

## Pedigree Analysis of 17 High Quality Korean Rice Cultivars Using Web Database Systems

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**ABSTRACT:** It is important to understand pedigree of rice cultivars commonly used for breeding. In this paper, pedigree tables for tracking the pedigree of 17 representative rice cultivars recommended by Rural development Administration (RDA) were completed and analyzed using two kinds of web database system; "IRIS" and "RRDB". Seven cultivars, namely, "Sangmibyeyo", "Ilpumbyeyo", "Saegewhabyeyo", "Surabyeyo", "Shindongjinbyeyo", "Ilmibyeyo" and "Jungwhabyeyo" had "Koshihikari" on the pedigree of their ancestor. Besides "Koshihikari", the most frequently used ancestral germplasms among the high quality rice cultivars were "Fujisaka 5", "Kameno o" and "Asahi". "Fujisaka 5" was used as ancestral parent in 12 out of 17 cultivars. Interestingly, "Kameno o" was used in pedigree of 16 out of 17 high quality varieties and "Asahi" was used in the ancestral pedigree of all 17 varieties. "Hwayeongbyeyo" was used as one of parent in the breeding of "Dongjin 1", "Hwabongbyeyo", "Saegewhabyeyo" and "Junambyeyo". "Ilpumbyeyo" was used in the breeding pathway of "Junambyeyo" and "Saegewhabyeyo". "Manggeumbyeyo" itself was not enlisted as one of high quality rice cultivars, but was used as a breeding parent of three high quality varieties, namely, "Saegewhabyeyo", "Hwabongbyeyo" and "Nampyeongbyeyo". Incorporated with evaluation data, pedigree will provide a valuable chance to genealogical tracking of agronomic traits such as disease resistance, grain quality and etc.

**Keywords:** rice, pedigree, high quality, genealogy, Web DB, IRIS, RRDB

The pedigree of crop cultivar is a genealogical record of breeding procedures that gives helpful information about genealogical relationship and crop improvement to the breeders. One of the critical use of pedigree informations is "Coefficient of parentage" (CP). CP is a form of numerical taxonomy based on pedigree relationships that can qual-

ify genetic relationships among the cultivars (Kempthorne, 1969). CP analysis gives genetic diversity among the varieties and prediction to the potential for continued breeding success. CP analysis was conducted in Korean-bred rice (Jong, 2003), barley (Jong and Park, 2000a, 2000b), and soybean (Jong *et al.*, 2000). In recent years, molecular markers such as AFLP (Amplified Fragment Length Polymorphism), RFLP (Restriction Fragment Length Polymorphism), SSLP (Simple Sequence Length Polymorphism) and SNP (Single Nucleotide Polymorphism) have been used in genealogical studies and gene identification. Although CP and molecular markers give valuable information of genealogical relationship to the plant breeders, pedigree itself gives more helpful information.

In the process of genealogical analysis, one of the most important factors is the accuracy of pedigree. Lacks of pedigree data often led to wrong conclusion. Before the development of crop germplasm database system and worldwide web services, completing detailed pedigree was a laborious and time consuming work. The database system related to crop germplasm resources provide a handy tools for tracking ancestral pedigree of crop varieties. Besides pedigree information, passport and evaluation data of germplasm also give much additional helpful information to the breeders. Major agronomic traits can be easily identified using database programs such as Gramene (<http://www.gramene.org/>) and Oryzabase (<http://www.shigen.nig.ac.jp/rice/oryzabase/top/top.jsp>) etc.

In this paper, we analyzed the pedigree table of 17 RDA-recommended high quality rice cultivar using web databases IRIS database system; International Rice Information System (IRIS) and Rice research database (RRDB).

### MATERIALS AND METHODS

Seventeen of RDA-recommended high quality rice cultivars were selected for the analysis of their pedigree (Table

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**Table 1.** Brief history and cross combination seventeen of rice cultivars with high quality.

No	Cultivar	Breeding No.	Cross combination	Breed. Year	Breed place
1	Odaebyeo	Suweon 303	<b>Akitsuho/Fuji 269</b>	1980	NICS <sup>†</sup>
2	Hwaseongbyeo	Suweon 330	<b>Aichi 37</b> /Samnambyeo	1984	NICS
3	Ilpumbyeo	Suweon 355	Suweon295/ <b>Inabawase</b>	1990	NICS
4	Hwayeongbyeo	Milyang 101	<b>Chukei 830</b> /YR 4811 Acp 8	1991	YARI
5	Daeanbyeo	Suweon 396	<b>Ooseto</b> /Seomjinbyeo	1995	NICS
6	Ilmibyeo	Milyang 122	Milyang96//Milyang95/Seomjinbyeo	1995	YARI
7	Jungwhabyeo	Sangju 15	<b>Etznan 126</b> /Minchikari//Daesungbyeo	1995	YARI
8	Donganbyeo	Iri 418	Milyang 95/HR5119-12-1-5	1996	HARI
9	Nampyeongbyeo	Iri 416	Iri 390/Milyang 95	1997	HARI
10	Surabyeo	Suweon 427	Suweon 345/ <b>Kanto PL4</b> //Sweon 345	1998	NICS
11	Hwabongbyeo	Milyang 138	Milyang 95/Iri 390//Milyang 101/Iri 390	1998	YARI
12	Sangmibyeo	Sangju 19	Sambaekbyeo/ <b>Ou 316</b>	1998	YARI
13	Saechucheong byeo	Suweon 433	(Daesung/Chucheongbyeo*5)+(Miinehikari/Chucheongbyeo*5)	1999	NICS
14	Sindongjin byeo	Iksan 438	Hwayeongbyeo/YR13604 Acp 22	1999	HARI
15	Junambyeo	Milyang 165	Hwayeongbyeoe//Sangjubyeo//Ilpumbyeo	2000	YARI
16	Dongjin 1	Iksan 444	Hwayeongbyeo/HR12800-AC21	2001	HARI
17	Saegehwa	Gewha 19	Ilpumbyeo//Iri 390/ <b>Chukei 830</b>	2001	HARI

