

PREFACE

Using several genetically advanced models (N_2 -fixing legume nodules, arbuscular mycorrhizae, rhizospheric associations) we demonstrated that in order to meet the diverse environmental challenges, land plants use a variety of nutritional and defensive symbioses with bacteria and fungi. These symbioses involve the cooperative partners' developmental programs resulted in establishing the convenient niches for microbes on the plant surfaces (in rhizosphere and rhizoplane), in tissues (inter-cellular spaces, tissue cavities) and sometimes inside the cells (symbiosomes) wherein the microbial co-habitants are hosted, managed using the multiple signaling circuits and provided with the optimal conditions for expressing their host-beneficial traits (nutrition, protection from pests and competitors).

The best model to study the plant-microbial symbioses (PMS) developmental programs is represented by the legume-rhizobia interactions: N_2 -fixing root nodule symbiosis (RNS) may be dissected into a series of stages and subprograms controlled by the cooperative (super-organism) plant-microbial genetic networks. The involved plant genes are classified into: organizer-genes responsible for signal transduction (*Sym* genes) and worker-genes involved in building the symbiotic compartments or in catalyzing the basic biochemical reactions required for an effective symbiosis (nodulins). Some of these genes are common to RNS, arbuscular mycorrhiza (AM) and associations with plant growth promoting rhizobacteria (PGPR) suggesting the common evolutionary roots for the diverse PMS types. Not only genes, but the microbial partners may also be shared by different symbiotic systems since in RNS evolution, the dicot plants incorporated the multiple genetic determinants and bacterial co-habitants from the less specific AM and PGPR associations.

Since the majority of PMS are not strictly required for the host growth and reproduction, they represent the excellent models for developmental genetics of plants which is often restricted by the impossibilities to identify by classical genetic methods those genes the mutations in which are non-compatible with the organisms' viability and fertility. The throughout genetic analysis of the developmental programs in PMS allows us to suggest a heuristic view of the symbiotic systems as of the "super-organisms" possessing their own phenotypes and genotypes. This approach enables us to suggest a novel genetic approach for constructing the sustainable agricultural systems: in order to restore and to further improve the symbiotic potential in plants, the breeders and genetic engineers should manipulate the integral super-organism systems. Analysis of syntenicity of symbiotically related genes in the model and crop legumes provided a background for genetic manipulations required for improving PMS and specifically for constructing the multipartite symbiotic communities in which the diverse nutritional and defensive functions are implemented with a minimal application of agrochemicals (fertilizers, pesticides) providing the background for sustainable agriculture.

This book will be useful for a broad audience including: (i) researchers and experts involved in molecular biology, genetics, biochemistry, cytology and ecology of plants and microorganisms, (ii) teachers and students engaged in biological and agricultural specialties at universities; (iii) specialists working in applied biology: breeders, genetic engineers, agronomists, plant growers.