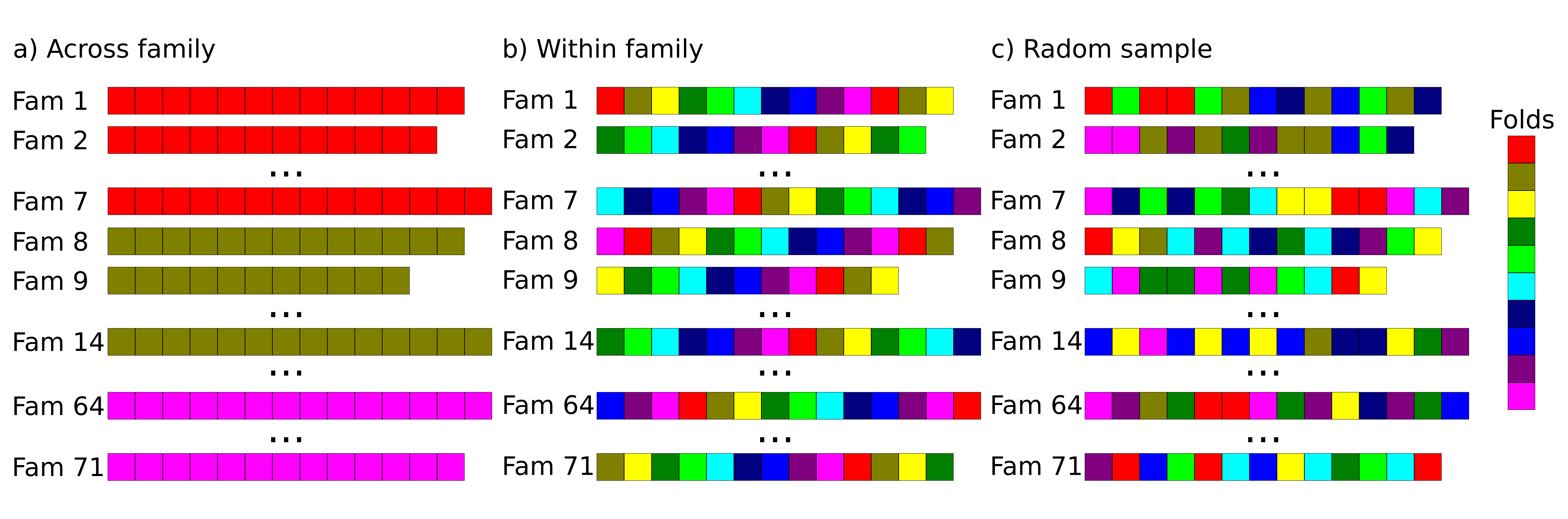
**Supplemental Figure S1 and Tables S1-10 for Almeida Filho et al., 2019**

****

**Figure S1.** General scheme for the three different 10-fold cross validations: a) Across families: Each fold is a group of distinct families; b) Within families: The folds contained groups from each family; and c) Random sample: Each fold is a group of distinct individuals randomly sampled ignoring family information. Each square is a representation of an individual and each row a full-sib family (Fam).

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **TABLE S1. Analysis of variance of linear model used to adjust the clonal means.** | | | | |
| Source | DBH (cm) | HT (cm) | RFbin (Binary) | RFgall (mm3) |
| Incomplete Block Variance | 0.24\*\* | 2448\*\* | - | - |
| F for Repetition | 184.87\*\* | 397.35\*\* | 3.2795\* | 20.7005\*\* |
| F for Clones | 2.41\*\* | 2.18\*\* | 3.851\*\* | 2.5576\*\* |
| Error Variance | 3.05 | 7575.11 | 0.1342 | 1.866 |
| Mean | 11.40 | 841.59 | 0.3531 | 0.8261 |
| CV(%) | 15.33 | 10.34 | 103.78 | 165.37 |
| R2(%) | 63.84 | 81.41 | 55.72 | 46.43 |
| \*\*,\*: means significant with p<0.01 and p<0.05 respectively, with F test for fixed effect and LRT for variance components. | | | | |

