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Note generali	Description based upon print version of record.
Nota di bibliografia	Includes bibliographical references and index.
Nota di contenuto	1. Well-designed experiments make proteomic studies on stressed plants meaningful -- 2. Cereal Root Proteomics for Complementing the Mechanistic Understanding of Plant Abiotic Stress Tolerance -- 3. A proteomic view of the cereal and vegetable crop response to salinity stress -- 4. Proteomics of Flooding-Stressed Plants -- 5. Proteomic analysis of crop plants under low temperature: a review of cold responsive proteins -- 6. How proteomics contributes to our understanding of drought tolerance? -- 7. The impact of heat stress on the proteome of crop species -- 8. Proteomics approach for identification of nutrient deficiency related proteins in crop plants -- 9. Plant response to bacterial pathogens: A proteomics view -- 10. Plant fungus interaction proteomics: an update -- 11. Insight into physiological, molecular, and proteomic changes associated with phytoplasma infection in crop plants -- 12. Insect pest proteomics and its potential application in pest control management -- 13. Proteomic Research on Honeybee Diseases -- 14 Application of Proteomic Biomarkers in Livestock Disease Management.
Sommario/riassunto	This book will cover several topics to elaborate how proteomics may

contribute in our understanding of mechanisms involved in stress adaptation. The knowledge being accumulated by a wide range of proteomics technologies may eventually be utilized in breeding programs to enhance stress tolerance. This book presents comprehensive reviews about 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. According to FAO's estimate, the number of people suffering from chronic hunger has increased to over a billion. Due to most of the extreme poor who suffers from hunger live in rural areas, the effort to enhance agricultural productivity will be a key element in reducing the number of global population suffering from hunger. This goal will not be achieved unless we develop new genotypes of food crops and animals that will both improve production under sub-optimal 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. Also several genotypes with good stress tolerance environmental stresses have been identified or developed, it is difficult to transfer these traits into 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 possible 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 comparison 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 at mRNA and 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.
