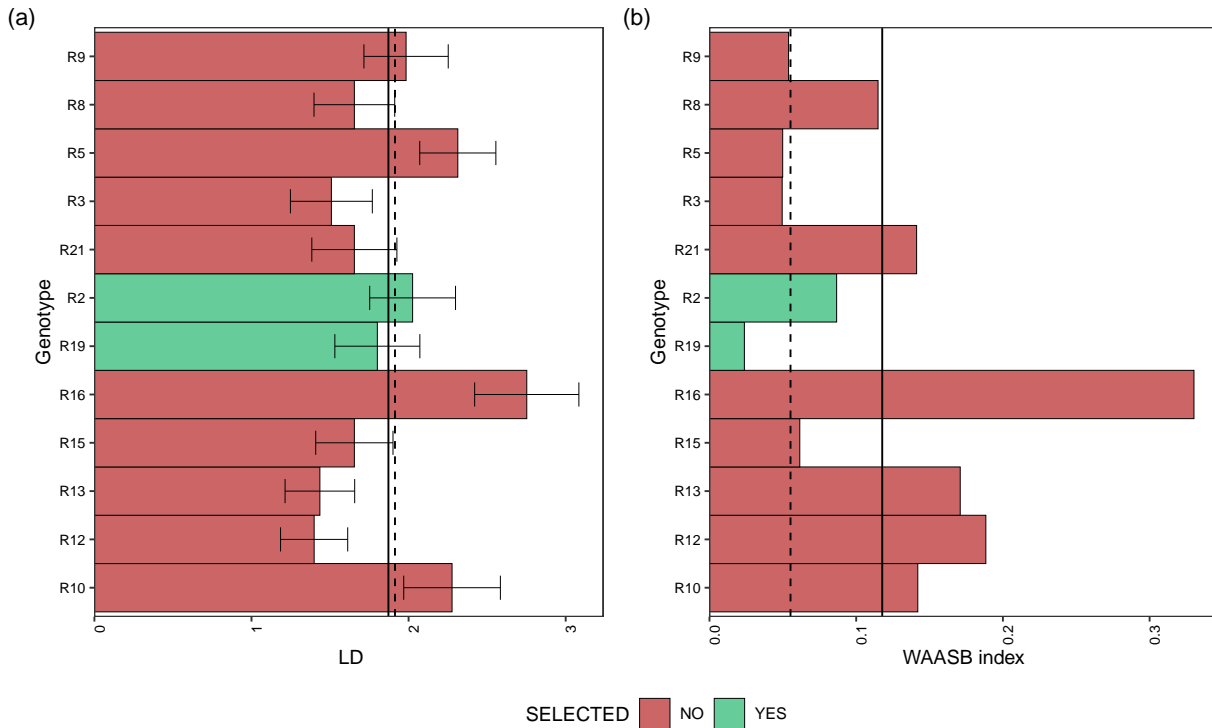


Mean performance (a) and stability (b) for plant height (PH) of 12 red beans genotypes. The vertical dashed and solid lines shows, respectively, the mean of the selected genotype and the overall mean for both mean performance and WAASB index

5.6.3.4 Mean performance and stability for PH

```
p1<- plot_selected(blups_sel, GEN, LD, blups_sel_mean_LD$mean_LD)
p2<- plot_selected(waasb_sel, GEN, LD, waasb_sel_mean_LD$mean_LD) + labs(y = "WAASB
  ↪ index")

arrange_ggplot(p1, p2,
  guides = "collect",
  tag_levels = "a",
  tag_prefix = "(",
  tag_suffix = ")")
```



Mean performance (a) and stability (b) for lodging (LD) of 12 red beans genotypes. The vertical dashed and solid lines shows, respectively, the mean of the selected genotype and the overall mean for both mean performance and WAASB index

