

6. SUMMARY AND CONCLUSIONS

The evolution, with in lineage patterns, resulting from process operating on time scales less than the duration of individual species, are referred to as “microevolution,” which is the focus of population genetics and population ecology. Dobzhansky (1937) Mayr (1942) and Simpson (1944) opined that perception of macroevolutionary pattern is merely a result of the coarse scale of systematic studies that emphasizes difference in degree between the two phenomena but not of one kind. From this perspective, macroevolutionary patterns better explained by reference to phylogeny, while microevolutionary patterns refer primarily to local adaptive advantages (Funk and Brooks, 1990).

The systematist’s null hypothesis is the assumption that more and more characters are sampled, no consistent pattern of relationships will emerge; as more and more characters are added to the tree, which fails to have any resolution of the tree and the polytomies will persist. When a consistent pattern (or group of similar patterns) does emerge, the systematist rejects the null hypothesis in favour of the pattern studied. The accepted pattern, described in a cladogram, is the working hypothesis of historical order among species that can be used in macroevolutionary investigations (Funk and Brooks, 1990). A major change was initiated with the broad application of cladistics from 1970 onwards that helped in establishing novel taxonomic hypothesis. This trends led to numerous realignments at the generic and family levels, and many taxa had to be re-circumscribed in order to confirm with the requirement of monophyly.

In the recent trends morphology and molecular systematics have been the major and successful tool of the systematics, and proposed classification could be assessed by visual comparison of the taxa, with anatomical, embryological, phytochemical, etc, character as additional criteria. Classification is a primary activity of systematics, it

consists of translating some view on how taxa are believed to be related in to a system of names. It “an art of systematics” i.e., taxonomic approach considered with writing or analysis of flora, biodiversity, herbarium, monographs requires broad knowledge in such varied fields as nomenclature, plant morphology, phytogeography, reproductive biology and botanical bibliography. This taxonomic methodology must continue to be a focus of the systematic as a goal in classification. Usually this involves setting up a hierarchic system and therefore utilizes groups at higher and lower levels of inclusion to reflect relationship. A key point is that in building a classification, the present study focused on real entities recorded in the taxa, which may represent the relationship exist among group. Classification is a very practical application of knowledge at hand, if one chooses to incorporate cladistic information in to a classification, it will be based on a cladogram, and not on an (unknowable) phylogenetic tree (Freudenstein, 1998).

In the present investigation, a multidisciplinary evaluation of 289 consistent attributes, from different disciplines were selected for taxonomic assessment (Table-11). Which reveals the consistent attributes, selected from different populations, in order to understand the degree of resemblance/variation with in the populations, inhabited in three different ecoclimatic-regions of south India. Further, overall attributes were employed in cladistic classification/analysis of 26 OTUS using external morphology (86-attributes), leaf architecture (48), trichome complex (66), stomatal complex (26), palynology (4), cytogenetics (6), seed morphology (15) and phytochemistry (37). The cladograms were constructed for the group based on individual parameters and also on total attributes. The cladogram constructed on total attributes revealed that the group was divided into 4 clusters, further, *Amaranthus* segregated into two clades, while non-amaranths (other than *Amaranthus*) into two clades.

The clade I constitute 8 OTUS, in which majority of taxa evidenced by the presence of tepals and stamens 5-each (5-merous), while remaining taxa like *Amaranthus caturus*, *A. mangostanus* and *A. retroflexus* (3-merous). However, *Amaranthus caudatus* var. *caudatus* and var. *aleopecurus* were exhibited maximum homology (88%) followed

by *A. edulis* (91%). Interestingly *A. edulis* was closely allied with *A. caudatus* var. *caudatus* than var. *aleopecurus* suggesting a close taxonomic kinship among the three taxa. This was supported by Coones (1975), Hauptli and Jain (1978), Madhusoodanan and Pal (1981) and Pal and Pandey (1981), i.e., the present day grain amaranths were evolved from monophyletic ancestor-*A. hybridus/edulis (quitensis)*, from which the two evolutionary divergent lines represented by *A. edulis/caudatus*, and *A. cruentus/hypochondriacus* were originated. Nevertheless these taxa differed in seed morphology, pigmentation and in trichome complex. Hauptli and Jain (1978) opined that *A. edulis (quitensis)* was doubtfully different from *A. hybridus*. However, significant distinction was noticed in cladogram suggests that the two taxa are distinct (80% homology, Table-18). Further, the minimum relationship (72.2 %) was exhibited by *A. caturus* with other members of the cluster, which was followed by *A. hybridus* (73 %) and *A. cruentus* (75 %). The weak relation with *A. caturus* probably due to 3-merous condition, chemical composition, trichome diversity and 4C DNA levels. The minimum degree of homology between *A. hybridus* and *A. cruentus* was also supported by the opinion of Coones (1975) Hauptli and Jain (1978), Madhusoodanan and Pal (1981) and Pal and Pandey (1981) regarding the origin of *A. cruentus* from the progenitor *A. hybridus*. *A. retroflexus* and *A. mangostanus* were considered as intermediate taxa in the subgroup, probably due to diversity in floral architecture, 3-merous condition, venation characteristics and chemical constitution, etc.

