Comparison Between Genotyping-by-sequencing and Array-based Scoring of SNPs for Genomic Prediction Accuracy in Winter Wheat

Ibrahim El-basyoni[1], Mary Guttieri[1], Katherine Frels[1], Aaron J. Lorenz[2], Peter Stephen Baenziger[1], Jesse Poland[3], Eduard Akhunov[4] and Mohamed Saadalla[5] .

[1]University of Nebraska - Lincoln, Lincoln, NE, [2]Department of Agronomy and Horticulture, University of Nebraska, Lincoln, NE, [3]USDA, Manhattan, KS, [4]Department of Plant Pathology, Kansas State University, Manhattan, KS, [5]Damanhour University, Egypt

Introduction

➤ The utilization of DNA molecular markers in plant breeding to maximize selection response via marker assisted selection (MAS) and genomic selection (GS) has the potential to revolutionize plant breeding.

➤ A key factor in GS applicability is the choice of marker platform.

➤ Genotyping-by-sequencing (GBS) provides a large number of SNPs, albeit with high rates of missing data.

➤ SNPs scored using array-based assays are of high quality, however the cost per sample is substantially higher than GBS.

Objectives

➤ Compare genomic prediction accuracy between GBS-derived SNPs (GBS) and array-based SNPs (SNPs).

➤ Compare genomic kinship matrices estimated using GBS and array-based SNPs.

Materials and Methods

➤**Plant Materials & Studied Traits:**

• 299 lines of the hard winter wheat association mapping panel (HWWAMP) that is part of ongoing TCAP (Triticeae Coordinated Agricultural Project) multi-year multi-environment association mapping study were used.

• The HWWAMP was phenotyped near Ithaca, NE, for flowering date, plant height, days to physiological maturity and grain yield in 2012 and 2013, and under two nitrogen rates (low and moderate nitrogen fertilization).
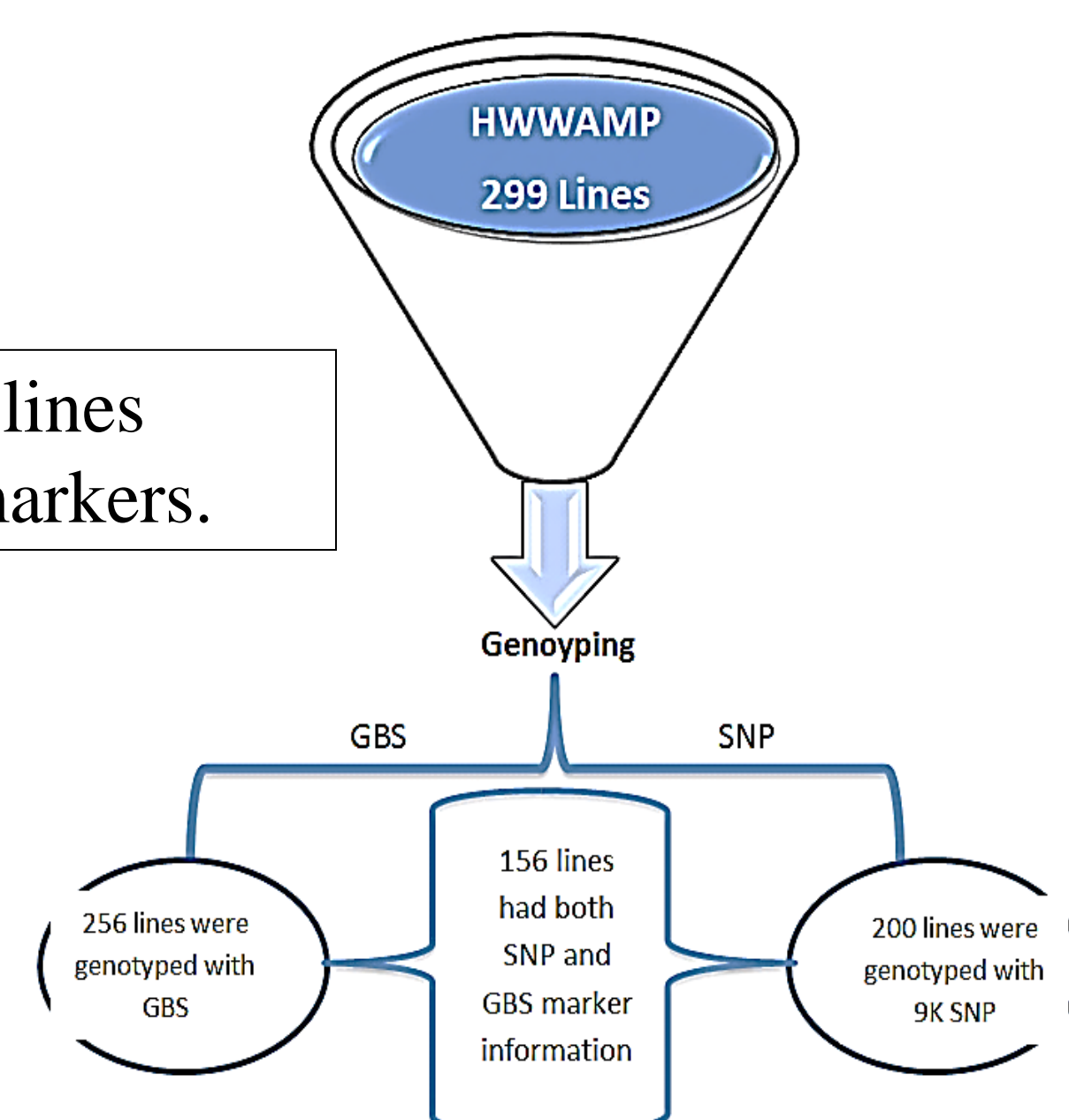
➤ **Experimental Design:**