5.6.3.5 Mean performance and stability for LD

5.7 MTME mixed model

5.7.1 Black beans

```
data_beans_BB <- droplevels(data_beans_compl[which(data_beans_compl$mkt=="BB")])
#TU
data_beans_BB.sc.TU <- droplevels(subset(data_beans_BB, loc=="TU"))
data_beans_BB.sc.TU <- scale(data_beans_BB.sc.TU[,5:8])
#dim(data_beans_BB.sc.TU)
#BA
data_beans_BB.sc.BA <- droplevels(subset(data_beans_BB, loc=="BA"))
data_beans_BB.sc.BA <- scale(data_beans_BB.sc.BA[,5:8])

#SA
data_beans_BB.sc.SA <- droplevels(subset(data_beans_BB, loc=="SA"))
data_beans_BB.sc.SA <- scale(data_beans_BB.sc.SA[,5:8])

#data_beans_BB.sc<- scale(data_beans_BB[,5:6])
data_beans_BB<- data_beans_BB %>%
  dplyr::select(name, loc, mkt,rep)
```

```

data_beans_BB.sc<- rbind(data_beans_BB.sc.BA,data_beans_BB.sc.SA, data_beans_BB.sc.TU)

#dim(data_beans_BB)
#dim(data_beans_BB.sc)

data_beans_BB<- cbind(data_beans_BB, data_beans_BB.sc)
#str(data_beans_BB)

#dim(data_beans_BB)

mod_MTME.bb <- asreml(fixed = cbind(GY, DM, PH, LD) ~ trait:rep + trait, # trait:rep -1,
  random = ~ us(trait):name + us(trait):name:loc, #name:us(loc)
  #residuals = ~dsum(~us(name)/loc),
  residuals = ~ units:us(trait),
  data = data_beans_BB,
  trace = F,
  maxit = 10000,
  predict = predict.asreml(classify = "name:loc:trait") )

#update.asreml(mod_MTME.bb)
d1<- data.frame(wald(mod_MTME.bb))

d2<- data.frame(summary.asreml(mod_MTME.bb)$varcomp)

# results as data.table
blup.mtme.bb<- data.table((mod_MTME.bb$predictions$pvals[1:6])) # set the BLUP

# d1
#
#           Df Sum.of.Sq Wald.statistic Pr.Chisq.
# trait           4      0.323           0.323 9.88e-01
# trait:rep       12     55.248          55.248 1.63e-07
# residual (MS) NA      1.000             NA      NA

# d2
#
#           component std.error z.ratio bound X.ch
# trait:name!trait_GY:GY      0.25787      0.0798 3.2327 P 0.0
# trait:name!trait_DM:GY      0.11359      0.0692 1.6409 P 0.0
# trait:name!trait_DM:DM      0.36827      0.1091 3.3752 P 0.0
# trait:name!trait_PH:GY      0.08661      0.0496 1.7466 P 0.0
# trait:name!trait_PH:DM      0.09752      0.0570 1.7104 P 0.0
# trait:name!trait_PH:PH      0.11734      0.0545 2.1547 P 0.0
# trait:name!trait_LD:GY     -0.07238      0.0585 -1.2380 P 0.0
# trait:name!trait_LD:DM      0.05215      0.0652 0.7996 P 0.0
# trait:name!trait_LD:PH      0.01736      0.0451 0.3845 P 0.0
# trait:name!trait_LD:LD      0.15495      0.0707 2.1911 P 0.0
# trait:name:loc!trait_GY:GY      0.07426           NA      NA B 0.0
# trait:name:loc!trait_DM:GY     -0.00742           NA      NA B 0.0
# trait:name:loc!trait_DM:DM      0.07241           NA      NA B 0.0
# trait:name:loc!trait_PH:GY     -0.01275           NA      NA B 0.0

