Characterization of the common *japonica*-originated genomic regions in the high-yielding varieties developed from inter-subspecific crosses in rice (*Oryza sativa* L.)

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Abstract: The inter-subspecific crossing between *indica* and *japonica* subspecies in rice have been utilized to improve the yield potential of temperate rice. In this study, a comparative study of the genomic regions in the eight high-yielding varieties (HYVs) was conducted with those of the four non-HYVs. Next-Generation Sequencing (NGS) mapping on the Nipponbare reference genome identified a total of 14 common genomic regions of *japonica*-originated alleles. Interestingly, the HYVs shared the *japonica*-originated genomic regions on the nine chromosomes, although they were developed from different breeding programs. A panel of 94 varieties was classified into four varietal groups with 39 single nucleotide polymorphism (SNP) markers from 39 genes residing in the *japonica*-originated genomic regions and 16 additional trait-specific SNPs. As expected, the *japonica*-originated genomic regions were only present in the *japonica* (JAP) and HYV groups, except for Chr4-1 and Chr4-2. The *Wx* gene, located within Chr6-1, was present in the HYV and JAP variety groups, while the yield-related genes were conserved as *indica* alleles in HYVs. The *japonica*-originated genomic regions and alleles shared by HYVs can be employed in molecular breeding programs to further develop the HYVs in rice.

Keywords: rice; yield; HYV; Tongil; *indica*; *japonica*; SNP; molecular breeding

1. Introduction

There are two subspecies in cultivated rice (*Oryza sativa*), *indica* and *japonica*. *Indica* rice is known to be adaptable to tropical regions, while *japonica* rice is grown in temperate regions. Therefore, *indica* and *japonica* have different characteristics [1]. In general, *japonica* varieties are known to have relatively low yield potentials, as compared to *indica* varieties. To improve the yield potential of *japonica* rice, inter-subspecific crosses between *indica* and *japonica* have been conducted by conventional rice breeders [2]. As a result of these efforts, several high-yielding varieties (HYVs) have been developed from *indica-japonica* crosses. One of the greatest historical successes of *indica–japonica* crosses was the development of Tongil, an HYV, in Korea. Tongil showed a 30% higher yield than those of the conventional *japonica* varieties. By growing Tongil rice, self-sufficiency in staple food in Korea was possible in 1977 [3]. There were important trade-offs in growing Tongil, such as cold intolerance, pathogen susceptibility, and low eating quality, which were inherited from *indica*

parents. A series of 'Tongil-like' HYVs have been developed from *indica–japonica* crosses to overcome the vulnerable points of Tongil from the late 1970s [2].

HYVs have been developed using *indica* and *japonica* varieties since the 1980s in Japan. Takanari is a Japanese semi-dwarf HYV, developed from the crosses between Milyang 42 and Milyang 25. Takanari shared the ancestry of Tongil [4]. To date, it recorded the highest grain yields for both yield trials (>10 t/ha as brown rice) and individual trials (11.7 t/ha as brown rice) in Japan [5]. Minghui 63, which was derived from the cross between IR 30 and Gui 630, is the male parent of the elite hybrid rice Shanyu 63 from China. IR 30 is a semi-dwarf variety developed in IRRI (International Rice Research Institute) and is a restorer line for WA-CMS A-lines, which have a good plant type, a high resistance to blast, a bacterial blight, and brown planthoppers. Gui 630 is a rice germplasm from Guyana that has a high grain weight, desirable grain quality, and high yield potential [6]. Gui 630 is known as an *indica* restorer variety [7].

Nipponbare is the *japonica* reference genome of rice and was first sequenced at the high-quality whole-genome level through all the crops [8]. In addition, the whole genome sequences of *indica* rice varieties were reported [9-13]. The genomic difference between *indica* and *japonica* at the sequence level has been extensively studied [14]. At least 384,431 single nucleotide polymorphisms (SNPs) and 24,557 insertion/deletion mutations (InDels) were reported between Nipponbare and 93-11 [15]. With the advent of Next-Generation Sequencing (NGS) technology, numerous genomes of diverse rice germplasm collections have become available. For instance, 3000 rice genomes were sequenced and deployed in genetic and genomic rice studies [16-19]. Recently, more than one hundred high-yielding loci, associated with green revolution phenotypes and derived from the two ancestral *indica* varieties, were identified with the help of pedigree analysis, whole-genome sequencing, and genome editing [20]. Furthermore, most of the quantitative trait loci (QTLs) and genes for high-yielding potential in HYVs originated from *indica* parents in previous studies using HYVs derived from *indica–japonica* crosses [3-5,21,22]. No report exists on the characterization of *japonica* genomic regions in HYVs derived from *indica–japonica* crosses yet.

Previously, we sequenced the whole genomes of Tongil and its parental varieties to analyze the genome composition and genetic factors of Tongil. As a result, the Tongil genome was found to be derived mostly from the *indica* genome, with a small portion of *japonica* genome introgressions [3]. This study was carried out to comparatively analyze the genome structure of eight HYVs and to identify the *japonica*-originated genomic regions that are shared in HYVs, which will be helpful in understanding the role of *japonica* genome in Tongil and other HYVs that are developed in temperate regions for the further development of promising HYVs.

2. Materials and Methods

2.1 Plant DNA materials

The eight HYVs, including Cheongcheongbyeo, Dasanbyeo, Hanareumbyeo, Milyang 23, Minghui 63, Nampungbyeo, Takanari, and Tongil, and four non-HYVs, including Nipponbare, Yukara, IR 8, and TN1 were used for the whole-genome sequence analysis. Cheongcheongbyeo, Dasanbyeo, Hanareumbyeo, Milyang 23, and Nampungbyeo are Tongil-like HYVs that were developed in Korea. Takanari and Minghui 63 are HYVs from Japan and China, respectively. The pedigree of each of the eight HYVs can be found in Figure S1. A total of 94 rice varieties were used for SNP marker validation (Table S1).

