A Proposal for an International Transcriptome Initiative for Forage and Turf: Microarray Tools for Expression Profiling in Ryegrass, Clover and Grass Endophytes

T. Webster
La Trobe University, Australia

N. Nguyen
Victorian Microarray Technology Consortium, Australia

C. Rhodes
La Trobe University, Australia

S. A. Felitti
Molecular Plant Breeding Cooperative Research Centre, Australia

R. Chapman
La Trobe University, Australia

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T. Webster, N. Nguyen, C. Rhodes, S. A. Felitti, R. Chapman, D. Edwards, and G. C. Spangenberg

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T. Webster[1,2], N. Nguyen[1,2], C. Rhodes[1,2], S. Felitti[1,3], R. Chapman[1,2,4], D. Edwards[1,3,4] and G.C. Spangenberg[1,2,3,4]
[1]Primary Industries Research Victoria, Plant Biotechnology Centre, La Trobe University, Bundoora, Victoria 3086, Australia [2]Victorian Microarray Technology Consortium, Australia [3]Molecular Plant Breeding Cooperative Research Centre, Australia [4]Victorian Bioinformatics Consortium, Australia
Email: german.spangenberg@dpi.vic.gov.au

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Introduction Knowledge of the expression pattern of genes provides a valuable insight into gene function and role in determining the observed heritable phenotype. High–density cDNA and oligonucleotide microarrays represent powerful tools for transcriptome analysis to gain an understanding of gene expression patterns for thousands of genes. Internationally coordinated efforts in transcriptome analyses and sharing of microarray resources will benefit the advancement of our understanding of gene function in forage and turf species.

Materials and methods Within a joint Pasture Plant Genomics Program co-funded by Agriculture Victoria Services Pty Ltd and AgResearch Ltd. (New Zealand), we have developed high-density cDNA microarrays representing over 15 000 unique genes for each perennial ryegrass and white clover (Sawbridge *et al*., 2003ab). Within the Molecular Plant Breeding Cooperative Research Centre, we have developed unigene microarrays allowing the interrogation of over 5 000 *Neotyphodium* and *Epichloe* genes (Nchip™ microarray and EndoChip™ microarray, Felitti *et al*., 2005).

Results Microarrays have been applied in hybridisations with labelled total RNA isolated from a variety of genotypes, plant organs, developmental stages, and growth conditions. The collated results enable validation of functions predicted through comparative sequence annotation and suggest roles for novel genes lacking comparative sequence annotation. We have applied this data to assess the expression of genes associated with selected metabolic pathways and developmental processes to dissect these at the transcriptome level and to identify novel genes co-regulated with template genes known to be involved in these processes. Furthermore, these microarrays have enabled applications for gene and promoter discovery when used in concert with BAC libraries established for each of the target species.

Conclusions An *International Transcriptome Initiative for Forage and Turf* (ITIFT) to facilitate international efforts in microarray-based transcriptome analyses for key forage and turf plants and their endosymbionts is proposed. The Plant Biotechnology Centre will support ITIFT contributing access to and transcriptional profiling with unigene microarrays for key forage and turf species, namely perennial ryegrass (*Lolium perenne*), white clover (*Trifolium repens*) and grass endophytes (*Neotyphodium*/*Epichloe*), as well as access to a range of platforms for microarray spotting, hybridisation and scanning operationally integrated through a Scierra laboratory workflow system. The Plant Biotechnology Centre further proposes to develop and maintain an ITIFT database with a web based front-end portal for secure access by the research community to appropriate data and information. Anyone interested in participating in, contributing to ITIFT or accessing ryegrass, clover and endophyte microarrays, should contact german.spangenberg@dpi.vic.gov.au.

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