

# Wonder Rice Initiative for Food Security and Health (WISH) Breeding Catalogue



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This publication is prepared for the JICA supported project “Wonder Rice Initiative for Food Security and Health (WISH)” project. The project is coordinated by the International Rice Research Institute (IRRI) in collaboration with Nagoya University and Kyushu University.

Developed WISH Lines for farmers,  
researchers, and stakeholders. (2012-2017)

# Foreword

Crop varietal improvement is a major goal for plant breeder. The success of these improved varieties and their adoption to farmers depends on having an improved varietal catalogue with information on the new varieties, including the varieties unique trait combinations, and taste and other cultural use. Adoption also depends on variety catalogues providing sources of seed supply that are readily available to farmers and extension workers.

With funding from the Japan International Cooperative Agency (JICA), and partnership between International Rice Research Institute (IRRI), Nagoya University,, have prepared the catalogue of improved varieties (2012-2017) and promising lines for Sub-Saharan Africa and Asian countries. The purpose of this catalogue is to provide information on improved varieties under the Wonder Rice Initiative for Food Security and Health (WISH) project. Our hope is that catalogues such as this one will be widely used by all stakeholders and farmers who are concerned with agricultural production, food security, sustainable development and agrobiodiversity conservation.



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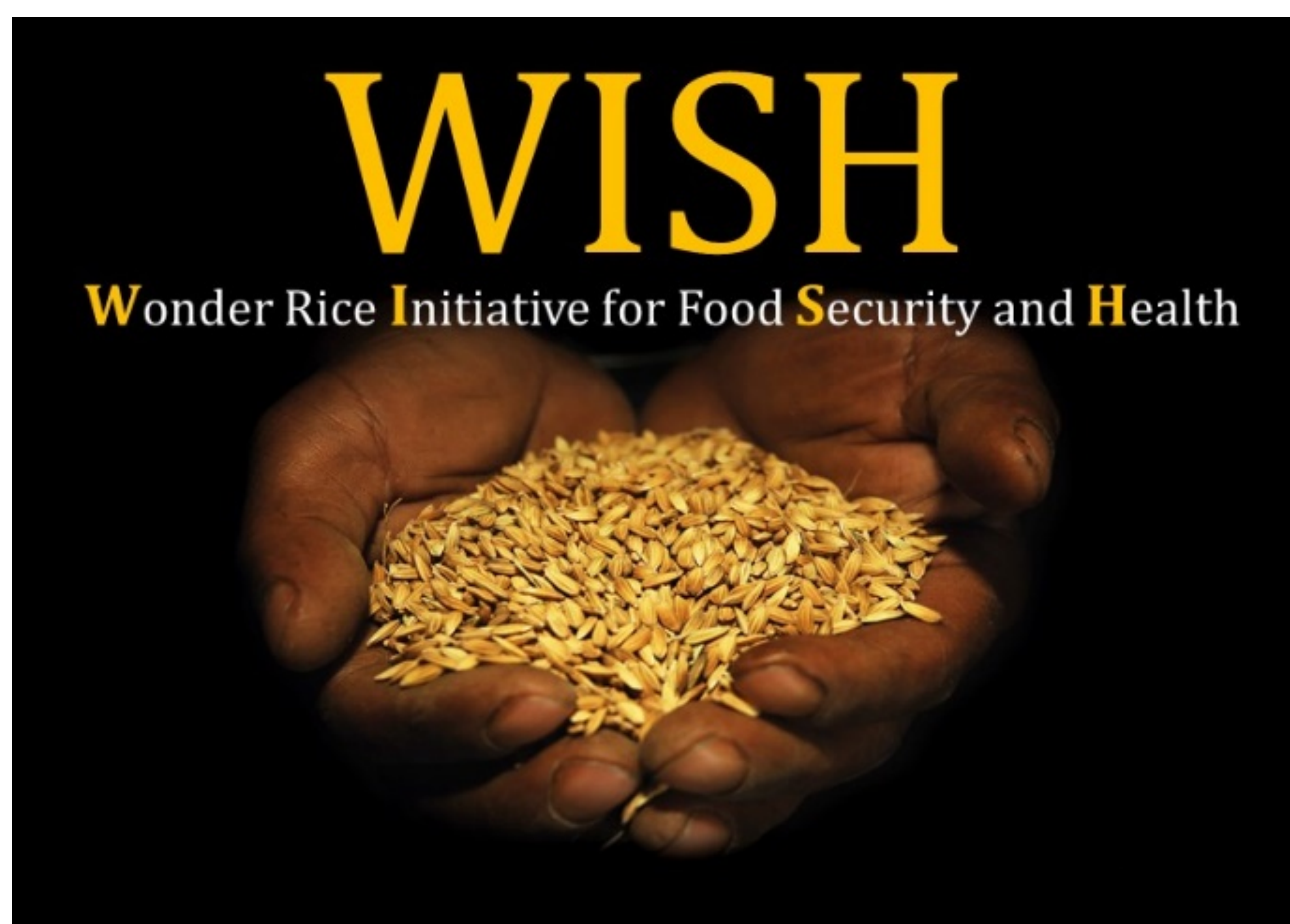
# Wonder Rice Initiative for Food Security and Health (WISH)

## Project Summary

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In the next 30 years, agriculture will face its biggest challenge yet: a projected 30% increase in global population compounded by an intensified competition for land and water resources, and an unstable climate that will push agricultural environments into a steady decline. To provide for a population that is estimated to reach 9 billion by 2050, agricultural production has to increase by 70%. Global cereal production alone has to increase by 38% over the next 30 or more years and this will have to come from arable lands that are already under intensive cultivation.

Rice is a principal food for more than 3 billion people and provides 23% of the caloric requirements worldwide. In Asia, the per capita rice consumption of more than 520 million people exceeds 100 kg annually. In Sub-Saharan Africa, the per capita rice consumption has doubled to 27 kg since 1970 and continues to rapidly increase in some countries due to population growth, urbanization, changes in employment patterns, rising income levels and changes in consumer preferences. In the least developed African countries of Nigeria, Tanzania and Niger, a continuing increase in income levels has also spurred shifts from a diet of tubers and cassava to rice. Even for low-income households in the region, rice is no longer a luxury food but the main source of calories, next to maize. Population and income projections in the next 15 years by the United Nations and the Food and Agricultural Policy Research Institute, respectively, indicate that the global demand for milled rice will increase to 555 million tons in Asia and 30 million tons in Africa. In Africa where rice is the fastest growing staple food, these projections will double in the next 30 years. Closing the gap between the current supply and the projected demand for rice will require consolidated efforts not only by international governments and organization but also research groups to boost rice production in both Asia and Africa.



The **Wonder Rice Initiative for Food Security and Health (WISH) Project** is a collaborative breeding program among *Nagoya University* in Japan, and the *International Rice Research Institute* in the Philippines, in full partnership with the *Japan International Cooperation Agency (JICA)*. It is a 5-year project that aims to increase the yield and improve the disease resistance of select rice varieties in Africa and Asia by marker-assisted backcrossing. The project capitalizes on the results of several years of basic research on the identification, cloning and functional analysis of genes controlling yield-related traits (i.e. grain number and number of primary branches per panicle) and disease resistance (blast and bacterial blight resistance) in rice

Since the project's launch in January of 2013, around 300 WISH lines in the background of rice cultivars that are preferentially grown by farmers across Asia and Africa have been improved for yield and yield-related traits, as well as for blast resistance by marker-assisted backcrossing. Around 300 pyramiding WISH lines in the same genetic backgrounds have been generated to carry genes for increased grain number (*Grain number 1a; Gn1a*), number of primary branches per panicle (*Wealthy Farmer's Panicle; WFP*) and blast resistance (*pi21*).