```

```

# trait:name:loc!trait_PH:DM 0.00149 NA NA B 0.0
# trait:name:loc!trait_PH:PH 0.06344 NA NA B 0.0
# trait:name:loc!trait_LD:GY 0.04234 NA NA B 0.0
# trait:name:loc!trait_LD:DM -0.00585 NA NA B 0.0
# trait:name:loc!trait_LD:PH -0.01030 NA NA B 0.0
# trait:name:loc!trait_LD:LD 0.09790 NA NA B 0.0
# units:trait!R 1.00000 NA NA F 0.0
# units:trait!trait_GY:GY 0.66440 0.0488 13.6191 P 0.0
# units:trait!trait_DM:GY 0.09813 0.0354 2.7707 P 0.0
# units:trait!trait_DM:DM 0.53533 0.0443 12.0755 P 0.0
# units:trait!trait_PH:GY 0.14825 0.0430 3.4472 P 0.0
# units:trait!trait_PH:DM 0.02495 0.0380 0.6564 P 0.0
# units:trait!trait_PH:PH 0.80001 0.0651 12.2932 P 0.0
# units:trait!trait_LD:GY 0.04123 0.0465 0.8857 P 0.0
# units:trait!trait_LD:DM 0.11857 0.0416 2.8483 P 0.0
# units:trait!trait_LD:PH 0.00104 0.0485 0.0214 P 0.2
# units:trait!trait_LD:LD 0.78932 0.0686 11.5024 P 0.0

```

5.7.2 Navy beans

```

data_beans_NB <- droplevels(data_beans_compl[which(data_beans_compl$mkt=="NB")])
#data_beans_NB <- na.omit(data_beans_NB)
#str(data_beans_NB)
#TU
data_beans_NB.sc.TU <- droplevels(subset(data_beans_NB, loc=="TU"))
data_beans_NB.sc.TU <-scale(data_beans_NB.sc.TU[,5:8])
#dim(data_beans_NB.sc.TU)
#BA
data_beans_NB.sc.BA <- droplevels(subset(data_beans_NB, loc=="BA"))
data_beans_NB.sc.BA <-scale(data_beans_NB.sc.BA[,5:8])

#SA
data_beans_NB.sc.SA <- droplevels(subset(data_beans_NB, loc=="SA"))
data_beans_NB.sc.SA <-scale(data_beans_NB.sc.SA[,5:8])

#data_beans_NB.sc<- scale(data_beans_NB[,5:6])
data_beans_NB<- data_beans_NB %>%
  dplyr::select(name, loc, mkt,rep)

data_beans_NB.sc<- rbind(data_beans_NB.sc.BA,data_beans_NB.sc.SA, data_beans_NB.sc.TU)

#dim(data_beans_NB)
#dim(data_beans_NB.sc)

data_beans_NB<- cbind(data_beans_NB, data_beans_NB.sc)
#str(data_beans_NB)

#data_beans_NB <- na.omit(data_beans_NB)

mod_MTME.nb <- asreml(fixed = cbind(GY, DM, PH, LD) ~ trait:rep + trait, # trait:rep -1,
  random = ~ us(trait):name + us(trait):name:loc, #name:us(loc)

