Preface

According to FAO’s estimate, the number of people suffering from chronic hunger has increased to over a billion.

Because most of the extreme poor who suffer from hunger live in rural areas, the effort to enhance agricultural productivity will be a key element to reduce the numbers of the global population suffering hunger.

This goal will not be achieved unless we develop new genotypes of food crops and animals that will both improve production under suboptimal conditions. The discovery of genotypes with the capacity to cope with these problems suggests that increasing the support of breeding for fragile environments is a viable strategy for uplifting the rural poor. However, breeding for environmental stresses is a slow and inefficient process. Although several genotypes with good stress tolerance to environmental stresses have been identified or developed, it is difficult to transfer these traits to elite backgrounds because they are genetically very complex. One possibility currently being evaluated for enhancement of stress tolerance is to apply biomarkers in breeding programs to follow the inheritance of major genes that are difficult to phenotype, such as pyramids of disease resistance genes of similar effect. Proteomics is a powerful approach to identify proteins associated with stress tolerance. It offers an entry point for identifying possibly significant changes in protein levels against a background of unresponsive proteins.

The application of proteomics is usually initiated by detection of stress-responsive proteins through the comparison of proteomics data between stressed and control organisms. Identification of these expressional candidate proteins may then reveal that some of them have functions clearly consistent with the stress tolerance trait. Other relevant information including the expression pattern of mRNA and the metabolomics may help to further verify the correlation of these candidate proteins with desirable traits. The step forward from collecting proteomics data to functional prediction will pave the way for the sustainable agricultural production under unfavorable environmental conditions.

This book will cover several topics to elaborate how proteomics may contribute to our understanding of mechanisms involved in stress adaptation. The knowledge
being accumulated through a wide range of proteomics technologies may eventually be utilized in breeding programs to enhance stress tolerance. This book presents a comprehensive review about the responses of crop and farm animals to environmental stresses. Challenges related to stress phenotyping and integration of proteomics and other omics data have also been addressed.

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