<sup>†</sup>NICS (National Institute of Crop Science, Suwon), HARI (Honam Agricultural Research Institute, Iksan), YARI (Yeongnam Agricultural Research Institute, Milyang)

Bold character; Cultivars that used Japanese germplasm on the primary cross directly

1). Since the pedigree presented by original breeders gives only limited information of genealogical history, we used five kinds of web database system; International Rice Information System (IRIS, <http://www.iris.irri.org>), MAFF Gene bank-Plant (<http://www.gene.affrc.go.jp>), Gramene (<http://www.gramene.org>) and Oryzabase (<http://www.shigen.nig.ac.jp>) and Rice research database (RRDB, <http://ineweb.narcc.affrc.go.jp>). IRIS is the rice implementation of the International Crop Information System, which is a database system that provides integrated management of global information on genetic resources and crop cultivars. This includes germplasm pedigrees, field evaluations, genetic (QTL) maps, structural and functional genomic data including links to external plant databases and environmental (GIS) data. The MAFF gene bank system was developed to provide passport and evaluation data of its collections by National genetic resources database system, Japan, which has been used by agricultural scientists in the public and private sectors. This database was being developed by National Institutes for Agrobiological Resources (NIAR), Japan and providing passport and evaluation data of their collections.

Gramene displays for phenotypes including mutant and quantitative trait-loci (QTL) modules. Sequence based relationships are displayed in the genome browser adapted from

Ensemble, in the comparative map viewer (CMap), Blast databases, and protein displays. The Oryzabase is consists of five parts; (1) genetic resource stock information, (2) gene dictionary, (3) chromosome maps, (4) mutant images, and (5) fundamental knowledge of rice science. RRDB is a publicly accessible database constructed to present characteristics of cultivated rice varieties. RRDB contains about 110,000 entries of information on more than 1,000 cultivated rice varieties in the world.

## RESULTS AND DISCUSSION

The pedigree table of 17 RDA-recommended high quality rice cultivars were completed and analyzed using web databases for the better understanding of genealogical relationships of high quality rice (Fig. 1). Our preliminary screening reveals that seven out of seventeen high quality cultivars used germplasm introduced from Japan. It is considered that it may be not due to lack of native germplasm but short history of rice breeding in Korea.

As shown in Table 1, four out of seven varieties, which used Japanese germplasm on the primary cross directly, were released before 1991. Actually, the first Korean-inbred cultivar "Nongbaek" was released in 1969 since Japanese-

