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Allelic share among two taxonomically related *Elymus* species , hexaploid *E. nutans* Griseb and tetraploid *E. burchan-buddae* (Nevski) Tzvelev

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Key words : *E. nutans* , *E. burchan-buddae* , ploidy , allelic frequency , genome , AFLP

Introduction Two taxonomically related *Elymus* species , *E. nutans* Griseb and *E. burchan-buddae* (Nevski) Tzvelev , are among the most abundant perennial grasses and widely distributed across the north western China . The two *Elymus* species are very similar in their morphology , although the important character that distinguishes them with certainty is chromosome number and genomic constitution (Lve , 1984) as *E. nutans* is hexaploid ($2n=6x=42$, StStYYHH) and *E. burchan-buddae* tetraploid ($2n=4x=28$, StStYY) . Effects of different ploidy genome on the plant genetics have been paid more attention . This study is to test the consanguinity between two *Elymus* species with different ploidy through shared AFLP (amplified fragment length polymorphisms) allelic frequencies , and induce the causal genome of .

Materials and methods Seed samples (30 seeds of each population used for DNA preparation) of fourteen populations of *Elymus nutans* Griseb ($2n=6x=42$, StStYYHH) and eight populations of *Elymus burchan-buddae* (Nevski) Tzvelev ($2n=4x=28$, StStYY) were collected from the Qinghai-Tibetan Plateau in Maqin County (N34°29'-34°33' , E100°23'-100°31' , altitude from 2800m to 4100 m) , Qinghai Province , China . Fluorescent AFLP was amplified using IRDye® Kit on the DNA sequencer LI-COR-4300 (LI-COR Biosciences Inc . , Lincoln , NE , USA) . We have used the Structure software (V 2 . 1) described in detail by Falush et al . (2003) , which records the allele frequencies in a hypothetical "ancestral" population .

Results and discussion

Above 5% probability of allele frequency as a criterion , 84 . 29% of all allele were shared by two different ploidy *Elymus* plants . The rest unshared were rarely found in tetraploid *E. burchan-buddae* , however the alleles shared were common detected in hexaploid *E. nutans* (Figure 1) . Comparing the allele frequency and base pair for two different ploidy *Elymus* species separately , it was found that hexaploid *E. nutans* with St , H and Y genomes had the 1 . 45 times of alleles frequency and more bands of large size than those of tetraploid *E. burchan-buddae* with St and Y genomes . The results demonstrated that tetraploid *E. burchan-buddae* contained a few rare alleles and large bands that were commonly present in hexaploid *E. nutans* . A slightly higher allele number per locus and frequency had been detected in hexaploid *Triticum aestivum* compared to the tetraploids (Alamerew et al . , 2004) . This confirmed our hypothesis before experiment which higher genetic variability in hexaploid *E. nutans* than tetraploid *E. burchan-buddae* . In *Elymus* genus , Y genome may have similar genera origin and evolution history to St genome (Lu and Björn , 2004) .

Conclusions We can deduce that it is H genome that leads to resultant difference in allele frequency and richness among two taxonomically related *Elymus* species , hexaploid *E. nutans* and tetraploid *E. burchan-buddae* .

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It seemed that extra H genome had brought complexity to the whole genetic pool of hexaploid *E. nutans* .

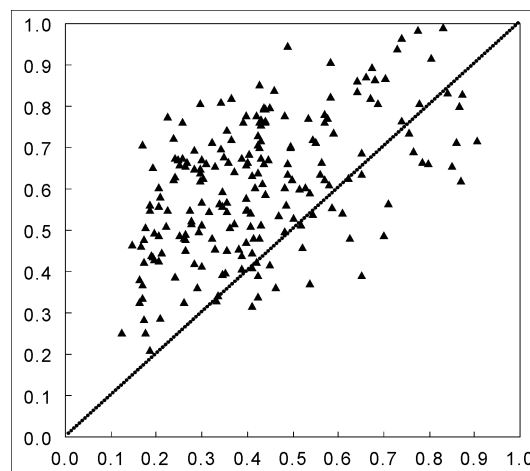


Figure 1 Comparisons of each allele frequency between tetraploid *E. burchan-buddae* and hexaploid *E. nutans* . X axis represents the frequency of one allele in tetraploid *E. burchan-buddae* . Y axis shows the frequency of the same allele in hexaploid *E. nutans* .