Morphological Variation and Genetic Patterns of Bermudagrass along Longitudinal and Latitudinal Gradients

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This complex environmental heterogeneity coupled with the long-standing history offers scenarios suitable for and favoring the evolution and existence of variation of morphological traits. Understanding the population genetic pattern and process of gene flow requires a detailed knowledge of how landscape characteristics structure populations. Geographic patterns in morphological variation and ploidy level of 570 *Cynodon dactylon* (L.) Pers. (common bermudagrass) individuals sampled from 28 geographic sites along a latitudinal and longitudinal gradient across China were observed. Genetic diversity and structure within these collections was estimated via expressed sequence tag-derived simple sequence repeat (EST-SSR). Considerable variations in morphological traits were observed at different longitudes and latitudes. Larger morphological sizes of *C. dactylon* appeared at the low and high-latitude regions, while the leaves of the erect shoot and the internode length enlarged significantly with the collection sites moving from east to west. Higher within-population genetic diversity appeared at low-latitude, as well as having positive correlation with temperature and precipitation. No isolation by distance and notable admixture structure existed among populations along latitudes, but low gene flow means a rich genetic differentiation among populations of *C. dactylon* along longitudinal gradient. The genetic diversity increased with the ploidy level of *C. dactylon* at different latitudes, suggesting polyploidy creates higher genetic diversity. Groups of individuals with the same ploidy at different longitudes were separated further away by genetic distance along with the increasing ploidy levels. The findings of this study are related to landscape population evolution, polyploidy speciation, preservation, and use of bermudagrass breeding.



Research Biography

Xuebing Yan received his PhD degree on grass science from China Agricultural University in 2005. He belonged to the Henan Agricultural University from 2007 to 2018 and had experience in the USDA Forage and Rangeland Research Lab, in the USA from 2013 to 2014. Since 2018, he has belonged to the College of Animal Science and Technology, Yangzhou University as a distinguished Professor. His research interest is to study the population genetic differentiation of grass and the forage processing and utilization.