2.2 Whole genome sequencing and DNA variation

Tongil and its three parental varieties (Yukara, IR 8, and TN1) were sequenced in a previous study [3]. The other eight varieties were sequenced using the Illumina Hiseq 1000 or NextSeq 500 platform in this study (Table 1). Whole genome sequencing, including the construction of shotgun DNA libraries, was performed according to the methods recommended by the manufacturer (Illumina, San Diego, CA, USA). The Illumina whole-genome shotgun paired-end DNA sequencing

data were filtered to obtain high-quality sequence data. Raw sequence reads were subjected to quality trimming using FastQC v0.11.3 (http://www.bioinformatics.babraham.ac.uk/projects/fastqc/), and the reads with a Phred quality (Q) score <20 were discarded. Adapter trimming was conducted by using Trimmomatic (http://www.usadellab.org/cms/?page=trimmomatic).

The clean reads were mapped on the *japonica* reference Nipponbare genome (Os-Nipponbare-Reference-IRGSP-1.0 [23]) using the Burrows–Wheeler Aligner (BWA) program [24]. The alignment results were merged and converted into binary alignment map (BAM) files [25]. The BAM files were used to calculate the sequencing depth and to identify SNPs using the GATK program with default parameters [26].

All the raw sequence data obtained in this study are available in the NCBI Short Read Archive (SRA) database under the following BioProject accession numbers: Nipponbare [PRJNA264254], Milyang 23 [PRJNA264250], Dasan (or Dasanbyeo) [PRJNA222717], Cheongcheong (or Cheongcheongbyeo) [PRJNA616202], Nampung (or Nampungbyeo) [PRJNA616219], Hanareum (or Hanareumbyeo) [PRJNA616209], Takanari [PRJNA616222], and Minghui 63 [PRJNA616216]. The raw sequence data of Tongil, Yukara, IR 8, and TN1 are available in a previous study [3].

2.3 SNP allele calling

Genotype calling, in order to identify SNPs that originated from the *indica* and *japonica* genomes, was performed. There were two types of values calculated in this study: (1) variety value and (2) reference value. The variety value calculated whether it was of *japonica*-type parental allele (Yukara allele) of Tongil or a Tongil-like variety or not. The variety value of SNP was calculated as the sum of the following values: '1' (IR 8 allele); '2' (TN1 allele); '4' (Yukara allele); and '0' (all others). If the SNP is the same as the Nipponbare reference, the value '1' was given to the SNP; otherwise, the value '0' was given. The SNPs showing variety value '4' and reference value '1' were called *japonica*-type SNPs. Then, the total number of *japonica*-type SNPs in each 100 kb block, which is the approximate chromosomal distance for the linkage disequilibrium (LD) decay rate in rice [27], in each chromosome was counted to identify the introgressed regions of *japonica*.

2.4 SNP marker development for Fluidigm platform

A total of 39 representative genes were selected from the selected regions. The representative genes were well-annotated in the public gene/QTL databases, as of 2017/01/06 (RAP: https://rapdb.dna.affrc.go.jp/ and UniProt: https://www.uniprot.org/). Then, only the genes containing non-synonymous SNPs in the predicted exon and UTR regions between HYVs and non-HYVs were selected. We assumed that these genes might be a part of the candidate genes that are associated with *japonica*-originated traits. Out of the many SNPs in the genes, only one SNP with a substitution polymorphism between *indica* (IR 8 and TN1) and *japonica* (Nipponbare and Yukara) per representative gene was selected for the genomic validation. The SNP markers for the Fluidigm platform (Fluigim corp., USA) were designed using the method by Seo et al. [28]. To design Fluidigm SNP genotyping assays, 60–150 bp sequences, flanking the selected SNPs on either side, were aligned by BLAST. Finally, the selected SNPs and flanking sequences were uploaded on the D3 Assay Design (https://d3.fluidigm.com/) website. After confirming the results, the designed assays were ordered. One Fluidigm SNP assay contained the Allele-Specific Primer 1 (ASP1), ASP2, Locus-Specific Primer (LSP), and Specific Target Amplification (STA) primer.

2.5 DNA extraction and Fluidigm genotyping

Young leaves of each plant from all materials used in this study were collected for DNA extraction at the tillering stage. Genomic DNA was extracted using the modified cetyltrimethylammonium bromide (CTAB) method, as described by Murray and Thompson [29]. The concentration and purity of DNA samples were measured with a NanoDrop 1000 spectrophotometer (NanoDrop Technologies, Wilmington, DE, USA). DNA samples, showing absorbance ratios above 1.8 at 260/280nm, were diluted to 50ng/uL and used for genotyping.

Genotyping was performed using the BioMark™ HD system (Fluidigm, San Francisco, CA, USA) and 96.96 Dynamic Array IFCs (Fluidigm, San Francisco, CA, USA), according to the manufacturer's protocol in National Instrumentation Center for Environmental Management (NICEM), Seoul National University (Pyeongchang, Korea). Specific Target Amplification (STA) was performed prior to SNP genotyping analysis. PCR was performed in a 5 μL reaction containing 50 ng of the DNA sample, according to the manufacturer's protocol. For genotyping, SNPtype assays were performed using STA products, according to the manufacturer's protocol. The genotyping result was acquired using Fluidigm SNP Genotyping Analysis software. All the genotype-calling results were manually checked and any obvious errors in the homozygous or heterozygous clusters were curated.

2.6 Data analysis

We analyzed basic marker statistics, such as major allele frequency (MAF), heterozygosity, and polymorphism information content (PIC) of SNP markers using PowerMarker V3.25 [30]. PowerMarker V3.25 was used to calculate the genetic distance, based on CS Chord [31] and the constructed un-weighted pair group methods with the arithmetic mean algorithm (UPGMA) dendrogram, which was visualized in Molecular Evolutionary Genetics Analysis version 7.0; MEGA7 [32].

3. Results

3.1 Whole genome sequencing and SNP calling

To analyze the genomic composition of the HYVs derived from *indica–japonica* crosses, the whole genomes of HYVs and four varieties were sequenced on the Illumina platform. A large number of short reads were mapped onto the reference Nipponbare genome and were then assembled into a consensus sequence. The number of sequence yields and the number of reads and mapping depths were varied. For example, a total of 66,464,246 reads of the Cheongcheongbyeo genome, corresponding to 9,991,040,272 bp (10 Gb), were generated, representing a 21-fold mapping depth. Nipponbare showed the largest number of sequence yields and number of reads and mapping depths (Table 1).