Preliminary evaluations showed that under modified cultural management in the field, WISH lines bred for increased grain number and number of primary branches per panicle have up to 54% increase in primary branching and 36% increase in grain number compared to the recurrent parents used in the program. Similarly, preliminary field and nursery screening of WISH lines bred to have *pi21* showed a broader spectrum of resistance to blast. Data to support these claims have been published in 3 original research and presented in 6 national and international conferences, as well as in 11 academic and regional organizational meetings. Information on the breeding strategy for the project has also been a part of 4 educational outreach for rice researchers and students alike. Now close to its 5<sup>th</sup> year, preparations are currently underway to deploy a total of 300 improved WISH lines carrying individual or combined target genes to 8 countries in Asia namely Cambodia, Vietnam, Sri Lanka, Myanmar, Nepal, Lao PDR and Indonesia, and in 3 countries in Africa namely Kenya, Burundi and Mozambique for initial testing, further improvement or adoption.

Interested researchers, farmers, and stakeholders may contact Prof. Motoyuki Ashikari (ashi@agr.nagoya-u.ac.jp) and Professor Kazuyuki Doi (kdoi@agr.nagoya-u.ac.jp) of Nagoya University.

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# **Wonder Rice Initiative for Food Security and Health(WISH) Developed Yield Lines**

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# NERICA 1 x ST (*Gn1a*)



A. Agronomic Data of Advanced WISH Yield Lines

Line	DTH	PH	TN	PL	PB	SB	FG	UFG	TNG	HGW
	Average Data $\pm$ SEM	Average Data $\pm$ SEM	Average Data $\pm$ SEM	Average Data $\pm$ SEM	Average Data $\pm$ SEM	Average Data $\pm$ SEM	Average Data $\pm$ SEM	Average Data $\pm$ SEM	Average Data $\pm$ SEM	Average Data $\pm$ SEM
NERICA 1	73	108.4 $\pm$ 1.08	14 $\pm$ 1.43	26.67 $\pm$ 0.57	13 $\pm$ 0.35	25 $\pm$ 1.93	99 $\pm$ 8.28	46.8 $\pm$	239 $\pm$ 15.15	2.7 $\pm$ 0.05
ST12	75	128.9 $\pm$ 3.21	11 $\pm$ 1.63	24.03 $\pm$ 0.39	20 $\pm$ 0.83	59 $\pm$ 5.41	173.27 $\pm$ 14.79	72.67 $\pm$	451 $\pm$ 15.03	2.6 $\pm$ 0.05
WISH 1:1-3-4-3-3	76 $\pm$	121.7 $\pm$ 2.48	10.4 $\pm$ 0.24	30.2 $\pm$ 1.18	15 $\pm$ 0.24	54 $\pm$ 3.66	187.86 $\pm$ 11.68	63.33 $\pm$ 7.37	754 $\pm$ 50.69	2.44 $\pm$ 0.07
WISH 1:4-12-3-1-12	74 $\pm$	120.1 $\pm$ 1.32	6.6 $\pm$ 0.40	22.66 $\pm$ 0.38	20 $\pm$ 0.81	59 $\pm$ 4.32	151.66 $\pm$ 6.88	112.1 $\pm$ 8.59	743 $\pm$ 75.37	2.6 $\pm$ 0.07
WISH 1:4-9-3-4-2	73 $\pm$	92.4 $\pm$ 2.90	10.4 $\pm$ 0.93	23.56 $\pm$ 1.08	8 $\pm$ 0.37	19 $\pm$ 2.20	68.4 $\pm$ 7.71	25.86 $\pm$ 3.76	283 $\pm$ 30.21	2.3 $\pm$ 0.13
WISH 1:6-16-10-4-1	76 $\pm$	111.5 $\pm$ 2.37	12 $\pm$ 1.67	25.23 $\pm$ 0.14	13 $\pm$ 0.20	48 $\pm$ 0.51	164.86 $\pm$ 9.98	63.66 $\pm$ 6.88	686 $\pm$ 10.73	2.62 $\pm$ 0.02
WISH 7:3-6-4-1-2	74 $\pm$	120 $\pm$ 0.00	11 $\pm$ 0.00	23.17 $\pm$	9 $\pm$	23 $\pm$	99.67 $\pm$	17.33 $\pm$	351 $\pm$	2.6 $\pm$

DTH= Days to 50% Heading ; PH=Plant Height; TN=Tiller Number; PL= Panicle Length; PB=Primary Branches; SB=Secondary Branches; FG= Filled Grains; UFG=Unfilled Grains; TNG= Total Number of Grains; HGW=100 grain weight; SEM= Standard Error of Mean

NERICA varieties have a yield advantage over their *O. glaberrima* and *O. sativa* parents, either through superior weed competitiveness, drought tolerance, and pest or disease resistance or simply through higher yielding potentials. ST12 on the other hand, from the stocked rice collections of Togo field in Nagoya University, is the donor for *Gn1a* and *WFP* alleles. Advanced lines of this WISH carries *Gn1a* alleles responsible for increase in grain number.

Other Information:

Generation: BC<sub>3</sub>F<sub>5</sub>

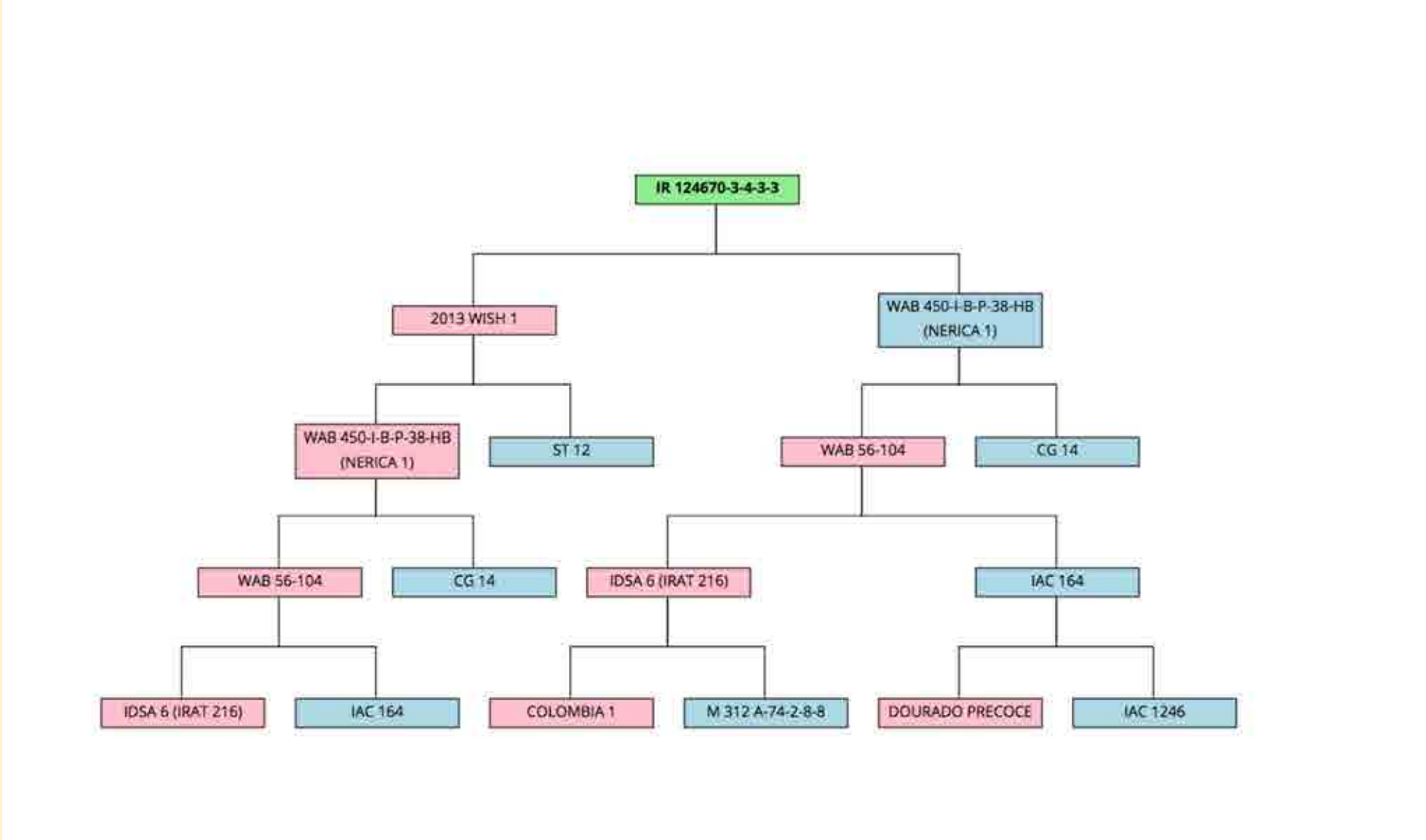
IR Designations:

