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## Abstract

Genetic diversity among 14 Withania accessions were studied using morphological, chemical, and RAPD (Rapid Amplification of Polymorphic DNA) markers. On the basis of morphological variation and maximum assimilation of chemical constituents, wild accessions were considered elite as compared to cultivated. The molecular study showed that a total of 12 DNA fragments were amplified with five random decamer primers 75% of which were polymorphic. Genetic similarity matrix based on the Dice index detected coefficients ranging from 0.556 to 0.941. These coefficients were used to construct a dendrogram using unweighted pair group method with arithmetic mean (UPGMA). These accessions were clustered into two major groups; the first group included AGB-009, AGB-012, AGB-042, AGB-030, AGB-053, AGB-019, AGB-017, AGB-002, and AGB-003; the second included AGB-025, AGB-001, AGB-036, AGB-015, and AGB-055. The highest similarity among the Ashwagandha accessions was observed between AGB-009 and AGB-030, AGB-009 and AGB-012, AGB-042 and AGB-030, AGB-025 and AGB-001, AGB-036 and AGB-015, AGB-015 and AGB-055 and between AGB-015 and AGB-055. The most distant populations in the dendrogram were AGB-053 and AGB-055. The combination of morphological, chemical, and molecular markers assessment will be useful in studying the genetic diversity of Withania for identification, conservation, breeding, improvement activities, and in order to achieve elite type in terms of bioactive metabolites.