Table 1. Basic sequencing statistics of the varieties used in this study.

Type	Variety name	Yield (bp)	Read	N (%)	GC (%)	Q30 (%)	Depth (X)	Sequencing method
HYV	Cheongcheongbyeo	9,991,040,272	66,464,246	0.07	43.83	83.37	21.76	Illumina NextSeq 500
HYV	Dasanbyeo	5,677,243,407	93,838,734	1.05	39.75	69.57	10.32	Illumina Hiseq 1000
HYV	Hanareumbyeo	8,701,463,207	57,884,660	0.07	43.74	81.74	18.58	Illumina NextSeq 500
HYV	Milyang 23	8,909,120,495	147,258,190	0.31	41.08	76.44	17.79	Illumina Hiseq 1000
HYV	Minghui 63	10,346,919,646	68,794,138	0.07	43.93	83.18	22.48	Illumina NextSeq 500
HYV	Nampungbyeo	10,366,586,498	68,923,446	0.07	43.88	83.52	22.62	Illumina NextSeq 500
HYV	Takanari	9,372,371,998	62,353,794	0.08	43.38	83.10	20.35	Illumina NextSeq 500
HYV	Tongil	13,362,670,165	264,607,330	0.16	42.57	70.41	24.58	Illumina Hiseq 1000
Japonica	Nipponbare	22,212,867,380	439,858,760	0.19	42.10	89.12	51.72	Illumina Hiseq 1000
Japonica	Yukara	9,155,887,048	151,336,976	0.28	41.13	77.37	18.51	Illumina Hiseq 1000
Indica	IR 8	8,287,794,812	136,988,344	0.40	41.14	78.94	17.09	Illumina Hiseq 1000
Indica	TN 1	8,337,247,875	137,805,750	0.31	41.51	77.25	16.83	Illumina Hiseq 1000

Abbreviations are as follow: HYV—high-yielding variety, N (%)—percentage of skipped base, GC (%)—percentage of GC content, Q30 (%)—percentage of bases showing Phred quality score (Q) >= 30.

More than one million SNPs were detected in each of the eight HYVs and two *indica* varieties against the Nipponbare genome. More than 90% of the SNPs were detected in the intergenic region. The smallest number of SNPs were in the 5' untranslated region (UTR). Two *indica* varieties, IR 8 and TN1, represented a relatively large number of SNPs, as compared to eight HYVs. Among the eight HYVs, Milyang 23 showed the smallest number of SNPs (Table 2). This implies that most of the HYVs, except for Minghui 63, possess some genomic segments inherited from *japonica*.

Table 2. Number and location of the SNPs in the varieties against Nipponbare pseudomolecule.

Varieties	Non-synonymous	Synonymous	Intron	5' UTR	3' UTR	Intergenic	Total
Cheongcheongbyeo	19,193	17,439	21,671	7,076	29,403	1,019,466	1,114,248
Dasanbyeo	18,534	16,944	21,247	7,006	28,598	975,433	1,067,762
Hanareumbyeo	18,059	16,492	20,657	6,825	27,766	937,990	1,027,789
Milyang 23	17,836	16,414	20,110	6,628	27,271	933,778	1,022,037
Minghui 63	20,117	18,601	22,351	7,350	30,731	1,042,153	1,141,303
Nampungbyeo	19,592	17,960	21,588	7,195	29,286	1,005,553	1,101,174
Takanari	18,631	16,936	20,881	6,887	28,157	966,035	1,057,527
Tongil	18,427	16,837	20,816	6,750	27,021	952,421	1,042,272
IR 8	20,578	18,834	22,847	7,494	31,152	1,061,383	1,162,288
Taichung Native 1	20,171	18,179	22,095	7,614	30,286	1,041,363	1,139,708

