

<<Advance in Barley Sc>>

图书基本信息

书名：<<Advance in Barley Sciences-Proceedings of 11th International Barley Genetics Symposium-大麦科学研究进展>>

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内容概要

The last half century has seen extraordinary progress in barley genetics research. In the first International Barley Genetics Symposium in 1963, scientists just started to discuss a map of barley chromosomes. Today, the International Barley Genome Sequencing Consortium is at the dawn of the completion of the barley genome sequence. The regular International Barley Genetics Symposium provide an important platform for barley breeders and scientists to share their research results and understand the future trends of barley genetics research. The proceedings are not only the permanent record; they also provide key references for interested outsiders at the symposium and future barley research scientists. The organizing committee received around 150 abstracts and put them into a special volume for all symposium participants to have access, which will be helpful for improving the discussions at the poster sessions. Moreover, we have selected 38 full length papers and published them as The Proceedings of 11th IBGS.

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作者简介

Advance in Barley Sciences : Proceedings of 11th International Barley Genetics Symposium presents up-to date developments in barley science. The book contains 38 papers submitted to the 11th International Barley Genetics Symposium, and covers all the presentation sessions of the conference, i.e, barley development and economics, utilization of germplasm, genetic resources and genetic stocks, end-uses, biotic stress tolerance, abiotic stresses, new and renewed breeding methodology, barley physiology, successful breeding examples, barley genomics and all other '-omics'. The information will be useful for barley breeders, brewers, biochemists, molecular geneticists and biotechnologists. This book may also serve as a reference text for students and scientists engaged in barley research.

Dr. Guoping Zhang is a barley breeder and crop physiologist in Department of Agronomy, Zhejiang University of, China.

Dr. Chengdao Li is a senior molecular geneticist and barley breeder in Department of Agriculture and Food, Western Australia. He is also an adjunct professor in Murdoch University of Australia and Zhejiang University.

Dr. Xu Liu, an Academician in China Academy of Engineering, is a scientist of plant resources in Chinese Academy of Agricultural Sciences.

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书籍目录

- Evolution of Wild Barley and Barley Improvement
- Genetic Diversity in Latvian Spring Barley Association Mapping Population
- Genome-Wide Association Mapping of Malting Quality Traits in Relevant Barley Germplasm in Uruguay
- The "Italian" Barley Genetic Mutant Collection : Conservation, Development of New Mutants and Use
- Stanca Antonio Michele, Tumino Giorgio, Pagani Donata, Rizza Fulvia, Alberici Renzo,
- α -Amylase Allelic Variation in Domesticated and Wild Barley
- Novel Genes from Wild Barley *Hordeum spontaneum* for Barley Improvement
- The Distribution of the Hordoinoline Genes and Identification of Puroindoline b-2 Variant Gene Homologs in the Genus *Hordeum*
- Exploiting and Utilizing the Novel Annual Wild Barley Germplasms on the Qing-Tibetan Plateau
- Agronomic and Quality Attributes of Worldwide Primitive Barley Subspecies
- Differences between Steely and Mealy Barley Samples Associated with Endosperm Modification
- Genotypic Difference in Molecular Spectral Features of Cellulosic Compounds and Nutrient Supply in Barley : A Review
- Use of Barley Flour to Lower the Glycemic Index of Food : Air Classification β -Glucan-Enrichment and Postprandial Glycemic Response after Consumption of Bread Made with Barley β -Glucan-Enriched Flour Fractions
- Screening Hulless Barley Mutants for Potential Use in Grain Whisky Distilling
- Natural Variation in Grain Iron and Zinc Concentrations of Wild Barley, *Hordeum spontaneum*, Populations from Israel
- Genes Controlling Low Phytic Acid in Plants : Identifying Targets for Barley Breeding
- Correlation Analysis of Functional Components of Barley Grain
- Genome-Wide Association Mapping Identifies Disease Resistance QTLs in Barley Germplasm from Latin America
- The CC-NB-LRR-Type Rdg2a Resistance Gene Evolved' through Recombination and Confers Immunity to the Seed-Borne Barley Leaf Stripe Pathogen in the Absence of Hypersensitive Cell Death
- Increased Auxin Content and Altered Auxin Response in Barley Necrotic Mutant *necl*
- Vulnerability of Cultivated and Wild Barley to African Stem Rust Race TTKSK
- Genome-Wide Association Mapping Reveals Genetic Architecture of Durable Spot Blotch Resistance in US Barley Breeding Germplasm

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Genetic Fine Mapping of a Novel Leaf Rust Resistance Gene and a
Barley Yellow Dwarf Virus Tolerance

(BYDV) Introgressed from *Hordeum Bulbosum* by the Use of the 9K
iSelect Chip

A major QTL Controlling Adult Plant Resistance for Barley Leaf
Rust

Large Population with Low Marker Density Verse Small Population
with High Marker Density for QTL Mapping : A Case Study for Mapping
QTL Controlling Barley Net Blotch Resistance

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