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **TABLE S2** Summary of models tested, where ‘X’ represent the presence of a given effect in the model. | | | | | | | | | | |
| Model code | | | SNP covariates | |  | Pedigree Kernels | |  | Gaussian Kernels | |
| Method | Pedigree  inclusion | id | Add | Dom |  | Add | Dom |  | Ka | Kd |
| BayesA  Add | None | 1 | X |  |  |  |  |  |  |  |
| Add | 2 | X |  |  | X |  |  |  |  |
| BayesA  Add-Dom | None | 3 | X | X |  |  |  |  |  |  |
| Add | 4 | X | X |  | X |  |  |  |  |
| Add-Dom | 5 | X | X |  | X | X |  |  |  |
| RKHS  Ka | None | 6 |  |  |  |  |  |  | X |  |
| Add | 7 |  |  |  | X |  |  | X |  |
| Add-Dom | 8 |  |  |  | X | X |  | X |  |
| RKHS  Ka-Kd | None | 9 |  |  |  |  |  |  | X | X |
| Add | 10 |  |  |  | X |  |  | X | X |
| Add-Dom | 11 |  |  |  | X | X |  | X | X |
| Pedigree | Add | 12 |  |  |  | X |  |  |  |  |
| Add-Dom | 13 |  |  |  | X | X |  |  |  |

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **TABLE S3.** Average of phenotypic prediction accuracies (or predictive ability ) of three models: addive- and additive-dominance-BayesA and RKHS-KA for six simulated traits (Polygenic and Oligogenic traits with three dominance levels). | | | | | | | | |
| Model | d2=0 | |  | d2=0.1 | |  | d2=0.2 | |
| Oligogenic | Polygenic |  | Oligogenic | Polygenic |  | Oligogenic | Polygenic |
| BayesA-add | 0.313 | 0.290 |  | 0.343 | 0.325 |  | 0.382 | 0.358 |
| BayesA-add-dom | 0.307 | 0.286 |  | 0.342 | 0.327 |  | 0.394 | 0.372 |
| RKHS Ka | 0.286 | 0.286 |  | 0.336 | 0.336 |  | 0.367 | 0.380 |
| RKHS Ka-Kd | 0.281 | 0.282 |  | 0.332 | 0.335 |  | 0.370 | 0.382 |

