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## **Quantitative trait loci for vegetative traits in perennial ryegrass (***Lolium perenne* **L.)** A.M. Sartie<sup>1</sup>, H.S. Easton<sup>1</sup>, M.J. Faville<sup>1</sup> and C. Matthew<sup>2</sup>

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**Introduction** Physiological (EP) research in forage grasses relates traits such as leaf elongation rate (LER), leaf elongation duration (LED), and leaf appearance interval (ALf), to forage yield (Chapman & Lemaire, 1993). This paper reveals preliminary quantitative trait locus (QTL) discovery for eight EP traits in perennial ryegrass. It also investigates the potential role of multivariate analyses such as principal component analysis (PCA) in QTL analysis of EP data.

**Materials and methods** A full-sib mapping population (n=200) created by pair-crossing plants from cv. 'Grasslands Impact' and cv. 'Grasslands Samson' (Faville *et al.* this volume) was replicated three times in a randomised complete block design glasshouse experiment. From April to June 2003, ALf, ligule appearance interval (ALg) and leaf length (LL) were recorded. Tiller number (TN) and plant dry weight (DW) above 25 mm were measured at the end of the experiment. Mean tiller weight (TW), and a productivity index (PI, Hernández Garay *et al.*, 1999), were derived from DW and TN. LER and LED were also calculated. Data were subjected to PCA. EP traits and PCA scores (PCs) were used for QTL discovery, by interval mapping (MapQTL 4.0).

**Results and discussion** Plants were significantly ( $p \le 0.001$ ) different for all traits measured. Twenty-two QTL were discovered involving all EP traits except TN (Table 1). The majority of the QTL occur on linkage groups (LG) 1, 3, 4 and 6, with single QTL on LG 2, 5 and 7. Plants varied significantly for the first three PCs yielded by PCA of EP traits (83% phenotypic variation explained, PVE). Generally QTL for PC's are well defined and co-locate with QTL for some but not all correlated traits. For example, PC2 (25% PVE) correlates most strongly with LL (R=0.60), while its strongest QTL co-locates with a QTL for TW, and PC3 correlates most strongly with DW (R=0.80) but co-locates with a QTL for LER. Future work will determine whether PC's, accounting in three parameters for most of the variation in nine EP traits, and located with well defined QTL, are repeatable over experimental conditions and between populations, and can be used in marker-assisted selection.

Table 1 Linkage groups, QTL peaks (cM), LOD scores and PVE for EP traits and PC scores			
LG	QTL peak (cM)	EP Trait (LOD; PVE)	PC (LOD; PVE)
	0.0	PI (3.0; 7.6)	PC2 (4.9; 7.7)
1	7.2	LER (3.7; 9.4), LL (7.4; 19.7)	
	22.5	ALg (3.7; 10.1)	PC2 (4.5; 10.0)
2	9.4	TW (3.2; 12.5)	
	36.1	ALf (3.4; 8.8), ALg (3.7; 9.3)	
3	45.7	LER (3.0; 8.0)	
	88.1	TW (6.2; 19.0)	PC2 (6.4; 20.5)
4	40.3	LED (7.9; 21.8), ALf (10.5; 26.4), LL (3.6; 9.3), ALg (5.8; 15.6)	PC2 (4.7; 12.6)
	43.5		PC1 (6.1; 15.0)
5	60.9	ALf (2.8; 10.4)	
	0.0	LL (4.0; 11.0)	PC2 (3.6; 8.6)
6	3.2	TW (3.2; 10.7)	
	16.4	ALf (3.6; 9.5), ALg (4.1; 10.5)	
	43.5	ALf (3.3; 10.4), ALg (3.9; 11.7), DW (3.9; 8.6)	PC1 (6.9; 12.5)
7	17.1	LER (4.0; 10.1)	PC3 (3.4;8.2)

Table 1 Linkage groups, QTL peaks (cM), LOD scores and PVE for EP traits and PC scores

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