



Robust heritability estimation in plant studies

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Heritability is of major importance in plant studies to help achieve better yield and other agronomic traits of interest. In candidate gene studies regression models are used to test for associations between phenotype and candidate single nucleotide polymorphisms (SNPs). SNP imputation guarantees that marker information is complete and so both the coefficient of determination, R^2 , and broad-sense heritability are equivalent. However, when the normality assumption is violated, the classical R^2 may be seriously affected. Recently two R^2 alternatives with good properties were proposed for the linear mixed model: a marginal R_m^2 for the variance explained by the fixed factors and a conditional R_c^2 for the variance explained by both the fixed and random factors. In this work we step forward a robust version of R_c^2 and assess the adequacy of both classical and robust counterparts in the estimation of true broad-sense heritability via simulation, where a particular contamination scenario is considered. An example of application with a real maize data set is also presented.

Keywords: Robust linear mixed model; Coefficient of determination; Single nucleotide polymorphism (SNP); Heritability estimation.