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **TABLE S4**. Results of results of narrow sense heritability (h2), proportion of phenotypic variance due dominance (d2), and broad sense heritability (H2) for six simulated traits (Polygenic and Oligogenic traits with three dominance levels). | | | | | | | | | | | | | |
| Trait | Method | Pedigree inclusion | Without dominance\* | | |  | Medium dominance | | |  | High dominance | | |
| h2 | d2 | H2 |  | h2 | d2 | H2 |  | h2 | d2 | H2 |
| Oligo-  genic | BayesA  Add | None | 0.21 | - | 0.21 |  | 0.27 | - | 0.27 |  | 0.27 | - | 0.27 |
| Add | 0.34 | - | 0.34 |  | 0.41 | - | 0.41 |  | 0.42 | - | 0.42 |
| BayesA  Add-Dom | None | 0.20 | 0.04 | 0.25 |  | 0.26 | 0.06 | 0.32 |  | 0.25 | 0.11 | 0.36 |
| Add | 0.30 | 0.04 | 0.34 |  | 0.37 | 0.06 | 0.43 |  | 0.38 | 0.09 | 0.47 |
| Add-Dom | 0.28 | 0.14 | 0.42 |  | 0.33 | 0.16 | 0.49 |  | 0.33 | 0.22 | 0.55 |
| RKHS  Ka | None | - | - | 0.60 |  | - | - | 0.67 |  | - | - | 0.70 |
| Add | - | - | 0.59 |  | - | - | 0.66 |  | - | - | 0.69 |
| Add-Dom | - | - | 0.60 |  | - | - | 0.67 |  | - | - | 0.70 |
| RKHS  Ka-Kd | None | - | - | 0.70 |  | - | - | 0.74 |  | - | - | 0.76 |
| Add | - | - | 0.68 |  | - | - | 0.73 |  | - | - | 0.75 |
| Add-Dom | - | - | 0.69 |  | - | - | 0.73 |  | - | - | 0.75 |
| Pedigree | Add | 0.31 | - | 0.31 |  | 0.34 | - | 0.34 |  | 0.37 | - | 0.37 |
| Add-Dom | 0.21 | 0.18 | 0.39 |  | 0.23 | 0.20 | 0.43 |  | 0.24 | 0.24 | 0.48 |
| Poly-  genic | BayesA  Add | None | 0.23 | - | 0.23 |  | 0.25 | - | 0.25 |  | 0.29 | - | 0.29 |
| Add | 0.35 | - | 0.35 |  | 0.39 | - | 0.39 |  | 0.43 | - | 0.43 |
| BayesA  Add-Dom | None | 0.22 | 0.03 | 0.26 |  | 0.24 | 0.07 | 0.31 |  | 0.27 | 0.11 | 0.38 |
| Add | 0.31 | 0.04 | 0.35 |  | 0.35 | 0.05 | 0.40 |  | 0.39 | 0.09 | 0.48 |
| Add-Dom | 0.28 | 0.13 | 0.41 |  | 0.30 | 0.17 | 0.48 |  | 0.34 | 0.21 | 0.55 |
| RKHS  Ka | None | - | - | 0.60 |  | - | - | 0.66 |  | - | - | 0.70 |
| Add | - | - | 0.58 |  | - | - | 0.64 |  | - | - | 0.69 |
| Add-Dom | - | - | 0.59 |  | - | - | 0.65 |  | - | - | 0.70 |
| RKHS  Ka-Kd | None | - | - | 0.70 |  | - | - | 0.73 |  | - | - | 0.77 |
| Add | - | - | 0.68 |  | - | - | 0.72 |  | - | - | 0.75 |
| Add-Dom | - | - | 0.68 |  | - | - | 0.72 |  | - | - | 0.75 |
| Pedigree | Add | 0.31 | - | 0.31 |  | 0.36 | - | 0.36 |  | 0.38 | - | 0.38 |
| Add-Dom | 0.22 | 0.16 | 0.38 |  | 0.25 | 0.21 | 0.45 |  | 0.26 | 0.25 | 0.51 |
| \*The parametric values: d2=0, d2=0.1 and d2= 0.2, for traits without dominance, medium dominance and high dominance respectively. For all traits h2=0.25. | | | | | | | | | | | | | |

