**Methods**

**Plant materials**

We sampled three different germplasm sources, including Chinese cultivated rice (*O. sativa* L.) varieties, cultivated rice varieties from sources outside of China, andwild rice(*O*. *rufipogon* Griff*.*) varieties (Figure S1a and Table S1). First, core Chinese rice landrace collections were selected from about 50,000 rice varieties conserved at the China National Rice Research Institute in Hangzhou, Zhejiang Province (Wang et al., 2014). Based on a NJ trees (Figure S1a) constructed from 103 SSR markers (Wang et al., 2014), we sampled 371 Chinese cultivated rice varieties to represent the full range of phenotypic diversity (Figure S1b-e) and geographic distribution in China. Next, from a collection of about 2,500 cultivated rice varieties from outside of China (Wang et al., 2018), we used PLINK v1.90 beta to obtain pairwise estimates of identity-by-state (IBS). The average IBS value was below 0.75, with different geographical origins used to identify 372 unrelated cultivated rice varieties from other countries. Finally, the existing geographical populations (185 varieties) of wild rice were selected, which reflect the habitats and genetic diversity of extant wild rice taxa. These wild rice seeds were obtained from the germplasm center of the Institute of Crop Science, Chinese Academy of Agricultural Sciences in Beijing, China. All the wild rice varieties were subjected to genomic and phenotypic identification to select representative wild rice varieties according to the following criteria. Firstly, on the basis of the cluster tree of genome sequences, the wild rice varieties representing all three important branches and all existing distribution areas of wild rice were selected. Secondly, wild rice varieties possess typical morphological characteristics of wild rice planting in Beijing (Figure S1f-h) were selected. Two rice genomes (*O. barthii* and *O. meridionalis*) from the National Center for Biotechnology Information (NCBI) database (BioProject accession numbers PRJNA264485 and PRJNA264483, respectively) were used as outgroups. In this study, 371 Chinese cultivated rice varieties and 185 wild rice varieties were sequenced to serve as additional resources of existing rice genome sequences, and the resulting data have been deposited into the NCBI (BioProject accession numbers PRJNA657701 and PRJNA658215).

**DNA isolation and genome sequencing**

Genomic DNA for each rice variety was extracted with a DNeasy Plant Mini Kit (Qiagen, Beijing, China) from plant leaves. Around 10 µg of DNA was sheared into approximately 500-bp fragments using the Covaris system (Thermo Fisher Scientific). These fragments were purified, A-tailed, ligated, and amplified by PCR for library construction using the TruSeq Library Construction Kit (Illumina, San Diego, CA, USA) following the manufacturer’s instructions. The libraries were indexed by mixing DNA from five samples at an equimolar concentration. After the library was constructed, the initial quantification was carried out using a Qubit 2.0 fluorometer. The qualified library was loaded on an Illumina HiSeq 2500 platform (San Diego, CA, USA) for 125-bp, paired-end sequencing.

**Mapping and variation calling**

The raw sequencing data were first filtered by removing adaptor sequences and reads with low-quality base calls, which primarily result from base-calling duplicates and adaptor contamination, with the following criteria: (i) reads with ≥10% unidentified nucleotides (N); (ii) reads with >10 nt aligned to the adaptor, with ≤10% mismatches allowed; (iii) reads with >50% bases having Phred quality <5; and (iv) putative PCR duplicates generated through PCR amplification in the library construction process, i.e., read 1 and read 2 of two paired-end reads that are completely identical. To identify SNPs, clean reads from all rice varieties were separately aligned to the *O. sativa* ssp. *japonica* reference genome (Nipponbare, Reference-IRGSP-1.0) by BWA v0.7.17 using the parameters “mem –t 4 –k 32 –M -R” (Li and Durbin 2010). The sequencing coverage and other detailed information for each rice variety are listed in Table S1. The reads aligned to multiple regions were removed by SAMtools v1.9 (parameter: rmdup) (Li et al., 2009). For SNP calling, the mpileup files were generated by SAMtools mpileup with the parameters “-q 1 -C 50 -S -D -m 2 -F 0.002”. Then, the HaplotypeCaller tool implemented in GATK v4.0.1.2 was used to call SNPs based on local *de novo* assemblies of haplotypes in each active region. A high SNP confidence score was applied in the above analysis with the parameters “-stand\_call\_conf 30 -stand\_emit\_conf 40”. The resulting SNPs were filtered to remove ambiguous or low-quality calls. We masked loci that had more than two alleles, less than 4X coverage in any sample, a Phred-scaled probability score of less than 25, or high levels of heterozygosity based on Hardy-Weinberg equilibrium. Finally, the software SnpEff v4.3T (Cingolani et al., 2012) was used to annotate all detected SNPs based on their physical locations and predict coding effects according to the *O. sativa* ssp. *japonica* genome (MSU Rice Genome Annotation Project Release 7; Table S2).