```

```

#residuals = ~dsum(~us(name)/loc),
residuals = ~ units:us(trait),
data = data_beans_NB,
trace = F,
maxit = 10000,
predict = predict.asreml(classify = "name:loc:trait") )
#update.asreml(mod_MTME.nb)
#update.asreml(mod_MTME)
d1<- data.frame(wald(mod_MTME.nb))

d2<-data.frame(summary.asreml(mod_MTME.nb)$varcomp)

# results as data.table
blup.mtme.nb<- data.table((mod_MTME.nb$predictions$pvals[1:6])) # set the BLUP

# d1
#           Df Sum.of.Sq Wald.statistic Pr.Chisq.
# trait      4    0.663          0.663 9.56e-01
# trait:rep  12   63.914          63.914 4.33e-09
# residual (MS) NA    1.000             NA      NA
#
# d2
#           component std.error z.ratio bound X.ch
# trait:name!trait_GY:GY    0.28345    0.0865    3.278    P    0
# trait:name!trait_DM:GY    0.18415    0.0733    2.514    P    0
# trait:name!trait_DM:DM    0.33087    0.1036    3.195    P    0
# trait:name!trait_PH:GY    0.12097    0.0620    1.951    P    0
# trait:name!trait_PH:DM    0.06994    0.0646    1.083    P    0
# trait:name!trait_PH:PH    0.22001    0.0765    2.875    P    0
# trait:name!trait_LD:GY    0.15304    0.0820    1.867    P    0
# trait:name!trait_LD:DM    0.23406    0.0922    2.539    P    0
# trait:name!trait_LD:PH   -0.06152    0.0715   -0.860    P    0
# trait:name!trait_LD:LD    0.42545    0.1305    3.261    P    0
# trait:name:loc!trait_GY:GY  0.08495    0.0408    2.081    P    0
# trait:name:loc!trait_DM:GY -0.00607    0.0315   -0.192    P    0
# trait:name:loc!trait_DM:DM  0.09322    0.0442    2.107    P    0
# trait:name:loc!trait_PH:GY -0.01022    0.0325   -0.315    P    0
# trait:name:loc!trait_PH:DM  0.04445    0.0323    1.376    P    0
# trait:name:loc!trait_PH:PH  0.05325    0.0464    1.148    P    0
# trait:name:loc!trait_LD:GY -0.01023    0.0285   -0.359    P    0
# trait:name:loc!trait_LD:DM -0.03865    0.0282   -1.372    P    0
# trait:name:loc!trait_LD:PH -0.00769    0.0288   -0.267    P    0
# trait:name:loc!trait_LD:LD  0.03354    0.0351    0.956    P    0
# units:trait!R             1.00000         NA      NA    F    0
# units:trait!trait_GY:GY    0.61060    0.0475   12.845    P    0
# units:trait!trait_DM:GY   -0.03874    0.0355   -1.093    P    0
# units:trait!trait_DM:DM    0.54619    0.0461   11.851    P    0
# units:trait!trait_PH:GY    0.12173    0.0416    2.928    P    0
# units:trait!trait_PH:DM   -0.02890    0.0380   -0.760    P    0
# units:trait!trait_PH:PH    0.73727    0.0625   11.803    P    0
# units:trait!trait_LD:GY    0.01485    0.0377    0.393    P    0
# units:trait!trait_LD:DM    0.04894    0.0351    1.396    P    0

```

```
# units:trait!trait_LD:PH      -0.04851    0.0408  -1.190    P    0
# units:trait!trait_LD:LD      0.57031    0.0503  11.330    P    0
```