IR 124670-3-4-3-3

IR 124672-9-3-4-2

IR 124672-12-3-1-12

IR 124673-16-10-4-1





# NERICA 1 x ST12 ( WFP)



A. Agronomic Data of Advanced WISH Yield Lines

Line	DTH	PH	TN	PN	PB	SB	FG	UFG	TNG	HGW
	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM
NERICA 1	73 ± 0	108.4 ± 1.08	14 ± 1.43	27 ± 0.57	13 ± 0.35	25 ± 1.93	99 ± 8.28	46.8 ± 7.56	239.4 ± 15.15	2.74 ± 0.05
ST12	75 ± 0	128.9 ± 3.21	11 ± 1.63	24.03 ± 0.39	20 ± 0.83	59 ± 5.41	173 ± 14.79	72.67 ± 7.17	451.2 ± 15.03	2.6 ± 0.05
WISH 1:2-1-7-2-1	72 ± 0	124.4 ± 2.03	8 ± 0.20	25.39 ± 0.62	20 ± 0.85	47 ± 5.18	181 ± 13.84	53.73 ± 8.96	704 ± 45.89	2.86 ± 0.07
WISH 1:2-1-7-5-1	68 ± 0	116.6 ± 3.46	8 ± 1.36	24.83 ± 0.73	21 ± 0.29	33 ± 7.00	139 ± 17.52	55.87 ± 13.06	584 ± 30.51	2.34 ± 0.14
WISH 1:4-15-1-7-1	79 ± 0	127 ± 2.70	5 ± 0.40	23.5 ± 0.75	29 ± 0.87	48 ± 2.68	170 ± 24.41	96.13 ± 31.28	797 ± 29.56	2.86 ± 0.05
WISH 1:6-12-8-10-4	73 ± 0	114.1 ± 4.88	7 ± 0.75	25.93 ± 0.36	20 ± 0.72	45 ± 1.19	145 ± 6.20	32.8 ± 4.93	532 ± 15.65	2.62 ± 0.09
WISH 7:5-5-1-1-2-1	76 ± 0	123.4 ± 4.42	5 ± 0.37	22.97 ± 0.39	24 ± 0.75	48 ± 3.46	157 ± 5.88	71.53 ± 15.27	686 ± 40.61	2.64 ± 0.07

DTH= Days to 50% Heading ; PH=Plant Height; TN=Tiller Number; PL= Panicle Length; PB=Primary Branches; SB=Secondary Branches; FG= Filled Grains; UFG=Unfilled Grains; TNG= Total Number of Grains; HGW=100 grain weight; SEM= Standard Error of Mean

NERICA varieties have a yield advantage over their *O. glaberrima* and *O. sativa* parents, either through superior weed competitiveness, drought tolerance, and pest or disease resistance or simply through higher yielding potentials. ST 12 on the other hand, from the Stocked rice collections of Togo field and Nagoya University, is the donor for *Gn1a* and *WFP* alleles. Advanced lines of this WISH carries *WFP* alleles responsible for increase in primary branching.

Other Information:

Generation: BC<sub>3</sub>F<sub>5</sub>

IR Designations:

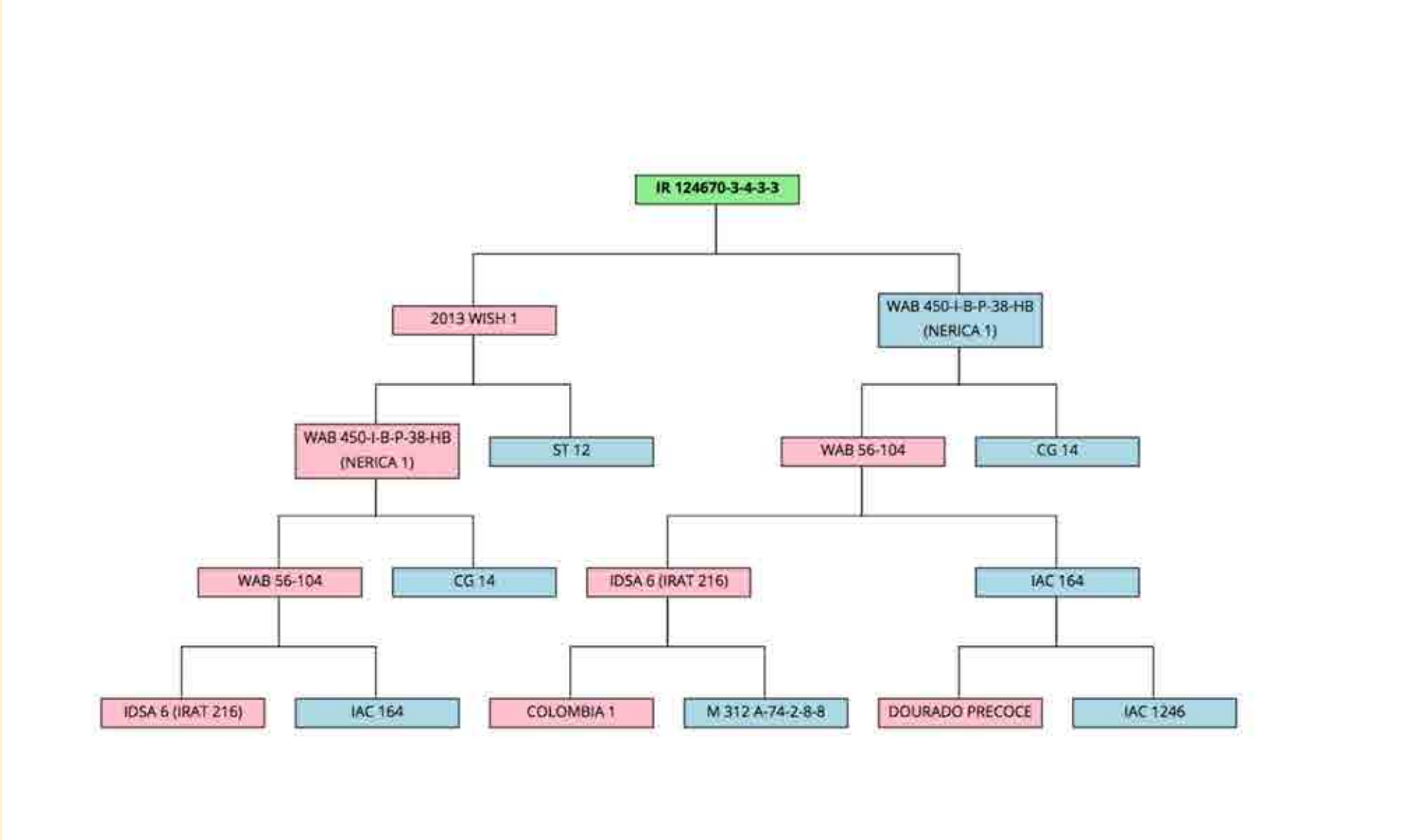
IR 124671-1-7-2-1

IR 124671-1-7-5-1

IR 124672-15-1-7-1

IR 124673-12-8-10-4

IR 124681-1-1-2-1





# NERICA 1 x ST12 (*Gn1a*+*WFP*)



A. Agronomic Data of Advanced WISH Yield Lines

Line	DTH	PH	TN	PL	PB	SB	FG	UFG	TNG	HGW
	Average Data $\pm$ SEM	Average Data $\pm$ SEM	Average Data $\pm$ SEM	Average Data $\pm$ SEM	Average Data $\pm$ SEM	Average Data $\pm$ SEM	Average Data $\pm$ SEM	Average Data $\pm$ SEM	Average Data $\pm$ SEM	Average Data $\pm$ SEM
NERICA 1	73	108.4 $\pm$ 1.08	14 $\pm$ 1.43	26.67 $\pm$ 0.57	13 $\pm$ 0.35	25 $\pm$ 1.93	99 $\pm$ 8.28	46.8 $\pm$	239 $\pm$ 15.15	2.7 $\pm$ 0.05
ST12	75	128.9 $\pm$ 3.21	11 $\pm$ 1.63	24.03 $\pm$ 0.39	20 $\pm$ 0.83	59 $\pm$ 5.41	173.27 $\pm$ 14.79	72.67 $\pm$	451 $\pm$ 15.03	2.6 $\pm$ 0.05
WISH 1:4-8-8-10-7	79	126.2 $\pm$ 2.52	7 $\pm$ 0.58	26.5 $\pm$ 0.70	20 $\pm$ 0.76	68 $\pm$ 5.47	198 $\pm$ 20.74	109.53 $\pm$	923 $\pm$ 76.45	2.5 $\pm$ 0.14
WISH 1:4-8-8-2-1	72	127 $\pm$ 2.84	7 $\pm$ 0.60	24.77 $\pm$ 0.53	19 $\pm$ 0.42	69 $\pm$ 4.16	159.47 $\pm$ 10.47	122.47 $\pm$	846 $\pm$ 34.86	2.7 $\pm$ 0.11
WISH 1:4-8-8-4-1	76	123 $\pm$ 3.15	8 $\pm$ 0.73	23.6 $\pm$ 0.20	19 $\pm$ 0.46	54 $\pm$ 4.89	169.53 $\pm$ 12.63	96.53 $\pm$	798 $\pm$ 48.18	2.8 $\pm$ 0.03
WISH 1:4-8-8-8-2	79	130.7 $\pm$ 1.94	6 $\pm$ 0.58	26.13 $\pm$ 0.52	18 $\pm$ 1.06	54 $\pm$ 5.14	151.53 $\pm$ 15.58	87.6 $\pm$	717 $\pm$ 47.41	2.4 $\pm$ 0.18
WISH 1:6-12-8-12-4	74	125.2 $\pm$ 3.26	6 $\pm$ 0.58	23.8 $\pm$ 0.54	22 $\pm$ 0.80	54 $\pm$ 3.73	192.8 $\pm$ 11.58	62.33 $\pm$	765 $\pm$ 39.74	2.7 $\pm$ 0.04
WISH 1:6-12-8-12-7	73	130.7 $\pm$ 3.59	5 $\pm$ 0.37	23.5 $\pm$ 0.51	20 $\pm$ 0.88	58 $\pm$ 8.93	200.13 $\pm$ 25.25	46.47 $\pm$	740 $\pm$ 95.77	2.9 $\pm$ 0.06

DTH= Days to 50% Heading ; PH=Plant Height; TN=Tiller Number; PL= Panicle Length; PB=Primary Branches; SB=Secondary Branches; FG= Filled Grains; UFG=Unfilled Grains; TNG= Total Number of Grains; HGW=100 grain weight; SEM= Standard Error of Mean

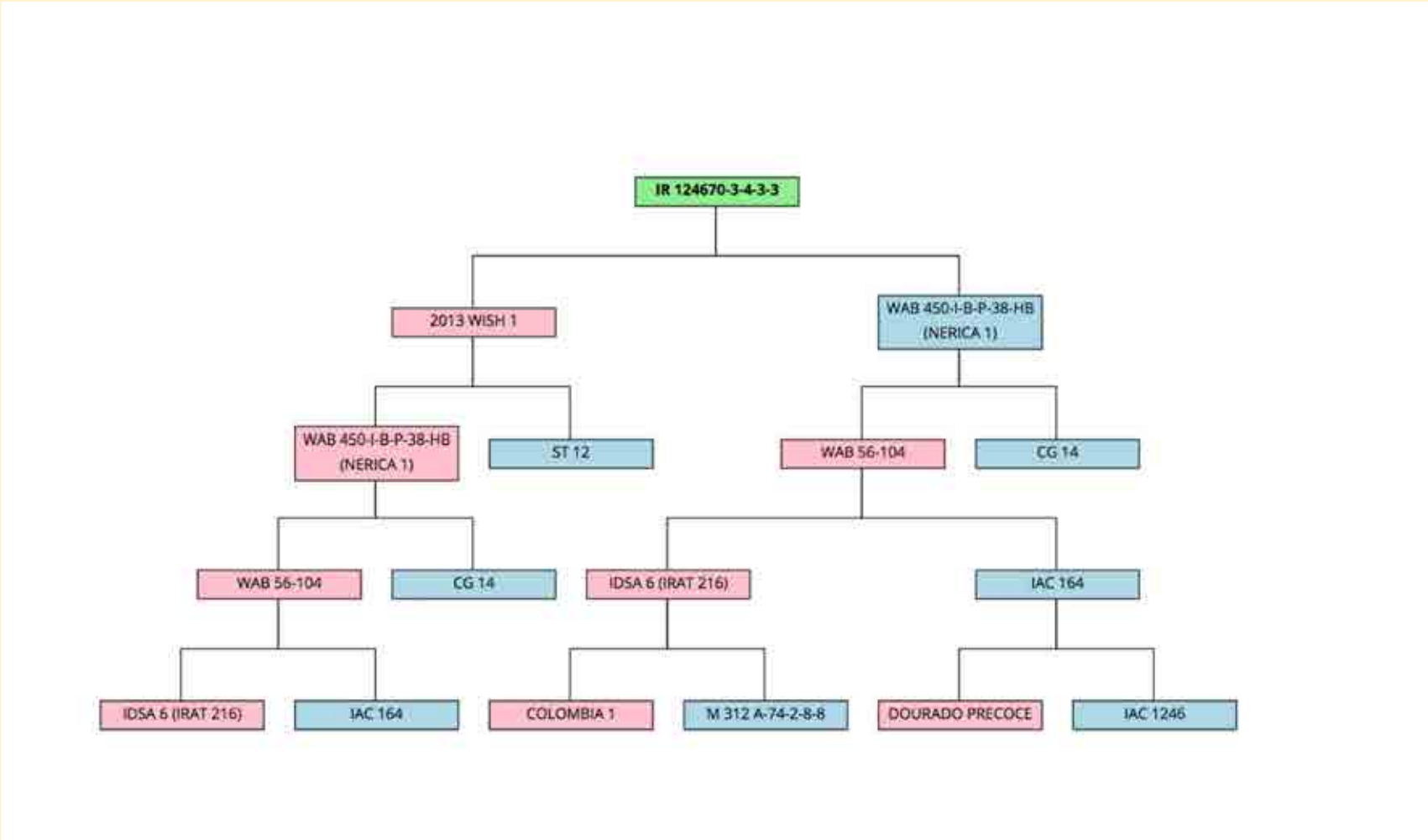
NERICA varieties have a yield advantage over their *O. glaberrima* and *O. sativa* parents, either through superior weed competitiveness, drought tolerance, and pest or disease resistance or simply through higher yielding potentials. ST 12 on the other hand, from the Stocked rice collections of Togo field and Nagoya University, is the donor for *Gn1a* and *WFP* alleles. Advanced lines of this WISH carries *Gn1a* alleles responsible for increase in grain number and *WFP* alleles responsible for increase in primary branching.

