Genotype by environment interactions amongst diverse forage brassicas across Australia's mixed farming zone

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Abstract

Forages that provide rotational benefits in intensive cropping systems and augment existing feed sources are needed across Australia's mixed farming region. Forage brassicas offer such potential, especially in areas where canola is not commonly grown, and as an alternative to forage cereals. Multi-environment analyses were used to explore the genotypic adaptations of several forage brassica genotypes grown in multiple environments throughout the mixed farming region over ten experimental site-years. Forages were assessed for productivity within an early- (800-1300 growing degree days after sowing) and late-grazing window (1600-2100 growing degree days after sowing). Forage brassica genotypes were often lower in edible biomass compared to forage oats, but were higher in metabolisable energy (ME) and crude protein (CP) content, and thus often higher in yields of ME and CP. In the early grazing window, there were no genotype by environment interactions for yields of ME and CP. However, in the late grazing window, several genotypes showed a genotype by environment interaction for these productivity measures. These multi-environment trial analyses identified that forage rapes cvv. Goliath, HT-R24 and Winfred were best suited to a broad range of environments in both an early and late grazing window, and raphanobrassica cv. Pallaton was well suited to a range of environments in a late grazing window, but particularly in low-moderate production environments. Further simulation modelling will explore the potential of these well-adapted genotypes to fill feed gaps in a broader range of environments and livestock systems across Australia's mixed farming region.

Keywords
Forage biomass, metabolisable energy yield, crude protein yield, multi-environment trial analyses

Introduction

Forage brassicas (members of the Brassicaceae family) are high in nutritive value with around 12.1-14.1 MJ ME/kg DM (Barry 2013) and 13-19% CP (Sun *et al.* 2012). They are most often used as a summer forage in high rainfall dairy and livestock systems as an alternative to dry pasture and/or crop residues or lucerne. Many forage brassica genotypes have high vernalisation requirements which lengthens their vegetative phase and enhances their capacity to fill seasonal feed gaps in livestock systems. A range of genotypes are commercially available in Australia, varying in their functional traits and role in livestock systems. These include leaf-type and hybrid genotypes with multi-graze potential, and bulb genotypes with both bulb and above ground edible biomass that are generally used as a single-graze crop. In mixed farming systems, forage brassicas may play a critical role in filling feed gaps, whilst also serving as a break-crop in cropping rotations. The role of forage brassicas may be particularly important in semi-arid subtropics where canola (*Brassica napus var. annua L.*) is not commonly grown due to the lower productivity and profitability as a result of terminal drought and a short growing season (Robertson and Holland 2004). Preliminary studies undertaken in northern New South Wales and southern Queensland revealed forage rapes produced > 5 t/ha of dry matter that was comparable or higher than other benchmark species including forage cereals and legumes (Bell *et al.* 2020). Despite the likely potential of forage brassicas for use in Australia's mixed farming region, no studies have explored the potential systems benefits of a broad range of genotypes when sown in autumn and winter within this production environment (i.e., drier environment). In this study, we used multi-environment trial analyses to identify the potential genotypic adaptations of a diverse set of

forage brassica genotypes grown across multiple environments within this region. Our analyses were based on the productivity measures of edible biomass (data not presented), and their associated concentrations and yield of ME and CP. From these analyses, we aimed to identify 'stand-out' genotypes that are best adapted to these drier environments. The performance of these select genotypes will be further explored using the cropping systems model APSIM (Agricultural Production Systems Simulator) (Holzworth *et al.* 2014) following validation testing and adaptation of the existing canola model (Robertson and Lilley 2016).

Methods
Site locations and forage measures
A diverse set of forage brassica genotypes were grown at core experiments in Tummaville and Condamine in southern Qld, York in the central wheatbelt in WA, and Iandra in central west NSW in 2018 and 2019. In 2019, an additional two sites located in Pine Ridge and Armatree in northern NSW were included. Over the growing season, Tummaville 2018 received 330 mm, Condamine 2018 and York 2019 received ~130 mm rainfall, Tummaville 2019, Iandra 2018 and York 2018 received ~ 300 mm rainfall, and the 2019 sites at Condamine, Iandra, Armatree and Pine Ridge received < 80 mm rainfall. Edible biomass (i.e., both above and below (bulb) biomass) were collected within an early- (800-1300 growing degree days after sowing) and late- grazing window (1600-2100 growing degree days after sowing) and these samples were also analysed for ME and CP content. Yields of ME and CP were calculated as the product of biomass and their respective nutritional content.