5.7.3 Red beans

```
## MTME mixed model Small Red - Pink Beans
# This model is not working! Too many missing genotypes and few genotypes available for
#  → thos market class.

data_beans_SR <- droplevels(data_beans_compl[which(data_beans_compl$mkt=="SR")])

#data_beans_SR <- na.omit(data_beans_SR)

#dim(data_beans_SR)
#TU
data_beans_SR.sc.TU <- droplevels(subset(data_beans_SR, loc=="TU"))
data_beans_SR.sc.TU <-scale(data_beans_SR.sc.TU[,5:8])
#dim(data_beans_SR.sc.TU)
#BA
data_beans_SR.sc.BA <- droplevels(subset(data_beans_SR, loc=="BA"))
data_beans_SR.sc.BA <-scale(data_beans_SR.sc.BA[,5:8])

#SA
data_beans_SR.sc.SA <- droplevels(subset(data_beans_SR, loc=="SA"))
data_beans_SR.sc.SA <-scale(data_beans_SR.sc.SA[,5:8])

#data_beans_SR.sc<- scale(data_beans_SR[,5:6])
data_beans_SR<- data_beans_SR %>%
  dplyr::select(name, loc, mkt,rep)
#dim(data_beans_SR)
data_beans_SR.sc<- rbind(data_beans_SR.sc.BA,data_beans_SR.sc.SA, data_beans_SR.sc.TU)

#dim(data_beans_SR)
#dim(data_beans_SR.sc)

data_beans_SR<- cbind(data_beans_SR, data_beans_SR.sc)
#str(data_beans_SR)

mod_MTME.sr <- asreml(fixed = cbind(GY, DM, PH, LD) ~ trait:rep + trait, # trait:rep -1,
  random = ~ us(trait):name + us(trait):name:loc, #name:us(loc)
  #residuals = ~dsum(~us(name)|loc),
  residuals = ~ units:us(trait),
  data = data_beans_SR,
  trace = F,
  maxit = 10000,
  predict = predict.asreml(classify = "name:loc:trait") )

#update.asreml(mod_MTME.sr)
d1<- data.frame(wald(mod_MTME.sr))

#
```



```
d2<- data.frame(summary.asreml(mod_MTME.sr)$varcomp)

# d1
#           Df Sum.of.Sq Wald.statistic Pr.Chisq.
# trait      4    0.0747         0.0747 9.99e-01
# trait:rep  12   58.7787         58.7787 3.77e-08
# residual (MS) NA    1.0000             NA      NA

# d2
#           component std.error z.ratio bound X.ch
# trait:name!trait_GY:GY    0.014673      NA      NA    B 0.0
# trait:name!trait_DM:GY    0.002083      NA      NA    B 0.0
# trait:name!trait_DM:DM    0.000615      NA      NA    B 0.0
# trait:name!trait_PH:GY    0.007643      NA      NA    B 0.0
# trait:name!trait_PH:DM    0.007450      NA      NA    B 0.0
# trait:name!trait_PH:PH    0.003715      NA      NA    B 0.0
# trait:name!trait_LD:GY   -0.020386      NA      NA    B 0.0
# trait:name!trait_LD:DM    0.015287      NA      NA    B 0.0
# trait:name!trait_LD:PH   -0.009582      NA      NA    B 0.0
# trait:name!trait_LD:LD    0.032827      NA      NA    B 0.0
# trait:name:loc!trait_GY:GY 0.257368      NA      NA    B 0.0
# trait:name:loc!trait_DM:GY -0.140886      NA      NA    B 0.0
# trait:name:loc!trait_DM:DM 0.427960      NA      NA    B 0.0
# trait:name:loc!trait_PH:GY -0.094343      NA      NA    B 0.0
# trait:name:loc!trait_PH:DM -0.293548      NA      NA    B 0.0
# trait:name:loc!trait_PH:PH 0.490821      NA      NA    B 0.0
# trait:name:loc!trait_LD:GY 0.257104      NA      NA    B 0.0
# trait:name:loc!trait_LD:DM -0.198700      NA      NA    B 0.0
# trait:name:loc!trait_LD:PH -0.051090      NA      NA    B 0.0
# trait:name:loc!trait_LD:LD 0.320474      NA      NA    B 0.0
# units:trait!R            1.000000      NA      NA    F 0.0
# units:trait!trait_GY:GY   0.754348    0.0923    8.173    P 0.0
# units:trait!trait_DM:GY   0.162496    0.0719    2.259    P 0.0
# units:trait!trait_DM:DM   0.792539    0.1027    7.714    P 0.0
# units:trait!trait_PH:GY   0.311365    0.0741    4.204    P 0.0
# units:trait!trait_PH:DM   0.046331    0.0705    0.657    P 0.0
# units:trait!trait_PH:PH   0.757329    0.1005    7.538    P 0.0
# units:trait!trait_LD:GY   -0.025897    0.0648   -0.400    P 0.1
# units:trait!trait_LD:DM   0.108011    0.0672    1.608    P 0.0
# units:trait!trait_LD:PH   -0.017539    0.0661   -0.265    P 0.0
# units:trait!trait_LD:LD   0.634711    0.0852    7.451    P 0.0
```