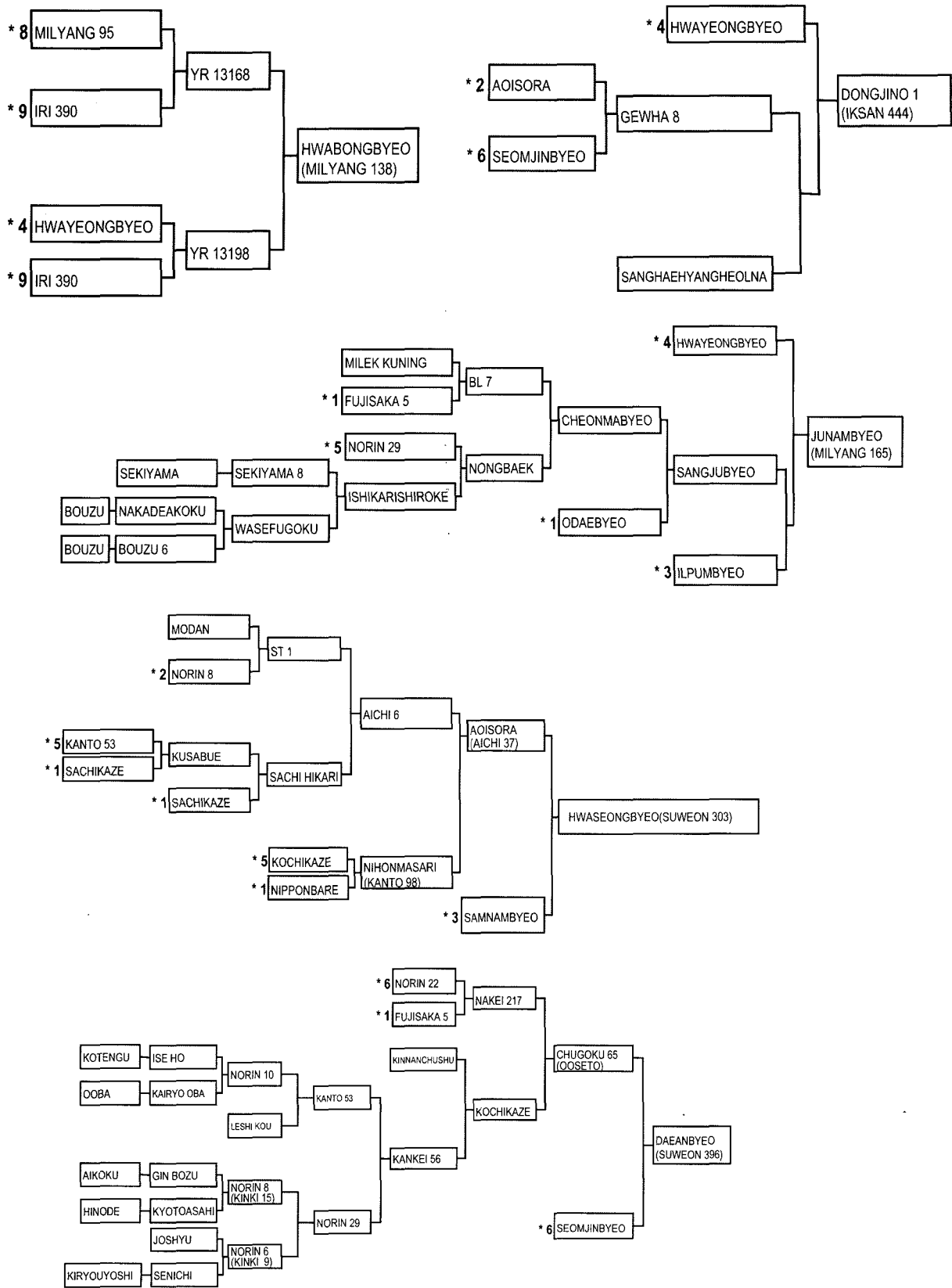


Fig. 1. Pedigree of 17 rice cultivars with high quality in 2004. (Filled box indicates newly expanded pedigree; numbers behind asterisk mark means cultivars which carries ancestral pedigree. The numbers order is the same as in Table 1.

