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**Phenotypic assessment and quantitative trait
locus (QTL) analysis of herbage and seed
production traits in perennial ryegrass
(*Lolium perenne* L.)**

A thesis presented in partial fulfilment
of the requirement for the degree of

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Abstract

The aims of this study were to develop a genetic linkage map of perennial ryegrass, identify quantitative trait loci (QTL) for herbage and seed production traits, and to identify DNA markers associated with QTL for use in marker-assisted selection (MAS).

Major traits identified for herbage production were leaf elongation rate (LER), leaf lamina length (LL), tiller number (TN) and tiller weight (TW), and for increased seed production were seed yield per head (SdYH), reproductive tiller number (RT), reproductive tillers with matured heads (TMH), florets per head (FH), spikelets per head (SH), florets per spikelet (FS), floret site utilization (FSU) and seed weight (TSW).

A genetic linkage map spanning 582 centimorgans (cM) was constructed with EST-SSR (simple sequence repeat markers derived from expressed sequence tags) and used to identify QTL for herbage dry weight (DW) and seed yield per plant (SdYP), and their key component traits. Significant genotype by environment effects were encountered for herbage yield, with fewer QTL identified in spring than in autumn. For some traits, ranking of genotypes differed greatly between seasons and different QTL were identified.

QTL for DW were identified on linkage groups (Lg) 1 and 6. The QTL on Lg 6 co-located with QTL for TN, while that on Lg 1 co-located with LER and LL. Markers at Lg 1 QTL (qDW-03-1.1) may be more useful for increasing herbage production by MAS because selection for high LER and long LL has been suggested to increase herbage production in perennial ryegrass. QTL for SdYP were identified on Lg 2 and Lg 6. The QTL on Lg 6 co-located with QTL for SdYH, FSU and TSW, while that on Lg 2 co-located with FH, SH and FS. For seed production, markers at Lg 6 QTL (qSdYP-03-6) may be very useful because this QTL co-located with QTL for SdYH, FSU and TSW, and SdYH has been identified previously as a key selection criterion for increasing seed yield.

Marker-trait validation confirmed markers pps0495 and pps0698 identified by QTL analysis to be potentially useful for selecting for fast leaf appearance and long LL, respectively, in perennial ryegrass.

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Dedication

This thesis is dedicated to my father, Mr Moinina Sartie, mother, Mrs Mattu Jeneba Sartie and my children, Samuel Gbormuma Sartie, Cornelia Mattu Jeneba Sartie and Lucy Mubao Sartie.

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List of Abbreviations

ALf	leaf appearance interval (days)
ALg	ligule appearance interval (days)
ANOVA	analysis of variance
AFLP	amplified fragment length polymorphism
ATi	tiller appearance interval
BC	backcross
BLUP	best linear unbiased predictor
CAPs	cleaved amplified polymorphic sequence
CIM	composite interval mapping
cM	centiMorgan
DNA	deoxyribonucleic acid
DH	days to heading
EST-SSR	SSR markers that are derived from expressed sequence tags
DW	herbage dry weight (g)
F ₁	first filial generation
F ₂	second filial generation
FH	florets per head
FS	florets per spikelet
Fst	tiller site filling
FSU	floret site utilisation
Ha	hectare
H _b	broad sense heritability
I	Grasslands Impact cultivar
KgN/ha	kilograms nitrogen per hectare
L	litre
LAI	Leaf area index
LED	leaf elongation duration (days)
LER	leaf elongation rate (cm/day)
LL	leaf lamina length (cm)
Lg	linkage group
LOD	logarithm-of-odds ratio

LRS	likelihood ratio statistic
LS	leaf sheath length (mm)
LSD	least significant difference
LW	leaf lamina width (mm)
MAS	marker-assisted selection
MJ/m ² /day	micro joules per metre square per day
MQM	multiple QTL Mapping
NaCl	sodium chloride
n _r	number of replications
ns	number of seasons
PCA	principal component analysis
PC1	principal component 1
PC2	principal component 2
PC3	principal component 3
PCR	polymerase chain reaction
PGH	plant growth habit
PI	plant productivity index
QTL	quantitative trait locus
RAPD	randomly amplified polymorphic DNA
RCB	randomised complete block
RFLP	restriction fragment length polymorphisms
REML	residual maximum likelihood
Rpm	revolutions per minute
RT	number of reproductive tillers
S	Grasslands Samson cultivar
SCAR	sequence characterised amplified region
SdYH	seed yield per head (mg)
SDC	size-density compensation
SdYP	seed yield per plant (g)
SE	standard error of the mean
SH	spikelets per head
SIM	simple interval mapping
SIL	stem internode length (cm)
SL	spike length (cm)

SMC	soil moisture content
SNP	single nucleotide polymorphism
SOH	spread of heading
SSR	simple sequence repeat
STN	September tiller number
t DM/ha	tonnes dry matter per hectare
TN	tiller number
TSW	1000 seed weight (g)
TMH	% tillers with matured head
TW	tiller weight (g)
VT	vegetative tiller number
v/v	volume per volume
wt	weight
w/v	weight per volume
σ^2_g	genotypic component of variance
σ^2_ϵ	residual variance of means of genotypes
σ^2_{gs}	genotypic component of variance across season
λ	lambda