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **TABLE S5.** Results of s of narrow sense heritability (h2), proportion of phenotypic variance due dominance (d2), and broad sense heritability (H2). These results are from evaluation of the diameter breast height (DBH), plant height (HT), Rust resistance evaluated as gall volume (RFgall) and presence or absence (RFbin) in loblolly pine, using different methods according with table S2. | | | | | | | | | | | | | | | | |
| Method | Pedigree inclusion | DBH | | |  | HT | | |  | RFbin | | |  | RFgall | | |
| h2 | d2 | H2 |  | h2 | d2 | H2 |  | h2 | d2 | H2 |  | h2 | d2 | H2 |
| BayesA  Add | None | 0.517 | - | 0.517 |  | 0.447 | - | 0.447 |  | 0.391 | - | 0.391 |  | 0.287 | - | 0.287 |
| Add | 0.680 | - | 0.680 |  | 0.602 | - | 0.602 |  | 0.509 | - | 0.509 |  | 0.412 | - | 0.412 |
| BayesA  Add-Dom | None | 0.462 | 0.097 | 0.559 |  | 0.367 | 0.166 | 0.533 |  | 0.378 | 0.026 | 0.403 |  | 0.285 | 0.044 | 0.329 |
| Add | 0.621 | 0.055 | 0.676 |  | 0.527 | 0.109 | 0.636 |  | 0.481 | 0.037 | 0.518 |  | 0.363 | 0.072 | 0.435 |
| Add-Dom | 0.550 | 0.170 | 0.720 |  | 0.430 | 0.254 | 0.684 |  | 0.432 | 0.154 | 0.587 |  | 0.290 | 0.137 | 0.426 |
| RKHS  Ka | None | - | - | 0.844 |  | - | - | 0.807 |  | - | - | 0.723 |  | - | - | 0.650 |
| Add | - | - | 0.814 |  | - | - | 0.795 |  | - | - | 0.679 |  | - | - | 0.617 |
| Add-Dom | - | - | 0.822 |  | - | - | 0.794 |  | - | - | 0.682 |  | - | - | 0.625 |
| RKHS  Ka-Kd | None | - | - | 0.841 |  | - | - | 0.827 |  | - | - | 0.764 |  | - | - | 0.712 |
| Add | - | - | 0.819 |  | - | - | 0.809 |  | - | - | 0.734 |  | - | - | 0.691 |
| Add-Dom | - | - | 0.816 |  | - | - | 0.803 |  | - | - | 0.726 |  | - | - | 0.685 |
| Pedigree | Add | 0.677 | - | 0.677 |  | 0.616 | - | 0.616 |  | 0.422 | - | 0.422 |  | 0.318 | - | 0.318 |
| Add-Dom | 0.513 | 0.202 | 0.715 |  | 0.392 | 0.290 | 0.682 |  | 0.296 | 0.186 | 0.481 |  | 0.221 | 0.180 | 0.401 |

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **TABLE S6**. Results of Slope of predicted Genotypic values and phenotypes for diameter breast height (DBH), plant height (HT), Rust resistance evaluated as gall volume (RFgall) and presence or absence (RFbin) in *Pinus taeda*, using different methods according with table S1. | | | | | | | | |
| Method | Pedigree | DBH |  | HT |  | RFbin |  | RFgall |
| BayesA  Add | None | 1.000 |  | 0.991 |  | 0.986 |  | 1.029 |
| Add | 1.013 |  | 0.996 |  | 0.971 |  | 0.962 |
| BayesA  Add-Dom | None | 0.989 |  | 0.971 |  | 0.965 |  | 1.007 |
| Add | 1.007 |  | 0.980 |  | 0.951 |  | 0.953 |
| Add-Dom | 1.010 |  | 0.992 |  | 0.935 |  | 0.908 |
| RKHS  Ka | None | 1.063 |  | 1.066 |  | 1.066 |  | 1.103 |
| Add | 1.066 |  | 1.064 |  | 1.038 |  | 1.037 |
| Add-Dom | 1.070 |  | 1.076 |  | 1.021 |  | 1.001 |
| RKHS  Ka-Kd | None | 1.152 |  | 1.173 |  | 1.172 |  | 1.227 |
| Add | 1.116 |  | 1.144 |  | 1.108 |  | 1.124 |
| Add-Dom | 1.117 |  | 1.148 |  | 1.092 |  | 1.084 |
| Pedigree | Add | 1.026 |  | 1.013 |  | 0.985 |  | 0.958 |
| Add-Dom | 1.035 |  | 1.039 |  | 0.961 |  | 0.914 |

