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Book Review.
Plant-Microbe Symbioses: Molecular Approaches

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The book contains an excellent collection of experimental and review papers concerning interactions of plants with different pathogens, mycorrhizal fungi and rhizobia. Three urgent directions of the symbioses research are traced in the book.

The first direction is an analysis of the signal exchange and cross-regulation of "symbiotic" genes in the interacting organisms. The flavonoid-induced synthesis of the rhizobia Nod factors which elicit the early stages of nodule development in the legumes (Heidstra and Bisseling) is best studied but is not the sole example of these interactions. The induction of recognition responses in the arbuscular mycorrhizal fungus *Glomus mosseae* (Giovannetti et al.) and of cell wall protein synthesis in the ectomycorrhizal fungus *Pisolithus tinctorius* (Tagu and Martin) demonstrate that the signal-regulated gene expression is a common feature of different plant-microbe symbioses. Elucidation of the molecular mechanisms of synthesis, perception and gene-inducing activity of the signal molecules constitute a universal experimental strategy broadly represented in the reviewed book.

The second direction is a comparative analysis of the genes and functions involved in the beneficial and pathogenic interactions. Involvement of various defence responses in formation of the arbuscular mycorrhizas (Gianinazzi-Pearson et al., Kapulnik et al.) and of nitrogen-fixing nodules (Heidstra and Bisseling) support de Bary's broad concept of symbiosis which includes both mutualistic and antagonistic interactions covering sufficient parts of the partners' life cycles. However, rhizobia or mycorrhizal fungi infections induce weakly those defence reactions which are strongly expressed when the plants are attacked by pathogens (Uknes et al., Hammond-Kosack et al.). Moreover, the plant mutants have been identified which are defective in mycorrhization and/or nodulation but are not affected in the pathogen resistance (Gianinazzi-Pearson et al.). Therefore, use of genetic and molecular approaches brings us closer to elucidation of those genes and functions which are common for and which can discriminate between mutualism and antagonism in the plant-microbe interactions.

The important evolutionary implications should be made from these data coupled with a taxanomic analysis of plant-associated organisms. The rhizobia are demonstrated to be a polyphyletic group of narrow-host-range symbionts some of which (*Rhizobium, Sinorhizobium*) are close to the pathogenic agrobacteria, while the others (*Azorhizobium, Bradyrhizobium*) are close to various free-living diazotrophs (Young and Haukka). Different rhizobia have diverged from their hypothetical common ancestor much earlier than the host plants (legumes) originated. Therefore, the rhizobia-legume symbioses apparently might have originated several times from various beneficial and parasitic plant-microbe interactions. In contrast, the arbuscular mycorrhizal fungi (Glomaceae) comprise a monophyletic group of broad-host-range symbionts and there are no data on their close relation to pathogens (Simon). In spite of evident differences in the evolutionary strategies of facultative legume-rhizobia symbioses and obligate mycorrhizas, they might have common stages of development because the legume mutants which are defective in both mycorrhization and nodulation were obtained (Gianinazzi-Pearson et al.). Possibly, the higher plants possess the universal system(s) for regulating the microbial interactions which may be beneficial or deleterious, depending on a symbiont genotype.

The third direction is research of interactions between plants and the free-living populations of symbiotic microbes. The preinfection interactions may be highly specific and may influence the structure of a symbiont population (Deacon). The host plants and the environmental factors contribute greatly to the population dynamics of the mycorrhizal fungi (Gardes and Dahlberg, Sanders et al., Dodd et al., Lloyd-MacGilp et al.) and rhizobia (Hirsch). Diversification into the symbiotic and saprophytic biotypes (Deacon) apparently improves the adaptive and evolutionary potentials of the microbial populations. Development of novel molecular and statistical approaches for analyzing populations of plant-interacting microbes (Leifert et al., Brown) is of great importance for selection of valuable strains from natural populations, for assessing stability of the introduced strains and for improving safety of the plant-associated microbes released into the environment.

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