• Incomplete block randomized design with two replications, in a split plot arrangement with nitrogen rates (44, 88 kg ha-1 residual + applied) as main plot, genotypes as subplot was used. Genotypes arranged in augmented design as incomplete blocks within each main plot. Each incomplete block included 22 entries (2 check genotypes + 20 lines).

➤ **Marker Data:**

• SNP: 9K iSelect Beadchip SNP Assay (Cavanagh, et al. 2013)

• GBS-based SNPs: GBS libraries were constructed in 95-plex using the P384A adaptor set (Poland et al., 2012) and each library was sequenced on a single lane of Illumina HiSeq 2000.

Figure 1: Flow chart shows the number of lines genotyped using SNPs and GBS markers.

➤ **Statistical Analysis:**

• GBS and array-based SNPs (SNPs) with less than 10% missing data and MAF > 0.05 were used to estimate kinship matrices.

• The breeding value for each genotype was estimated using a G-BLUP mixed model.

• The prediction accuracy was estimated using 10-fold cross validation (CV), replicated 100 times (all analysis were done within R software).

Results

➤ Analysis of variance for phenotypic traits indicated significant statistical differences among lines and between years, however no significant statistical differences were detected for the two nitrogen rates. Therefore, genomic predictions models were applied for each year separately after averaging across nitrogen rates.
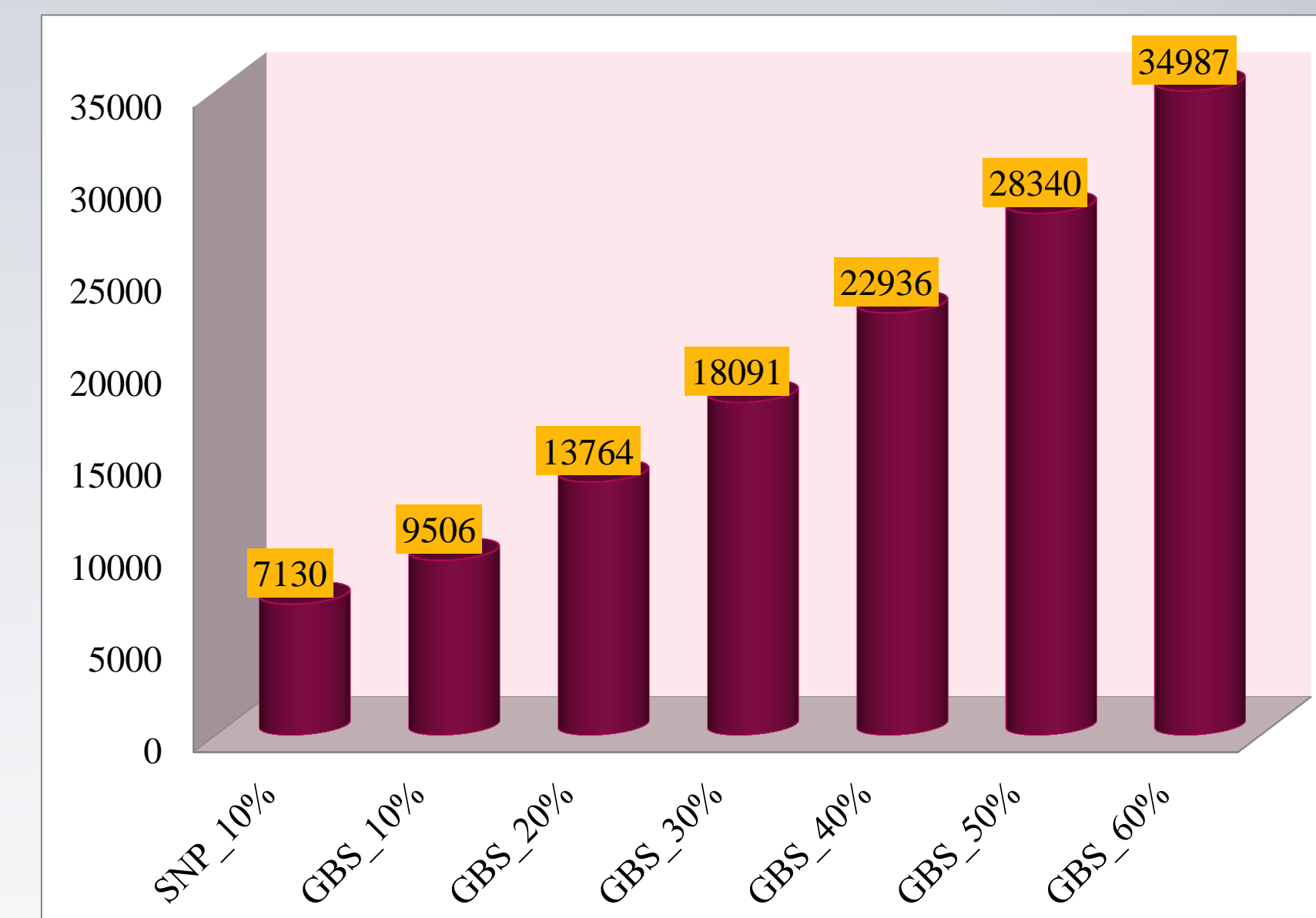

