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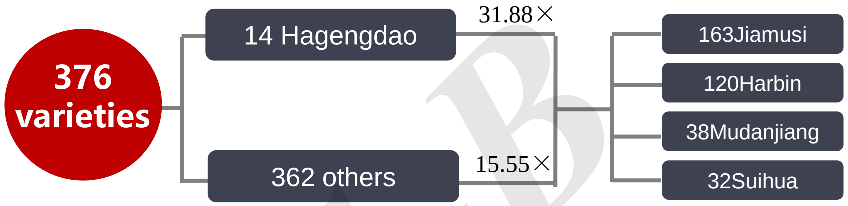
Genomic insights into the diversity of rice cultivars developed in Heilongjiang Province, China

Key words: *Japonica* rice; Heilongjiang; Genomic diversity; Rice breeding

Results



376 varieties

14 Hagengdao

31.88×

362 others

15.55×

163Jiamusi

120Harbin

38Mudanjiang

32Suihua

- A total of 200T data were obtained
- 4.90 million SNPs, 0.98 million Indels

Table 1 Number of SNPs on each chromosome in 376 Heilongjiang varieties

Chromosome	Intergenic	5’-UTR	3’-UTR	Exon	Intron	Total
Chr1	199735	4960	8938	68544	62572	344749
Chr2	249988	5683	9408	76412	75662	417153
Chr3	247019	6177	10576	66294	71560	401626
Chr4	245774	4755	5978	98143	74056	428706
Chr5	221450	4262	7231	74122	60515	367580
Chr6	269320	4500	8038	87624	75658	445140
Chr7	198882	3781	6989	68632	63503	341787
Chr8	263969	4401	8058	94173	79304	449905
Chr9	170951	2430	3926	59185	48877	285369
Chr10	295566	5829	8121	98007	77664	485187
Chr11	319502	6508	10705	126336	98007	561058
Chr12	226831	3819	6584	83822	65419	386475
Total	2908987	57105	94552	1001294	852797	4914735
Percent	59.19%	1.16%	1.92%	20.37%	17.35%	100.00%

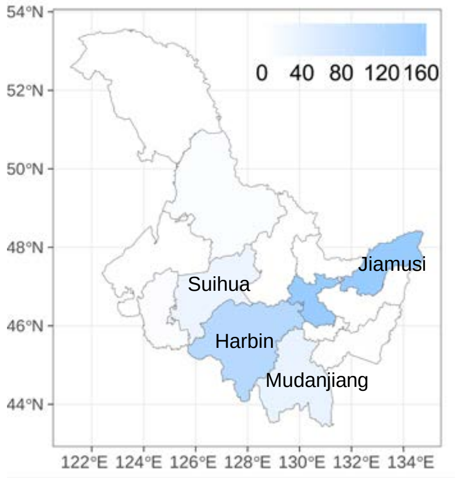


Fig. 1 Geographical distribution map of 376 Heilongjiang rice varieties collected.

Results

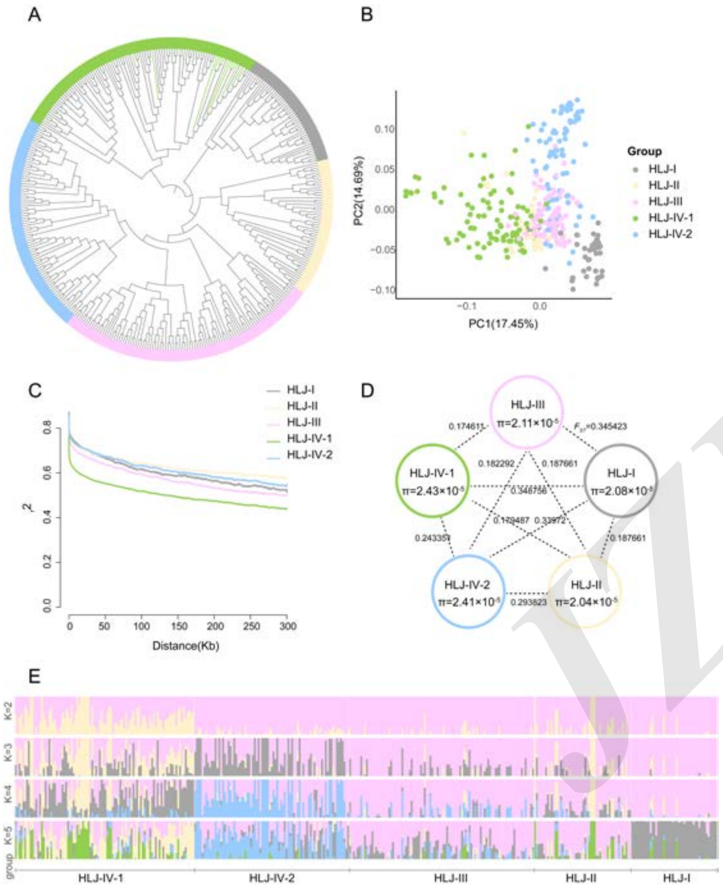
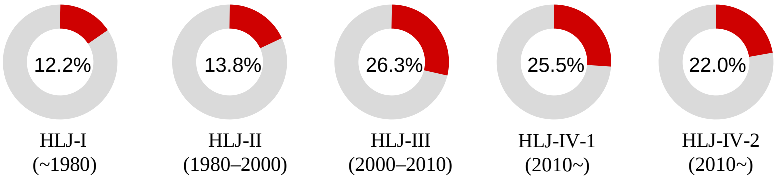


