Geographic Patterns in the Genetic Diversity of Elymus Species From Qinghai-Tibetan and Inner Mongolian Plateau

Xuebing Yan
Zhengzhou College of Animal Husbandry, China

Yuxia Guo
Henan Agriculture University, China

Z. He
China Agricultural University, China

W. Kun
China Agricultural University, China

The XX International Grassland Congress took place in Ireland and the UK in June-July 2005. The main congress took place in Dublin from 26 June to 1 July and was followed by post congress satellite workshops in Aberystwyth, Belfast, Cork, Glasgow and Oxford. The meeting was hosted by the Irish Grassland Association and the British Grassland Society.

Proceedings Editor: D. A. McGilloway

Publisher: Wageningen Academic Publishers, The Netherlands

Geographic patterns in the genetic diversity of Elymus species from Qinghai-Tibetan and Inner Mongolian Plateau

Y. Xuebing[1,2], G. Yuxia[3], Z. He[1] and W. Kun[1]
[1]China Agricultural University, Beijing 100094, PRC, Email: yxbbjzz@163.com, *[2]Zhengzhou College of Animal Husbandry, zhengzhou 450002, PRC, [3]Henan Agricultural University Zhengzhou 450002, China,*

Keywords: *Elymus*, genetic diversity, allozyme, SSR, geographic variation

Introduction The genus *Elymus* is the largest genus in the tribe Triticeae with about 150 species distributed in most temperate regions of the world (Dewey, 1984). The genetic diversity of *Elymus* spp. from alpine regions is very important for improving resistance to adverse condition. The goals of this study were to investigate micro-satellite and enzyme polymorphism and population structure of different regions and *Elymus* spp. in China.

Materials and methods Forty eight natural populations of 10 *Elymus* spp. from different elevations of the Qinghai-Tibetan Plateau except for 8 populations of 3 spp. from the Inner Mongolian Plateau were examined for morphological, allozyme, micro-satellite (SSRs) markers.. Five enzyme systems, alcohol dehydrogenase (ADH), aspartate amino transferase (AAT), Aryl esterase (EST), peroxidase (PRX) and malic dehydrogenase (MDH), were analysed against five plants of each population. SSR variations were observed using six primer pairs specific for *Elymus* spp., ie. ECGA22, ECGA210, ECGA125, EAGA13, EAGA53, EAGA101, described by Sun *et al*. (1998a,1998b). Diversity analyses were performed against 48 populations using SPSS ,the software package Popgene and NTSYS-PC program for morphology, allozyme and micro-satellite, respectively. To graphically display the relationship of the spp. and populations, a dendrogram was generated from a pair-wise distance matrix using an unweighted pair group method with arithmetic average (UPGMA) (Rohlf, 1993).

Results The five enzyme systems and six SSR markers assayed in this study were found to be encoded by 14 loci and 28 alleles, respectively. Data of allozyme showed that the average total genetic diversity (*H*T) was 0.37, ranging from 0.23 to 0.48. The mean within population component of diversity (*H*S) was 0.03, ranging from 0.0 to 0.07. The mean gene diversity among populations (*D*ST) and species were 0.34 and 0.47, ranging from 0.21 to 0.41 and 0.27 to 0.62. The proportion of total genetic variation among populations (*G*ST) was, on average, 0.92. For micro-satellites, a total of 28 alleles were found at the six loci analyzed. Among all spp. and populations, the percentage of polymorphic loci was 100% expected heterozygosis and Shannon's Information index were 0.25 and 0.38. Between populations of each species, the percentage, heterozygosis and Shannon's Information index ranged from 16.67 to 83.33, 0.07 to 0.37 and 0.10 to 0.53, respectively (Table 1). Primer pair ECGA22 amplified six fragments in many species. The others produced one to four polymorphic markers. All amplified products were within the range of 100-500bp.

Table 1 *Micro-satellite diversity of Elymus spp. at different levels*

		%	h*	I*
Elymus level		100.00	0.25	0.38
	E.nutans	50.00	0.13	0.20
	E.sibiricus	66.67	0.21	0.30
Species	*E.breviaristatus*	50.00	0.17	0.25
	E.purpuraristatus	66.67	0.21	0.30
level	*E.cylindricus*	83.33	0.37	0.53
	E. glaucus	50.00	0.19	0.27
	E.geminatus	50.00	0.19	0.27
	E.tangutorum	16.67	0.07	0.10
	E.atratus	33.33	0.14	0.20
	E.submuticus	33.33	0.18	0.21

h* =Nei's (1973) gene diversity, I* = Shannon's Information index

Conclusion The majority of the total genetic diversity of selfing *Elymus* spp. reside among populations based on allozyme analyses. This also indicates a high degree of differentiation among the populations. Micro-satellite is useful for differentiating very close species.

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