# Importance of different plant traits for dual-purpose cereal dry matter production and grain recovery in southern NSW

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**Abstract**

With growers` increased focus on dual-purpose (DP) cereal varieties and the development of new DP varieties, a set of experiments investigating the grazing and grain recovery of DP cereals were run at Wagga Wagga in 2016 and 2017. The experiments were designed in a randomised complete block with one or two factors. With two factors e.g. variety and sowing time, the experiments were arranged in split-plot or factorial (depending on the second factor). Sixty three different wheat, barley and triticale genotypes were tested over the two years, with a core subset of 24 genotypes studied in detail. Various measurements and plant traits such as plant population, plant growth stage, dry matter production, morphological attributes, grain yield and quality were recorded. The study found that there were differences between both crop type and genotypes and how they accumulated dry matter and then recovered from grazing to produce grain. The key variables and traits were plant population, tillers number and leaf dry weight for dry matter production before anthesis and total dry matter, fertile tiller number and stem dry weight at anthesis for grain yield.

**Key words**: Dual-purpose cereals, mixed farming, multivariate, morphological traits

**Introduction**

Dual-purpose cropping systems – sowing crops for both grazing and grain recovery – are an old and common farming practice worldwide. In recent years, cropping systems that include DP crops have attracted more interest because of greater profitability and sustainability in Australia and other parts of the world (Franzluebbers 2007; Radcliffe et al. 2012). Dual-purpose cereals offer growers management flexibility. This allows them to respond to seasonal uncertainty and fluctuating grain and livestock markets, making DP cereals an integral part of mixed farming systems in New South Wales (NSW).

There has been a number of studies identifying differences in dry matter production and grain recovery in cereal genotypes following grazing (Kelman and Dove 2009; Harrison et al. 2011). However, limited work has been undertaken on species and cultivar differences and understanding how these differences affect dry matter (DM) and grain yield (GY).

**Methods**

Field experiments were sown at Wagga Wagga in 2016 and 2017 investigating cereal crop type and genotype response to grazing, subsequent grain recovery and were sown at the first opportunity in autumn (Table 1).

Table 1. Annual rainfall, growing season rainfall (GSR) (Apr–Oct) and sowing dates at Wagga Wagga, NSW.

| Year | Annual rainfall (mm) | GSR(Apr–Oct) (mm) | Sowing date 1 | Sowing date 2 |
|------|------|------|------|------|
| **2016** | 779 | 592 | 2 May | 24 May |
| **2017** | 445 | 230 | 30 March | 27 April |

 Sixty three different unreleased or commercial wheat, barley and triticale genotypes were tested over the two years. The experiments were all conducted in a row by column arrangement based on randomized complete block design with four replications. Key measurements recorded included dry matter (DM) production at mid tillering and then before stem elongation i.e. growth stage (GS)31 on

the Zadoks scale (Zadoks et al. 1974). The experiments were grazed by sheep following DM measurement and allowed to recover for either further DM assessment or carried through to grain production. The experiments were crash grazed to minimise sheep grazing preferences. Fertiliser and all other crop management were implemented according to best management practices to maximise dry matter production and grain recovery.

In addition to DM and GY measurements such as plant establishment, tiller numbers , NDVI, anthesis date and various morphological traits at anthesis, on a subset of 24 genotypes were recorded to better understand how the different genotypes accumulate DM and then recover for grain production. Only selected genotypes and traits, were subjected to multivariate analysis from the DP cereal experiment data.

*Table 2. Genotypes studied in detail at Wagga Wagga, NSW in 2016 and 2017. Those used in both years are underlined.*

| Crop type | Genotype |
|---|---|
| **Barley** | Urambie |
| **Triticale** | Cartwheel, Endeavour, Tobruk, Tuckerbox, Crackerjack2 |
| **Wheat** | EGA_Wedgetail, LRPB Kittyhawk, Naparoo, Sunlamb, Manning, EGA_Gregory , Longsword, ADV12.1446, ADV08.0008, VO9150-01, SF-Adagio, SF-Scenario, ADV11.9419, ADV09.0345, V07041-39, HV16, Biere, Whistler |

The relationships between the traits and variables before anthesis for GY, the first dry matter (DM1) and the second dry matter cuttings (DM2) are presented only for 2016 as we did not have a balanced dataset common between two years for these traits and only for 21 genotypes. The results of anthesis measurements, DM1, DM2 and GY are presented for 14 common genotypes for both years. Different statistical approaches, including principal components analysis (PCA), partial least squares (PLS) and different clustering approaches (mainly the results from 'ward.D2' linkage method are presented here) were used to do multivariate analyses using the R programme environment (R Core Team 2018).

