

A germplasm and breeding strategy for improved drought resistance in *Phaseolus vulgaris*

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Abstract

A selectively imported germplasm collection was evaluated under field conditions at Kingaroy, Qld., to assess the extent of genetic variation for drought resistance traits. Significant genotypic variation for T, W and HI was observed. Some of these lines are being currently being used as parents in a pilot breeding program, where indirect selection for these traits using a selection index approach, will be applied in the segregating populations. It is hoped that a more rapid rate of genetic improvement for improved drought resistance can be achieved using this indirect selection approach.

Keywords: navy bean germplasm drought resistance physiological traits

Opportunities exist for plant breeders to utilise analytical tools and models developed by crop physiologists. Novel approaches which allow analysis of genotype response in breeders multi-environment trials in terms of physiological determinants of growth and yield have been advocated (1, 2). This improved understanding can allow for better interpretation of genotype by environment interactions, as well as providing new indirect selection criteria to complement empirical based selection approaches. These analyses can be conducted on large numbers of genotypes for only minor investments in extra measurements. This paper illustrates this approach for a *Phaseolus vulgaris* germplasm collection using the functional component model where water limits productivity.

Materials and methods

The model used is based on that proposed by Passioura (3), where $Y = T \times WUE \times HI$, and Y is seed yield (g/m²), T is the crop transpiration (mm), WUE is ability of the crop to produce biomass per unit of water transpired (g/mm/m²), and HI is the harvest index or proportion of seed yield to total biomass.

A random sample of 343 *P. vulgaris* imported germplasm lines were grown under irrigated conditions at the DPI, Kingaroy, Queensland during January to May, 1997. An unreplicated design with a check variety (Sirius) alternating after every 7 plots was used to provide within site data adjustment for environmental variation. Plot size was a single row, 5 m long, 0.9 m apart sown at 20,000 seeds/ha.

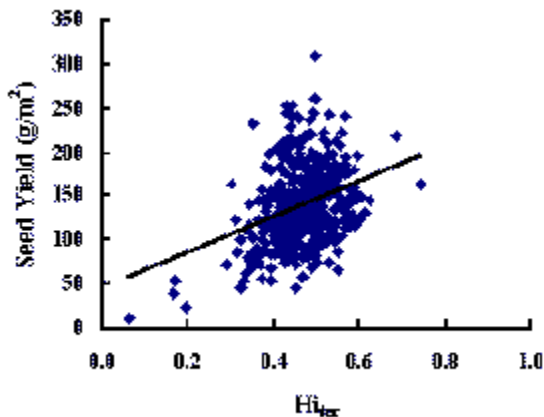
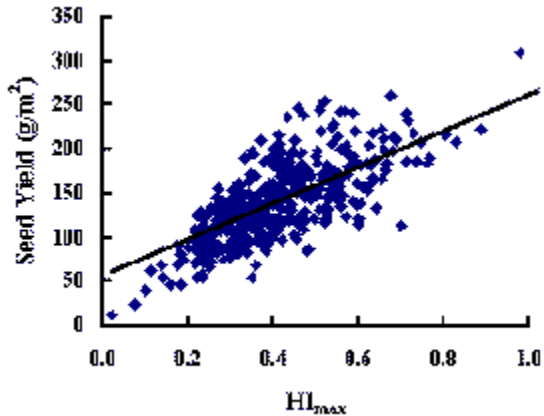
Measurements of the following parameters were made on each genotype: -maximum total biomass of at mid pod fill (BIO_{max}); total biomass at terminal maturity (BIO_{ter}.); specific leaf area (cm²/g) and seed yield (Y). HI was calculated both as the ratio of Y to BIO_{max} (HI_{max}) and as the ratio of Y to BIO_{ter} (HI_{ter}). WUE was estimated from the high correlation between WUE and SLA (4), while T was a derived variate from the above equation (see 1).

Results and discussion

Wide genetic variability was found for all traits. BIO_{max} had a 3 fold range from 100 to 660 g/m², while seed yield showed a similarly large range from 10 to 260 g/m². The range in WUE was from 2.9 to 4.5 g/mm/m², representing a large genotypic range (55%) for this species. Estimated T ranged from as low as 50 mm to greater than 200 mm. HI_{max} had a wide range from 0.1 to 0.7. Seed yield was significantly correlated with HI_{max}, which was derived from measurements of BIO_{max} ($r = 0.49$, Fig. 1), but was very weakly correlated with HI_{ter} based on measurements of BIO_{ter} ($r = 0.12$, Fig. 2). Accordingly, the correlation between HI_{max} and HI_{ter} was very poor ($r = 0.05$). These observations have significant implications for screening of HI in grain legumes which shed leaf biomass prior to physiological maturity. They suggest total biomass estimates are valid only if measured at maximum biomass, before significant

leaf loss and stem remobilisation have occurred. Estimates of HI based on total biomass measurements at maturity are not only erroneous but could lead to significant measurement errors, and hence lack of progress in selection of parents and screening of progenies.

Figure1: The relationship between seed yield and $H_{i_{max}}$ for a range of *P. vulgaris* germplasm. Figure 2: The relationship between seed yield and $H_{i_{ter}}$ for a range of *P. vulgaris* germplasm.



There was no significant association between T and WUE, indicating there was genetic independence and hence the possibility of combining high expressions of both traits as a breeding objective. Similarly, $H_{i_{max}}$ appeared to be independent of both T and WUE.

The results of this *P. vulgaris* germplasm evaluation suggest that there is scope for incorporation of the physiological components of yield under water limited conditions ($H_{i_{max}}$, WUE and T) to assist in the indirect selection for yield. A pilot breeding program utilising previously identified sources of high WUE, HI and T traits has begun at QDPI, Kingaroy.

Conclusions

Relatively simple estimates of crop physiological components of seed yield can be made on large numbers of genotypes/segregating progenies for very little extra investment in measurements and resources in conventional breeding programs. A case study for genetic variation in drought resistance traits in *Phaseolus vulgaris* is presented, and has shown that significant variation for T, WUE and HI exists and could be further exploited in plant improvement programs.

References

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