Statistical analyses
Multi-environment trial analyses (Smith *et al.* 2005) for yields of ME and CP were carried out using linear-mixed models with ASReml-R (Butler *et al.* 2017) and factor analytic models (Smith *et al.* 2001) to explore genotype by environment interactions by estimating the genetic variance for each experiment and genetic covariances between experiments (Kelly *et al.* 2007). Experimental design and spatial location of plots was also included in the analysis (Gilmour *et al.* 1997), which allowed each experiment to have its own residual model structure. Best linear unbiased predictors (BLUPs) were calculated for all productivity measures. The environmental mean for each site was calculated as the mean of the BLUPs for all genotypes grown at that site. Genotype by environment interactions within the early and late grazing windows was explored using a linear regression on the environmental mean (Finlay and Wilkinson 1963).

Model validations in APSIM
Data collected from core experimental sites, including biomass and ME content, were used to validate forage rapes cvv. Goliath, HT-R24 and Winfred, and raphanobrassica cv. Pallaton in the existing canola APSIM model. Initial model testing focussed on thermal time for emergence, end juvenile, and floral initiation to better approximate the phenology and thus, biomass and nutritive value of the crop.

Results
The genotype predictions of some forage brassica genotypes were often ranked lower in edible biomass than forage oats (data not presented), but they were often higher for ME yield, and in particular, CP yield (Figure 1). This was due to the much higher ME and CP content of the forage brassicas compared to forage oats. In the early grazing window, there were very few interactions between genotype and the environment with most genotypes ranking consistently for yields of ME and CP across the low to high production environments tested (correlation table not presented). Within this early grazing window, Rival bulb turnip was highly productive for yields of ME and CP compared to the other genotypes at all sites except one, and it was highly responsive in high production environments. Forage rapes cvv. Goliath, HT-R24 and Winfred had consistently higher yields of ME and CP in this early grazing window compared to the other genotypes, and this was most evident in low and medium production environments (Figure 1a and b). In the late grazing window, genotypes performed less consistently for yields of ME and CP across environments. Discrepancies in genotypic adaptations between sites in this late grazing window was most apparent between the high

