

# Genomic Selection for Drought Tolerance in Maize

Shikha Mittal<sup>1</sup>, Atmakuri Ramakrishna Rao<sup>2</sup>, Kanika Arora<sup>1</sup>, Rinku Sharma<sup>1</sup>, Kaliyugam Shiriga<sup>1</sup>, Swati Mittal<sup>1</sup>, Sreelatha Dogga<sup>3</sup>, Tikka Shobha Rani<sup>3</sup>, Sumalini Katragadda<sup>3</sup>, Firoz Hossain<sup>1</sup>, Trilochan Mohapatra<sup>1</sup> and Nepolean Thirunavukkarasu<sup>1\*</sup>

<sup>1</sup>Division of Genetics, Indian Agricultural Research Institute, New Delhi-110 012, India

<sup>2</sup>Centre for Agricultural Bioinformatics, Indian Agricultural Statistics Research Institute, PUSA, Library Avenue, New Delhi- 110 012, India

<sup>3</sup>Acharya N G Ranga Agricultural University, Rajendra Nagar, Hyderabad 500030, India

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**Abstract**—Genomic selection (GS) has emerged as one of the important approaches to predict hybrid performance in maize. Here, we tested the predictive accuracies for 240 maize subtropical lines phenotyped for drought at different environments. GS Predictive abilities of seven models—ridge regression, LASSO, elastic net, random forest, reproducing kernel Hilbert space, Bayes A and Bayes B were tested for seven agronomic traits. Bayes B had outperformed other six GS models with highest prediction accuracy of 0.97, thereby allowing the selection of Bayes B for further analysis. From the Bayes B, a set of top 1053 significant SNPs with higher marker effects were selected across all datasets to validate the genes and QTLs. Out of these 1053 SNPs, 77 SNPs mapped ten drought-responsive transcription factors in their vicinity. These transcription factors were associated with different physiological and molecular functions—stomatal closure, root development, hormonal signaling and photosynthesis. Results of our experiment are important for the prediction and development of hybrid performance under drought stress in maize.