



Measuring varietal success on-farm with rank-based metrics

Farmer rankings of varietal traits can be adapted for use by breeders

Plant breeders need to assess newly developed varieties across different environments. This is typically done with on-station trials, using intensive phenotyping across growing conditions. However, this may not always represent the performance of the final breeding products on farms, where input levels are lower, and growing conditions are more varied. Therefore, testing in the later stages of the crop breeding cycle should involve on-farm testing for realistic evaluation of varietal performance and suitability.

It is a challenge for on-farm testing to obtain sufficient volumes of good data. Large-scale implementation of tricot has the potential to generate extensive volumes of varietal performance data from farmers over many environments and years. Such data can be of much value to breeders - but only if the observations can be analysed and interpreted in ways compatible with breeders' analytical and decision-making pipelines.

Under the tricot approach, it is easier for farmers to use rankings rather than scoring or metric measurements. Farmers only need to indicate relative differences between varieties (e.g. "this variety is taller than this one"). However, it is

still a challenge to get estimates for crop yield. In addition, rankings are challenging to analyse statistically with the methods that breeders currently use. The 1000FARMS project seeks to address this by developing methods to process ranking-based data.

Adapting rankings for breeders with new statistics

We developed a methodology (Figure 1) that uses ranking data to produce estimates of important quantities of interest to breeders, including genetic variation across time and farm conditions, as an output (Figure 2). The results demonstrated clearly that farmer-generated ranking data can provide accurate estimates for any quantitative or qualitative trait. This confirms that rankings can provide a good alternative to data collected using metric measurements or scoring.

Trial designers still face a trade-off. Rank-based observations have reduced information content per data point, compared to metric measurements - about 2.5 times as many observations are required on average to achieve similar precision, and at least 10 to 20 replicates

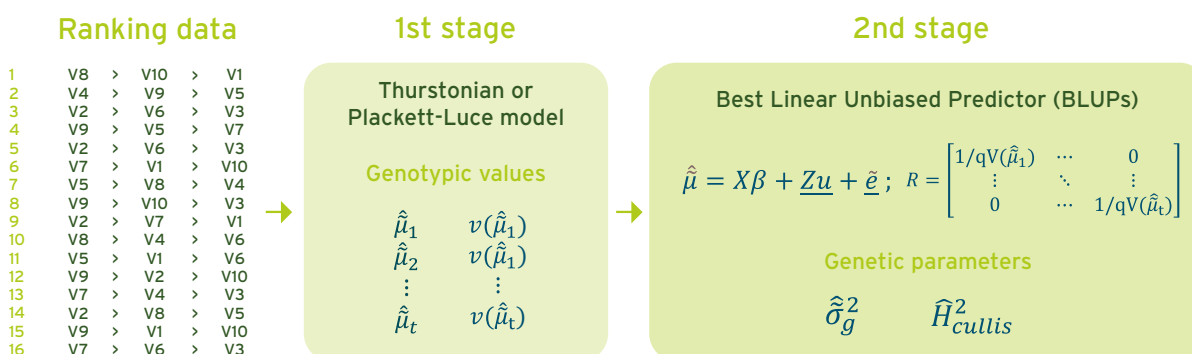


Figure 1. New approach to estimate genotypic values, genetic variances, and heritability using ranking data

per genotype are needed to ensure that trait means can be estimated reliably. However, field agents' farm visits are an important cost driver in on-farm trials. Because farmer rankings make it possible to limit farm visits, the trade-off between price and accuracy will often favour a large set of farmer-generated rankings over a smaller set of more precise metric data.

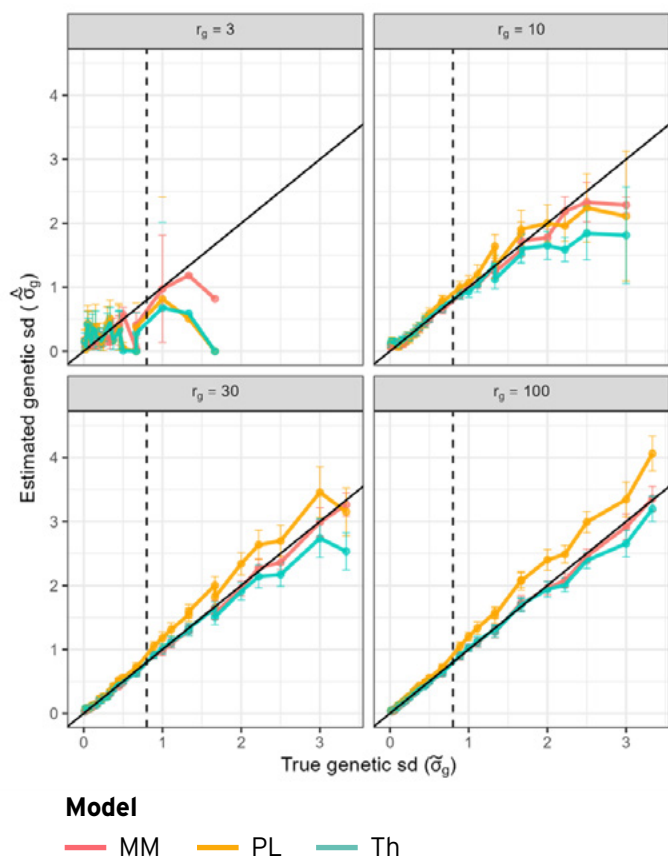
This does not mean that metric estimates are replaced by ranking estimates under the tricot approach. Rather, a more cost-effective subset

of the trial farms can be visited to collect metric data, which can be combined with tricot ranking data to calculate the magnitude of varietal differences on the actual scale of measurement (e.g. t/ha for yield) accurately. Other work has shown that farmers are also able to provide accurate data by measuring yield in volume (e.g. filling tin cans). We have already developed some early applications on actual data for several crops, and software to implement these analyses will soon be made available to breeding programs.

Engaging farmers for on-farm data that will feed back to farmers

Our work provides a proof-of-concept for an approach whereby ranking data can be used as input into quantitative analysis of genotypic on-farm performance. Provided sufficient observations per genotype, our two-stage approach allows breeders to estimate many

genetic parameters of interest from multi-year, multi-location ranking data. This means that breeders will be able to use system-wide on-farm variety ranking data, potentially supplemented with metric measurements, as a new powerful tool to determine which varieties have the best potential to excel in their actual target environments. As breeding programs make more use of these data, they can produce new crop varieties that show production advantages under farm conditions, which are in turn more likely to be adopted by farmers.



Note: The panels compare the performance of two statistical models for ranking data (PL and Th) to a benchmark of metric estimates (MM). Each panel represents a different intensity of genotype replication (r_g). We compare MM (marginal means, which is a mixed model using the metric data, with two rank-based models, PL (Plackett-Luce) and Th (Thurston Case V). The vertical dashed line represents the typical standard deviation in on-farm trials based on the literature. The continuous diagonal line represents the 1:1 line (perfect relationship). The results show that rank-based estimates are very close to metric-based estimates when replication is sufficient.

Figure 2. Relationship between true and estimated genetic standard deviations for simulated yield variety trials of maize

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