

Estimation of breeding values for forage yield of oat allows better selection of parents

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Forage varieties of cultivated oat (*Avena sativa* L.) are widely grown in Australia during the winter months, providing high quality forage for grazing animals when native and improved pastures are dormant. The Queensland Department of Agriculture and Fisheries operates a breeding program to develop high yielding, locally-adapted commercial cultivars of forage oat for beef, dairy and sheep producers. Advanced selections are evaluated for forage yield using a forage harvester in multi-cut replicated plot trials at several locations under irrigated and rain-fed conditions across several years. Analysis of forage yield multi-environment trial (MET) data is performed using a linear mixed model for the study of the genotype by environment interaction. This model accounts for design effects and spatial variability in each trial, and allows for different residual variances for the different cuts, different residual correlations between cuts within trials, different genetic variances for cuts, and different genetic correlations between cuts (Smith et al 2001). The genetic relationship between the varieties in the MET is incorporated into the analysis via an additive relationship matrix derived from the pedigree of the individual lines that reflects the expected degree of co-ancestry among them (Oakey et al 2007). Breeding values obtained from this analysis are used to identify the parents that contribute the highest amount to the forage yield of their progeny (Oakey et al 2006). Breeding values for total forage yield, early vigour (first cut), and regrowth (second cut), estimated from a MET analysis of 12 trials over 4 years (2014-2017) are presented for a sample of commercial cultivars, advanced breeding lines and germplasm lines. This information will be used in selecting the best parents for future crossing, with the aim of accelerating genetic gain for forage yield and its components in the long term.

Key Words: forage oat, forage yield, breeding values, Australia

References

- Smith, A., B. Cullis and R. Thompson. 2001. Analyzing variety by environment data using multiplicative mixed models and adjustments for spatial field trend. *Biometrics* 57: 1138-1147.
- Oakey, H., A. Verbyla, W. Pitchford, B. Cullis and H. Kuchel. 2006. Joint modeling of additive and non-additive genetic line effects in single field trials. *Theoretical and Applied Genetics* 113: 809-819.
- Oakey, H., A.P. Verbyla, B.R. Cullis, X.M. Wei and W.S. Pitchford. 2007. Joint modeling of additive and non-additive (genetic line) effects in multi-environment trials. *Theoretical and Applied Genetics* 114: 1319-1332.