The variance components used to estimate broad-sense heritability or repeatability for each trait and trial were calculated using the following mixed linear models to the RCBD field design for NDVI and Ground Cover(GC) data or alpha lattice design for Canopy Temperature (CT) data, with the package *ASReml*-R Version 4.1 (Gilmour et al, 2015; Butler et al, 2009). The terminology used to define models and heritability equations followed Holland et al, (2003).

Model orthomosaic (single plot-level value) for NDVI and GC

where, is the is the phenotypic value of the *i-th* entry in *k*-th row and *l-th* column, for the *j*-th replicated block, is the overall mean effect, is the random effect of the *i*-th entry distributed as iid , is the random effect of the *j*-th block distributed as iid , is the random effect of the *k*-th row nested within block distributed as iid , is the random effect of the *l*-th column nested within block distributed as iid , and is the residual error effect distributed as iid ).

Model orthomosaic (single plot-level value) for CT

where all the terms are the same as for the orthomosaic model for NDVI and GC but including a new term for sub-block effect . is the random effect for the *m-th* sub-block nested within block distributed as iid .

The variance components derived from the model were used to as:

where, is the genotypic variance, is the residual variance, and *r* is the number of replicated blocks. In this model, plot effects and plant-within-plot effects are cofounded in the residual error effect.

Model photo mean (single plot-value by averaging multiple values per plot) used the same linear model and heritability equation used for the orthomosaic model.

Model photo subsampling (multiple plot-level values) for NDVI and GC

where all the terms are the same as for the orthomosaic model but including a new term for within-plot effect variation . is the random effect of the *m-th* subsample nested within *i-th* genotype, *j-th* block, *k-th* row, and *l-th* column.

Model photo subsampling (multiple plot-level values) for CT

The variance components derived from the model were used to calculate as:

where, is the genotypic variance, is the plot variance, is the within-plot variance (now the residual error variance), *r* is the number of replicated blocks, and is the number of subsamples calculated as the harmonic mean for each plot.

Model photo image (including the effect of image file) for NDVI, GC, and CT

where, is the is the phenotypic value of the *i-th* entry in the *j*-th replicated block for the *k-th* image, is the overall mean effect, is the random effect of the *i*-th entry distributed as iid , is the random effect of the *j*-th block distributed as iid , is the random effect of the *k*-th image file distributed as iid , and is the residual error effect distributed as iid ).

The variance components derived from the model were used to calculate as:

Model photo image + angle (including the effect of image file and camera horizontal angle) for NDVI, GC, and CT

where, is the fixed effect covariate for camera horizontal angle. was calculated with the same equation used for the photo image model.

References

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