The clade II comprises 8 OTUs, in which most of the taxa exhibited tepals and stamens 3 each (3-merous) while *Amaranthus spinosus* and *A. dubius* by 5-merous condition. Interestingly two divergent lineages evidenced by *A. spinosus* and *A. dubius* (maximum kinship-77%) on one hand and *A. tricolor* var. *tricolor* and var. *tristis* on other hand. The former ones possess 5-merous condition in this cluster, though *A. spinosus* is distinct species in the genus with paired spines. Apart from this, they exhibit close affinity in external morphology and seed morphology. It was supported by Pal (1973), who opined that these taxa often involved in hybridization, therefore these are pantropical widespread weeds. However, dissimilarity was also noticed between these

taxa in chromosomal number, ploidy level, 4C DNA content, chlorophyll diversity, etc. *A. tricolor* is said to be the complex taxon which includes two legitimate varieties i.e., *var. tricolor* and *var. tristis*, differentiated based on the nature of stem, arrangement of flowers in spike and the nature of bracteoles. This was substantiated by the macroscopic observation on leaf architectural patterns i.e., conspicuous nature of arches and joining pattern, nature of tertiary veins transverse the leaf blade as depicted in dendrogram (Fig-14, 15, 31). However, in this cluster the minimum relation was recorded among *A. viridis*, *A. graecizans* and *A. blitum*, which may be due to the nature of fruit dehiscence and in seed morphology. But these taxa are distinct in morphology especially in leaf shape, size, vigour index and chemical composition, etc.

The clade III comprises 5 OTUs (non-amaranths) represented with maximum kinship (58%) between coastal species like *Psilostachys sericea* and *Psilotrichum elliotii*, however, exhibited dissimilarity in habit and habitat nature, leaf shape, venation pattern, floral morphology, trichome complex, stomatal complex, etc. The minimum homology (57%) was noticed between *Achyranthes bidentata* and *Pupalia lappacea* followed by *Cyathula prostrata* (53%). Several features like straggling nature, phyllotaxy, floral defence modifications evidenced the nearest affinity among these taxa. But there were certain differences among the taxa especially stem nature, leaf morphology, floral arrangement, seed morphology, etc.

Five OTUs constitute the clade IV in which the maximum degree of kinship (52%) was recorded between *Aerva lanata* and *Nothosaerva brachiata*, which may be due to similarity in floral and seed morphology. The remaining taxa viz., *Allmania nodiflora*, *Digera muricata* and *Trichurus monsoniae* exhibited minimum relationship (46-48%). These taxa are said to be far related ones as evidenced by broad spectrum of variation in habit and habitat, external morphology, seed morphology, palynology, chromosomal number, etc. The dendrogram supported the classification of *Amaranthus* complex with their allied taxa in the tribe *Amarantheae*.

The present observations revealed that taxonomic boundaries among the members of *Amaranthus* complex provided by the earlier taxonomists were proved valid. The critical molecular and anatomical studies helped in the assessment of taxonomic hierarchy in the group. The interspecific relationship recorded between *A. caudatus* var. *caudatus* and *A. edulis* prompted to conduct further, micromolecular studies in order to understand the relationship. In addition *Amaranthus hybridus* and *A. cruentus* were designated as close relatives based on cladistic analysis. The present observations provided distinct demarcations among the taxa with detailed descriptions. The extensive and intensive systematic analyses based on wide range of consistent attributes were critically analyzed for providing distinct circumscription for each taxon. This substantiates the artificial key constructed based on exomorphic characters. The observations, though required further studies for evolution of phylogeny, may help the plant users for easy identification and effective utilization.