**Results and Discussion**
Figures 1a and 1b show the PLS results on different plant traits.  There is  a close relationship between the GY of genotypes (as the response variable) and some plant traits *at anthesis*, such as total dry weight, spike dry weight, stem dry weight and fertile tiller ratio. However, there is a negative relationship between GY and sterile tiller ratio, DM2 and leaf dry weight. Higher DM at anthesis was related to a higher final GY (Ferrise et al. 2010). Reduced GY has also been related to fewer tiller numbers in wheat (White et al. 2008). Low correlations were found between GY and DM1, spike length and peduncle length (Figure 1a).

The PLS method was used to investigate relationships between GY and some plant traits *before anthesis*. The GY showed high correlation with plant establishment, tiller numbers per square meter at cuttings one and two, NDVI1 and DM1. Grain yield showed a low correlation with DM2 and NDVI2, showing the possible different effects from grazing at the second time, on the GY of genotypes (Figure 1b).
The PCA results show different performance for the selected genotypes based on plant traits at anthesis (Figure 2a) and before anthesis (Figure 2b) with GY, DM1 and DM2. About 70% of variation among genotypes was explained by the two first components of PCA for the traits at anthesis, and 62% for traits before anthesis, with GY, DM1 and DM2. Triticale genotypes showed a different cluster from the wheat and barley genotypes.
Triticale genotypes showed greater GY, stem length, total dry weight and peduncle length compared to wheat and barley genotypes. Longsword[A] and ADV08.0008 had a higher DM1 and fertile tiller ratio relative to other genotypes. The ratio of sterile tillers and leaf dry weight were higher for Manning[A] compared with the other genotypes (Figure 2a and 2b). NDVI readings at the first and second cutting showed high correlation with the corresponding dry matter production (Figure 1b and 2b).
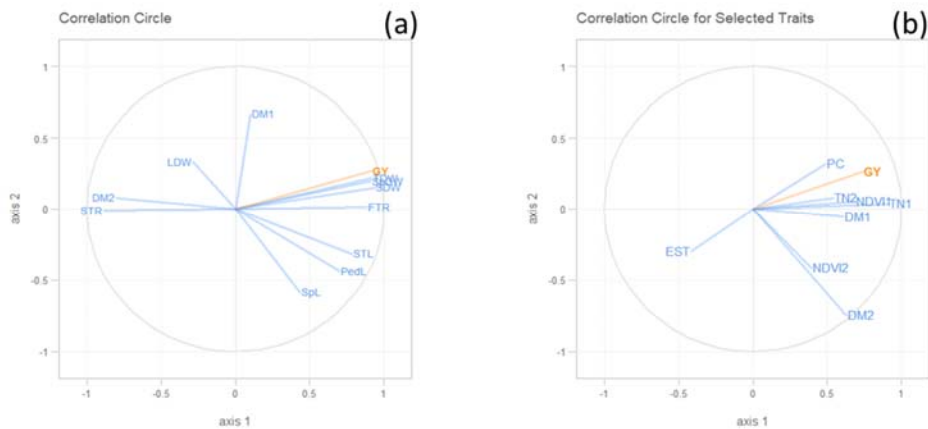
**Figure 1. Partial least squares (PLS) correlations circle of plant traits <u>at anthesis</u> including: sterile tiller ratio (STR), fertile tiller ratio (FTR), leaf dry weight (LDW), spike length (SpL), peduncle length (PedL), stem dry weight (SDW), stem length without spike (STL), spike dry weight (SpDW) and total dry weight (TDW) with grain yield (GY), dry matter at the first cutting (DM1) and dry matter at the second cutting (DM2) (a), and for selected plant traits <u>before anthesis</u> including; establishment score (EST), plant count (PC), NDVI at the first cutting (NDVI1), NDVI at the second cutting (NDVI2), Tillers number at cutting one (TN1), Tillers number at cutting two (TN2) with GY, DM1 and DM2 (b).**
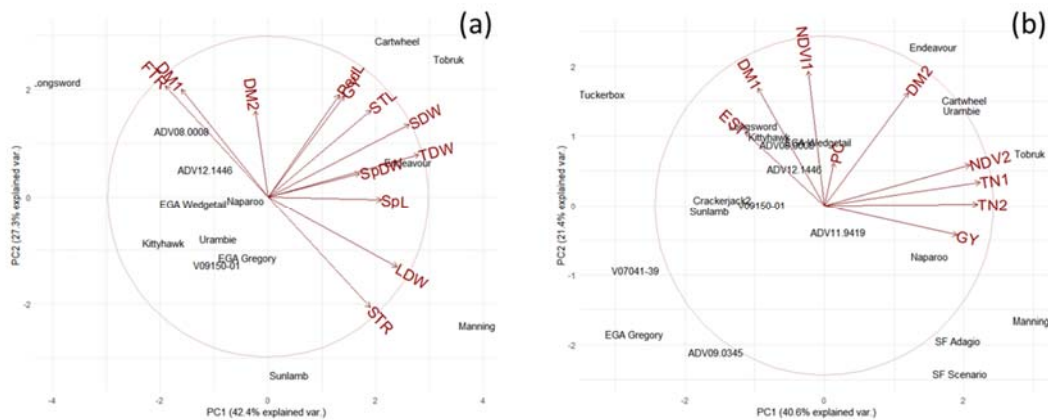


