Genomic Constitution of the New Zealand *Triticeae*

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Abstract: The New Zealand flora contains 3 genera within the *Triticeae*, *Elymus, Australopyrum* and *Stenostachys*. The genomic constitution of the New Zealand hexaploid *Elymus* has been previously determined as StYW, the *Australopyrum* as W and *Elymus enysii* as HW (Svitashev *et al*. 1998; Edgar & Connor 2000). To date the genomic constitution of the tetraploid *Stenostachys* has been unknown, but this research suggests it is HW.

Keywords: New Zealand; *Elymus; Stenostachys*

New Zealand *Elymus* and *Stenostachys* species were studied using the sequences of the trnL (UAA) gene intron of chloroplast DNA (cpDNA) and the internal transcribed spacer (ITS) region of nuclear ribosomal DNA. The cpDNA region was PCR-amplified using primers c and d (Taberlet *et al*. 1991), while the ITS region was PCR-amplified using primers EC-1 and EC-2 (Williams *et al*. 2001). PCR products were purified and sequenced directly. DNA sequences were aligned, with manual adjustment to optimise alignments where necessary, using MegAlign (DNASTAR). Maximum parsimony analyses were performed using heuristic PAUP* (version 4.0b10; Swofford 2002), and nodal support was estimated using 100 bootstrap replicates.

The analysis of the ITS sequences placed the New Zealand species in two distinct clades (Figure 1). The first containing the hexaploid (*solandri, sacandros, falcis, apricus, multiflorus*) and octoploid (*tenuis*) *Elymus* species and the second containing the three tetraploids *Stenostachys laevis, S. gracilis* and *Elymus enysii*, and the diploid *Australopyrum* species, *A. calcis* from New Zealand and *A. pectinatum* from Australia. The *Hordeum* species, with the H genome, appear as a sister group to the rest of the *Triticeae* species.

Since the *Elymus* species did not form part of the *Pseudoroegneria* clade, we interpret this to mean that ITS majority sequence in the hexaploid and octoploid *Elymus* clade is possibly the Y genome, while the majority ITS sequence in the clade containing *Australopyrum, Stenostachys* and *E. enysii* is the W genome.

The analysis of the cpDNA sequences placed the New Zealand taxa in three distinct but different clades (Figure 2). The first clade contains the *Stenostachys* spp. and *Elymus enysii*, the second clade contains the *Australopyrum calcis* and the third clade contains the hexaploid *Elymus solandri, E. multiflorus* and *E. sacandros*. GenBank searches of non-New Zealand species with closely aligning sequences show that both the *Stenostachys* spp. and *Elymus enysii* form a clade with many H genome *Hordeum* species.

The cpDNA result suggests that the maternal genome of the tetraploid *Stenostachys* species and *Elymus enysii* is the H genome.

These results suggest that the genomic constitution of *Stenostachys* is HW, the same as *Elymus enysii*. The results obtained for New Zealand hexaploid *Elymus* species is consistent with previous publications of StYW. Furthermore, both analyses suggest that the Australasian *Australopyrum* and the Eurasian *Agropyron* are sister groups.

GB = sequence obtained from GenBank
The *Poa pratensis* sequence was specified as an out-group. Bootstrap values are shown for major clades; letters refer to the probable Genomes

