# POTENTIAL USE OF PREDICTION FOR SELECTION OF SOYBEAN GENOTYPES WITH RESISTANCE TO THE STINK BUG COMPLEX

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Introduction

➢ One of the main factors that compromise soybean productivity in Brazil.
➢ Use of resistant cultivars.
➢ The resistance is quantitative and difficult to be implemented in breeding programs.
➢ The challenge is revealing the genetic mechanisms related to this trait and selecting superior genotypes using genomic tools that allow the reduction of the time needed to obtain a cultivar.
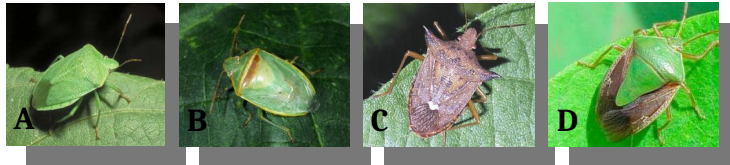
(A) *Nezara viridula*; (B) *Piezodorus guildinii*; (C) *Euschistus heros*; e (D) *Edessa meditabunda*

Objective

Evaluate the predictive abilities (PA) of genomic selection (GS) targeting at resistance to the stink bug complex and yield in soybean crop and to identify superior genotypes based on genomic estimated breeding values (GEBVs).

Materials and methods

➢ 290 soybean genotypes and 14 checks.
➢ 16x19 design alpha-lattice, three replications;
➢ Crops 2018/2019, 2019/2020 and 2020/2021;

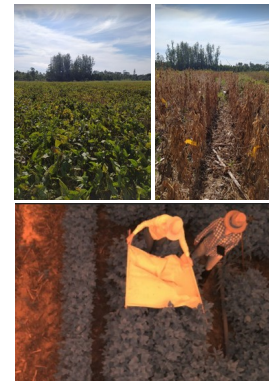$$y_{irsj} = \mu + P_{s(j)} + B_{r/s(j)} + L_j + \underline{G}_{ij} + \underline{\varepsilon}_{irsj}$$

➢ Genotyping-by-sequencing: 7231 SNPs.

➢ Weight of healthy seeds (WHS), leaf retention (RF), tolerance (TOL) and grain yield (GY).

$$TOL = \left(1 - \left(\frac{GY - HSW}{GY}\right)\right) \times 100$$

➢ GBLUP $\quad y = Xb + Zg + e$

➢ Cross-validation: 5-fold

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Results and discussion

Table 1: Variance components, PA e H[2] to evaluated traits in a soybean breeding panel.

Trait	Variance Components			[c] PA	[d] H[2]
	[a] G	[b] GxY	Residual		
TOL	0.0057	0.0027	0.0038	0.59	0.75
WHS	51404.3	60021.9	103142.2	0.54	0.46
LR	0.2097	0.0950	0.3570	0.57	0.63
GY	88756.7	64134.4	245802.6	0.54	0.32

[a] G: genetic variance component; [b] GxY: variance component of interaction genotype by year; [c] PA: predictive abilities; [d] H[2]: Heritability.
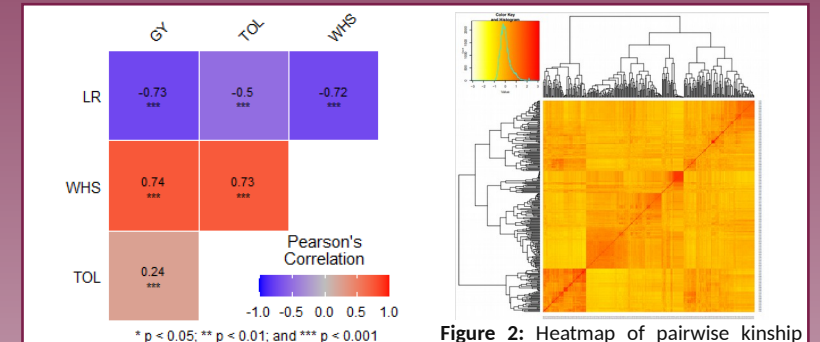

Figure 1: Additive genetic correlations obtained from GBLUP models

Figure 2: Heatmap of pairwise kinship matrix values, based on a 7231 SNPs, according with VanRaden algorithm.

Table 2: Means predicted by GEBV

	Xo	Xs	GS
GY	2068.57	2295.26	226.68
LR	2.59	2.27	-0.32
TOL	0.36	0.43	0.075
WHS	846.84	1151.27	304.42

Xo: original population mean; Xs: selected population mean; GS: selection gain.

Conclusion

Although the evaluation of other models is indispensable, these results show that the use of genomic selection becomes a promising tool for the selection of superior genotypes. Furthermore, these genotypes can be included in future crosses, aiming to obtain offspring with greater resistance.

Acknowledgments