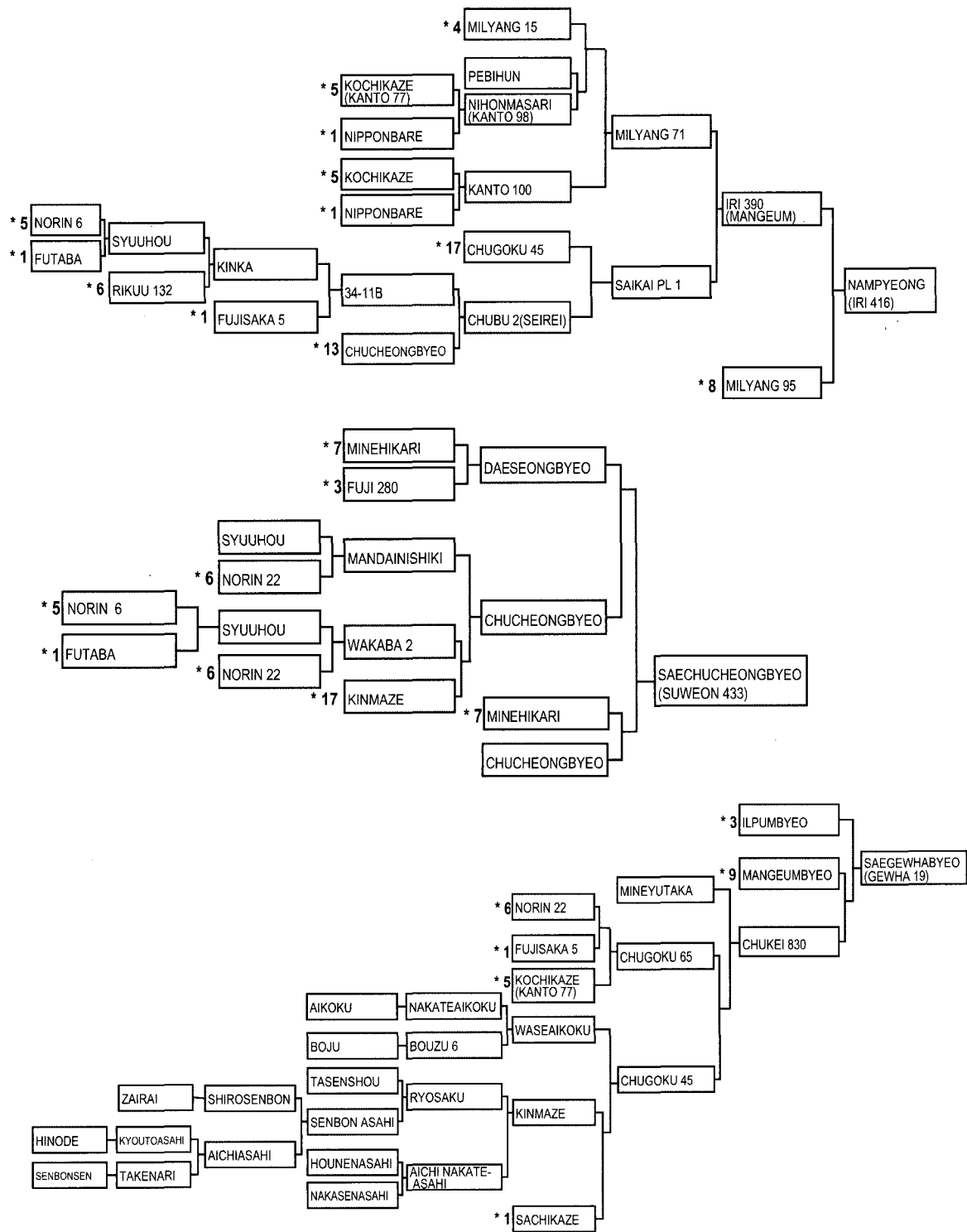


Fig. 1. Continued-1.

bred “Norin 1” was released in 1931. The other reason is the spreading of “Tongil” type rice. In 1970's, most of breeding goals were concentrated on increasing yield capacity and disease resistance introducing Indica germplasm unfamiliar

to Korean diet.

We tracked “Koshihikari” among the pedigree of 17 high quality rice cultivars (Fig. 2). It is believed that Japanese cultivar “Koshihikari” is one of the world best high quality rice.

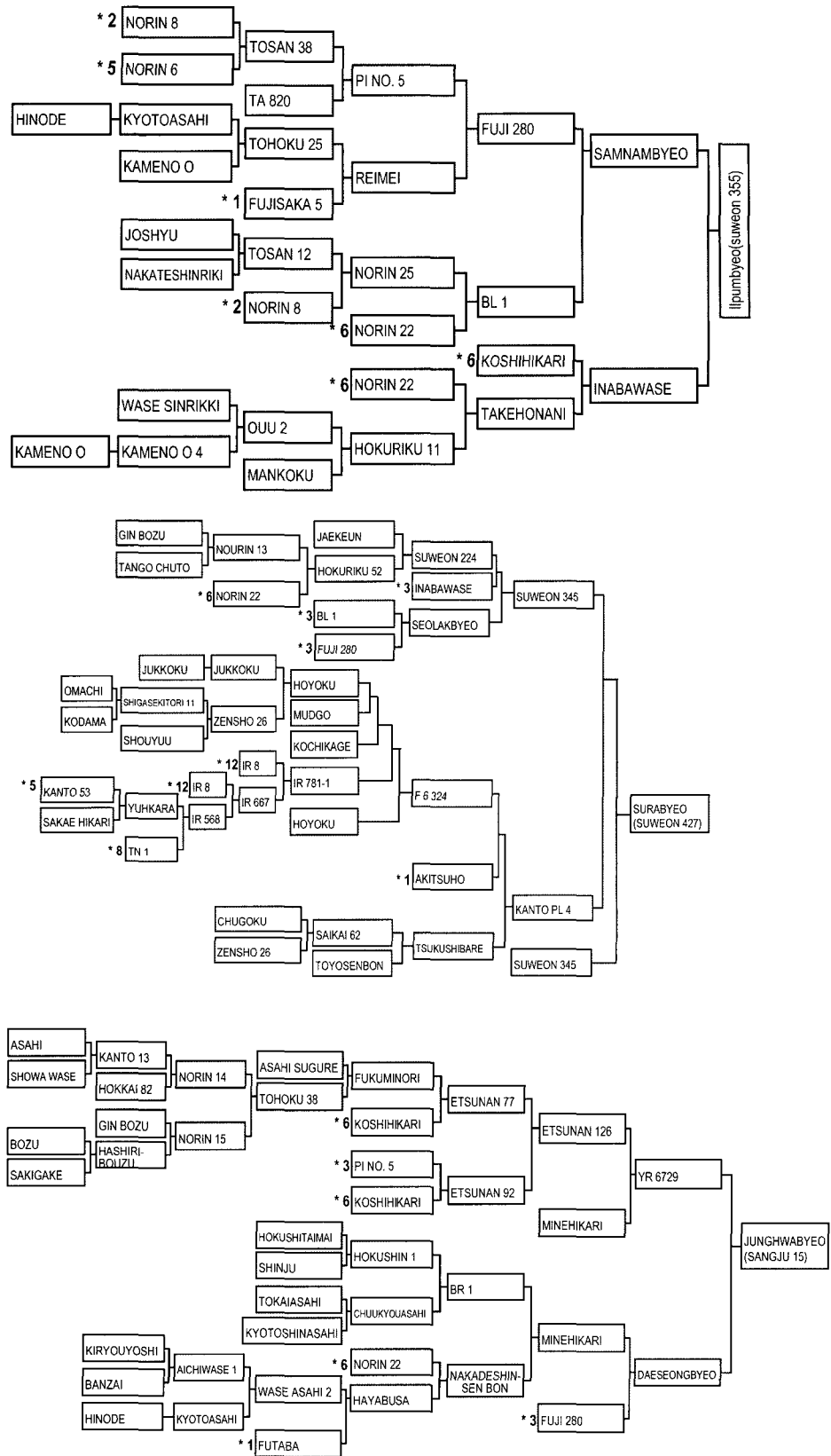


Fig. 1. Continued-2.

