

|                         |   |
|-------------------------|---|
| 1. Record Nr.           | UNINA9910557745603321   |
| Autore                  | Ichitani Katsuyuki  |
| Titolo                  | Genetics in Rice  |
| Pubbl/distr/stampa      | Basel, Switzerland, : MDPI - Multidisciplinary Digital Publishing Institute, 2020   |
| Descrizione fisica      | 1 electronic resource (188 p.)  |
| Soggetti                | Research & information: general<br>Biology, life sciences   |
| Lingua di pubblicazione | Inglese   |
| Formato                 | Materiale a stampa  |
| Livello bibliografico   | Monografia  |
| Sommario/riassunto      | <p>Rice feeds more than half of the world population. Its small genome size and ease in transformation have made rice the model crop in plant physiology and genetics. Molecular as well as Mendelian, forward as well as reverse genetics collaborate with each other to expand rice genetics. The wild relatives of rice belonging to the genus <i>Oryza</i> are distributed in Asia, Africa, Latin America and Oceania. They are good sources for the study of domestication and adaptation. Rice was the first crop to have its entire genome sequenced. With the help of the reference genome of Nipponbare and the advent of the next generation sequencer, the study of the rice genome has been accelerated. The mining of DNA polymorphism has permitted map-based cloning, QTL (quantitative trait loci) analysis, and the production of many kinds of experimental lines, such as recombinant inbred lines, backcross inbred lines, and chromosomal segment substitution lines. Inter- and intraspecific hybridization among <i>Oryza</i> species has opened the door to various levels of reproductive barriers ranging from prezygotic to postzygotic. This Special Issue contains eleven papers on genetic studies of rice and its relatives utilizing the rich genetic resources and/or rich genome information described above.</p> |