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Genetic variation in perennial ryegrass for root profile characteristics

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Abstract. Fifteen plants, replicated twice, of each of 20 half-sib families of perennial ryegrass were grown in deep sand tubes irrigated with a low ionic strength nutrient solution in a glasshouse. Top growth was measured. Roots were turned out, cut into 10 cm profile increments, washed free of sand, dried and weighed. For top growth, total root growth and root-shoot ratio, there were significant differences among families translating to narrow sense heritability coefficients between 0.3 and 0.4. However, the ratio between root in the top 10 cm and total root, and a parameter for a well-fitting exponential model describing root profile showed variation between individuals but very little or no variation between families. This translated to narrow sense heritability coefficients of less than 0.1.

Introduction

Breeding perennial ryegrass (*Lolium perenne* L.) for root characteristics that might improve nutrient efficiency in pastures has received little attention. Bonos et al. (2004) reported that two cycles of selection resulted in a substantial increase in root mass between 30 and 60 cm depth in cultivar Bastion tetraploid perennial ryegrass. Root/shoot ratios in ryegrass are very sensitive to nutrient supply conditions (Jarvis & Macduff 1989). At the onset of nitrogen deprivation, diploid perennial ryegrass can very rapidly lower the proportion of assimilates allocated to the shoot, and restoration of the incremental shoot weight ratio is also rapid once the nitrogen supply is re-established (van Loo *et al*. 1992). In van Loo's study, the ranking of three cultivars for root shoot ratio changed with nitrogen supply status, but one cultivar (Splendour) had the highest root/shoot ratios irrespective of nitrogen level. High genetic variation in shoot and root dry matter between individual genotypes of a full-sib mapping population of perennial ryegrass was reported by van Loo *et al*. (2003). Broad sense heritabilities were 0.48 and 0.46 for shoot and root weights, respectively.

Nutrient acquisition by pasture grasses is also influenced by root longevity (Wu *et al*. 2005), root responses to patchy nutrient supply (Grime *et al*. 1991), and competition from other plants (Fitter 1976). No references to possible genetic variation within ryegrass have been found for any of these parameters. In the work reported here, variation in root mass distribution was determined for 20 half-sib families of perennial ryegrass. Competition between plants was avoided by growing plants in individual tubes, and trimming the shoots to avoid interference above ground. Root temperature and nutrient supply were controlled to minimise any possible variation between families in root longevity/temperature relationships, or response to nutrient supply perturbations.

Materials and methods

Plant material

Two clonal replicates of 15 genotypes from each of 20 half-sib families from an open pollinated breeding pool of perennial ryegrass were used. Individual tillers were taken from the stock plants, and the leaf laminae trimmed to one-third, and nodal roots to 5mm, before each tiller was weighed.

Experimental system

Details of the method for recording vertical root mass distribution by depth are in Crush *et al*. (2005). Briefly plants were grown from tillers in 1m deep × 90 mm diameter tubes of sand irrigated daily with 100 ml of a low ionic strength nutrient solution based on the chemical composition of the soil solution in New Zealand pasture topsoils (Blamey *et al*. 1991). Average day/night temperatures during the experiment were 18ºC and 12ºC. Day length was maintained at 12 h with supplementary lighting between 6 and 8am, and 4 and 6 pm.

The shoots were trimmed once after 71 d growth and the clippings dried and weighed. The plants were harvested after 104 d growth. Shoots were severed from the roots at the tiller base, oven dried and weighed. To extract the roots, the vertically hinged tubes were opened, and the sand/root column was cut into 10 cm increments. The sand was washed away and the roots were collected, re-washed to remove fine sand, and dried and weighed.

Statistical analysis

The data were analysed using the REML procedure of GenStat 8 (Eighth Edition, Version 8.1.0.154), with all factors considered to be random effects. All interactions of families with rows, columns and blocks were examined and were not significant. Shoot weights required square root transformation for analysis, and the means presented are back transformed from the square root scale. Root weights and root:shoot ratios both required log transformation and the back transformed means, without bias correction, are presented with a least significant ratio. For both the shoot and root weight data the initial tiller weight was used as a covariate. An exponential model ($Y=A+B.R^x$) was fitted to the root weight data over the depths. Details of the procedure are in Crush *et al*. (2005). The decay constant (R) from the exponential model was log transformed after being subtracted from 1. The means presented are those back transformed from the log scale (without bias correction) along with the least significant ratio. The proportion of roots in the top 10 cm did not require transformation before analysis.