production (Tummaville 2019) and low-medium production environments (Figures 1c and d). This was mostly due to the much poorer relative productivity of some genotypes, such as leafy turnip cv. Hunter, in low-medium production environments compared to the high production environment (Figures 1c and d). In low to medium production environments within this late grazing window, raphanobrassica cv. Pallaton had high relative productivity compared to many other genotypes but was much less responsive to high production environments (Figures 1c and d). Forage rapes cvv. Goliath and HT-R24 performed well across the different production environments.
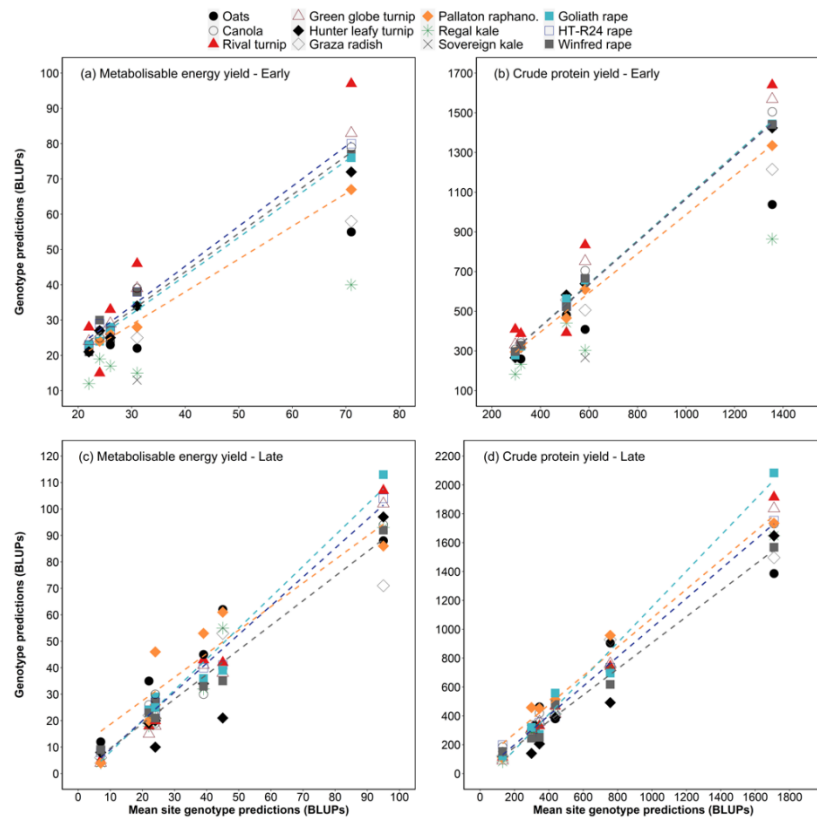
Figure 1. Genotypic adaptations of a diverse set of forage brassica genotypes, canola and cereal crops for metabolisable energy yield (a and c) and crude protein yield (b and d) in an early (a and b) and late (c and d) grazing window identified using best linear unbiased predictors (BLUPs) from multi-environment trial analyses. Regression lines are shown for forage rapes cvv. Goliath, HT-R24 and Winfred and raphanobrassica cv. Pallaton that performed the best in low-medium rainfall environments.
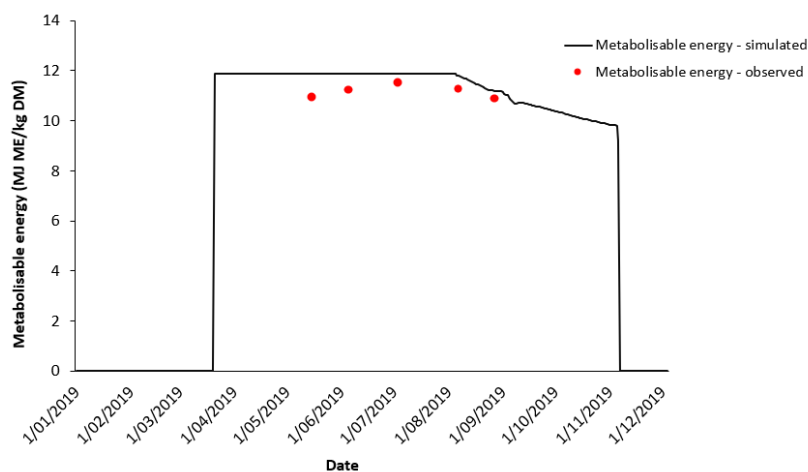
Figure 2. Preliminary validation simulations of the metabolisable energy content of forage rape cv. Winfred using the canola APSIM model and data collected from Tummaville 2019.
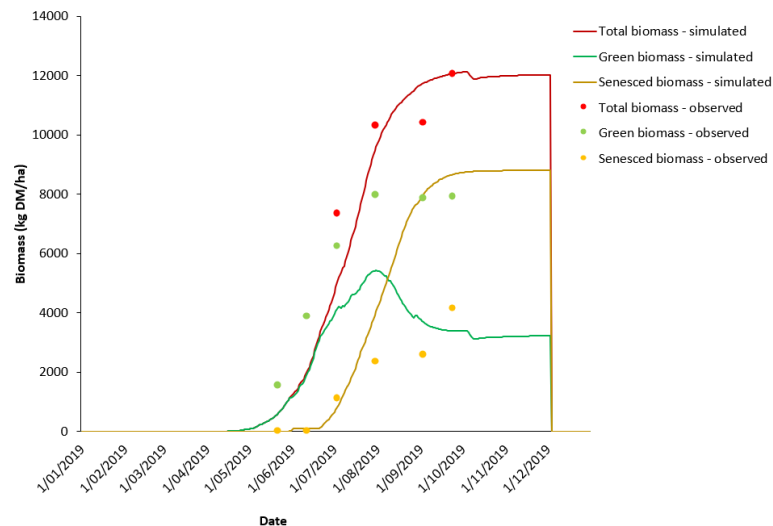
Figure 3. Preliminary validation simulations of the total, green and senesced biomass of forage rape cv. Winfred using the canola APSIM model and data collected from Tummaville 2019.

Preliminary model validations for Winfred forage rape indicate that the adapted canola APSIM model sufficiently simulates forage ME content (Figure 2) for this genotype, but further testing is required to better simulate biomass fractions, particularly green and senesced biomass material (Figure 2).

Conclusion

These multi-environment trial analyses identified that the forage brassica genotypes with the greatest potential for use in Australia's mixed farming region, particularly in low-medium production environments (<230 mm growing season rainfall), were forage rapes cv. Goliath, HT-R24 and Winfred and Pallaton. These genotypes will be the focus of future modelling activities that will explore the capacity of these well-adapted forage brassicas to fill feed gaps and complement the existing feedbase across different production environments and livestock systems within Australia's mixed farming region.

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