

DOCTORAL THESIS

Pharmacognostic study of acorus: from a phylogenetic perspective

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Pharmacognostic Study of *Acorus* – from a Phylogenetic Perspective

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ABSTRACT

Acorus has been used for treatment of dyspepsia, colic and brain diseases for thousands of years. And yet more recently in history, its effects of causing cancers and dermatitis, and its gastrointestinal toxicity have been concerning professionals and patients. Quality Control of the medicinal herbs is of paramount importance to health and well being of the patients. Authentication of the medicinal species is a first step. Benefiting from a robust phylogenetic study of Acoraceae, the cornerstone of the present research that is detailed subsequently, two Quality Control methods based on well characterized DNA sequences are established, essentially featuring reliability and reproducibility.

The possibility of making better use of *Acorus* – with enhanced therapeutic effects while with decreased side effects and toxicity – is proposed. The essential oil fraction of the herb demonstrates more potential effects than a single component. The oils are so diverse even among different populations of the same species that it is likely to find out or concoct oil cocktails from *Acorus* bearing fitness being truly beneficial to human beings. Once such possibility becomes reality, the next step in Quality Control should be to develop methods to analyze and ensure the quality of the oils.

The cornerstone research is elaborated below.

Phylogenetic relationships among Acoraceae, the most primitive extant group of monocots, are assessed by cladistic analysis of combined DNA sequences from the nuclear ITS region, and chloroplast *matK* gene, *ndhF* gene, *trnL-trnF* intron/spacer, *trnT-trnL* spacer, *psbA-trnH* spacer, and *rps16* intron. Legitimate outgroups are not available for the non-protein-coding loci, thus not allowing using outgroup rooting for the polarization of genetic variation. The utilization of midpoint rooting bifurcates the group of plants into a “calamus clade” and a “gramineus clade”, consistent with the “two species view” of Acoraceae phylogeny. The phylogeny within the calamus clade demonstrates that the split corresponds to geography – one subclade is from North America, while the other is from eastern Asia. *Acorus americanus* (Raf.) Raf. collected from Michigan appears to be co-specific with *A. calamus* L. from Maryland, U.S.A. Three principal lineages are shown within the gramineus clade. 1) The basal lineage consists of *A. sp.*, *A. latifolius* Z. Y. Zhu, and one accession of *A. tatarinowii* Schott, collected within the same geographic area. 2) Another two accessions of *A. tatarinowii* appearing to be of polyphyletic origins with the accession in the basal lineage form the second lineage. 3) The third lineage is composed of two subclades – the first subclade includes two accessions of *A. gramineus* Soland., and the second subclade includes *A. gramineus* var.

flavomarginatus, *A. xiangyeus* Z. Y. Zhu and *A. macrospediceus* (Yamamoto) F. N. Wei et Y. K. Li – radiating from their common ancestors. Suites of morphological traits and other characters for defining the clades and the species/varieties are presented; these include the venation patterns, the ratio of sympodial leaf length to spadix length, the length, width and the color pattern of vegetative leaves, and the contents of essential oil. This study provides an example of phylogeny reconstruction of a major group of plants starting at the base of monocots, and constitutes a first step towards monographing Acoraceae.

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