

| | |
|--------------------------------------|--|
| Category | : 8th Rice Genetics Symposium |
| Select Theme | : Genetic improvement |
| Endorsement email | : |
| Keyword 1 | : Pre-breeding |
| Keyword 2 | : Genomics-assisted breeding |
| Keyword 3 | : Marker-assisted selection |
| Title of Entry | : Genome-wide association study of important agronomic traits in japonica rice grown in temperate regions |
| Presenting author | : Concha Domingo |
| Presenting author email | : domingo_concar@gva.es |
| Co author 1 | : Juan Luis Reig-Valiente; Manuel Talón |
| Co author 2 | : Luis Marqués |
| Affiliation presenting author | : Instituto Valenciano de Investigaciones Agrarias |
| Affiliation 1 | : Instituto Valenciano de Investigaciones Agrarias |
| Affiliation 2 | : Cooperativa de Productores de Semillas de Arroz, Spain |
| Select only one type of presentation | : 3-5 minute flash talk |
| Abstract | : Genome-wide association is an efficient tool to study the genetic bases underlying diversity, a fundamental resource for breeding. Rice plants are sensitive to the agro-climate conditions, being photoperiod one of main factor contributing to their adaptation to the region where they are grown. In this study, we have analysed a collection of japonica varieties adapted to temperate regions to perform association studies with traits that are involved in the good performance of plants in this climate such as heading date and other agronomical traits such as plant height, number of panicles, panicle length and number of grains per panicle. We have performed a genome wide association study using a panel of 1713 SNPs that, based on linkage disequilibrium estimations, provides a full coverage of the whole genome. We have found a total of 43 SNPs associated with variations in the different traits. The identified SNPs were distributed across the genome except in chromosome 12, where no associated SNPs were found. The inspection of the vicinity of these markers also revealed a set of known genes previously associated with physiological functions strongly linked to agronomic traits. Of special relevance are two genes involved in gibberellin homeostasis that are associated with plant height and panicle length. We also detected novel associated sites with heading date, panicle length and number of grain per panicle. We have identified loci associated with important agronomic traits among cultivars adapted to temperate conditions. Some of these markers co-localized with already known genes or QTLs, but our findings also provide novel molecular markers that can be of help to elucidate the complicated genetic mechanism controlling important agronomic traits, as flowering regulation in the nondependent photoperiod pathway. The detected associated markers may provide important tools for the genetic improvement of rice cultivars in temperate regions. |

Uploaded Files »

No files found.