

REMATTOOL-R: A smart tool for identifying superior maize genotypes from multi-environment yield trials.

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Abstract

Breeders routinely evaluate many experimental hybrids that may be of different maturities. In maize (*Zea mays* L.), days to 50% anthesis and percent grain moisture content are used as proxies for relative maturity. The lack of an easy-to-use statistical tool that gives yield potential of all entries in a trial while classifying them into different relative maturity categories in a single visualization makes it difficult to quickly assess superior genotypes. We report on a tool called REMATTOOL-R to aid breeders in visualizing and assessing the relationship between yield and certain agronomic traits, viz., days to anthesis, percent harvest grain moisture content, and number of harvested plants, and help them in advancing experimental hybrids to the next stage. REMATTOOL-R uses either Best Linear Unbiased Estimators (BLUEs) or Best Linear Unbiased Predictors (BLUPs) of yield and agronomic traits from multilocation trials to perform various computations. The various computations produce graphical and tabular visualizations of the relationship between grain yield and days to anthesis, moisture content and number of harvested plants that can be used to support selection decisions by the breeder. REMATTOOL-R outputs tables showing entries with at least 5% higher yield than the check varieties in the trial. REMATTOOL-R is a robust, simple, user-friendly, and easily comprehensible tool, convenient for identifying superior genotypes during all the trial stages of a maize breeding program. REMATTOOL-R will be useful to breeders and researchers in related disciplines. The instructions and steps for using REMATTOOL-R are published and can be accessed at <https://doi.org/10.1080/15427528.2022.2134072>.

Keywords: maize variety testing; multi-environment trial analysis (META); relative maturity; REMATTOOL-R; superior varieties identification