**Phenotypic data analysis**

Phenotypic traits were statistically analyzed using a stagewise approach. The responsive variable was fitted using a general linear model to obtain the adjusted means by genotype in a single-trial analysis using genotypes and blocks as fixed effects.

where is a vector () of response variable observed in genotype at the block, is the overall mean, is a vector of genotypes, is the effect of the genotype nested in the check plot , is the effect of the block, and is the vector () of residuals for the trial. The adjusted means for genotypes obtained from single-trial analysis were used in stagewise MET analysis. Stagewise BLUPs were estimated using a variance-covariance structure for MET using ASReml-R software [13]. Here we used a the unstructured (US) variance-covariance matrix with no assumption of equal variances and/or covariances.

where the diagonal elements () are given by the genetic variances for each environment explained by the G×E and the off-diagonal elements are the covariance between pairs of environments assuming that off-diagonal elements are different in each pair of environments. The vectors of FD, and LOC were assumed as fixed effects and YEAR, and CUT were assumed as random effects. A Wald test for fixed effects was generated and terms were added sequentially to obtain p-values. Wald test was used in determining the degrees of freedom for calculating confidence intervals, half-Least Significant Difference (LSD) and p-values. If denominator DFs for TERM are available in Wald table, they were used. For random effects the residual DF or the maximum of the denominator degrees in Wald test (excluding the intercept) are used. In other words, the denominator degrees of freedom were obtained using dDF.na method residual. These DF are used for the t-distribution to obtain the p-values and pairwise differences of the predictions, standard error and p-values were generated.

Predicted mean values (Least-Squares Means) and p-values of pairwise differences were obtained for the explanatory variables (FD, LOC, YEAR, and CUT) and their combinations (C).

Combinatoric without repetitions of four explanatory variables in single, double, triple, and quadruple interactions can be summarized as , where and . Significant pairwise interactions were defined with p-values > 0.05.

The random effects components include the interaction of each ENV (LOC:YEAR:CUT) and GEN: idv(ENV):id(GEN) defines a heterogenous variance for each ENV with no correlation among GEN.