*3.2 Evaluation of japonica-*type *SNP value*

To identify the SNPs that originated from the *indica* and *japonica* genomes, the SNP value was evaluated. The SNPs showing a variety value of 4 and a reference value of 1 were *japonica*-originated SNPs. The total number of *japonica*-originated SNPs in each 100 kb block of each chromosome were counted in order to identify introgressed regions from *japonica*. Previously, we discriminated the Tongil genome into segments that originated from *indica* and *japonica* using the sliding window method [3]. In this study, we allowed for one exception from the HYV in order to include Takanari, Cheongcheong, and Minghui 63. Accordingly, a total of 14 *japonica*-originated genomic regions, which were shared by at least six HYVs, were detected. The common *japonica*-originated genomic regions were distributed on nine chromosomes, not including chromosomes 8, 10, and 12. There were three *japonica*-type regions on chromosome 2 and two regions on chromosomes 1, 4, and 7. Furthermore, the regions were clustered or closely located on each chromosome. The size of the regions was varied from 0.1Mb for Chr7-1 and Chr11-1 to 2 Mb for Chr1-2. Out of the 14 regions, seven were common in eight HYVs (Figure 1, Table 3).
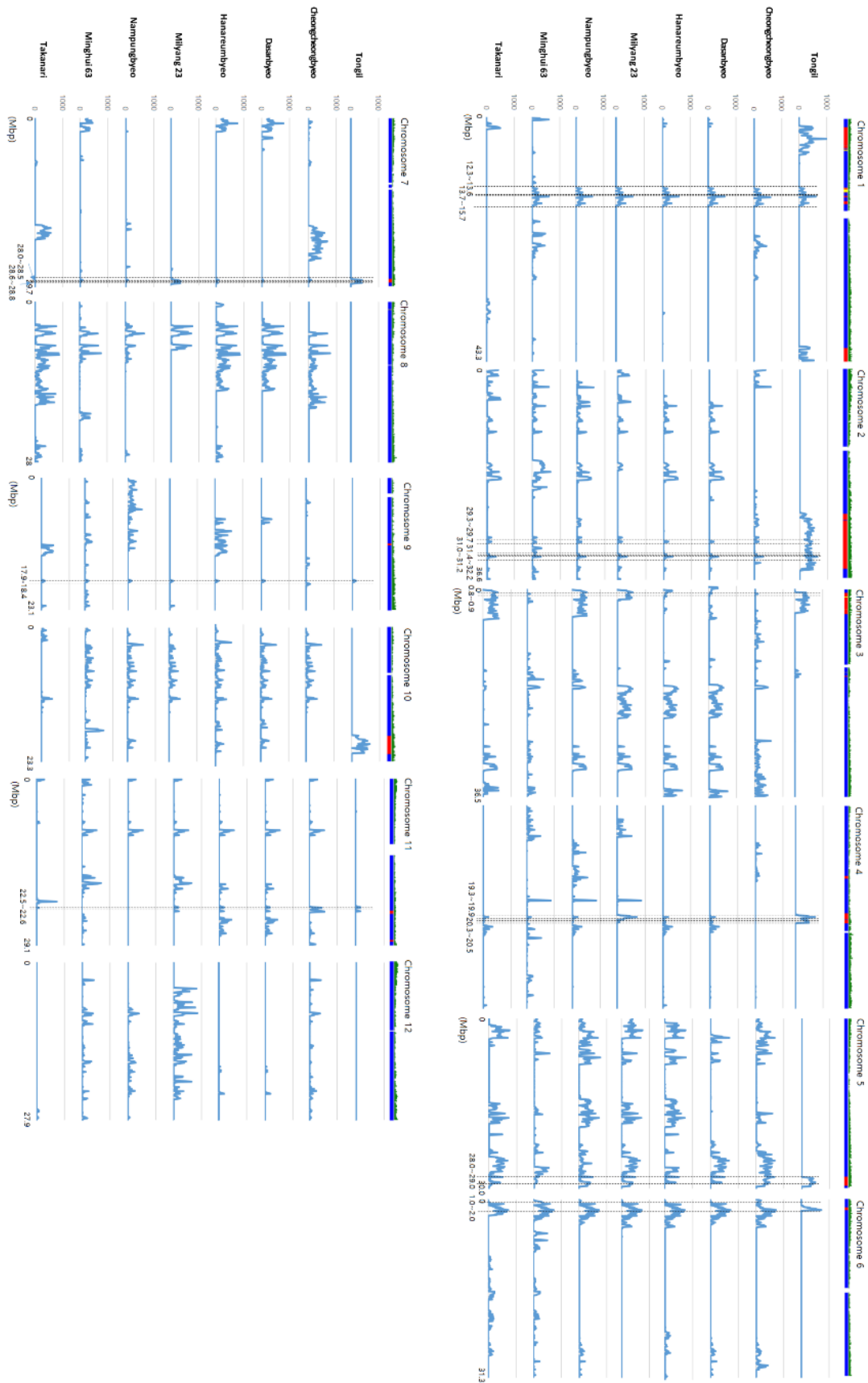
Figure 1. Location of *japonica*-type SNPs on 12 chromosomes of HYVs and their co-location with the *japonica* block of the Tongil genome, shown as a bar above the graphs. The blue and red block of the Tongil genome represents the *indica* and *japonica* blocks, respectively. The blue peak on each graph indicates the number of *japonica*-type SNPs. The position and range for the co-location of *japonica*-type blocks are denoted by black dotted lines.

Table 3. *Japonica*-type SNP frequency of Tongil and the other HYVs at common *japonica*-type regions among the eight HYVs.

Region	Narrowed Range (Mb)	Size (Mb)	Tongil	Cheongcheongbyeo	Dasanbyeo	Hanareumbyeo	Milyang 23	Nampungbyeo	Minghui 63	Takanari	Type
Chr1-1	12.3~13.6	1.3	23.3	23.3	23.3	23.3	23.3	23.3	23.3	0.0	All (ex. Takanari)
Chr1-2	13.7~15.7	2	31.4	31.4	31.4	31.4	31.4	31.5	31.5	0.0	All (ex. Takanari)
Chr2-1	29.3~29.7	0.4	64.1	14.1	14.1	14.1	14.1	14.1	14.4	14.1	All
Chr2-2	31.0~31.2	0.2	46.5	1.1	1.1	1.1	1.1	1.1	2.1	1.1	All
Chr2-3	31.4~32.2	0.8	77.4	17.3	17.6	17.6	17.6	17.6	21.6	17.6	All
Chr3-1	0.8~0.9	0.1	73.9	19.3	16.6	16.6	73.9	73.9	19.2	73.9	All
Chr4-1	19.3~19.9	0.6	75.9	0.0	8.2	8.2	77.3	8.2	7.0	8.2	All (ex. Cheongcheong)
Chr4-2	20.3~20.5	0.2	87.9	0.0	12.8	12.8	12.8	5.1	0.3	5.1	All (ex. Cheongcheong)
Chr5-1	28.0~29.0	1	76.9	82.1	23.9	23.9	23.9	23.9	13.7	23.9	All
Chr6-1	1.0~2.0	1	55.2	51.7	70.1	70.1	70.1	70.1	70.1	70.1	All
Chr7-1	28.5~28.6	0.1	32.0	6.5	5.0	6.5	4.8	6.5	6.5	0.0	All (ex. Takanari)
Chr7-2	28.6~28.8	0.2	93.5	9.7	7.7	7.6	33.2	9.7	7.6	0.0	All (ex. Takanari)
Chr9-1	17.9~18.4	0.5	13.9	0.7	13.9	13.9	13.9	13.9	13.9	13.9	All
Chr11-1	22.5~22.6	0.1	25.3	65.6	25.3	25.3	25.3	0.0	0.0	12.9	All (ex. Nampung/Minghui63)

Abbreviation is as follow: ex.—except.