Figure 2: Number of markers under different levels of missing values for SNP sand GBS markers.
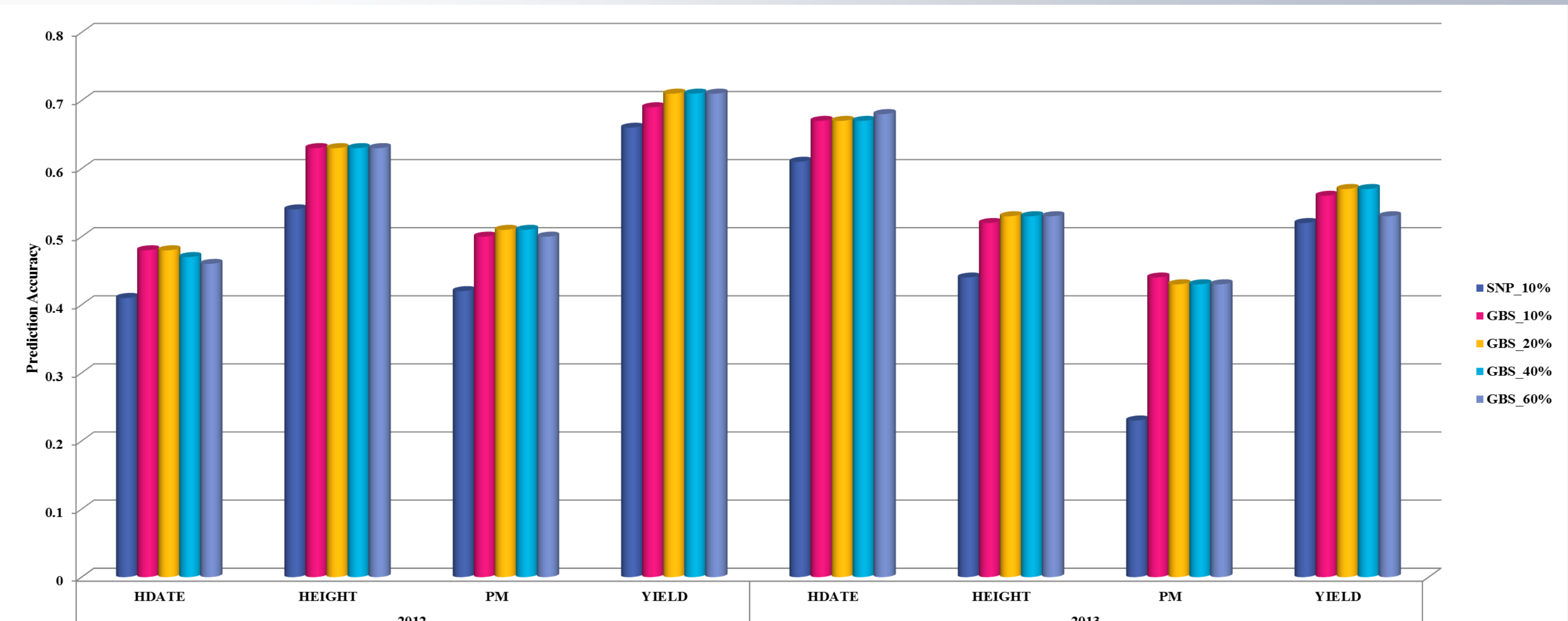

Figure 3: Correlation between predicted and observed values (accuracy) for GBS and SNP markers using different levels of missing values.