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **TABLE S7.** Results of Slope of prediction of Breeding, Dominance deviation, Genotypic and phenotypic values of for six simulated traits (Polygenic and Oligogenic traits with three dominance levels), using different methods according with table S1. | | | | | | | | | | | | | |
| Domiance  Level | Method | Pedigree inclusion | Bredding  Value | |  | Dominance  Deviation | |  | Genotypic  Value | |  | Phenotypic  Value | |
| Olig | Poly |  | Olig | Poly |  | Olig | Poly |  | Olig | Poly |
| d2=0 | BayesA  Add | None | 1.073 | 1.052 |  | - | - |  | 1.073 | 1.052 |  | 0.993 | 0.969 |
| Add | 1.015 | 1.002 |  | - | - |  | 1.015 | 1.002 |  | 0.94 | 0.918 |
| BayesA  Add-Dom | None | 1.089 | 1.096 |  | - | - |  | 1.032 | 1.023 |  | 0.965 | 0.937 |
| Add | 1.044 | 1.038 |  | - | - |  | 1.001 | 0.988 |  | 0.921 | 0.903 |
| Add-Dom | 1.115 | 1.101 |  | - | - |  | 0.973 | 0.942 |  | 0.888 | 0.882 |
| RKHS  Ka | None | 1.11 | 1.069 |  | - | - |  | 1.11 | 1.069 |  | 0.997 | 0.978 |
| Add | 1.059 | 1.049 |  | - | - |  | 1.059 | 1.049 |  | 0.963 | 0.947 |
| Add-Dom | 1.178 | 1.147 |  | - | - |  | 1.028 | 1.006 |  | 0.936 | 0.919 |
| RKHS  Ka-Kd | None | 1.183 | 1.161 |  | - | - |  | 1.183 | 1.161 |  | 1.087 | 1.061 |
| Add | 1.13 | 1.103 |  | - | - |  | 1.13 | 1.103 |  | 1.024 | 1.008 |
| Add-Dom | 1.239 | 1.21 |  | - | - |  | 1.094 | 1.076 |  | 0.996 | 0.981 |
| Pedigree | Add | 1.001 | 1.009 |  | - | - |  | 1.001 | 1.009 |  | 0.919 | 0.926 |
| Add-Dom | 1.238 | 1.231 |  | - | - |  | 0.952 | 0.958 |  | 0.872 | 0.873 |
| d2=0.1 | BayesA  Add | None | 0.984 | 0.932 |  | - | - |  | 1.029 | 1.013 |  | 0.995 | 0.987 |
| Add | 0.947 | 0.887 |  | - | - |  | 0.987 | 0.971 |  | 0.959 | 0.955 |
| BayesA  Add-Dom | None | 1.024 | 0.974 |  | 1.195 | 1.010 |  | 1.004 | 0.979 |  | 0.963 | 0.962 |
| Add | 0.97 | 0.924 |  | 2.986 | 1.188 |  | 0.974 | 0.959 |  | 0.935 | 0.939 |
| Add-Dom | 1.047 | 1.019 |  | 0.648 | 0.605 |  | 0.962 | 0.944 |  | 0.923 | 0.925 |
| RKHS  Ka | None | 0.982 | 0.933 |  | - | - |  | 1.069 | 1.047 |  | 1.043 | 1.027 |
| Add | 0.958 | 0.908 |  | - | - |  | 1.038 | 1.017 |  | 1.013 | 1.001 |
| Add-Dom | 1.081 | 1.028 |  | - | - |  | 1.022 | 0.994 |  | 0.998 | 0.983 |
| RKHS  Ka-Kd | None | 1.037 | 0.977 |  | - | - |  | 1.155 | 1.114 |  | 1.12 | 1.098 |
| Add | 1.011 | 0.962 |  | - | - |  | 1.109 | 1.087 |  | 1.079 | 1.067 |
| Add-Dom | 1.137 | 1.049 |  | - | - |  | 1.101 | 1.056 |  | 1.057 | 1.046 |
| Pedigree | Add | 0.921 | 0.861 |  | - | - |  | 0.953 | 0.955 |  | 0.919 | 0.951 |
| Add-Dom | 1.145 | 1.083 |  | 0.506 | 0.539 |  | 0.933 | 0.941 |  | 0.914 | 0.937 |