Other Information:

Generation: BC<sub>3</sub>F<sub>5</sub>

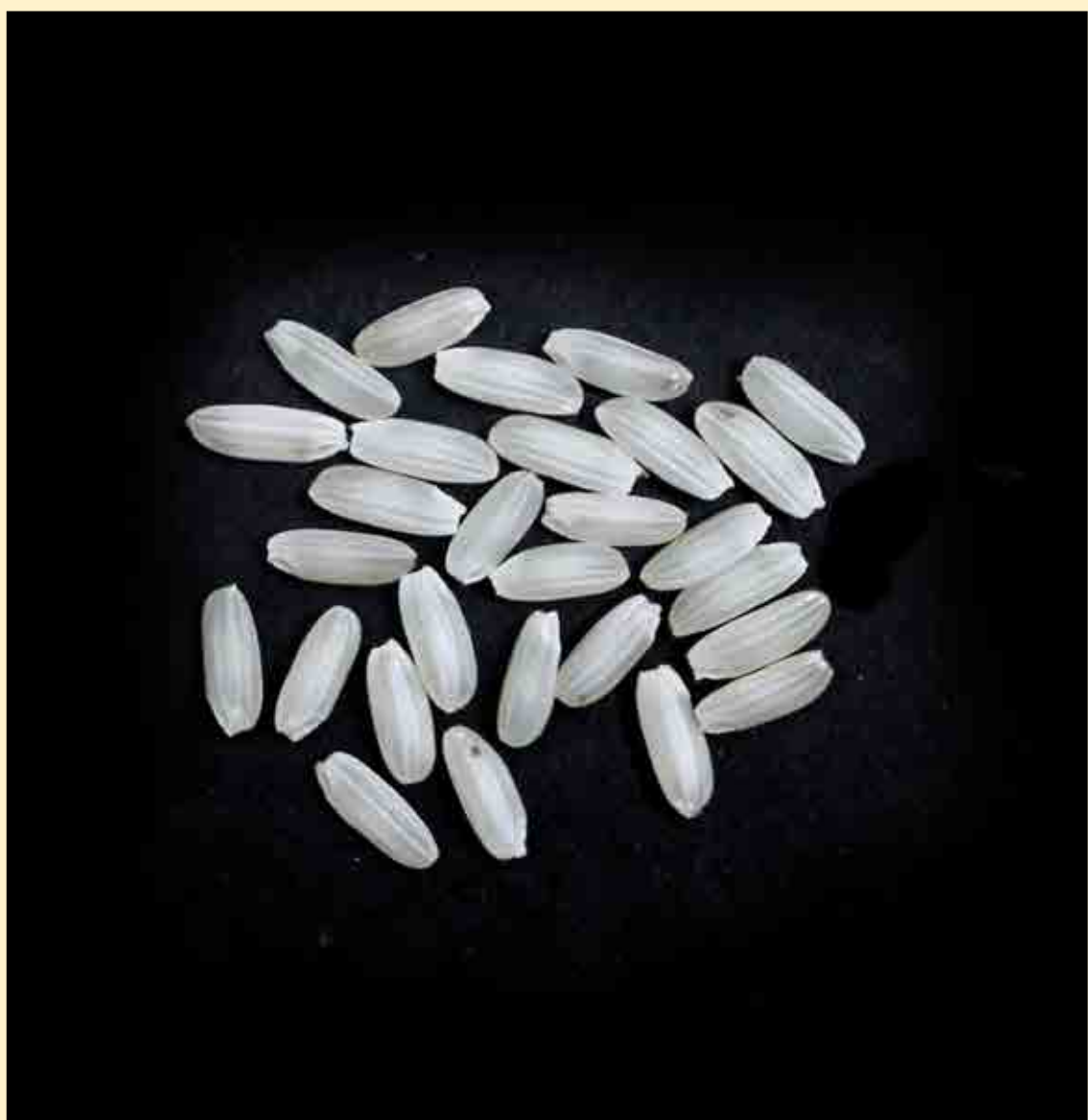
IR Designations:

- IR 124672-8-8-2-1
- IR 124673-12-8-12-7
- IR 124672-8-8-4-1
- IR 124672-8-8-8-2
- IR 124672-8-8-10-7
- IR 124673-12-8-12-4





# NERICA 4 x ST12 (*Gn1a*)



A. Agronomic Data of Advanced WISH Yield Lines

Line	DTH	PH	TN	PL	PB	SB	FG	UFG	TNG	HGW
	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM
NERICA 4	75	105.7 ± 2.61	11.8 ± 0.8	25.03 ± 0.41	14 ± 0.4	32 ± 2.73	105 ± 3.08	59.07 ± 6.87	282.2 ± 23.21	2.24 ± 0.04
ST12	72	128.9 ± 3.22	11.4 ± 1.63	24.034 ± 0.39	20 ± 0.86	59 ± 5.44	173.27 ± 14.79	72.67 ± 7.17	391.2 ± 29.16	2.6 ± 0.05
WISH 12:5-10-2-1-7	70	100.2 ± 3.67	10 ± 1.22	22.4 ± 0.61	11 ± 0.32	23 ± 2.52	97.47 ± 4.00	28.27 ± 5.59	377.2 ± 21.29	3.1 ± 0.44
WISH 12:5-10-2-2-5	73	92.9 ± 3.90	9.8 ± 1.62	20.85 ± 0.42	11 ± 0.32	22 ± 1.16	96.27 ± 2.92	19.93 ± 3.36	326.6 ± 27.97	2.7 ± 0.07
WISH 12:5-6-1-2-5	68	103.3 ± 5.10	6.8 ± 0.66	23.102 ± 0.67	12 ± 0.58	27 ± 3.8	97.13 ± 9.05	46.60 ± 9.53	431.2 ± 45.37	3.3 ± 0.04
WISH 12:5-6-2-2-5	73	98.5 ± 2.39	6.4 ± 0.68	24 ± 0.38	12 ± 0.24	32 ± 1.46	126.13 ± 4.81	34.27 ± 3.56	481.2 ± 16. 96	3.14 ± 0.06
WISH 12:5-6-3-1-7	71	102.7 ± 1.18	8.2 ± 0.66	24.77 ± 0.44	13 ± 0.32	32 ± 1.73	126.13 ± 7.74	35.8 ± 7.18	485.8 ± 27.74	2.78 ± 0.07

DTH= Days to 50% Heading ; PH=Plant Height; TN=Tiller Number; PL= Panicle Length; PB=Primary Branches; SB=Secondary Branches; FG= Filled Grains; UFG=Unfilled Grains; TNG= Total Number of Grains; HGW=100 grain weight; SEM= Standard Error of Mean

NERICA varieties have a yield advantage over their *O. glaberrima* and *O. sativa* parents, either through superior weed competitiveness, drought tolerance, and pest or disease resistance or simply through higher yielding potentials. ST12 on the other hand, from the stocked rice collections of Togo field in Nagoya University, is the donor for *Gn1a* and *WFP* alleles. Advanced lines of this WISH carries *Gn1a* alleles responsible for increase in grain number.