• Results from correlating the kinship matrices estimated from SNP and GBS marker platforms indicated that 92.3% (144 lines) of the lines had correlation more than 0.75.
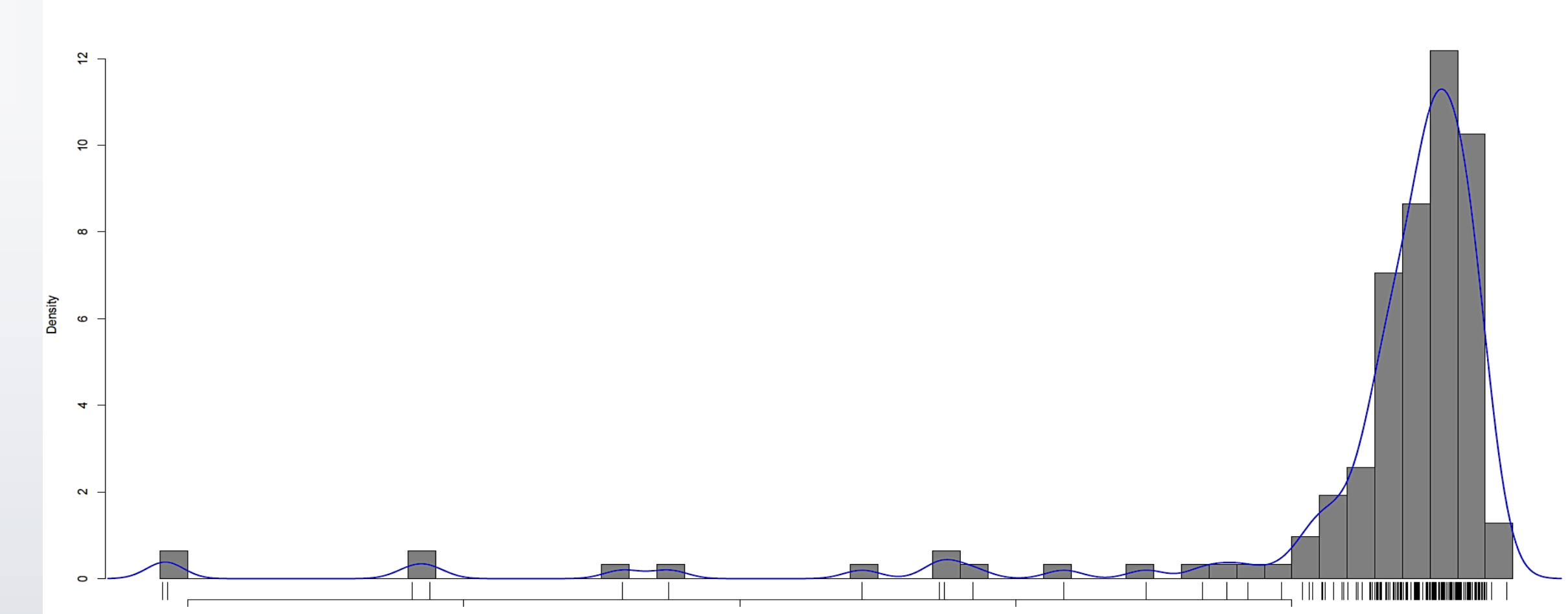

Figure 4: Distribution of the correlation coefficient (ρ) across kinship matrices estimated from SNP and GBS markers.

Conclusions

• Both marker platforms were equivalent in genomic selection prediction accuracy.

• Kinship matrices estimated from both GBS and SNP markers were equivalent for 92.3% of the genotyped lines.

References

• Cavanagh, C. et al . 2013. Genome-wide comparative diversity uncovers multiple targets of selection for improvement in hexaploid wheat landraces and cultivars. PNAS.

• Poland, J. et al .2012. Genomic Selection in Wheat Breeding using Genotyping-by-Sequencing. The Plant Genome Journal 5(3): 103

Acknowledgment