

The Ns-genome specific DNA sequences from *Leymus*

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The Ns-genome specific DNA sequences have been isolated from two *Leymus* species: *L. mollis* and *L. arenarius*. Five out of six clones characterized, i.e. pLmIs1, pLmIs44, pLmIs51, pLmIs53 and pLaIs56, are dispersed retrotransposon-like repeats, and one (pLaIs7) is a chloroplast gene. These sequences are highly specific to *Leymus* and *Psathyrostachys* as they hybridize essentially to these species, while little or no signal can be detected in other Triticeae species. Fluorescence *in situ* hybridization (FISH) mapping of these sequences shows that they are dispersed indiscriminately over all chromosomes. Southern hybridization experiments using total genomic DNA as probes confirm that there is nothing else in the *Leymus* genomes but Ns-genomic DNA. Based on these evidence, *Leymus* must be considered autopolyploid having the (Ns)_n genome designation or segmental allopolyploid consisting of a variation of the basic N^s-genome. To examine further how species in these two genera are related, genetically and genomically, and to what extent the basic Ns-genome has distributed in the Triticeae, we have included in the study more than 30 species and accessions of known, or suspected, to have the Ns-genome. Restriction fragment length polymorphisms (RFLPs) generated by these Ns-genome specific sequences are used to construct phylogenetic trees, and as expected the Ns-genome is clearly differentiated from all other genomes examined. This Ns-genome cluster includes all of the *Leymus*-*Psathyrostachys* species, except two accessions that have been misidentified. *Hordelymus* and *Hystrix* (one species) have the *Leymus* Ns-genome. Furthermore, the Ns-genome cluster appears to divide into two major groups: one containing all Eurasian *Leymus* species and the other comprising the rest, i.e. N-American and Asiatic *Leymus*, all species of *Psathyrostachys*, and other Ns-genome species.

References:

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