# *Lotus japonicus* handbook

**Editorial Director**
**ANTONIO J. MÁRQUEZ**

**Section Editors**
**J. STOUGAARD**
**M. UDVARDI**
**M. PARNISKE**
**H. SPAINK**
**G. SAALBACH**
**J. WEBB**
**M. CHIURAZZI**
**A. J. MÁRQUEZ**

**Springer**

**Dordrecht**

# Preface

Legumes are very important plants (VIPs). They account for about one-third of the world's primary crop production, human dietary protein, and processed vegetable oil, and are a major source of feed for livestock and raw materials for industry. Legumes are a key component of sustainable agricultural systems because of symbiotic nitrogen fixation, which provides these plants and associated or subsequent crops with a free and renewable source of nitrogen. Legumes are also able to establish beneficial symbioses with soil fungi that enable them to mine phosphorous and other essential nutrients from the soil more effectively. However, despite their importance in agriculture, increases in legume yield through breeding over the past few decades have lagged behind those of cereals. While classical plant breeding can and will lead to further improvements in legume genotypes in the future, the genomics revolution offers alternative and complementary approaches that can aid and accelerate plant breeding. Genomics and functional genomics, together with the more classical scientific disciplines of genetics, biochemistry, physiology, and molecular and cell biology, have already accelerated discoveries in legume molecular and systems biology.

Legumes have played a key role in biological research, a good example of which is Mendel's work on the common garden pea that provided the groundwork for modern genetics. Mendel's work also highlighted the importance of choosing a tractable model species for scientific research. While diploid pea was a fine model for classical genetics, the large size of the pea genome together with other less than optimal features have hindered the isolation and characterisation of genes with important roles in legume biology and agriculture. For this reason *Lotus japonicus* was chosen as a model species for legume research some ten years ago. Since then, many groups within Europe and around the world have adopted *L japonicus* as a model and have developed numerous resources and protocols to facilitate basic and applied research on this species. Over 200 research papers focusing on *L japonicus* have now been published, many of them groundbreaking. Amongst the most important discoveries that have come from Lotus research have been the isolation of genes with crucial roles in symbiosis development, which have provided amazing new insight into the nature and evolution of signalling in plant-microbe symbioses.

This handbook represents the first effort to compile basic descriptions and methods for research in *L japonicus*. We wish to thank all the authors for their efforts in making the book as complete and up-to-date as possible. We are also grateful to the EU, which has provided funding to promote Lotus research, including the research and training networks HPRN-CT2000-00086 (coordinated by Michael Udvardi) and MRTN-CT-2003-505227 (coordinated by Martin Parniske). In fact, this book was conceived within the framework of the first of these networks. Finally, we wish to thank Megan McKenzie, our Technical Editor for her extraordinary professional work, as well Junta de Andalucía (Spain) for support in preparing the camera-ready version of this handbook for publication.

THE EDITORS