Abstract

Title of thesis: Phylogenetic analysis of different species of Asparagus based on molecular cytogenetic and systematic study

The genus Asparagus, well known for its medicinal and ornamental importance comprises of three subgenera of cladode bearing plants: Protasparagus, Asparagus and Myrsiphyllum. The interspecific delimitation of the subgenus Protasparagus is ill-defined till date due to lack of discontinuous morphological characters. A few phylogenetic studies have been conducted so far, inferring partly the phylogenetic status of the subgenus Asparagus and Myrsiphyllum while the interspecific relationship within Protasparagus remained unresolved. Therefore, the aim of the present study was to explore the molecular phylogenetic relationships within the members of Asparagus subgenus Protasparagus. In the present study, the interspecific phylogenetic relationships among nine taxa of the Asparagus subgenus Protasparagus have been analyzed for the first time based on different cladode characteristics, rDNA ITS and cpDNA trnL intron sequences, mitotic chromosome numbers, nuclear DNA content as well as the analysis of two principal secondary metabolites i.e. shatavarin-IV and sarsasapogenin. The present study provides an unbiased grouping of the studied members of this subgenus into four distinct subclades with their monophyletic nature suggesting that the rDNA ITS and cpDNA trnL intron sequence based molecular phylogenies are explicitly congruent with the cladode characteristics of the subgenus Protasparagus. It also emphasizes the paramount importance of several cladode morphological and anatomical characters along with the phylogenetic significance of different stomatal as well as surrounding epidermal cell traits in Protasparagus species-level phylogeny. The present study reports the flow cytometric estimation of genome size of six different taxa of Asparagus other than A. officinalis namely, A. falcatus, A. aethiopicus, A. setaceus cultivar Robustus, A. racemosus, A. gonoclados and A. africanus for the first time. It also highlights that the nuclear DNA content (2C value) is positively correlated with the chromosome count for each taxon analyzed and can be used as a taxonomic marker in the Protasparagus species relationship. The analysis of two important bioactive phytocompounds i.e. shatavarin-IV and sarsasapogenin can also provide its importance in the delimitation of the studied taxa even at the subclade level. Therefore, the present explicit phylogenetic analyses can add important background information for further studies on biogeography of a wide range of Asparagus species.