

## Genetic diversity evaluation of *Roegneria kamoji* Ohwi germplasm from different ecoregions in China

Z. Xu<sup>1</sup>, H. J. Xiao<sup>2</sup>, D. Michalk<sup>3</sup>

<sup>1</sup>Grassland Research Institute of CAAS, Hohhot, Inner Mongolia, 010010, P.R. of China; <sup>2</sup>Beijing Agricultural Vocational college, Beijing, P.R. of China; <sup>3</sup>NSW Department of Primary Industries, Orange Agricultural Institute, Orange NSW Australia, 2800. E-mail: yxuzhu@yahoo.com.

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**Introduction** *Roegneria kamoji* Ohwi (2n=6x=42) has many excellent characteristics, but little is known about its genetic diversity. The goal of this study was to identify the genetic differences among 90 specimens of *R. kamoji* collected from 8 geographical groups (8 provinces, including Yunnan, Sichuan, Gansu, Xinjiang, Inner Mongolia, Ningxia, Hebei, Shanxi) in China using morphology marker; Gliadins marker and DNA marker. We also studied the correlations between genetic diversity and five ecological factors (longitude, latitude, altitude, AMT and AMP).

**Materials and methods** At the same time, morphological data were collected for 15 quantitative characters we also tested the genetic diversity based on Gliadins marker and DNA marker and tested with A-PAGE and ISSR. Statistical analyses were conducted with SPSS11.5, NTSYS-pc and Popgene Version 32.

**Results** The diversity indices based on a morphology marker, Gliadins marker, and DNA marker are shown in table 1. From table 1 we can conclude that the genetic diversity of *Roegneria kamoji* Ohwi is very abundant, the diversity index of inter-population is higher than that of intro-population, and variation within population is the main reason for variation of *Roegneria kamoji* Ohwi. The genetic diversity of Yunnan and Sichuan specimens was higher than for the rest of the collection, so we can deduce that Sichuan and Yunnan are the diversity center of *Roegneria kamoji* Ohwi in China. This conclusion agrees with that of Cai (Cai L B, 2002).

**Table 1** The comparisons of Shannon's index based on three markers among *Roegneria kamoji* Ohwi germplasm

Region	Yunnan	Sichuan	Xinjiang	Gansu	Inner Mongolia	Ningxia	Shanxi	Hebei	TG	WP	AP
a	1.374	1.572	1.371	1.321	1.271	1.228	0.875	0.854	1.781	1.355	0.426
b	0.717	0.666	0.604	0.577	0.592	0.458	0.243	0.241	0.726	0.512	0.214
c	0.674	0.593	0.368	0.217	0.453	0.145	0.234	0.079	0.471	0.345	0.126

Note: a: Morphological marker index, b: ISSR marker index, c: Gliadins marker index, TG: Total genetic diversity, WP: Genetic diversity within population, AP: Genetic diversity among population.

Pearson correlation coefficient showed that there is significant correlation between diversity index and altitude, latitude, mean rainfall, this fact suggested that altitude, latitude and rainfall play an important role in shaping patterns of morphological variations in *Roegneria kamoji* Ohwi. Cluster analysis by the un-weighted pair group method for arithmetic averages (UPGMA) indicated that the relationship among 90 specimens was closely correlated with the sites where the plant materials were collected.

**Conclusion** (1) The variation within populations was significantly higher than that between populations, which was the main cause that resulted in variation of *R. kamoji* germplasm resources. (2) Sichuan and Yunnan are the diversity center of *Roegneria kamoji* Ohwi in China. (3) The genetic diversity was also correlated with latitude and altitude. (4) Cluster analysis showed that some materials from the same regions could cluster together, the longer their geographical distance, the closer their relationship.

### Reference

Cai L. B., 2002. The geography distribution of *Roegneria*. Acta Bot. Boreal. Occident. Sin., 22(4): 913-923.