



Genetic diversity of *Tadehagi triquetrum* in Northeast Viet Nam

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Introduction

Tadehagi triquetrum (L.) H. Ohashi (Fig. 1), a legume subshrub native to SE Asia, has an economic potential because of its therapeutic uses, capacity to provide crude protein for livestock feeding during dry seasons, and good adaptation to depauperate soils. Despite the ever increasing interest in conservation issues of wild plant species as potential sources for novel germplasm providing answers to future challenges, little is known about genetic diversity in *T. triquetrum*.

Still, information about the genetic diversity of species is essential for sustainable use and efficient conservation of plant genetic resources. *Ex situ* conservation in genebanks requires a careful balance between the size of collections and the feasibility of maintaining and managing germplasm storage. The objective of this study was to analyse the relatedness among accessions collected in Bac Kan, Northeast Viet Nam, in order to create baseline data for future conservation efforts.



Fig. 1: *Tadehagi triquetrum* (L.) H. Ohashi

Materials & Methods

Genetic diversity was analysed using random amplified polymorphic DNA markers (RAPD) to determine the extent of genetic variation among 24 *T. triquetrum* accessions originating from Bac Kan province, Northeast Viet Nam. Seedlings were raised from scarified seeds under greenhouse conditions. Of each accession young leaf tissue of ten individual plantlets was bulked. Template DNA was processed according to a small-scale DNA extraction method. Six out of 80 primers that yielded polymorphic markers were chosen for marker amplification. Data analysis was performed employing the software package NTSYS-pc version 1.80 (Rohlf, 1993). Jaccard's similarity (JS) coefficients were calculated and used to generate dendrograms by means of the unweighted pair group method with arithmetic averages (UPGMA).

Based on the calculation of pairwise binary genetic distances for dominant data a Mantel test (999 permutations) was applied to analyse correlations between genetic and geographical distances for each accession using GenAlEx V5 (Peakall and Smouse, 2001).

Results & Conclusions

Moderate levels of interaccession diversity, represented by 33.3% of polymorphic fragments (P%) and an average JS coefficient of 0.64, were found. UPGMA clustering (Fig. 2) and Mantel test did not reveal a correlation between geographic and genetic distances ($R=0.135$, $P=0.107$). Regarding the moderate level of differentiation found among accessions, a high incidence of outcrossing along with long distance seed dispersal must be assumed. Despite of the fragmented landscape of Bac Kan province gene flow seems to counteract stronger differentiation.

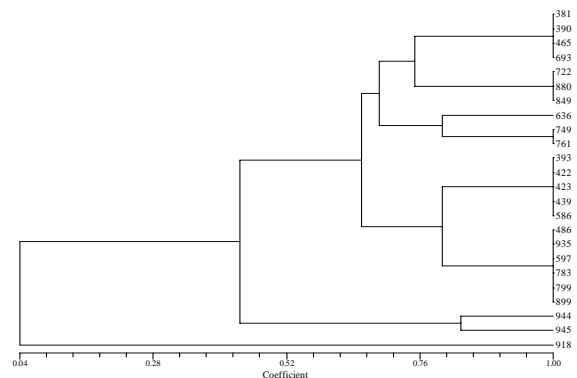


Fig. 2: UPGMA dendrogram illustrating genetic relationships among 24 accessions of *T. triquetrum*. The numerical scale of JS coefficients indicates increasing similarity.

Three unique markers were found in an outlier accession (accession no. 918) which may contain unique genetic characteristics and therefore should be conserved *ex situ* as a single accession. Of all other clusters, representative sub-samples should be selected or accessions bulked, for genebank storage. If a wider range of the genetic diversity in Vietnamese *T. triquetrum* is to be explored, further collection missions should cover more extended areas with larger geographical distances.

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