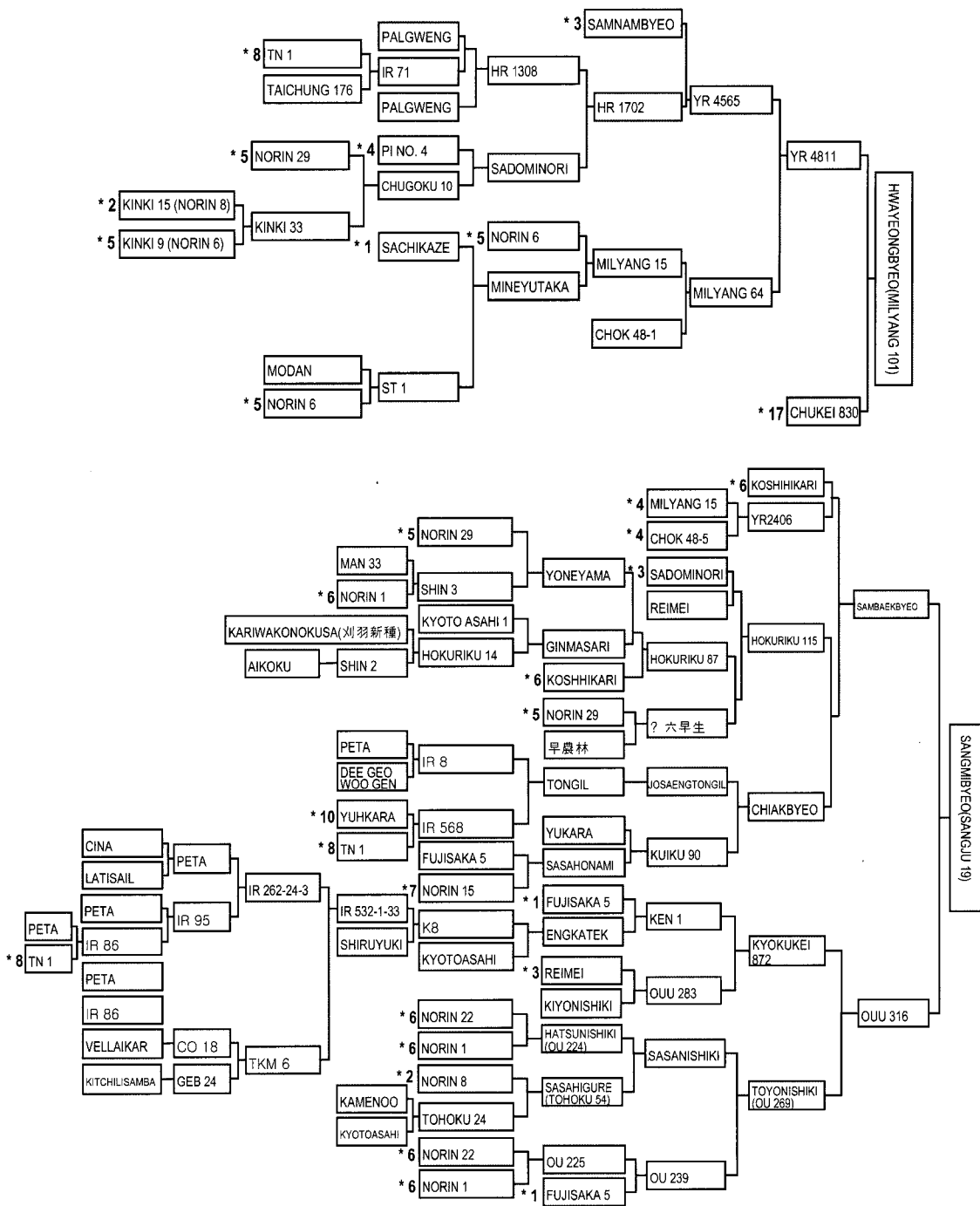


Fig. 1. Continued-3.

Seven cultivars such as “Sangmibyeo”, “Ilpumbyeo”, “Sae-gewhabyeo”, “Surabyeo”, “Shindongjinbyeo”, “Ilmibyeo”, “Jungwhabyeo” had “Koshihikari” on the pedigree of their ancestor. However, none of these varieties used “Koshihikari” for the direct primary cross. All of them used bridge parent such as “Inabawase”, “Hokuriku 87” and “Kinuhikari”, etc. This might be the effort of breeders to discard

the unfavorable agronomic traits of “Koshihikari” except for grain quality.