Fig. 2 Inferred population structure of HLJ rice cultivars.

- Based on 56,376 core SNP markers of 376 varieties, the optimum K value of population structure was determined to be 5, which was divided into five subgroups.
- All varieties are temperate *japonica* rice (GJ) with 0.05% to 5.24% *indica* rice gene penetration.
- The varieties bred in recent years were divided into two subgroups, and their nucleotide diversity and linkage disequilibrium attenuation rate were high, which indicated that the new varieties had high genetic diversity and high recombination rate.



Results

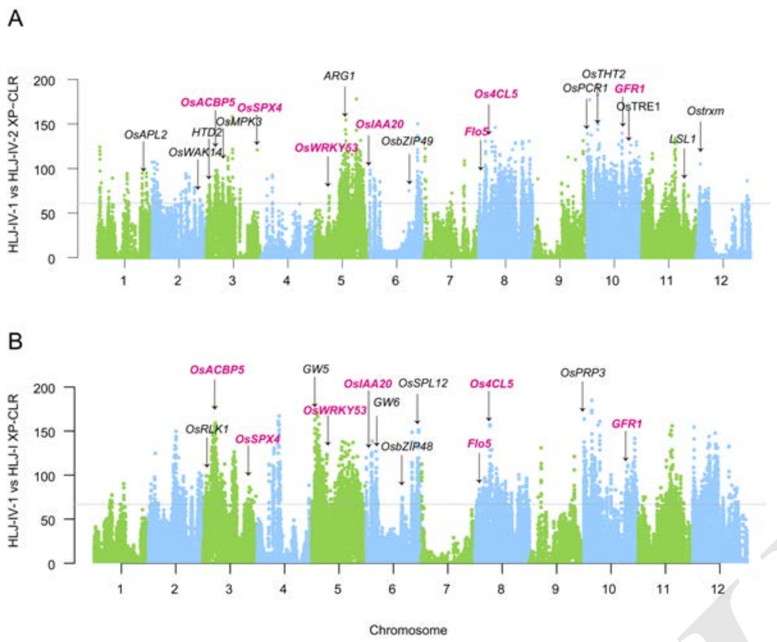


Fig. 3 Identification of putatively selected genomic regions based on the cross-population composite likelihood ratio (XP-CLR) scores in different stages of HLJ's rice cultivars.

- More than 10% of the genomic regions were selected.
- Rice blast resistance genes, such as *OsACBP5* and *Os4CL5*, are often selected in the breeding process, indicating that broad-spectrum disease resistance is the key goal of breeding.
- There are great differences in the selected genes of varieties at different growth stages. For example, the comparison between HLJ-IV-1 and HLJ-I shows that grain-shaped genes (*GW5* and *GW6*) are selected, and some genes are enriched in carbohydrate metabolism pathway.

- Most *japonica* rice varieties (11/14) showed close genetic distance with Wuyoudao4, while ha1,3,6 were far from other varieties.
- The series of varieties showed high genetic consistency, especially in aroma traits and yield.