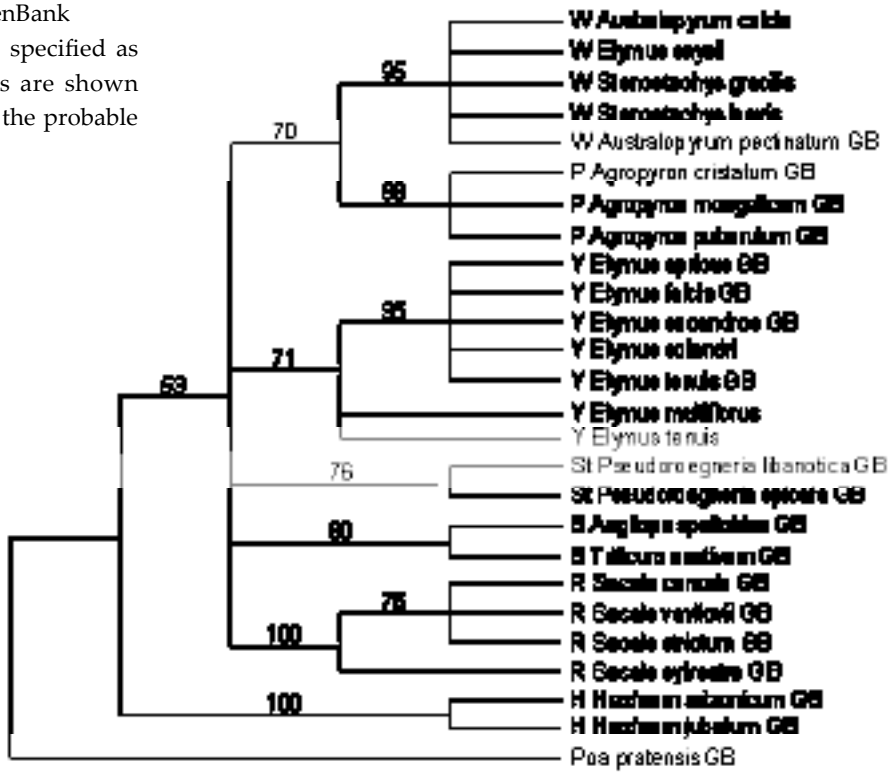

Figure 1. ITS strict consensus tree based on maximum parsimony analysis

GB = sequence obtained from GenBank
The *Poa pratensis* sequence was specified as an out-group. Bootstrap values are shown for major clades; letters refer to the probable Genomes

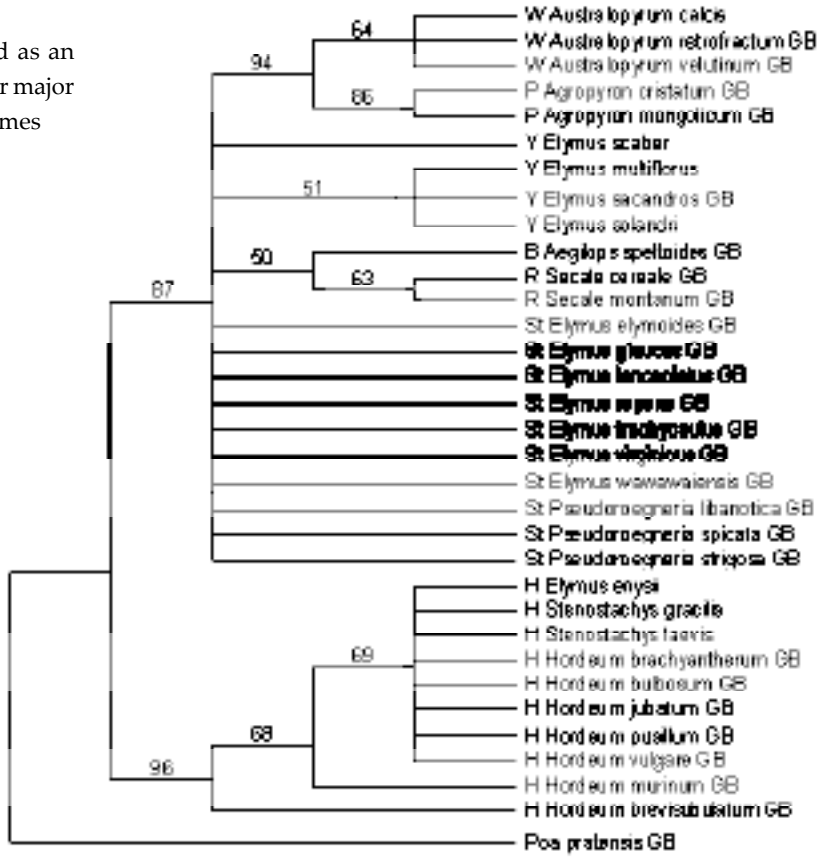

Figure 2. cpDNA strict consensus tree based on maximum parsimony analysis

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