Other Information:

Generation: BC<sub>3</sub>F<sub>5</sub>

IR Designations:

WISH 12:5-6-1-2-5

WISH 12:5-6-2-2-5

WISH 12:5-6-3-1-7

WISH 12:5-10-2-1-7

WISH 12:5-10-2-2-5



# NERICA 4 x ST12 (*WFP*)



A. Agronomic Data of Advanced WISH Yield Lines

Line	DTH	PH	TN	PL	PB	SB	FG	UFG	TNG	HGW
	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM
NERICA 4	75 ±	105.7 ± 2.61	11.8 ± 0.80	25.03 ± 0.41	13 ± 0.34	32 ± 2.66	105 ± 3.08	59.07 ± 6.87	282.2 ± 23.13	2.24 ± 0.04
ST12	72 ±	128.9 ± 3.21	11.4 ± 1.63	24.03 ± 0.39	20 ± 0.83	59 ± 5.41	173.27 ± 14.79	72.67 ± 7.17	391.27 ± 29.18	2.6 ± 0.04
WISH 12:22-4-10-1	70 ±	124 ± 2.53	6.2 ± 0.49	26.83 ± 0.18	12 ± 0.27	32 ± 1.20	128.33 ± 5.78	18.13 ± 3.05	439.4 ± 12.79	3.02 ± 0.05
WISH 12:22-4-5-5	70 ±	125.9 ± 2.64	6.4 ± 1.17	27.23 ± 0.46	12 ± 0.53	41 ± 1.80	154.8 ± 6.73	26.8 ± 5.22	544.8 ± 18.52	3.06 ± 0.12
WISH 12:22-4-9-7	72 ±	123.7 ± 1.68	6.6 ± 0.40	28.56 ± 0.56	11 ± 0.21	37 ± 0.81	149.53 ± 6.38	21.33 ± 3.71	512.6 ± 10.34	2.96 ± 0.07
WISH 12:23-2-2-5	76 ±	105 ± 2.77	7.2 ± 0.86	25.46 ± 0.69	12 ± 0.19	24 ± 0.92	95 ± 4.72	24.53 ± 2.87	358.6 ± 9.45	2.94 ± 0.24
WISH 12:23-2-5-2	73 ±	106.75 ± 2.95	13.5 ± 2.53	26.08 ± 0.90	13 ± 0.21	27 ± 3.08	123.08 ± 9.47	14.25 ± 4.06	412 ± 27.19	2.93 ± 0.08
WISH 12:23-2-5-7	73 ±	101.8 ± 2.78	8.6 ± 0.51	24.97 ± 0.64	12 ± 0.31	22.4 ± 1.62	99.8 ± 8.57	22.53 ± 3.67	367 ± 16.60	2.9 ± 0.06

DTH= Days to 50% Heading ; PH=Plant Height; TN=Tiller Number; PL= Panicle Length; PB=Primary Branches; SB=Secondary Branches; FG= Filled Grains; UFG=Unfilled Grains; TNG= Total Number of Grains; HGW=100 grain weight; SEM= Standard Error of Mean

NERICA varieties have a yield advantage over their *O. glaberrima* and *O. sativa* parents, either through superior weed competitiveness, drought tolerance, and pest or disease resistance or simply through higher yielding potentials. ST 12 on the other hand, from the Stocked rice collections of Togo field and Nagoya University, is the donor for *Gn1a* and *WFP* alleles. Advanced lines of this WISH carries *WFP* alleles responsible for increase in primary branching

Other Information:

**Generation:** BC<sub>3</sub>F<sub>4</sub>-BC<sub>3</sub>F<sub>5</sub>  
**IR Designations:**  
WISH 12:22-4-5-5            WISH 12:23-2-2-5  
WISH 12:22-4-9-7            WISH 12:23-2-5-7  
WISH 12:22-4-10-1  
WISH 12:23-2-5-2



# NERICA 4 x ST6 (*Gn1a*)



A. Agronomic Data of Advanced WISH Yield Lines

Line	DTH	PH	TN	PN	PB	SB	FG	UFG	TNG	HGW
	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM
NERICA 4	78	105.7± 2.61	12 ± 0.80	25.03 ± 0.41	14 ± 0.40	32 ± 2.73	105 ± 3.08	59.07 ± 6.87	282 ± 23.21	2.24 ± 0.04
ST6	83	119.3 ± 1.50	11 ± 0.73	26.07 ± 0.42	26 ± 0.45	58 ± 4.72	200.2 ± 15.97	89.93 ± 12.76	449 ± 43.75	2.62 ± 0.04
WISH 13:1-3-1-8-1-6	74	111.6 ± 1.09	8 ± 0.75	26.53 ± 0.31	14 ± 0.60	40 ± 1.72	145.87 ± 7.03	32.37 ± 5.91	534 ± 30.08	2.68 ± 0.05
WISH 13:1-3-2-5-1-7	79	114.6 ± 2.54	8 ± 1.02	26.13 ± 0.79	16 ± 0.40	49 ± 3.28	187.53 ± 13.51	50.6 ± 12.60	714 ± 72.06	2.66 ± 0.04
WISH 13:1-4-5-6-1-7	77	105.6 ± 1.72	8 ± 0.84	25.47 ± 1.00	14 ± 0.49	42 ± 1.02	137.67 ± 4.91	37.33 ± 3.79	525 ± 25.04	2.66 ± 0.10
WISH 13:1-4-5-6-5-7	70	110.2 ± 4.54	7 ± 0.49	26.34 ± 0.77	14 ± 0.40	40 ± 1.66	135.8 ± 12.77	59.6 ± 8.98	586 ± 51.47	2.78 ± 0.14

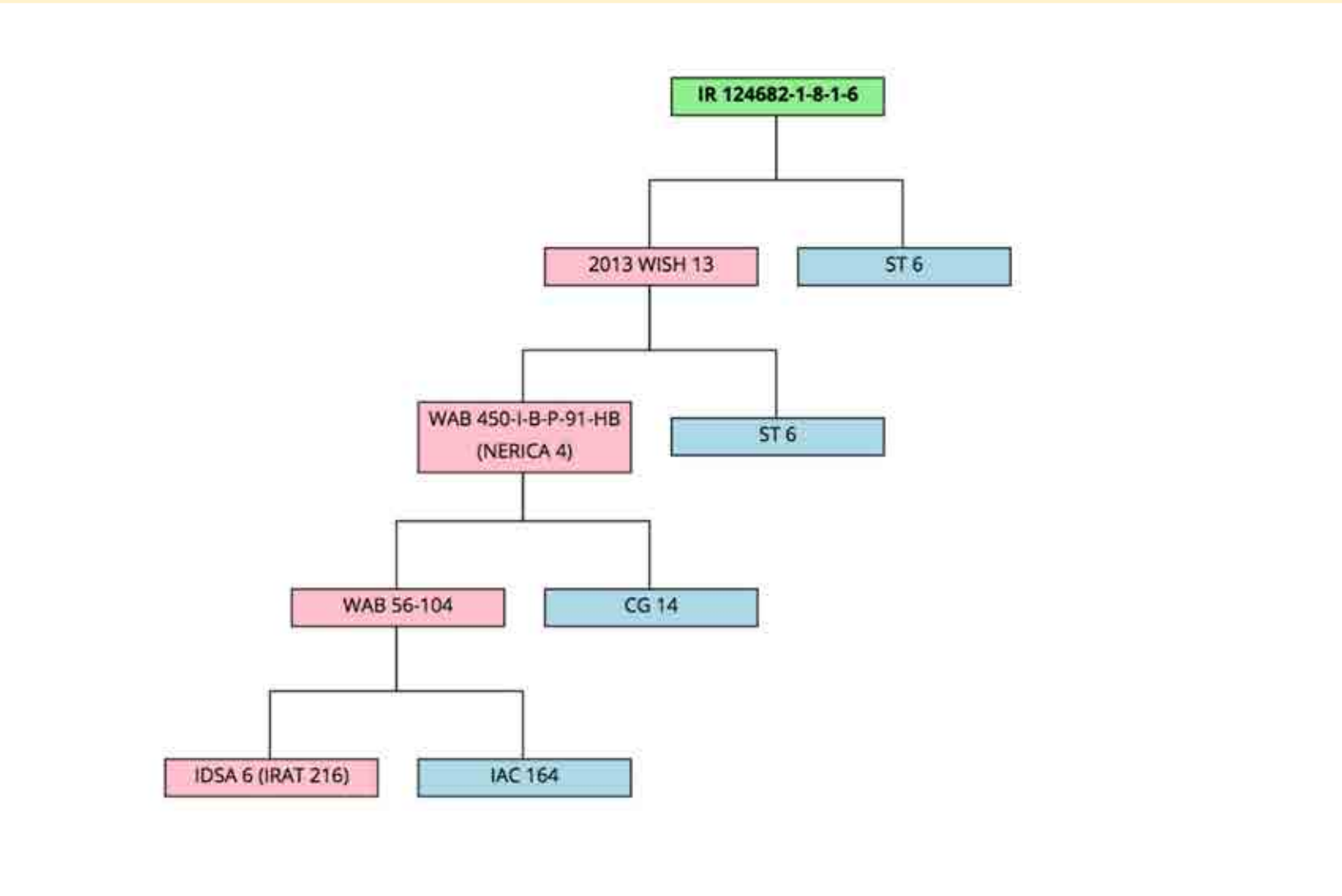
DTH= Days to 50% Heading ; PH=Plant Height; TN=Tiller Number; PL= Panicle Length; PB=Primary Branches; SB=Secondary Branches; FG= Filled Grains; UFG=Unfilled Grains; TNG= Total Number of Grains; HGW=100 grain weight; SEM= Standard Error of Mean

