Chapter 38

Evolutionary Aside 38.1--Evolution of Nodulation

Nodulation has evolved multiple times. A hypothesized predisposition for nodulation arose $100\,\mathrm{MYA}$ in a common ancestor, followed by rapid radiation. Most nodulating plants are found in the legume family, which arose $60\,\mathrm{MYA}$, and nodulation appears to have evolved multiple times within the legumes.

Species with independently derived nodulation share many of the same genes used for nodulation. The current explanation for the shared genes is that they were co-opted from developmental pathways used for arbuscular mycorrhizal symbiosis. Over millions of years, the common homologous genes persist, but pathways have been modified so that recognition of nitrogen-fixing bacteria is species specific.

Within the legumes, the papilionoid clade includes many common crops such as soybean, green beans, and garden peas that thrive because of nodulation. The papilionoids experienced several whole-genome duplications over evolutionary time resulting in polyploidy plants. The duplicated genes may have played a role in the evolution of nodulation as duplicates were co-opted for specific functions. However, analysis of a broader range of species indicates that polyploidy was not necessary for the rise of nodulation in nonpapilionoid species.