**Detection of selective sweeps**

Three different methods were used to investigate regions under selection pressure. First, the nucleotide diversity in each cultivated rice subgroup was calculated and the average absolute differentiation (*dxy*) (Puzey et al., 2017) between cultivated rice varieties and their wild ancestors was used to test for deviations from expected patterns of cultivated populations (DD residual test) (Arnold et al., 2016). The outlier regions with high divergence relative to the average diversity were fitted out and residuals were calculated based on vertical deviations from the regression line fit. The outlier values were used to identify regions with high differentiation relative to their level of diversity in the population (Figure S3). Outliers were identified by the overlap with other metrics and top candidates were selected from the5% outlier lists of *FST* between cultivated rice varieties and their wild ancestors and the XP-CLR test (Chen et al., 2010), which were examined in the XP-CLR v1.0 program with a likelihood-based model (Figures S2 and S4).

**Adaptation associations**

We used genotype-environment associations to represent adaptation associations using the method described by Mahony et al. (2019). Environmental data of minimum temperature in May(all layers with 30 s) and average daylength in August were downloaded from <http://worldclim.org/bioclim> and <https://sunrise-sunset.org/>, respectively, for georeferenced sample points. Bayenv v2.0 (Coop et al., 2010; Gunther and Coop, 2013) was used to identify loci responding to the environmental selection (-k 100000 and -r 63479). In this analysis, the neutral covariance matrix was estimated using a set of 4,737,349 non-redundant SNPs with 1×105 iterations. Bayenv attempts to account for sample size and population history while testing for a correlation between allele frequencies and an environmental variable. To control for a general relationship among populations, standardized allele frequencies was estimated from a set of control markers as the null model. Further, a global *FST*-like statistic was estimated to account for shared population structure. We compared the sample covariance matrix with the standardized sample covariance matrix based on population frequencies and found that the majority of the covariance between populations has been removed. Then Markov chain Monte Carlo (MCMC) was performed to integrate over the posterior of the parameters. For each centered and standardized environmental variable, Bayenv was run in the test mode with 1×106 iterations across three independent chains, in which the above calculated covariance matrix was used to correct for neutral population structure. To ensure that only loci with the strongest evidence for environmental effects were isolated, the above loci were re-ranked and only those ranked in the top 300 for both absolute rho and Bayes factor (BF) across the three chains (i.e., geographical position, minimum temperature in May, and average daylength in August) were selected. Then, we used empirical probability to determine the likelihood of the occurrence of an event based on computational data.

**Identification of *COLDF* function by mutants and analyses of agronomic traits**

*COLDF* function was identified through an in-house TILLING platform (www.croptilling.org) by screening the region from 22,687,902 bp to 22,689,535 bp on Chr. 8 (<http://rice.plantbiology.msu.edu/>) and gene editing. The two identified *COLDF* mutants (*coldf-1* from the TILLING platform and *coldf-2* from gene editing) were backcrossed to *O. sativa* ssp. *japonica* var. Zhonghua 11 twice before phenotypic analyses were performed. Three-leaf-stage seedlings were used as phenotyping materials in this study according to previous research (Ma et al., 2015; Zhao et al., 2017). Thirty seeds of each rice variety were equally divided and planted in two 10 cm × 10 cm pots. The plants were grown in a greenhouse at 30 °C under a photoperiod of 16 h light/8 h dark for two weeks until the three-leaf-stage. Then, for cold treatment, the three-leaf-stage rice seedlings were transferred to a plant growth chamber (RDN-600, Ningbo Ledian Instrument Manufacturing Co., Ltd., Ningbo, China) and grown at 4 °C with a 12 h light/12 h dark photoperiod for 48 h. After cold treatment, the plants were transferred back to the normal environment for recovery. After another 7 d, the rating scores for cold tolerance were determined based on the percent of survival rate as used in the previous study (Ma et al., 2015).

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