Next to “Koshihikari”, “Fujisaka 5” and “Kameno o” were frequently used as ancestral parents for the high quality rice cultivars. “Fujisaka 5” was used as ancestral parent in 12 out of 17 cultivars (Fig. 3). Interestingly, “Kameno o” was used in pedigree of 16 out 17 high quality varieties and “Asahi”

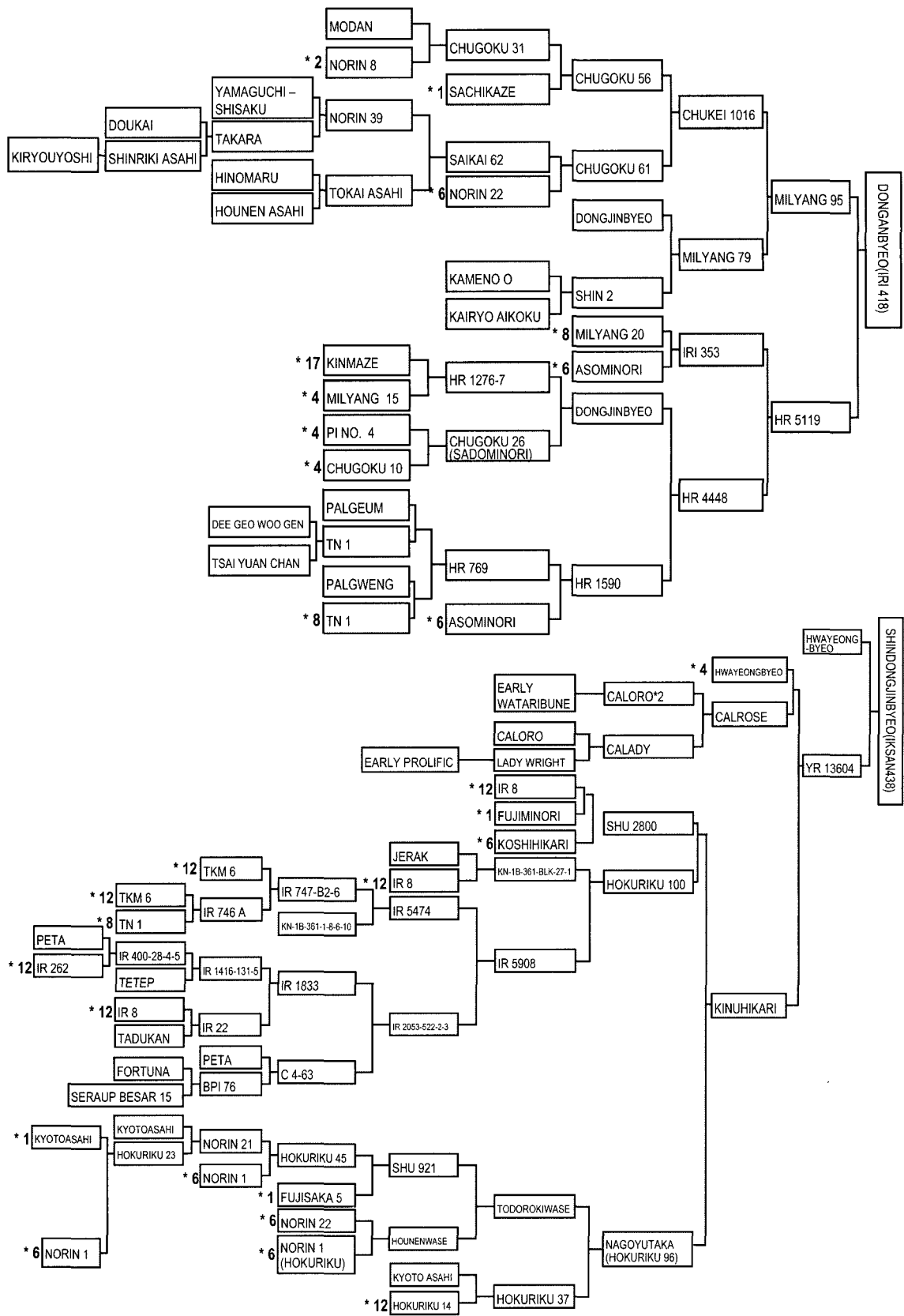


Fig. 1. Continued-4.





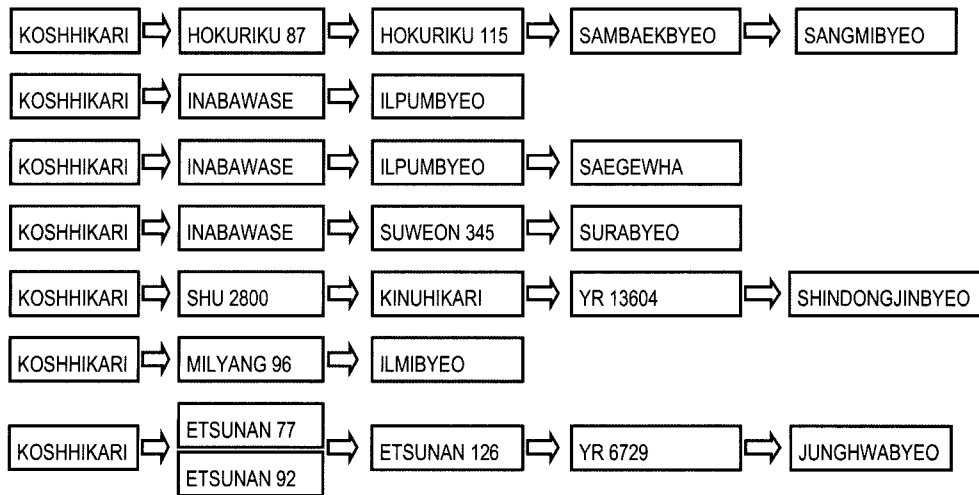


Fig. 2. Introduced pathways of “Koshihikari” to Korean rice cultivars with high quality.