3.3 QTL comparison and representative gene selection in common japonica-originated genomic regions

To elucidate the function of common *japonica*-type region*s* in HYVs, we first investigated the reported QTLs in the Q-TARO database [33]. A total of 101 QTLs for seven categories were co-located, with 14 common *japonica*-type region*s* on nine chromosomes. Only three regions on chromosome 2 were co-located with QTLs for all the seven trait categories. For eating quality, abiotic stress, and the yield-related category, 80 QTLs were identified. The largest number (10) of co-located QTLs was detected in the Chr6-1 region for eating quality. All the regions were co-located with the QTLs for abiotic stress tolerance (Table 4). This information of co-located QTLs, with common *japonica*-type regions, suggests that common genomic regions in HYVs might be mainly associated with quality, yield, and abiotic stress tolerance.

Table 4. Classification of the reported QTLs co-location with common *japonica*-type regions in eight HYVs.

Region	Eating quality	Abiotic tolerance	Biotic resistance	Yield related	Root	Flowering	Other	Total
Chr1-1/1-2	0	4	0	2	0	0	1	7
Chr2-1/2-2/2-3	8	6	3	5	1	1	1	25
Chr3-1	1	8	0	0	2	1	0	12
Chr4-1/4-2	0	2	0	4	1	0	1	8
Chr5-1	3	2	0	6	2	0	0	13
Chr6-1	10	1	1	0	1	2	0	15
Chr7-1/7-2	0	1	0	3	0	1	0	5
Chr9-1	0	4	2	7	0	0	0	13
Chr11-1	1	1	0	1	0	0	0	3
Total	23	29	6	28	7	5	3	101

Furthermore, we selected 39 genes containing non-synonymous SNPs, which could affect the molecular function of genes, and are clearly annotated in the databases of 12 common *japonica* chromosomal introgressions. There was no target gene that satisfied the above-mentioned condition in Chr4-2 and Chr7-1. The largest number (13) of selected genes was located on Chr1-2, which is the largest region, spanning 2 Mb. Only one gene was selected from Chr2-2, Chr7-2, and Chr11-1. The size of these three blocks was 0.1–0.2 Mb. The genes annotated from the major criteria of interest were *Os01g0348900, Os06g0130000, Os06g0130100* (stress tolerance), *Os06g0130400* (eating quality), and *Os01g0367100* (yield potential) (Table 5).

3.4 SNP marker development and genotyping using Fluidigm platform

A total of 39 SNP markers were designed in the 39 selected genes from common *japonica*-originated genomic regions, by one marker per one gene. The SNPs for the marker were selected from among the non-synonymous SNPs. Five SNP markers, out of the 39 SNP markers, were designed in 3' or 5' UTR. In addition, 12 agronomic traits, related to SNP markers in *indica-japonica* SNP set 2 [28] and four previously developed yield related SNP markers [34], were also used for the genotyping of 94 diverse germplasms. A total of 55 SNP markers were genotyped for 94 germplasms using the Fluidigm system, and consequently, 54 SNPs showed polymorphism and a clear genotype, except one monomorphic SNP marker designed in *Os01g0348900* on the Chr1-2 block. Therefore, we conducted a further analysis using a total of 54 polymorphic SNP markers (Figure 2, Table S2).

Table 5. Selected 39 genes in the common *japonica*-type regions.

Region	Gene (RAP DB)	Alternative name	Known function	
			UniProt	**RAP DB**
Chr1-1	Os01g0328500			Bucentaur or craniofacial development family protein
	Os01g0329800	IAI1		YT521-B-like protein family protein
	Os01g0337100	OsTPS1		Similar to Sesquiterpene synthase
Chr1-2	Os01g0347000	OsPHS1b, OsPP4, OsSTA14		Similar to PROPYZAMIDE-HTPERSENSITIVE 1
	Os01g0348900	salT(sal1), SalT1, sal1, Sal1, SALT, ML, SalT, OsSalT	Salt stress-induced protein	SalT gene product
	Os01g0351200	PARP2-A	Poly [ADP-ribose] polymerase 2-A	Similar to Poly
	Os01g0356800	OsEnS-6		Domain of unknown function DUF3406, chloroplast translocase domain containing protein
	Os01g0363900	OsWAK5		Similar to HASTY
	Os01g0364400	OsRLCK35		Protein kinase, catalytic domain domain containing protein
	Os01g0367100	PHD1		Chloroplast-localized UDP-glucose epimerase (UGE), Galactolipid biosynthesis for chloroplast membranes, Photosynthetic capability and carbon assimilate homeostasis (Os01t0367100-01);NAD(P)-binding domain containing protein
	Os01g0369200	CUL1	Cullin-like protein	Similar to Cullin-1
	Os01g0370000	OsOPR9, OsOPR01-2	Putative 12-oxophytodienoate reductase 9	NADH:flavin oxidoreductase/NADH oxidase, N-terminal domain containing protein
	Os01g0371200	OsGSTF1, RGSI	Probable glutathione S-transferase GSTF1	Similar to Glutathione-S-transferase 19E50
	Os01g0371400	OsGSTF9		Similar to Glutathione s-transferase gstf2
	Os01g0371500	OsGSTF10		Similar to Glutathione-S-transferase 19E50
	Os01g0375100	OsDjC6	DNAJ heat shock N-terminal domain-containing protein-like	Similar to DnAJ-like protein slr0093
Chr2-1	Os02g0713500	OsFbox108, Os_F0236		F-box domain, cyclin-like domain containing protein.
	Os02g0713900	HMGR I, Hmg1, HMGR1, HMGR 1, OsHMGR1	3-hydroxy-3-methylglutaryl-coenzyme A reductase 1	Similar to 3-hydroxy-3-methylglutaryl-coenzyme A reductase 1
Chr2-2	Os02g0743700			Similar to RING-H2 finger protein ATL1Q
Chr2-3	Os02g0755200	OsHDMA702, HDMA702	Lysine-specific histone demethylase 1 homolog 1	Similar to amine oxidase family protein
	Os02g0761100	OsCYP40b, OsCYP-8, OsCYP40-2		Similar to Cyclophilin-40 (Expressed protein)