| d2=0.2 | BayesA  Add | None | 0.892 | 0.867 |  | - | - |  | 1.01 | 0.963 |  | 1.008 | 1.008 |
| Add | 0.865 | 0.832 |  | - | - |  | 0.986 | 0.935 |  | 0.978 | 0.98 |
| BayesA  Add-Dom | None | 0.96 | 0.926 |  | 1.262 | 1.193 |  | 0.996 | 0.95 |  | 0.987 | 0.985 |
| Add | 0.91 | 0.877 |  | 1.358 | 1.264 |  | 0.978 | 0.933 |  | 0.965 | 0.971 |
| Add-Dom | 0.98 | 0.969 |  | 0.954 | 0.936 |  | 0.977 | 0.934 |  | 0.958 | 0.969 |
| RKHS  Ka | None | 0.867 | 0.852 |  | - | - |  | 1.067 | 1.018 |  | 1.051 | 1.063 |
| Add | 0.856 | 0.841 |  | - | - |  | 1.049 | 0.998 |  | 1.028 | 1.041 |
| Add-Dom | 0.988 | 0.968 |  | - | - |  | 1.048 | 0.997 |  | 1.018 | 1.039 |
| RKHS  Ka-Kd | None | 0.911 | 0.895 |  | - | - |  | 1.159 | 1.095 |  | 1.139 | 1.143 |
| Add | 0.893 | 0.879 |  | - | - |  | 1.129 | 1.065 |  | 1.105 | 1.112 |
| Add-Dom | 1.007 | 0.988 |  | - | - |  | 1.12 | 1.059 |  | 1.091 | 1.104 |
| Pedigree | Add | 0.826 | 0.814 |  | - | - |  | 0.977 | 0.923 |  | 0.954 | 0.974 |
| Add-Dom | 1.08 | 1.055 |  | 0.856 | 0.853 |  | 0.991 | 0.937 |  | 0.947 | 0.979 |
| **TABLE S8.** Results of prediction accuracies — correlation between predicted values and observed (phenotypes) — from model model that combines BayesA-add + RKHS-Ka for all evaluated traits (Diameter breast height – DBH, Height tree- HT, Rust Fusiform presence of gall – RFbin and Rust Fusiform gall volume - RFgall). The model validations were based in ten-fold with random sample approach. | | | | | | | | | | | | | |
| Trait | | | | | | Accuracy | | | | | | | |
| DBH | | | | | | 0.546 | | | | | | | |
| HT | | | | | | 0.460 | | | | | | | |
| Rfbin | | | | | | 0.367 | | | | | | | |
| Rfgall | | | | | | 0.290 | | | | | | | |
| \*Details of the BayesA-add + RKHS-Ka model could be found at Xavier *et al.* (2016). | | | | | | | | | | | | | |

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **TABLE S9.** Prediction accuracies of breeding and genotypic values from model that combines BayesA-add + RKHS-Ka for six simulated traits (oligogenic and polygenic with three dominance levels). The model validations were based in ten-fold with random sample approach. | | | | | |
| Dominance level | Breeding Value | |  | Genotypic Value | |
| Oligogenic | Polygenic |  | Oligogenic | Polygenic |
| d2=0 | 0.675 | 0.63 |  | 0.671 | 0.629 |
| d2=0.1 | 0.666 | 0.623 |  | 0.599 | 0.58 |
| d2=0.2 | 0.685 | 0.622 |  | 0.584 | 0.54 |
| \*Details of the BayesA-add + RKHS-Ka model could be found at Xavier *et al.* (2016). | | | | | |

# LITERATURE CITED

Xavier, A., W. M. Muir, and K. M. Rainey, 2016 Assessing Predictive Properties of Genome-Wide Selection in Soybeans. G3 Genes, Genomes, Genet. 6: 2611–2616.