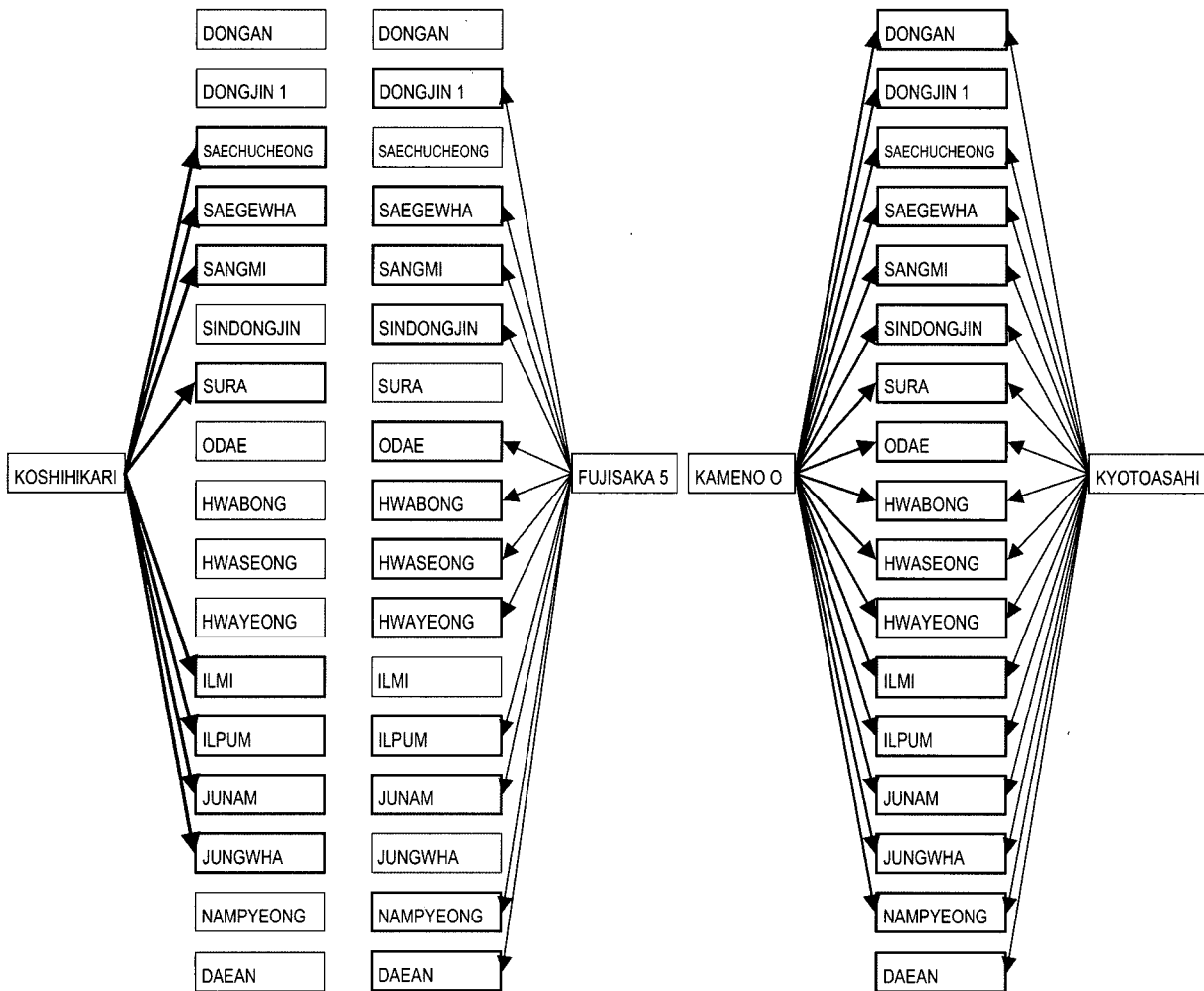


Fig. 3. Common ancestral germplasms among the 17 rice cultivars with high quality.

was used in the ancestral pedigree of all 17 varieties. Ito (1993) reported that the major ancestral parent of Japanese

high quality rice is “Kameno o” showing small grain type and “Asahi” with a large grain type . Since breeding itself is

