Cluster analysis and AMMI method in divergence
wheat genetics

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Abstract: The effects of interaction between genotypes and environments (G × E) on plant genetic improvement is one of the most complex processes and requires a lot of attention from the breeder. In this study we used multivariate techniques to evaluate the selection of wheat genotypes (Triticum aestivum) of the most divergent and of greatest productive potential for the understanding of the adaptability and stability among 50 genotypes evaluated in 60 environments (distributed in 18 countries). The measured data were submitted to the cluster analysis (which aims to group similar data, according to its characteristics), performed by the Ward method combined with the k-medoid concept, applied to the distance matrix by the correlation based on the original data , provided 25 genotypes and 6 environments. The AMMI (Additive Main Effects and Multiplicative Interaction) models were used to analyze the interaction G × E, on the adjusted data, model based on biplot graphs. The AMMI model explained the variability of the data very well 71.4%, which could increase reliability in the selection of superior cultivars and test environments. Based on the joint analysis, genotypes G2 and G13 were the closest to the definition of the "ideal genotype".
Keywords: multivariate analysis; genetic improvement; G × E interaction; multi-environmental trials; wheat.

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