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Hongyan Li

Chinese Academy of Agricultural Sciences, China

Zhiyong Li

Chinese Academy of Agricultural Sciences, China

Fugui Mi

Inner Mongolia Agricultural University, China

Xinxiong Lu

Chinese Academy of Agricultural Sciences, China

Hongmei Ning

Inner Mongolia Agricultural University, China

See next page for additional authors

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Presenter Information

Hongyan Li, Zhiyong Li, Fugui Mi, Xinxiong Lu, Hongmei Ning, Wengui Shi, and Xingyou Li

Genetic diversity of *Medicago Ruthenica* in Inner Mongolia on using SSR markers

LI Hong-yan^{1,2}, LI Zhi-yong¹, MI Fu-gui^{2*}, LU Xin-xiong³, NING Hong-mei², SHI Wen-gui¹, LI Xing-you¹

¹ Grassland Research Institute, CAAS, Hohhot, Inner Mongolia 010010 P.R. of China;

² College of Ecol. and Env. Sci., Inner Mongolia Agric. Univ., Hohhot, Inner Mongolia 010018 P.R. of China;

³ Institute of Crop Science, CAAS, Beijing 100081 P.R. of China

* Corresponding author E-mail: mfgui@yahoo.com.cn

Key word : *Medicago Ruthenica*, SSR, genetic diversity

Introduction *Medicago Ruthenica* is a perennial leguminous herb, characterized by its eco-wide adaptability, barren resistance, cold resistance, drought resistance and high nutritional value. In this study, we used SSR molecular markers to categorize wild *Medicago Ruthenica* of Inner Mongolia for the first time, and suggest a theoretical foundation for the research of wild *Medicago Ruthenica*.

Materials and methods The germplasm of *Medicago Ruthenica* originate from National forage Germplasm Medium Term Gene Bank in the Institute of Grassland of Chinese Academy of Agricultural Sciences. Six populations of *Medicago Ruthenica* were collected from 6 different range areas in Inner Mongolia, XiMeng (XM), TongLiao (TL), ChiFeng (CF), suburbs of Huhhot (HJ), TouZuoQi (TZQ) and Da Qing Shan (DQS). All of these specimens were planted on experimental fields in south suburbs of Huhhot. Total DNA was extracted using an improved standard CTAB from young leaflets of 148 individual *Medicago Ruthenica*. And then used for SSR amplification. The amplification results showed that the polymorphic 18 primer pairs screen from 89 primer pairs of SSR primer in the model legume *Medicago truncatula* from EST database. The data was analyzed by Popgen32 software for UPGMA cluster analysis.

Results 6 different populations of *Medicago Ruthenica* were abundant polymorphism in SSR products. The 18 primer pairs amplified in 148 individuals and produced a total of 109 site, distinct statistics and publication bands. The polymorphic site of XiMeng (XM) population is 104, while the highest ratio is 95.41%. The polymorphic site of TouZuoQi (TZQ) population is 86, while the lowest ratio is 78.90%. The result of populations cluster analysis indicated that genetic homogeneity ranged from 0.9971 to 0.9827, genetic distance ranged from 0.0174 to 0.0029. The populations of ChiFeng (CF) and Xi Meng (XM) have the highest genetic amount of similarity, the nearest genetic distance.

Conclusion The result of genetic distance cluster indicated that populations with similar ecological and geographical conditions prior to cluster.

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