NERICA varieties have a yield advantage over their *O. glaberrima* and *O. sativa* parents, either through superior weed competitiveness, drought tolerance, and pest or disease resistance or simply through higher yielding potentials. ST6 on the other hand, from the stocked rice collections of Togo field in Nagoya University, is the donor for *Gn1a* and *WFP* alleles. Advanced lines of this WISH carries *Gn1a* alleles responsible for increase in grain number.

Other Information:

Generation: BC<sub>3</sub>F<sub>5</sub>  
IR Designations:

- IR 124682-1-8-1-6
- IR 124682-2-5-1-7
- IR 124683-5-6-1-7
- IR 124683-5-6-5-7





# NERICA 6 x ST12 (*Gn1a*)



A. Agronomic Data of Advanced WISH Yield Lines

Line	DTH	PH	TN	PL	PB	SB	FG	UFG	TNG	HGW
	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM
NERICA 6	73 ±	132 ± 3.83	10 ± 1.41	26.2 ± 0.20	14 ± 0.40	43 ± 4.30	150 ± 12.42	40.47 ± 2.28	271 ± 10.75	2.44 ± 0.07
ST12	72 ±	128.9 ± 3.21	11 ± 1.63	24.2 ± 0.37	20 ± 0.86	59 ± 5.44	173.27 ± 14.79	72.67 ± 7.17	391 ± 29.16	2.6 ± 0.05
WISH 14:1-1-2-1-5	71 ±	120.9 ± 3.50	7 ± 0.86	22.2 ± 139.70	10 ± 0.37	50 ± 3.38	119.80 ± 9.80	17.93 ± 3.76	413 ± 37.20	2.7 ± 0.10
WISH 14:1-1-2-2-1	72 ±	117 ± 3.31	7 ± 0.37	24.8 ± 0.20	9 ± 0.40	55 ± 1.69	89.06 ± 3.82	8.73 ± 0.89	293 ± 10.98	3.08 ± 0.06
WISH 14:23-7-6-4-7	71 ±	142.9 ± 1.65	6 ± 0.84	30.8 ± 1.16	13 ± 0.58	51 ± 3.38	203.13 ± 8.24	36.73 ± 6.26	719 ± 30.68	3.04 ± 0.08
WISH 14:6-2-1-6-2	69 ±	112.5 ± 5.63	5 ± 0.37	25 ± 0.95	10 ± 0.40	59 ± 2.77	108.4 ± 5.90	34.33 ± 9.23	428 ± 38.81	2.86 ± 0.39
WISH 14:6-4-7-1-5	71 ±	140.5 ± 3.33	5 ± 0.20	28.2 ± 0.66	11 ± 0.97	56 ± 4.40	125.73 ± 14.87	14.77 ± 2.51	419 ± 49.27	3.16 ± 0.08

DTH= Days to 50% Heading ; PH=Plant Height; TN=Tiller Number; PL= Panicle Length; PB=Primary Branches; SB=Secondary Branches; FG= Filled Grains; UFG=Unfilled Grains; TNG= Total Number of Grains; HGW=100 grain weight; SEM= Standard Error of Mean

NERICA varieties have a yield advantage over their *O. glaberrima* and *O. sativa* parents, either through superior weed competitiveness, drought tolerance, and pest or disease resistance or simply through higher yielding potentials. ST12 on the other hand, from the stocked rice collections of Togo field in Nagoya University, is the donor for *Gn1a* and *WFP* alleles. Advanced lines of this WISH carries *Gn1a* alleles responsible for increase in grain number.

## Other Information:

Generation: BC<sub>3</sub>F<sub>5</sub>

IR Designations:

