Abstract

Adulteration in the medicinal plant material is the prevailing factor posing negative effects on the commercialization of medicinal plants. Both intentional and accidental mixing and substitution of original drug raw material with the less effective species reduces the quality of the final products. Use of authentic and original species is the very first and critical step to produce good quality, reliable and efficacious herbal drugs. Scientific validity of the species is the first and very essential parameter for quality assurance of the plant based therapeutics.

Many conventional techniques like macroscopy, microscopy and isolation of chemical marker compounds have been using since long to identify authentic plants and to separate them from their adulterants. Genome based identification methods provide an alternative tool which can be used independently or synergistically with the conventional methods. Amalgamation of DNA based techniques with the conventional techniques of identification present an effective approach for quality control and assurance of medicinal plants.

This project is based on the application of a part of genome that is internal transcribed spacer (ITS) region for the authentication of plant material to ensure the quality of herbal drugs. ITS is one of the proposed barcoding locus for identification of plants. Sequence of ITS region acquires species specific variations as the results of evolutionary processes. This region is flanked with the genes for ribosomal RNA. To carry out the project medicinal plants and their adulterant species were collected from various locations. Two medicinally important plants were selected for the project one is *Terminalia arjuna* which is a cardioprotectent and can be adulterated with other *Terminalia* species. Secondly, *Convolvulus microphyllus* vs *Evolvulus alsinoides* which have controversial identity due to ambiguous vernacular name ‘Shankhpushpi’. ITS region of each was amplified and sequenced. The sequences thus generated were compared to identify species specific polymorphism. On the basis of variations species specific primers were designed which were further used to develop PCR assays for rapid identification of the authentic and adulterated species.