

Forage Breeding for Changing Environments and Production Systems: an Overview

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Abstract. The 4th International Symposium of Forage Breeding was held at AgriBio, The Centre for AgriBioscience, Melbourne Australia from 23–25 September 2013. More than 100 delegates from around the world attended the symposium which featured sessions on genetic resources and novel species, breeding and managing symbiosis, overcoming abiotic stresses, forage quality and nutritive value, breeding for new environments and production systems, biotic stresses and disease tolerance, economic impact of genetic improvement of forages, new traits and technologies in forage breeding and whole genome selection in forages.

Introduction

Producing meat, milk and wool profitably from ruminants worldwide is based on the efficient conversion of forage based nutrients. Rapid changes in land use patterns such as the intensification of dairy and prime lamb production in Australasia, the move to producing cattle in new environments associated with the conversion of the humid pampas of Argentina from grazing to cropping or the emergence of new industries such as biofuel production have all created challenges for forage based agricultural systems. Among these challenges is the need to more rapidly incorporate novel traits or species into systems and the need to increase the rate of genetic gain in breeding programs.

Meeting these challenges will require the integrated use of tools from molecular breeding (Smith *et al.* 2007) and quantitative genetics and breeding (Casler and Brummer 2008; Conaghan and Casler 2011) along with the need to describe genetic advances and the relative value of traits using terms that equate to their likely profitability on farm. The science of forage breeding now encompasses the ‘Omics-Based’ approaches such as genomics and metabolomics, with phenotypic analysis of key traits and the genetic and environmental effects on the expression of these traits, quantitative genetics and economics to develop new and improved cultivars for use in a broad range of production systems. The **4th International Symposium of Forage Breeding** brought together more than 100 experts to discuss these issues across the following themes:

- genetic resources and novel species
- breeding and managing symbiosis

- overcoming abiotic stresses, forage quality and nutritive value
- breeding for new environments and production systems
- biotic stresses and disease tolerance
- economic impact of genetic improvement of forages
- new traits and technologies in forage breeding
- whole genome selection in forages

In this introduction we do not mean to summarise the presentations in each of these themes but rather to integrate messages from some of the presentations against what we saw as some of the major themes of the conference and to refer the reader to published work in this edition and other sources for further detail.

Integrating novel technologies for the effective utilisation of traits from new species and symbiota

Forage breeding has long been based on the incorporation of novel genetic resources from new and existing species into breeding programs and commercial systems. For instance in Australia, subterranean clover (*Trifolium subterraneum*) and phalaris (*Phalaris aquatica*) are two species that have been the beneficiaries of germplasm introduction and characterisation to greatly extend zones of agronomic adaptation and improve seasonal growth patterns (Oram *et al.* 2009; Nichols *et al.* 2013). At ISFB 2013 this concept was exemplified and extended to the successful incorporation of molecular tools for interspecific hybridisation in white clover and the breeding of the perennial ryegrass/endophyte (*Neotyphodium lolii*) symbiosis in the plenary presentations by Profs Warren Williams

(Williams 2014) and German Spangenberg respectively and in the use of *Trifolium arvense* genes to develop transgenic white clover with increased condensed tannin production (Hancock *et al.* 2014). These examples of the use of modern tools such as molecular markers, genomic *in situ* hybridisation and transgenesis are examples of the successful convergence of molecular and classical techniques to solve challenges that have proven to be quite intractable in the past.

Breeding for persistence

Persistence can be viewed as the sustained productivity of perennial pastures and forage breeders are often challenged with the perception that modern cultivars are not always as persistent as older ecotypes despite (or because of) their improved productivity. We are now aware of several concerted efforts to improve the persistence and productivity of perennial pastures under grazing; including lucerne (*Medicago sativa* L.) (Bouton 2012); red clover (*Trifolium pratense* L.) (Ortega *et al.* 2014) and phalaris (Culvenor and Simpson 2014). In each of these cases great responses to selection have been achieved through evaluation, phenotyping and recurrent selection of plants under grazing in harsh environments as a consequence of the foresight of these breeders and those that support their research. Further efforts are required to elucidate the genetic and physiological basis of these changes to enable the development of improved phenotypic and genomic selection methodologies to improve the rate of genetic gain for this important pasture trait.

Valuing Genetic Gain and Improved Selection Methodologies

There is a resurgence of interest in quantitative genetics, economic evaluation of genetic gain and improved selection methodologies that culminate in whole genome selection in forages. The experience of those who pioneered genomic selection in dairy cattle will be invaluable as forage breeders develop the tools and strategies to incorporate this technology to greatly increase the rate of genetic gain in forages (Forster *et al.* 2014; Lin *et al.* 2014), critical to the success of these efforts will be improvements in the accuracy of phenotyping complex traits and the incorporate improved statistical models that more accurately estimate the true potential of forage genotypes (e.g. Real *et al.* 2014), with the ultimate aim of expressing this potential in terms of the impact in farming systems (Smith *et al.* 2014).

Conclusions

We were delighted by the quality and breadth of the papers and are certain that they will be a stimulus for scientific discussion and exchange and selected papers are published in this special edition

of *Crop and Pasture Science* that will be a valuable resource for forage breeders and geneticists into the future. This is an exciting time for forage breeders as we face the needs of breeding changing production systems and non-traditional uses such as biofuels and industrial products.

We thank the authors of these invited papers for contributing to this issue and also to the authors of the further 17 oral papers and 40 posters that were presented at the symposium.

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