**Figure 2. Principal components analysis (PCA) for morphological traits <u>at anthesis</u>, GY, DM1 and DM2 (a), and for selected plant traits <u>before anthesis</u> with GY, DM1 and DM2 (b) (See Figure1 for details).**

The differences among genotypes from the PCA analysis method became more evident using cluster analysis. Cluster analysis mainly shows two clusters of genotypes for different plant traits. The two clusters are clear in figures 3a and 3b.

The triticale genotypes and Manning[A] are in one group and the rest of genotype are placed in the second group. Longsword[A] and Sunlamb[A] performed differently from the other genotypes such as EGA Wedgetail[A], LRPB Kittyhawk[A], Naparoo[A], and Urambie[A] which were all at the middle of the biplot, showing similar and close to the overall performance for this group of varieties. The heatmap shows the genotypes clustering with the corresponding plant traits (Figure 3b).
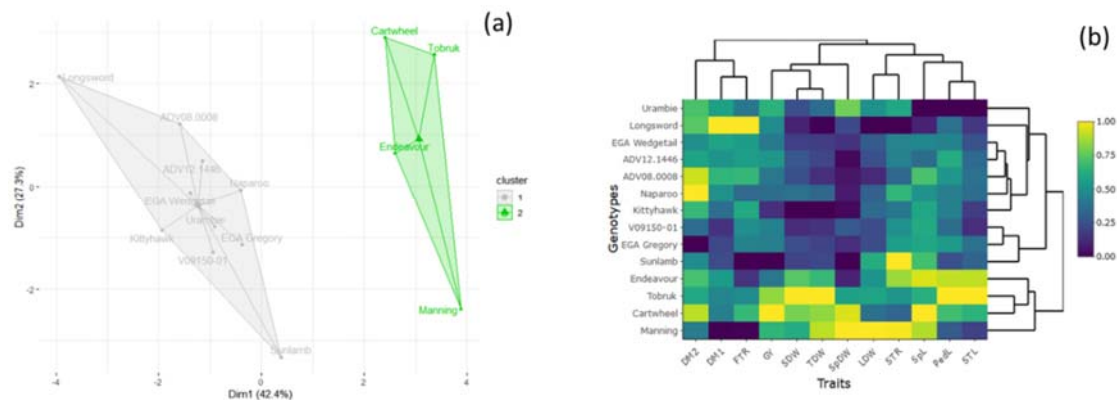
**Figure 3. Clustering of genotype based on morphological traits <u>at anthesis</u> with GY, DM1 and DM2 (a). Heatmap of genotypes and different plant traits (b). (See Figure 1 title for explanation of different abbreviations). The values on the heatmap guide are the scaled values for each plant traits (the colors close to zero show lower values and the colors close to one show higher values for each trait).**

## Conclusion

Early biomass production was well correlated with tillers number, number of plants per unit area and leaf dry weight. Grain yield correlated with a number of traits at anthesis, tiller numbers, total dry weight and stem dry weight. For the measured variables and traits, different responses were identified for crop types and to a lesser extent genotype. These findings indicate there are opportunities for growers to maximise fodder production and then grain recovery by selecting different crop types or genotypes that suit their farming systems.

## Acknowledgements

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