SCOPE AND LIMITATIONS
5 Scope, limitations and future perspective

In future, comparative nucleotide sequence analysis of the developed markers amplified from a large number of different Zingiber species and varieties of Z. officinale could reveal polymorphisms that are species- or variety diagnostic.

DNA analysis is currently considered to be cutting-edge technology, and can be suitably applied for identification of botanicals. DNA marker based identification of unadulterated crude materials is a simple, time and cost effective process. The complexity of application increases when used for semi-processed or processed botanicals, botanical mixtures composed of multiple plant species, and further when contaminants and adulterants are unknown. In order to establish a marker for identification of a particular species, DNA analysis of closely related species and/or varieties and common botanical contaminants and adulterants is necessary, which is a costly and time-consuming process. However, it is not impossible. Databases of DNA fingerprints and DNA sequences for a broad spectrum of plant species can be created and will be useful. Isolation of good-quality DNA suitable for analysis from semi-processed or processed botanicals is also a challenge. Another important issue is that DNA fingerprint will remain the same irrespective of the plant part used, while the phytochemical content will vary with the plant part used, physiology and environment. Thus DNA fingerprinting ensures presence of the correct genotype but does not reveal the chemical constituents or amount of active principle. However, DNA markers are more stable than chemical markers that are affected by environmental conditions, physiology and management practices. Hence DNA analysis and pharmacognostic techniques for chemoprofiling such as TLC, HPTLC, etc. will have to be used hand in hand rather than in isolation. Identification of quantitative-trait loci
that are closely linked to a biologically active phytochemical will prove to be useful. Several attempts have been made in recent years, to correlate DNA markers with qualitative and quantitative variations in phytochemical composition among closely related species. Proper integration of molecular techniques and analytical tools will lead to the development of a comprehensive system of botanical characterization that can be conveniently applied at the industry level for quality control of botanicals.

Recently, microarrays have been applied for the DNA sequence-based identification of medicinal plants. To utilize DNA microarrays for identification and authentication of herbal material, it is necessary to identify a distinct DNA sequence that is unique to each species of medicinal plant. The DNA sequence information is then used to synthesize a corresponding probe on a silicon-based gene chip. These probes are capable of detecting complementary target DNA sequences if present in the test sample being analyzed. The DNA chip technology can provide a rapid, high throughput tool for genotyping and plant species authentication. Recent advances in lab-on-chip technology have further enhanced the feasibility of automated, miniaturized, fast and sensitive genetic authentication of species.