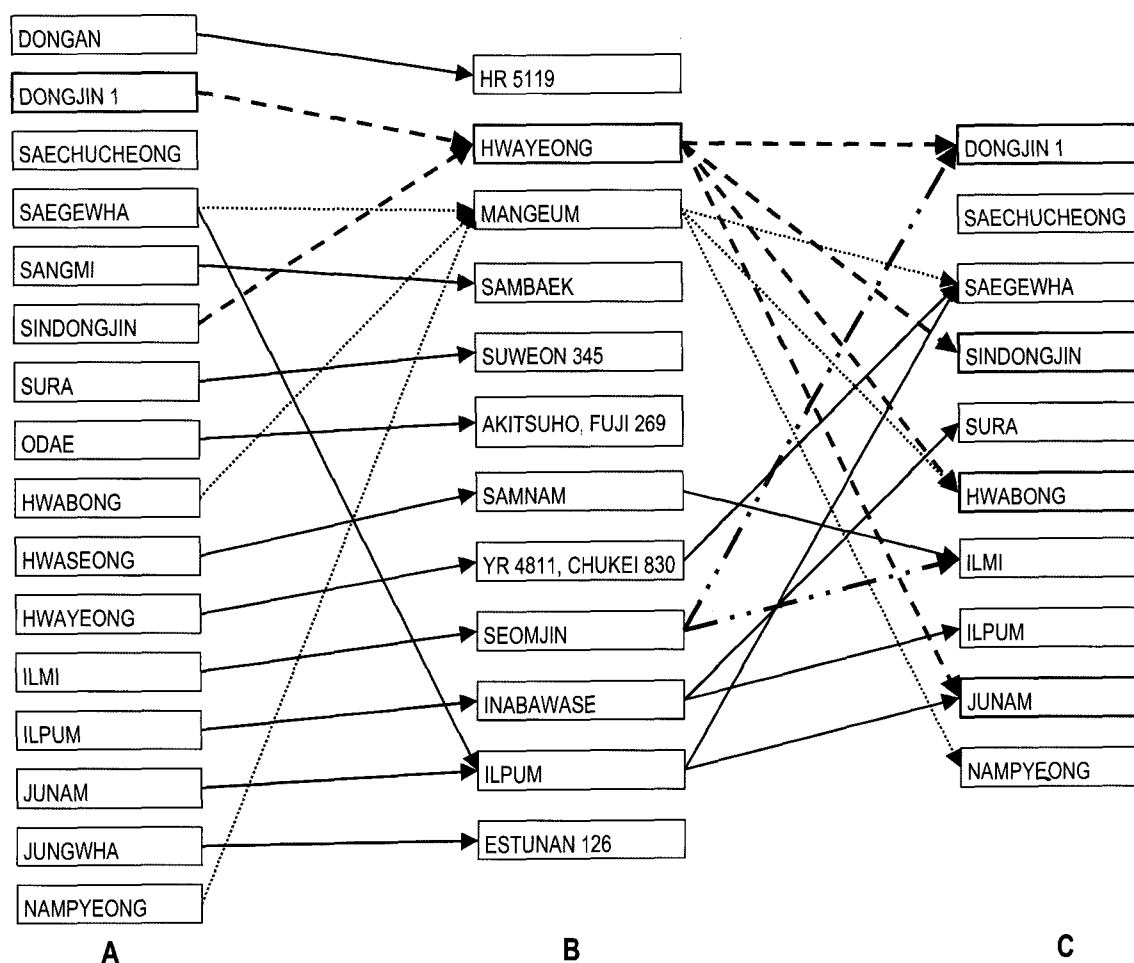


Fig. 4. The ancestral parents of high quality source described by breeders (A: 17 rice cultivar high quality, B: Source of ancestral high quality parents described by breeders, C: Cultivars shares high quality sources).

the process of selection, the genes associated with high quality of “Kameno o” were introgressed to “Ryuku 132” and “Norin 1” and finally reached to “Koshihikari”. On the other hand, “Asahi” was introduced to “Norin 8”.

Among the 17 high quality rice cultivars, only “Hwayeongbyeo” and “Ilpumbyeo” were used as a parent of the other high quality rice (Fig. 4). “Hwayeongbyeo” was used as a one of parent in the breeding of “Dongjin 1”, “Hwabongbyeo”, “Saegewhabyeo” and “Junambyeo”. “Ilpumbyeo” was used in the breeding pathway of “Junambyeo” and “Saegewhabyeo”. Although “Mangeumbyeo” itself was not enlisted as one of high quality rice cultivars, it was used as breeding parent of three high quality varieties, such as “Saegewhabyeo”, “Hwabongbyeo” and “Nampyeongbyeo”.

According to the analysis of genealogical relationship in 203 Korean rice varieties (Jong, 2003), most of the high quality rice cultivars belong to cluster V and VI. Further cluster analysis revealed that group V was related with “Hwayeongbyeo” (Chukey 830/YR 4811 Acp 8) and group VI was

related with “Dongjinbyeo” and “Milyang 95”. “Mangeumbyeo” was used as a parent of some cultivars, “Milyang 95” was used as one parent of “Mangeumbyeo”. It is concluded that the results agreed well with pedigree information.

Although CP provides genetic relationships among the varieties, there are many dissent opinion whether CP analysis provides realistic measure of genetic distances (Cox *et al.*, 1985). The major uncertainty arose from the same combination cross, lack of information on the pedigree and no estimates of breeder’s selection effects on relatedness (Kamphorne, 1969). The lacks of pedigree information can be overcome by the use of crop germplasm database. Web DB such as RRDB or IRIS provide more detailed pedigree information. However, incorporated with evaluation data, pedigree itself give a valuable chance to genealogical tracking of agronomic traits such as disease resistance etc. In conclusion, our pedigree table might provide valuable information for the future breeding of high quality rice in Korea.

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