Chr3-1	Os03g0114900		Mitochondrial import inner membrane translocase subunit Tim17 family protein, expressed	Similar to putaive mitochondrial inner membrane protein
	Os03g0115500			Similar to pyridoxine 5'-phosphate oxidase-related
Chr4-1	Os04g0395900			Polynucleotide adenylyltransferase region domain containing protein
	Os04g0400800			Heavy metal transport/detoxification protein domain containing protein
Chr5-1	Os05g0563400	OsARF15, ETT1, OsETT1, ARF3b	Auxin response factor 15	Similar to Auxin response factor 5
	Os05g0571700	OsFbox282, Os_F0643		Cyclin-like F-box domain containing protein
Chr6-1	Os06g0125132	SDH8B	Succinate dehydrogenase subunit 8B, mitochondrial	Conserved hypothetical protein
	Os06g0128300	OsABCB23, OsISC32		Similar to Mitochondrial half-ABC transporter, Similar to STA1 (STARIK 1); ATPase, coupled to transmembrane movement of substances
	Os06g0129900	Cytochrome P450	Cytochrome P450	Similar to Cytochrome P450 CYPD
	Os06g0130000	LMR		AAA-type ATPase, Defense response, Similar to Tobacco mosaic virus helicase domain-binding protein (Fragment)
	Os06g0130100	OsSIK1, OsER2, ER2		Receptor-like kinase (RLK), Drought and salt stress tolerance, Oryza sativa stress-induced protein kinase gene 1
	Os06g0130400	OsACS6		ACC synthase, Protein homologous to aminotransferase, Ethylene biosynthesis, Control of starch grain size in rice endosperm
	Os06g0131100	OsWD40-124		Similar to guanine nucleotide-binding protein beta subunit-like protein 1, WD40/YVTN repeat-like domain containing protein
	Os06g0136800	OsClp9, CLP9	ATP-dependent Clp protease proteolytic subunit	Peptidase S14, ClpP family protein
Chr7-2	Os07g0677500	POX3006, prx114	Peroxidase	Similar to Peroxidase precursor (EC 1.11.1.7)
Chr9-1	Os09g0471600	OsWAK84		EGF-like calcium-binding domain containing protein
	Os09g0471800	OsWAK85, YK10		Similar to WAK80 - OsWAK receptor-like protein kinase
Chr11-1	Os11g0592500		NB-ARC domain containing protein, expressed	Similar to NB-ARC domain containing protein, expressed
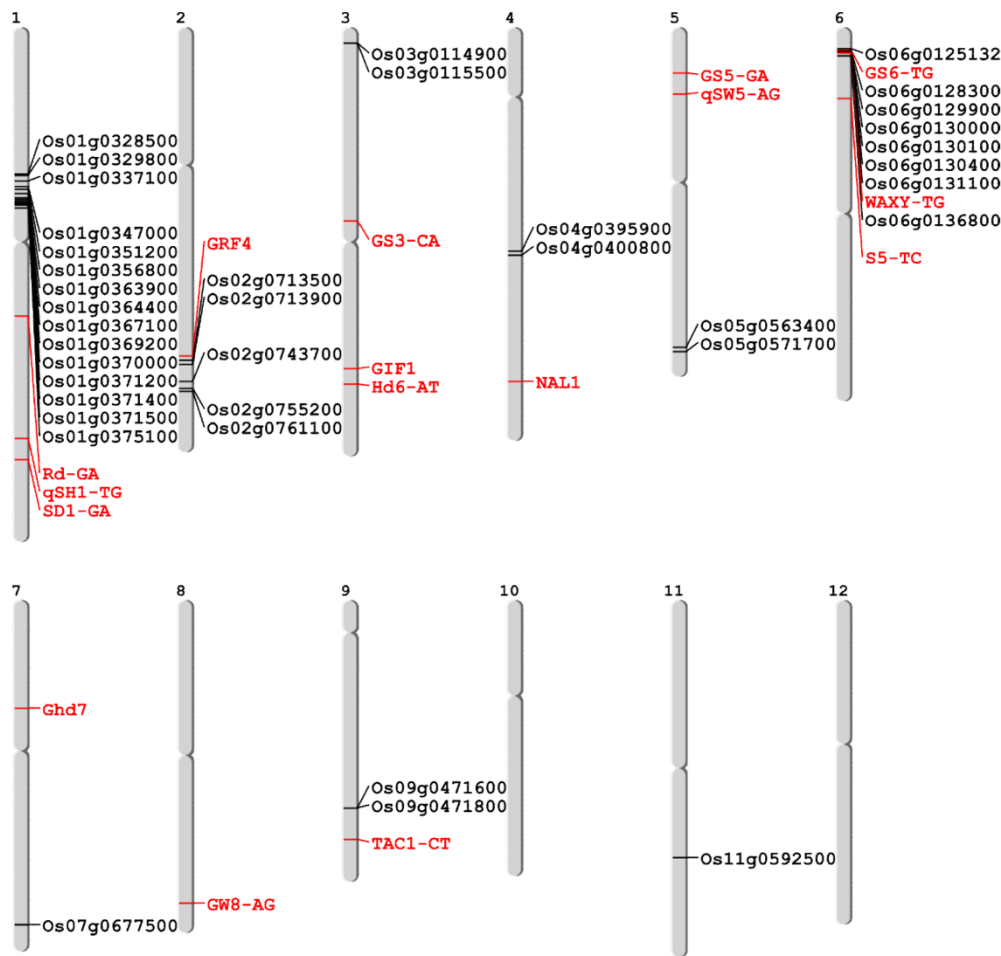
Figure 2. Genomic location of 54 polymorphic SNP markers used in this study. The markers represented by black and red indicate those newly developed on common *japonica* regions and those previously developed for agronomic trait related genes, respectively.

