

PREDICTING WHEAT PHENOLOGY BASED ON VRN-1, PPD-1 AND EPS GENES.

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RESUMO

Major developmental genes like *Vrn-1* and *Ppd-1* are determinants of wheat adaptation to different environments. Such genes play an important role in the crop ability to escape from seasonal abiotic stresses like frosts, terminal drought and extreme temperatures, which are expected to be more frequent in the short term future due to climate change. Therefore, it would be important to develop allelic-based phenological models as a potential tool to design lower costs breeding programs and accelerate the breeding process in a constantly changing climate scenario. With the objective to characterize and associate the phenotypic responses of different combinations of *Ppd*, *Vrn* and *Eps* alleles with the environmental variables that affect phenology in wheat, field trials were performed using a wide range of genetic ideotypes along multiple locations and sowing dates during 2018 and 2019 growing seasons. Based on trial results, we calibrated a marker-based mixed model that predicts heading date using the number of winter, photoperiod and *Eps* alleles at the *Vrn-1* and *Ppd-1* loci, and the *Eps-1* locus. ANOVA analysis marked that four genes had a statistically significant relationship to predicting wheat phenology: *VRN-A1*, *PPD-B1*, *PPD-D1* and *Eps-1*. The gene-based model had a prediction accuracy of 4.6 d using 10-year validation datasets that cover a high latitude and environmental range, thus providing a wide range in temperature and day length gradients. This marker-based model will allow breeders to target gene combinations to current and future environmental scenarios, using simple parameters that are independent of current commercial genotypes.

PALAVRAS-CHAVE: wheat, breeding, crop model, vernalization, photoperiod, earliness per se

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