5.8 MTME Var Comp and corr

- Variance Component and correlations analysis

```
# Black
#traits
a=summary(mod_MTME.bb)$varcomp[1:10,1]

z=matrix(0, 4,4)
```

```

z[upper.tri(z)| row(z)==col(z)] <- a
cora=z/sqrt(diag(z)%*%t(diag(z)))
#cora

#int traits - locations
b=summary(mod_MTME.bb)$varcomp[11:20,1]

z=matrix(0, 4,4)
z[upper.tri(z)| row(z)==col(z)] <- b
corb=z/sqrt(diag(z)%*%t(diag(z)))
#corb

# Navys
#traits
c=summary(mod_MTME.nb)$varcomp[1:10,1]

z=matrix(0, 4,4)
z[upper.tri(z)| row(z)==col(z)] <- c
corc=z/sqrt(diag(z)%*%t(diag(z)))
#corc

#int traits - locations
d=summary(mod_MTME.nb)$varcomp[11:20,1]

z=matrix(0, 4,4)
z[upper.tri(z)| row(z)==col(z)] <- d
cord=z/sqrt(diag(z)%*%t(diag(z)))
#cord

corr=as.matrix(bdiag(cora,corb, corc, cord))

rownames(corr)=c(
  "BB_GY",
  "BB_DM",
  "BB_PH",
  "BB_LD",
  "BB_Loc-GY",
  "BB_Loc-DM",
  "BB_Loc-PH",
  "BB_Loc-LD",
  "NB_GY",
  "NB_DM",
  "NB_PH",
  "NB_LD",
  "NB_Loc-GY",
  "NB_Loc-DM",
  "NB_Loc-PH",
  "NB_Loc-LD")

colnames(corr)=rownames(corr)

corr1<- as_tibble(corr)

```

```

corr1<- corr1 %>%
  tidyr::pivot_longer(
    cols = everything(),
    names_to = "var",
    values_to = "corr")

corr1<-corr1 %>%
  dplyr::filter(corr != 0) %>%
  dplyr::filter(corr != 1)

names=c(
  "G GY-DM_BB",
  "G GY-PH_BB",
  "G GY-LD_BB",
  "G PH-DM_BB",
  "G DM-LD_BB",
  "G PH-LD_BB",
  "GxE GY-DM_BB",
  "GxE GY-PH_BB",
  "GxE GY-LD_BB",
  "GxE PH-DM_BB",
  "GxE DM-LD_BB",
  "GxE PH-LD_BB",

  "G GY-DM_NB",
  "G GY-PH_NB",
  "G GY-LD_NB",
  "G PH-DM_NB",
  "G DM-LD_NB",
  "G PH-LD_NB",
  "GxE GY-DM_NB",
  "GxE GY-PH_NB",
  "GxE GY-LD_NB",
  "GxE PH-DM_NB",
  "GxE DM-LD_NB",
  "GxE PH-LD_NB"

)

names2=c(
  "GY-DM",
  "GY-PH",
  "GY-LD",
  "PH-DM",
  "DM-LD",
  "PH-LD",

  "GY-DM",
  "GY-PH",
  "GY-LD",
  "PH-DM",
  "DM-LD",
  "PH-LD",

