

Molecular Markers in the Improvement of the Medicinal Plants

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Plants since time immemorial have always been considered as a key source of energy and medicine. Plant are factories skilled in synthesizing infinite number of extremely complex, rare and bioactive compounds whose structures could otherwise escape the imagination forever and are the foundation for many new compounds synthesized artificially. Over three-quarters of the world population relies mainly on plants and plant extracts for health care. More than 30% of the entire plant species, at one time or otherwise used for medicinal purposes. Since ancient times, herbal medicine has played a major role in traditional systems of medicine such *Unani* and *Ayurveda*. It's very sorry state of the medicinal plant dependent industries that for production, they are totally dependent on the plant material that is collected from the natural habitat. This imposes a constraint on the available natural resources resulting in depletion or total loss of medicinal plant germplasm. Apart from indiscriminate collection from the wild that disturbs the natural balance, there is no control over the quality of the material that is being used. Studies on medicinal plants are rapidly increasing because of the search for new active molecules, and for the improvement in the production of plants or molecules for the herbal pharmaceutical industries. Better quality medicinal plants produced as result of biotechnological approach used could guarantee endless plant resource of uniform quality medicinal plants and individual natural compound for further processing and industry. In addition to this, conservation of the medicinal plant biodiversity using molecular markers will support to restore endangered or threatened plant populations. The need of medicinal plants cannot be met with from wildly growing plants alone, even with their improved management.

With the advancement of DNA based different molecular markers and molecular breeding strategies offered many new strategies to plant breeders and geneticists to resolve many of decades old problems faced during conventional breeding of medicinal plants. Molecular markers are unique and relate directly to the plant's genotype. Genetic diversity among individuals or populations can be determined using morphological, biochemical and DNA based molecular markers. To date, however, there have been relatively few reports of molecular marker-based approaches to medicinal plant improvement, and not even the most skeletal of genetic maps is available for any of the important industrially important species except for *Artemisia annua* [1]. This study not only proved the importance of molecular basis for marker-assisted breeding of *A. annua* but also highlights the significant reduction in time that are now feasible for developing this platform of knowledge and tools. Selection assisted by genetic markers is an extension of traditional crop breeding, which has been used extensively in food crop improvement. Again, it is a way to recognize desirable genotypes at an early stage to speed up the selection process.

Identifying a novel functional gene and useful marker sequences linked to them in a plant species is a lengthy and costly technical affair. Plant genome sequencing has progressed rapidly since the first genome (*Arabidopsis thaliana*) was completed in 2000 [2] followed by the 389-Mb rice genome was completed in 2004 [3]. There is a high degree of match in the DNA sequences of functional genes between different plant species; therefore, DNA probes from one species can often be used to identify homologous sequences in another closely related species.

The key developmental challenges for molecular markers now lies in developing new breeding strategies where the objectives will be increasing the germplasm base and increasing the number of traits that can be effectively selected simultaneously. The new marker technologies that offer greatly reduced costs in marker screening and high multiplexing capabilities will be central to these developments. Essentially we will move to whole genome-based selection strategies where specific recombinational events are sought and changes will be assessed on a genome-wide scale. In this way we can look for better management of chromosome regions that may come from wild relatives or land races, track several traits at once and keep the population size as small as possible. We also believe that despite the relatively small adoption of markers in different medicinal plant breeding to date, there will be a greater level of adoption in the next decade and beyond. Factors that should lead to a greater adoption of MAS in medicinal plants include:

- Establishment of facilities for marker genotyping and staff training within many medicinal plant breeding institutes in different parts of the world.
- Currently available (and constantly increasing) data on genes/ QTLs controlling traits and the identification of tightly-linked markers in different plants
- development of effective strategies for using markers in breeding
- establishment and creation of public databases for QTL/marker data especially for different medicinal plants
- Available resource for generating new markers from DNA sequence data arising in parts from different medicinal plant genome sequencing and research in functional genomics.

It is also critical that future endeavors in marker assisted selection are based upon lessons that have been learnt from past successes and (especially) failures in using MAS. Further optimization of marker genotyping methods in terms of cost-effectiveness and a greater level of integration between molecular and conventional breeding (especially in designing efficient and cost-effective strategies) represent the main challenges for the greater adoption and impact of MAS on different medicinal plants in the near future. The choice of the most appropriate marker system, however, needs to be decided on a case-by-case basis and will depend on many issues including the availability of technology

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platforms, costs for marker development, species transferability, information content and ease of documentation.

References

1. Graham IA, Besser K, Blumer S, Branigan CA, Czechowski T, et al. (2010) The Genetic Map of *Artemisia annua* L. Identifies Loci Affecting Yield of the Antimalarial Drug Artemisinin. Science 327: 328-331.
2. Arabidopsis Genome Initiative (2000) Analysis of the genome sequence of the flowering plant *Arabidopsis thaliana*. Nature 408: 796-815.
3. International Rice Genome Sequencing Project (2005) The map-based sequence of the rice genome. Nature 436: 793-800.