QTL Analysis of Mineral Content in Perennial Ryegrass (*Lolium Perenne* L.)

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Introduction Variation in mineral content of grasses can be strongly influenced by genetic factors. Grass tetany (hypomagnesemia) of cattle and sheep is due to disturbances in serum magnesium levels. In Southern Australia, resultant levels of mortality in cattle vary between 0.5-1.5% of total stock numbers. Serum magnesium variation may be due to feed deficits, or dietary imbalances that interfere with magnesium metabolism. High levels of potassium appear to exert negative effects on the levels of magnesium in the blood. Italian ryegrass genotypes with high levels of magnesium can alleviate the incidence of grass tetany. The genetic control of mineral content, including magnesium, in perennial ryegrass has been investigated using molecular marker-based analysis.

Material and methods The p150/112 population, which formed the basis for reference map construction through the International Lolium Genome Initiative (ILGI), and the second generation reference mapping population [F_1(NA$_6$xAU$_6$)] were used for phenotypic analysis. The F_1(NA$_6$ x AU$_6$) mapping population is based on a two-way pseudo-testcross structure, generating two parental genetic maps, and is largely populated by gene-associated markers. The maps of each population have been aligned through common simple sequence repeat (SSR) markers. Mineral content in each population was assessed through the use of inductively-coupled plasma mass spectroscopy (ICP-MS). The p150/112 population was sampled in Hokkaido Japan, while the F_1(NA$_6$ x AU$_6$) population was sampled in Hamilton, Australia.

Results A total of 14 mineral content traits were examined and heritability values were calculated varying from 0.19 to 0.75. QTL analysis based on simple interval mapping (SIM) and composite interval mapping (CIM) permitted the identification of a total of 68 QTLs. These QTL identified coincident regions of the genome associated with content level variation for several different mineral traits, with a number of common regions apparent across the three different genetic maps (Fig 1). This analysis provides the basis for targeted marker-assisted breeding for mineral content traits in pasture grass improvement.
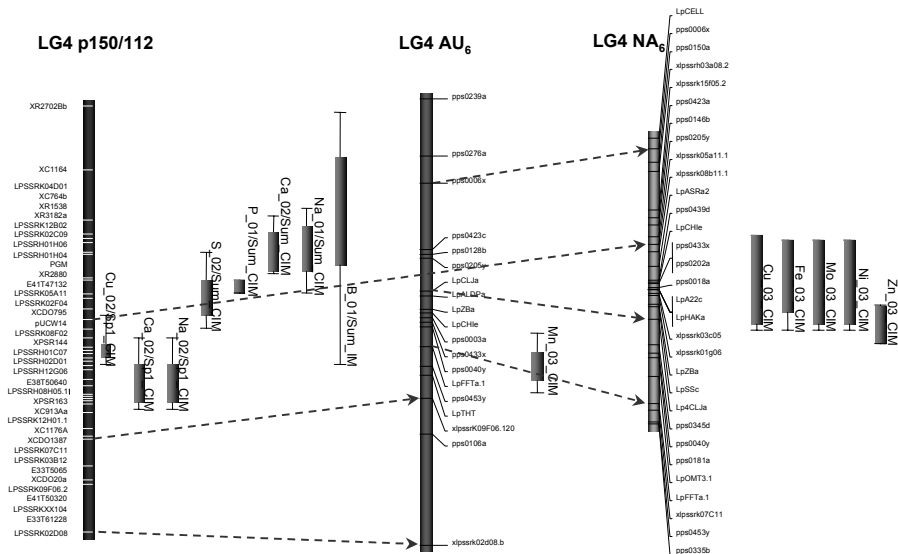

Figure 1 Selected linkage groups from the mapping populations p150/112 and F_1(NA$_6$xAU$_6$), with QTL regions controlling mineral content indicated. Common markers are shown for comparison of co-locations.