The results of genotyping showed a dividing pattern for 94 varieties. A phylogenetic analysis of 94 varieties was carried out using 54 polymorphic SNP markers. There were four groups, including IND1, IND2, HYV, and JAP, in the phylogenetic tree (Figure 3). All the sequenced HYVs, except Takanari, which possesses *indica* allele of Chr1-1 and Chr1-2, were clustered in the HYV-group with some Tongil-like and *indica* varieties. A total of 38 SNP markers were developed in the common Tongil-like *japonica*-like regions and discriminated IND1, IND2, and HYV by the frequency of *japonica*-alleles. The HYV group showed 93.8% for *japonica*-alleles frequency, which is similar to that of JAP. A total of 16 SNP markers were related to yield and some agronomic traits could distinguish JAP from the other three groups. For the 16 SNP set, the JAP group represented 86.1% of *japonica* allele, while the other three groups showed a lower *japonica* allele frequency, which was less than 30%. The HYV group contained *indica* alleles and were informed by the makers that were linked to the genes associated with plant architecture (SD1-GA, NAL1, and TAC-CT), yield potential (GIF1, Hd6-AT, Ghd7, and GW8-AG), and subspecies differentiation (Rd-GA, qSH1-TG, and S5-TC). They contained more than 50% japonica alleles using the markers linked to the genes for grain shape and quality (GRF4, GS3-CA, qSW5-AG, GS6-GT, and WAXY-TG) of HYV-type. Practically, the markers designed in the *japonica*-originated genomic regions and the yield-related markers from *indica* varieties can differentiate HYV from *indica* and *japonica* varieties. In fact, a high proportion of *japonica* alleles on Chr1-1, Chr1-2, and Chr3-1 was found in IND2, which consist of many varieties, known as the *aus* variety group.
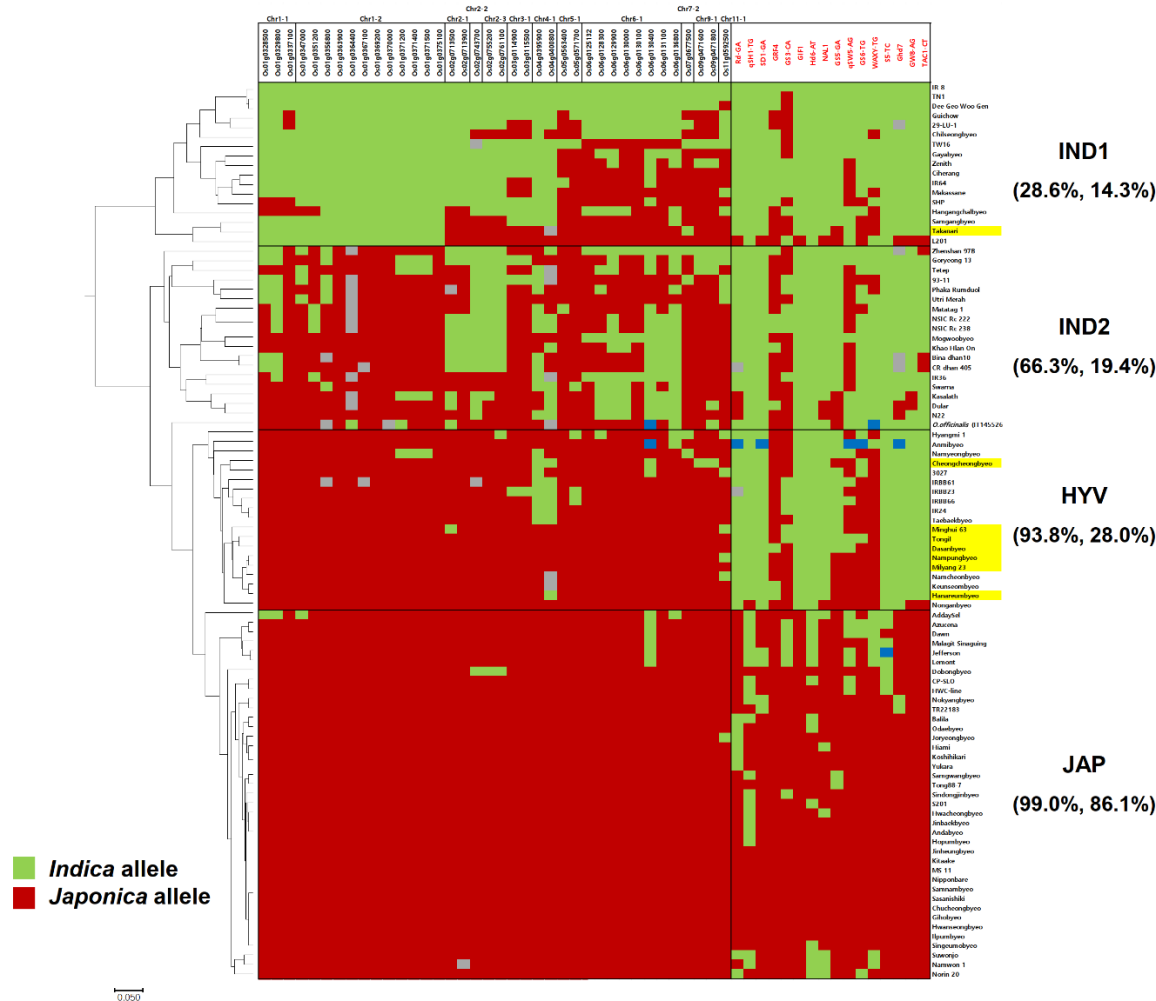
Figure 3. Phylogenetic tree of 94 germplasms based on 54 SNP markers and a genotype heat map. A 38 SNP marker set (left) and 16 SNP marker set (right) were developed on common *japonica* regions and agronomic trait related genes, respectively. The color of the marker ID is the same as in Figure 2. The varieties highlighted with yellow are eight resequenced HYVs. Homozygous alleles, which are identical to Nipponbare, were represented as red, and this is different from Nipponbare, represented as green and heterozygous alleles as blue. Grey indicates a missing genotype. The percentage values in parenthesis under each subgroup represent the percentage for homozygous *indica* allele in the 38 SNP marker set and 16 SNP marker set.