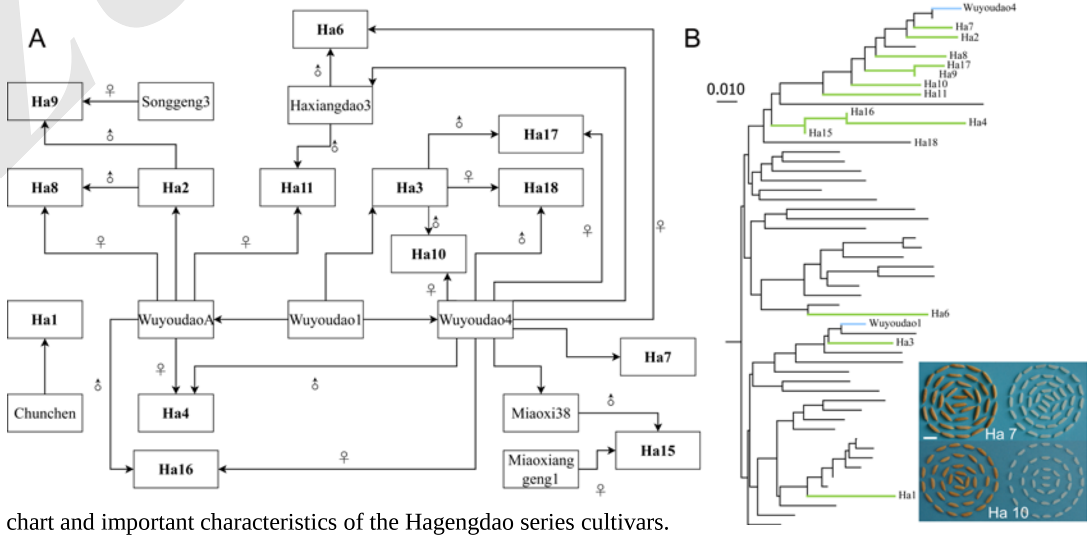
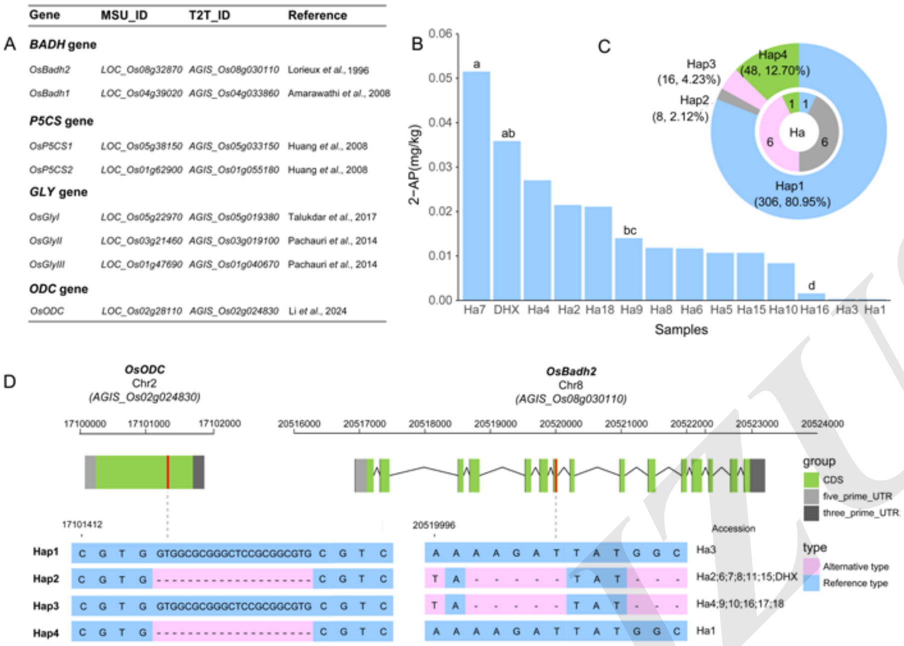


Fig. 4 Pedigree chart and important characteristics of the Hagengdao series cultivars.