Results

There were significant ($P< 0.001$) family effects for shoot dry matter (DM) and root DM (Table 1). Plants in family 10 had the heaviest shoots and roots, and family 18 had the lightest shoots and roots. The range in average size was 37% for shoots and 49% for roots. Shoot and root DM were significantly but not closely correlated across families ($R^2 = 0.63$) and there were significant ($P<0.001$) family effects on root/shoot DM ratios (Table 1). Root/shoot ratios varied from 0.43 (family 8) to 0.55 (family 11).

There were no significant over all effects of family on the pattern of root mass distribution down the profile. The range of values for the percentage of total root mass recovered from the 0-10 cm profile was 47-51% across all families (Table 1) with an $LSD_{0.05}$ of 2.5. Family 8 had the highest R value (0.1034) for the exponential model fitted to root mass distribution. This value was significantly higher than the mean value for the eight families (families 2, 3, 6, 9, 13, 14, 15, and 17) with the lowest R values (Table 1). The R values for these eight families did not differ significantly from the R value for family 20 which had the second highest value.

Discussion

There was significant variation among families for growth in shoot weight and root weight, and for root/shoot ratio. While shoot and root dry weights were positively correlated, there was significant ($P<0.05$) variation in root weight, independent of shoot weight, indicating the potential for specific genetic improvement of the root system. Within the controlled conditions of this experiment, the narrow-sense heritabilities for shoot weight, root weight and shoot-root ratio were respectively 0.41, 0.35, 0.29, indicating the potential for genetic improvement of these traits. This experiment gives no assessment of genetic interaction with environment, but similar heritabilities were also reported for root mass in ryegrass by van Loo *et al*. (2003). Both sets of results indicate that ryegrass could be selected for greater investment in the root.

There was no evidence of variation between families in parameters reflecting distribution of root mass with depth. There was substantial variation between plants within families for these parameters. Perennial ryegrass is an out breeding species, and breeding populations encompass considerable genetic diversity. This is usually reflected in a largely additive control of genetic variation (Breese & Hayward 1972), which distinguishes families as well as individuals within families. The breeding population studied here had not been previously selected for root traits. The large variation between individuals, which was not reflected in family variance, was therefore unexpected, particularly as Bonos *et al*. (2004) reported a substantial increase in root mass between 30-60 cm in a turf ryegrass after only two cycles of selection.

The wide extent of genotypic variation in vertical distribution of root mass may reflect the evolution of root systems under the small scale spatial heterogeneity of grassland soils. Grass populations with highly variable root vertical distributions would be more successful under conditions of intermittent nutrient and water supply, and sporadic root herbivory. In high input contemporary pastures, edaphic variations may have been sufficiently minimised to allow selection for a narrower range of root shapes that would give optimum plant performance per unit investment in root mass.

Table 1. Family means for shoot and root DM (mg), root/shoot DM ratios, percentage of total root mass in the top 10 cm, and values of the coefficient R for the equation $Y = A + BR^x$ fitted to the root mass vertical distribution data.

Family	Shoot	Root	Root/shoot	$\text{Roots}_{0\text{-}10}$	R
1	1254	537	0.44	49.7	0.0970
2	1244	561	0.47	47.3	0.0947
3	1277	665	0.54	49.5	0.0915
4	1121	531	0.50	49.4	0.0964
5	1385	603	0.46	49.7	0.0973
6	1238	549	0.46	48.0	0.0919
7	1217	555	0.47	49.5	0.0985
8	1283	534	0.43	51.1	0.1034
9	1339	613	0.48	47.7	0.0925
10	1500	730	0.50	51.0	0.0961
11	1320	714	0.55	51.6	0.0969
12	1335	664	0.50	49.3	0.0962
13	1249	649	0.53	49.2	0.0933
14	1124	529	0.49	51.1	0.0942
15	1252	557	0.46	48.5	0.0931
16	1342	586	0.46	51.3	0.0984
17	1123	517	0.47	49.2	0.0936
18	1093	495	0.47	50.7	0.0962
19	1250	605	0.50	48.8	0.0977
20	1095	490	0.47	50.6	0.0987
$\text{LSD}_{0.05}$	134.5				
$\text{LSR}_{0.05}$		1.16	1.10		1.08

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