

Phylogenetic Relationships in Subgenus *Ceratotropis* Species (Genus *Vigna*, Fabaceae) Inferred by trnT-F Sequences (Poster)

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Introduction

Understanding of phylogenetic relationships in scrop species and their wild relatives could provide the insights into origin and geographic variation and sustainable utilization of plant genetic resources.

Objectives

To investigate the phylogenetic relationships in subgenus *Ceratotropis* species (genus *Vigna*, Fabaceae) using the newly collected samples from South East Asia.

Methods

DNA sequencing analysis was made in three non-coding regions of chloroplast trnT-F genes using 51 accessions, 19 taxa representing 15 wild and cultivated species of subgenus *Ceratotropis* from 9 countries. Phylogenetic analyses were made by both maximum parsimony and Bayesian methods.

Results

The phylogenetic trees obtained by maximum parsimony and bayesian approaches reveal the monophyly of subgenus *Ceratotropis* species (100 % supporting posterior probability and bootstrap values). Subgenus *Ceratotropis* species were grouped into 2 major clades; A and B with 100 % posterior probabilities, respectively. Clade A consists of 8 species; *V. angularis*, *V. nepalensis*, *V. minima*, *V. nakashimae*, *V. riukuensis* (*V. minima* var. *minor*), *V. umbellata*, *V. hirtella*, *V. exilis* which were clustered into 3 subclades (I, II and III). Clade B consists of 7 species (*V. reflexo-pilosa*, *V. trinervia*, *V. aconitifolia*, *V. stipulacea*, *V. trilobata*, *V. radiata*, and *V. mungo*) with 1 subclade IV consisting allotetraploid species, *V. reflexo-pilosa* and *V. trinervia* (100% posterior probability and 96% bootstrap value.)

Conclusion

Only two major groups in subgenus *Ceratotropis* was observed by this analysis. Clade A species are mainly distributed in Asia, and clade B species showed major distribution in Indian subcontinent. Clade A consisted of three groups, *angularis-nepalensis*, *minima*, *umbellata-nakashimae-exilis*. Clade B consisted of six radiating groups including sections *Ceratotropis*, *Aconitifolia* and *Angulares*. No clear lineage differentiation was found in three races of *V. angularis* (azuki bean), and *V. nepalensis*. *V. riukuensis* showed more close similarity with *V. nakashimae* than with *V. minima*. Our data suggested that *V. trinervia* was the maternal genome donor of allotetraploid species, *V. reflexo-pilosa*. Many key characters for taxonomical grouping in this subgenus are positioned as homoplasy in the molecular tree.

Keywords: Monophyly, two major groups, evolution, SE Asia

Selected References

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