Results



A

Gene	MSU_ID	T2T_ID	Reference
***BADH* gene**			
OsBadh2	*LOC_Os08g32870*	*AGIS_Os08g030110*	Lorieux *et al.*, 1996
OsBadh1	*LOC_Os04g39020*	*AGIS_Os04g033860*	Amarawathi *et al.*, 2008
***P5CS* gene**			
OsP5CS1	*LOC_Os05g38150*	*AGIS_Os05g033150*	Huang *et al.*, 2008
OsP5CS2	*LOC_Os01g62900*	*AGIS_Os01g055180*	Huang *et al.*, 2008
***GLY* gene**			
OsGlyI	*LOC_Os05g22970*	*AGIS_Os05g019380*	Talukdar *et al.*, 2017
OsGlyII	*LOC_Os03g21460*	*AGIS_Os03g019100*	Pachauri *et al.*, 2014
OsGlyIII	*LOC_Os01g47690*	*AGIS_Os01g040670*	Pachauri *et al.*, 2014
***ODC* gene**			
OsODC	*LOC_Os02g28110*	*AGIS_Os02g024830*	Li *et al.*, 2024

Fig. 5 Number of aromatic cultivars, aroma genes, and their mutation types in the Hagengdao and Heilongjiang series cultivars.

1. The aroma of Harbin japonica rice series is similar to that of popcorn. Through sensory evaluation and GC-MS detection, it is found that all varieties except Ha1 and 3 have aroma characteristics.
2. There are specific deletion mutations in OsBadh2 and OsODC of most varieties (12/14) of Harbin japonica rice series, and double mutation can significantly increase the content of 2-AP.
3. Through the analysis of 376 Heilongjiang varieties, it was found that four haplotypes (Hap1 to Hap4) were formed based on OsBadh2 and OsODC gene mutations.
4. Hap1 accounts for 2.12%, and most of them are not aromatic rice varieties (80.95%).

Results

① Hagengdao7 rice has an aspect ratio of 3.2:1, while other varieties usually have an aspect ratio of 2.6:1-2.8:1. Its *OsGL3.1* has SNP in exon 11, which may lead to premature termination of translation.

② Some rice varieties in Heilongjiang carry *sd1-r* allele, which has high yield and strong lodging resistance, but Hagengdao series varieties have weak lodging resistance.

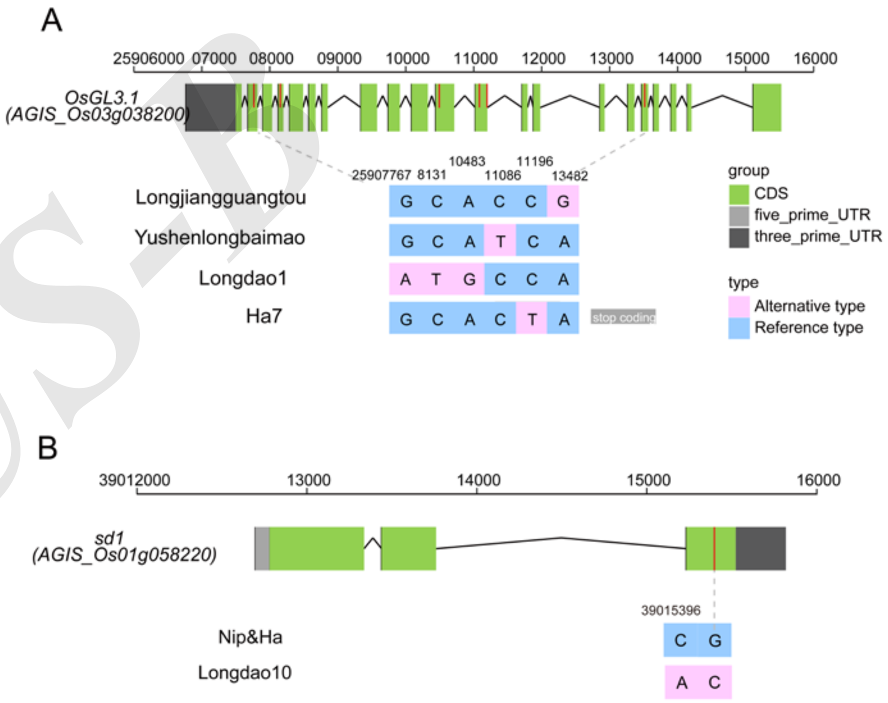


Fig. 6 Types of variation in important genes in the Hagengdao and Heilongjiang series cultivars

Research Summary

- By adding over 130 varieties to the previous HLJ-IV subgroup, we increased its reliability, distinctly categorizing varieties developed HLJ-IV into two groups
- We could potentially yield superior germplasm with even higher 2-AP content than that found in Hagengdao7 by knocking out the *OsODC* gene by genome editing
- The Dongnong and Xiushui series harbor the *sd1-r* and *sd1-j* alleles, showcasing their effective application in contemporary *japonica* rice breeding