Analysis of Genetic Relationships in Germplasms of Mugua in China Revealed by Internal Transcribed Spacer and its Taxonomic Significance

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Genetic relationships were studied among eight species of three taxa in the genus *Chaenomeles* by nuclear ribosomal internal transcribed spacer (ITS) analysis. A genetic distance matrix based on ITS sequences was estimated according to the formula of Kimura-2 parameter and a neighbour-joining phenogram, which were obtained with Clustalx4.1 software. The results showed that the germplasms of Mugua originate from *Ch. speciosa* (Sweet) Nakai, not including *Ch. sinensis* (Thouin) Kochne and *Ch. cathayensis* (Hemsl.) Schneid. The results also showed that 'Yao Mugua' and 'Ornamental Mugua' are the most distantly related species in germplasms.

Key words: Genetic Relationships, ITS, Mugua