4. Discussion

All eight HYVs used in this study were clustered into the *indica* group, based on *indica–japonica* SNP sets in a previous study [28]. Interestingly, some *japonica*-type SNPs were detected within the genomes of HYVs after resequencing analysis. Furthermore, collocations of 14 *japonica*-originated genomic regions commonly present in Tongil-like HYVs, inherited from *indica–japonica* crosses, were investigated. This suggests that these *japonica*-type genomic segments were commonly and repeatedly selected during independent breeding programs in the temperate rice cultivation area. To investigate the role of these *japonica* segments in HYVs, a comparative study of the reported QTLs and representative gene selection were conducted. Eating quality, stress tolerance, and yield related traits might be main drivers for the selection of the rice HYV breeding program.

A total of 54 SNP markers, including 38 SNP markers developed from 38 selected genes for 14 common *japonica*-type regions and 16 trait-specific SNP markers, were used for the genotyping of 94

diverse varieties across *indica* and *japonica*. For the 38 SNP marker set, 16 SNP markers were located on chromosome 1, which was not identified as a *japonica* genomic segment in Takanari. Consequently, Takanari was clustered into the IND1 subgroup, although it showed a similar genotypic pattern to the other HYVs. The Chr1-1 and Chr1-2 regions were co-located with some abiotic tolerance and yield related QTLs. Furthermore, there were several selected genes that conferred abiotic stress tolerance and yield potential in the blocks. For instance, *Os01g0337100* (*OsTPS1*) reported an association with abiotic stress response and tolerance by knock-out and overexpression [35,36]. *Os01g0367100* (*PHD*) was shown to be a gene that was involved in galactolipid biosynthesis and affected photosynthetic efficiency [37]. Recently, the effect of the haplotype of *PHD1* on grain yield was also reported using the 3K rice genome panel [17]. Takanari could not have acquired this *japonica* genomic segment from a different natural environment and/or breeder's selection.

In addition, 18 varieties out of the 19 HYV-types, showed *japonica*-type Wx^b allele on the SNP marker WAXY-TG, which was designed on the splicing site in the intron of *Wx* gene in the *japonica*-type region. The *Wx* gene only contains synonymous SNPs, although it is located within Chr6-1; thus, it was not selected in our study. We previously developed a functional SNP marker for the *Wx* gene [28]. The genomic region containing the *Wx* gene is a hotspot for grain quality [38] and has been selected during and after the domestication of rice [39]. The other genomic research using two Tongil-like varieties also showed a *japonica*-type SNP pattern on the common *japonica*-type region on chromosome 6 [40]. Tongil-like varieties showed medium amylose contents, approximately 19%–20%, which is similar to that of non-waxy Korean *japonica* varieties [41,42]. Further, *Os06g0130400*, one of the selected genes in Chr6-1, was also reported as the gene controlling starch grain size in endosperm [43]. *Os06g0130000* and *Os06g0130100* were reported for resistance to rice blast and bacterial blight, and tolerance to drought and salt stress, respectively [44,45]. Therefore, Chr6-1, including the *Wx* gene, might be mainly selected for eating quality and latent stress tolerance.

When HYVs were developed by inter-subspecific hybridization, the scientists aimed at not only transferring some of the desirable characteristics, like resistance to lodging, blast, and yield, but also at retaining the ecological adaptability and eating quality of *japonicas* [46]. The *japonica* chromosomal introgression regions identified in this study were regarded as putative temperate region adaptable and improved the eating quality of *indica*. For this reason, the varieties developed by *indica*–*japonica* crosses could also be considered as 'temperate *indica*'. Recently, new elite rice varieties showing high yield potential and high grain quality were developed by the precise pyramiding of major genes controlling yield and grain quality traits [47]. Furthermore, there was an attempt to develop cold tolerant *indica* using an inter-subspecific cross and marker-assisted selection (MAS) [48]. In other words, breeding *indica* varieties, which are adaptable to the temperate region with high yield potential and good eating quality, can be efficiently achieved through inter-subspecific crosses and marker-assisted selection using the SNP markers developed in this study. Nevertheless, to dissect the exact contribution of *japonica*-type regions in HYVs, a comprehensive genetic and physiological analysis, by applying the molecular markers developed in *japonica*-type regions to the segregation populations derived from cross between HYVs and *indica,* is necessary. In addition, the functional studies of genes in the regions, as well as the selected ones in this study, are also required.

5. Conclusions

Consumer preference in grain shape and quality during conventional breeding procedures, without sacrificing the high-yield potential of *indica*, were revisited by the genomic analysis of HYVs. The 14 *japonica*-originated genomic regions and alleles identified in this study shared by HYVs could be applied in further development of more HYVs through inter-subspecific rice breeding.

Supplementary Materials: The following are available online at www.mdpi.com/xxx/s1, Figure S1: Pedigrees of eight HYVs used in this study. (**A**) Tongil, (**B**) Minghui 63, (**C**) Cheongcheongbyeo, (**D**) Milyang 23, (**E**) Nampungbyeo, (**F**) Hanareumbyeo, (**G**) Dasanbyeo, (**H**) Takanari., Table S1: The list of 94 diverse rice germplasms used in this study. The order of ger1mplasm is identical with order in Figure 3. The varieties

highlighted by yellow are eight HYVs used in this study., Table S2: The list of 54 Fluidigm SNP markers used in this study. MAF, Heterozygosity and PIC were calculated in 94 rice varieties.

Author Contributions: Conceptualization, J.H.C. and H.-J.K.; methodology, J.S. and J.H.C.; software, J.S.; validation, B.K. and J.H.C.; formal analysis, J.S. and S.-M.L.; investigation, J.S., S.-M.L., J.-H.H., N.-H.S., and Y.K.L., resources, J.H.C and H.-J.K.; data curation, J.S. and B.K.; writing—original draft preparation, J.S.; writing—review and editing, J.H.C. and H.-J.K.; visualization, J.S., S.-M.L., and J.H.C.; supervision, H.-J.K.; project administration, J.H.C.; funding acquisition, H.-J.K. All authors have read and agreed to the published version of the manuscript.

Funding: This study was funded by a grant from the Next-Generation BioGreen 21 Program (No. PJ013165) of the Rural Development Administration, Korea.

Acknowledgments: We appreciate to members of Crop Molecular Breeding Lab., in Seoul National University for their kind advice and assistance for this study.

Conflicts of Interest: The authors declare no conflict of interest.

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