```

```

"GY-DM",
"GY-PH",
"GY-LD",
"PH-DM",
"DM-LD",
"PH-LD",

"GY-DM",
"GY-PH",
"GY-LD",
"PH-DM",
"DM-LD",
"PH-LD"
)

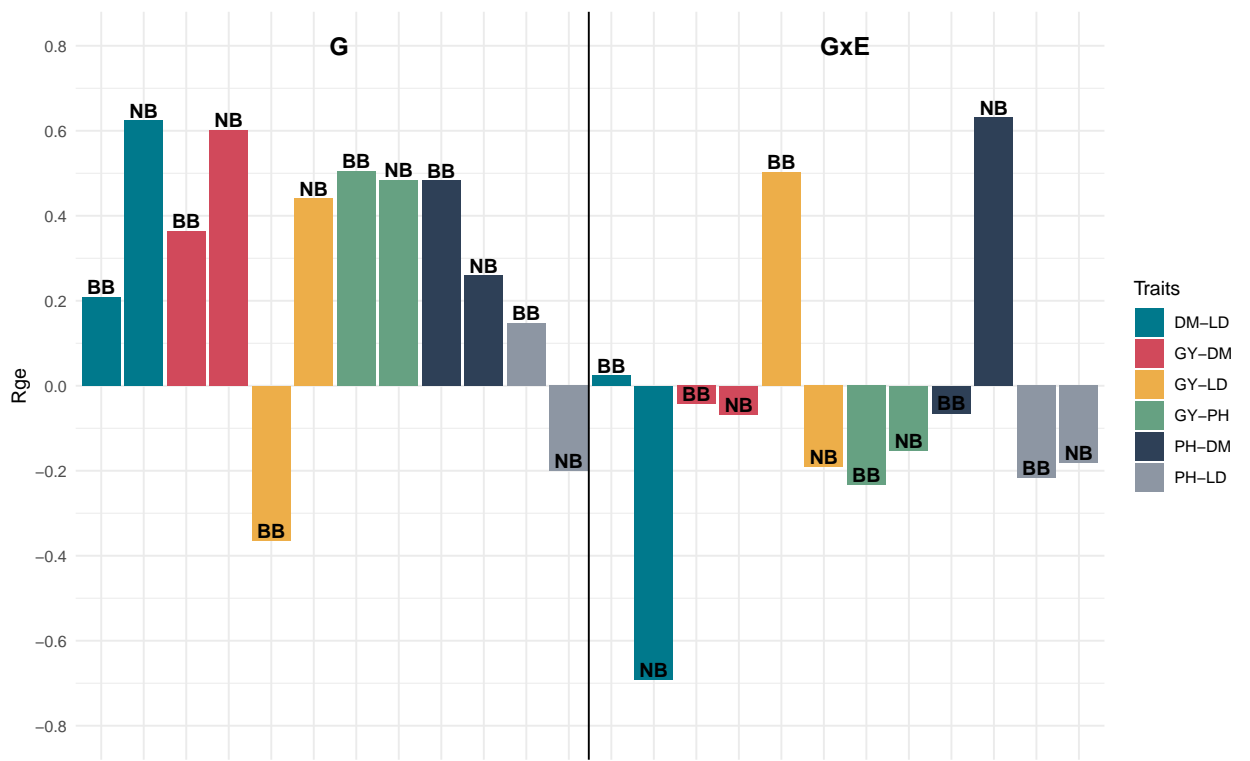
corr1$names<-names
corr1$names2<-names2

# Create new_id using dplyr only
corr1 <- corr1 %>%
  mutate(mkt = str_split(names, "_", simplify = TRUE)[ , 2])

#str(corr1)
branded_colors <- c("#00798c", "#d1495b", "#edae49",
                    "#66a182", "#2e4057", "#8d96a3")

ggplot(data=corr1, aes(x=names, y=corr, fill = names2)) +
  geom_bar(stat="identity", position=position_dodge())+
  geom_text(aes(label=mkt), vjust=-0.2, color="black",
            position = position_dodge(width = 1), size=4, fontface="bold")+
  scale_fill_brewer(palette="Paired")+
  theme_minimal() +
  theme(axis.text.x=element_blank(),
        strip.text=element_text(face="bold")) +
  scale_fill_manual(values=branded_colors) +
  labs(caption=NULL, x=NULL, y="Rge", fill = 'Traits') +
  scale_y_continuous(limits=c(-0.8, 0.8), n.breaks = 10) +
  geom_vline(xintercept = 12.47) +
  annotate(geom="text", x=6.6, y=0.8, label="G",size=5, fontface="bold",
          color="black") +
  annotate(geom="text", x=18.5, y=0.8, label="GxE",size=5, fontface="bold",
          color="black")

```



```
cat("\n\n\\pagebreak\n")
```

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