

Preface

Plant-based medicines are used in all civilizations and cultures, and have been one of the indispensable lines of defense in maintaining health and combating diseases worldwide. With the increasing demand of medicinal plants at the global level for use in pharmaceuticals and dietary supplements, biotechnology has emerged as a powerful tool for their conservation and improvement. By adopting techniques such as in vitro propagation and genetic transformation, biotechnology plays an important role in multiplication and genetic enhancement of medicinal plants. The rapid advances in plant genomics, transcriptomics, proteomics, and the recent emergence of metabolomics along with molecular biology and analytical chemistry will greatly facilitate and enhance the metabolic engineering of medicinal plants.

The purpose of “Biotechnology for Medicinal Plants: Micropropagation and Improvement” is to present in a single volume the comprehensive knowledge and the experience of renowned researchers and scientists in the field of medicinal plant biotechnology. The book provides an overview of modern plant biotechnology and discusses the potential applications of plant biotechnology in the improvement of medicinal plants. Each chapter is independently written by experts in their field of endeavor ranging from micropropagation protocols, advantages of different biotechnological tools in the plant micropropagation, the biosynthesis of useful secondary metabolites, the metabolomics, the transcriptomics, the metabolomic engineering, the bioinformatics, to the quality control of phytopharmaceuticals.

The book begins with introductory chapters on the overview of downstream processes of plant cell and tissue culture (Chap. 1, Yesil-Celiktas and Vardar-Sukan) and the *Agrobacterium rhizogenes*-mediated transformation in medicinal plants (Chap. 2, Roychowdhury et al.) followed by the biotechnology of *Scutellaria* propagation (Chap. 3, Joshee et al.), microbial endophytes (Chap. 4, Rathod et al.), *Cannabis* propagation for the production of phytocannabinoids (Chap. 5, Chandra et al.), and the micropropagation of medicinal *Epilobium* species (Chap. 6, Constantin et al.). In the next few chapters the discussion is focused on the advantages and amplification of photoelicitation (Chap. 7, Matsuura et al.), microspore culture

(Chap. 8, Ferrie), and cellular heterogeneity (Chap. 9, Patil and Roberts) in plant cell and tissue culture.

Hairy root cultures are a useful means for studying the biochemical and gene expression profiles of the biosynthetic pathways, and for metabolic engineering of medicinal plants. Chapter 10 (Sheludko and Gerasymenko) outlines the biosynthetic potential of hairy roots for the production of novel natural products, while in Chap. 11 (Bunsupa et al.) focus is laid on the molecular biology and biotechnology of quinolizidine alkaloid biosynthesis in leguminosae/Leguminosae plants.

Chapter 12 (Aravindaram and Yang), summarizes the various analytical techniques most frequently used in phytomedicinal research and the potential as well as the limitations of various approaches are discussed.

Free radicals are well known for their involvement in the pathogenesis of a large number of degenerative diseases such as cancer, cardiovascular diseases, neurological disorder and diabetes, in addition to their role in immunomodulation. Over the years, research on antioxidants present in medicinal plants has gained enormous popularity and emerged as an arena for providing potential therapeutic agents to prevent/quench free radical generation that may damage the biological system of the human body. Chapter 13 (Bhatt et al.), focuses on the antioxidants present in various important medicinal plants and their implication in the treatment of certain diseases.

Chapters 14–16 provide in-depth discussion on metabolic engineering in medicinal plants. In Chap. 14, Chow and Sato describe the metabolic engineering/metabolic engineering and synthetic biology for the production of isoquinoline alkaloids, whereas in the following chapter (Chap. 15) Shoji and Hashimoto explore the role of Isoquinoline Alkaloids ‘jasmonate-responsive transcription factors’ as new tools for metabolic engineering and gene discovery in medicinal plants. In Chap. 16, Zarate et al. review methodologies and advances with the future directions of metabolic engineering of plant cellular metabolism.

Using *Hypericum* as a model, use of metabolomics and transcriptomics to analyze the regulation and biosynthesis of medicinal compounds is described in Chap. 17 (Crispin and Wurtele). Metabolomics, the comprehensive analysis of diverse metabolites, has greatly expanded metabolite fingerprinting and profiling as well as the selection and identification of marker metabolites in medicinal plants. The methodology typically employs multivariate analysis to statistically process the massive amount of analytical chemistry data, not only including the major, but also fingerprinting the minor metabolites, resulting from high-throughput and simultaneous metabolite analysis. Using the advances in computational science, Chap. 18 (Okada et al.) of this book focuses on multivariate analysis of analytical chemistry data and utility of the KNApSAcK family database to understand metabolic diversity in medicinal plants. This chapter also describes the effectiveness and potential of computational systems biology in medicinal plant research.

Authenticity and consistency in the quality of biomass are the key parameters for the safety and efficacy of any phytopharmaceutical. Somatic mutation is a common problem in micropropagation that can alter the genetics and the chemical profile of the propagated crops. The quality assurance of starting material is

therefore a prerequisite. The concluding chapter ([Chap. 19](#), Sucher et al.) of this book discusses the use of genomic and transcriptomic profiling of propagated plants for the quality control of plant-based drugs.

It has been a pleasure to edit this book, primarily due to the splendid cooperation of contributors in preparation of the manuscript according to the guidelines provided, strict adherence to time schedules and the richness of the material provided by them, for that we are highly thankful. We express our gratitude and heartfelt thanks to each author for their generous contribution of time and effort.

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