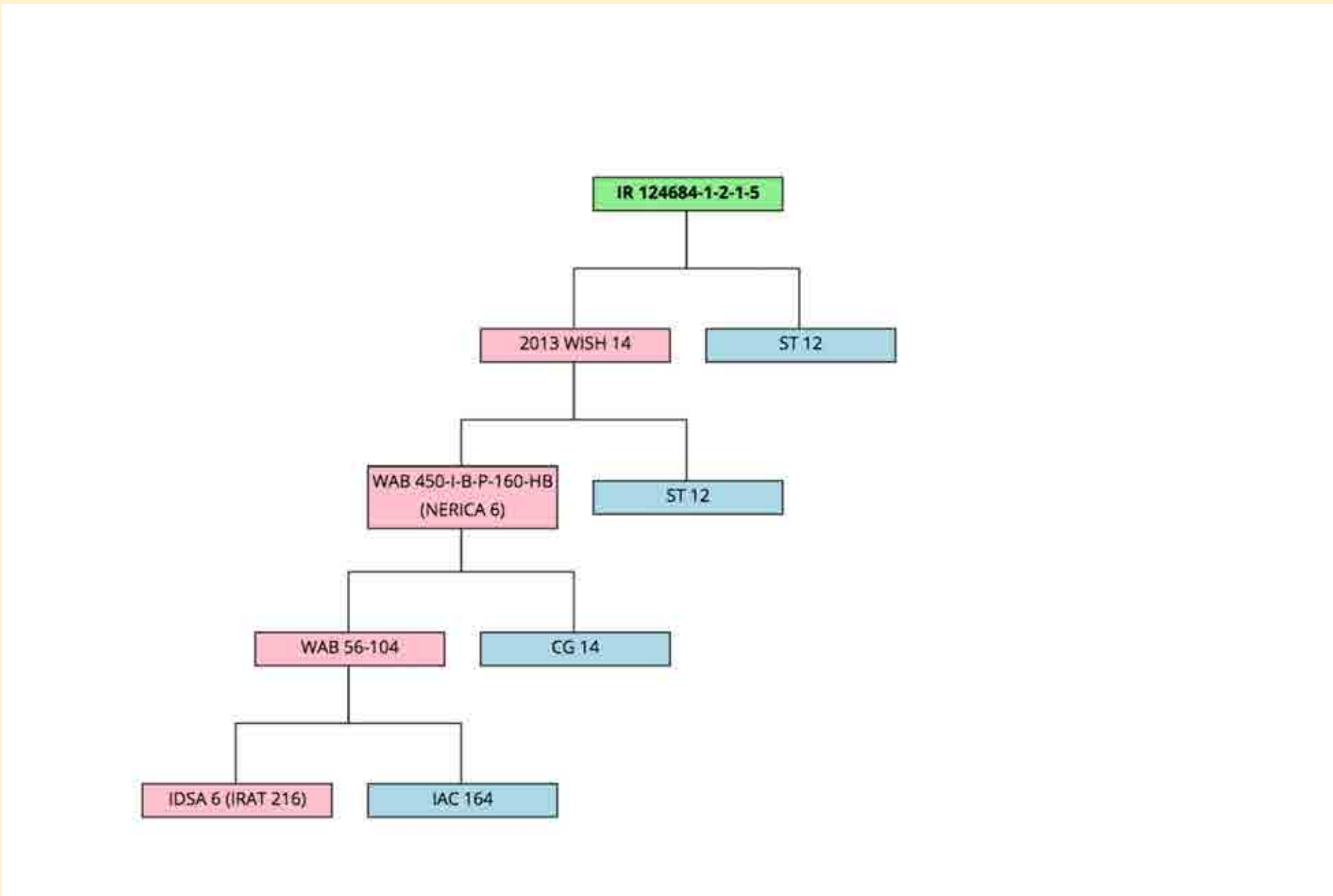
IR 124684-1-2-1-5

IR 124684-1-2-2-1

WISH 14:6-2-1-6-2

WISH 14:6-4-7-1-5

IR 124686-7-6-4-7





# NERICA 6 x ST12 (*WFP*)



A. Agronomic Data of Advanced WISH Yield Lines

Line	DTH	PH	TN	PL	PB	SB	FG	UFG	TNG	HGW
	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM
NERICA 6	73±	132±3.83	10±1.41	25.93±0.16	14±0.40	43±4.30	150±12.42	40.47±2.28	271±10.75	2.44±0.07
ST12	72±	128.9±3.21	11±1.63	24.03±0.39	20±0.86	59±5.44	173.27±14.79	72.67±7.17	391±29	2.6±0.05
WISH 14:1-1-4-8	68±	101.4±2.15	5±0.55	23±0.59	9±0.20	16±1.55	78±6.71	21.67±2.54	299±21	2.9±0.06
WISH 14:1-3-1-2	68±	114.7±1.31	6±0.58	23.33±0.67	10±0.24	23±0.75	109.73±2.17	23.67±2.26	400±10	3±0.04
WISH 14:23-10-2-1	71±	139.75±4.88	7±0.58	31.30±1.36	15±0.63	45±3.3	162.58±20.79	76.59±17.10	717±47	2.8±0.1
WISH 14:23-10-2-5	68±	137.4±4.88	8±0.24	29.77±1.04	14±0.37	42±2.37	186.87±7.64	40.46±3.68	682±22	2.7±0.2
WISH 14:23-15-4-5	69±	123±2.06	4±0.24	27.94±0.41	12±0.81	40±1.63	135.33±8.01	57.06±3.51	577±24	2.8±0.08
WISH 14:23-15-4-7	70±	138.9±4.24	5±0.24	29.46±0.58	13±0.24	42±2.35	179.8±8.33	42.33±4.17	666±20	3.1±0.07
WISH 14:23-2-5-1	70±	130±1.92	6±0.58	27.7±0.55	13±0.55	32±1.96	154.40±9.75	18.2±4.5	517±35	3±0.06
WISH 14:23-4-1-5	71±	135.9±3.16	6±0.73	28.93±0.68	14±0.40	32±2.46	149.73±12.76	26.40±2.8	528±37	3±0.04
WISH 14:23-5-9-8	69±	143.1±6.53	7±0.71	29.2±1.61	15±0.75	52±3.08	203.13±17.73	66.33±5	808±59	3±0.15
WISH 14:6-2-3-1	69±	129.625±5.03	5±0.29	28.13±0.72	11±0.71	45±4.14	134.17±4.5	81.9±16.53	648±51	3±0.05
WISH 14:6-5-9-1	70±	138.3±2.53	9±0.75	28.09±0.54	13±0.51	38±0.75	142.60±17.43	41.06±13.93	551±14	3±0.04
WISH 14:6-5-9-12	69±	120±2.35	6±0.49	23.6±0.33	10±0.37	26±1.81	110.6±7.98	15.13±2	377±23	3.1±0.03

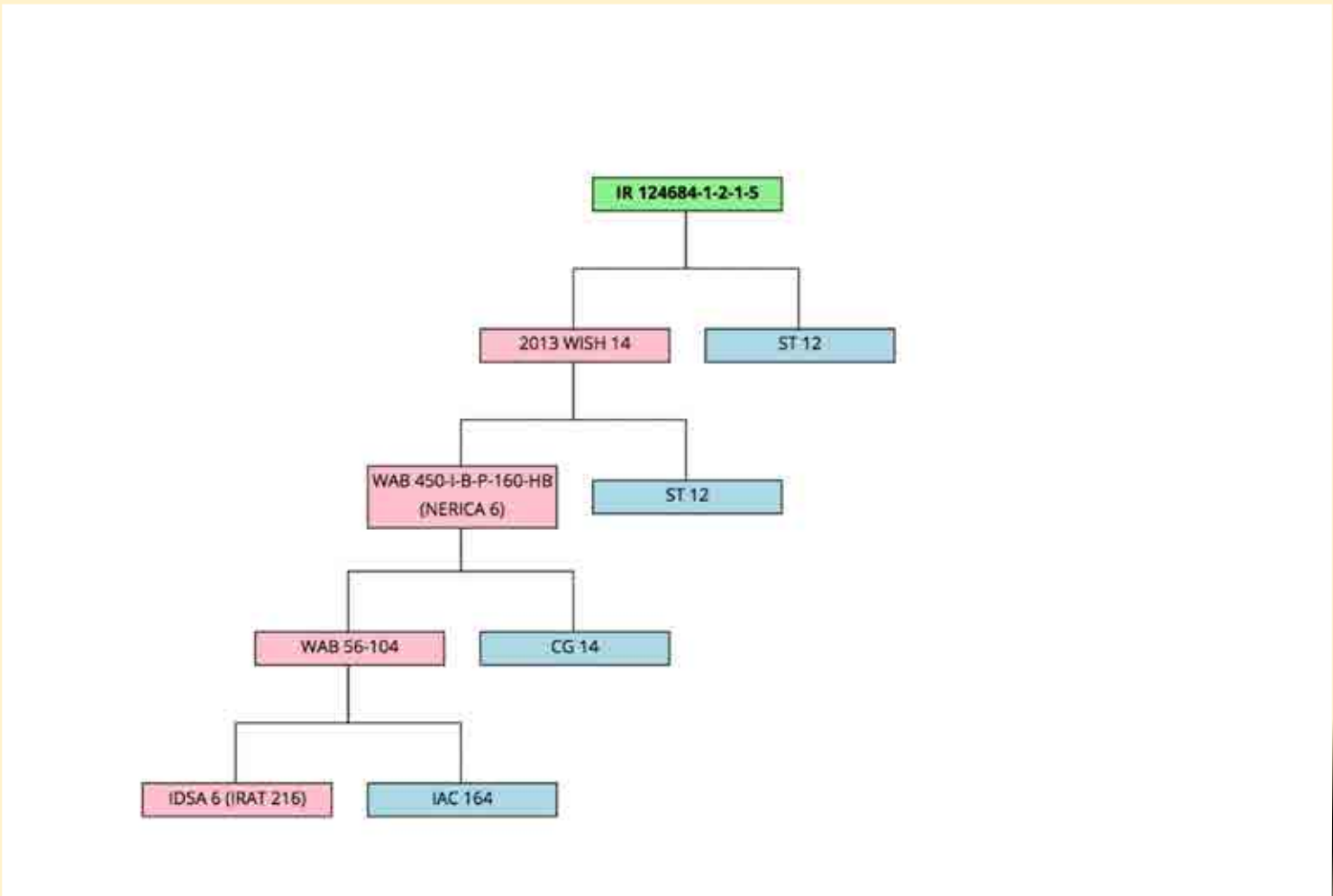
DTH= Days to 50% Heading ; PH=Plant Height; TN=Tiller Number; PL= Panicle Length; PB=Primary Branches; SB=Secondary Branches; FG= Filled Grains; UFG=Unfilled Grains; TNG= Total Number of Grains; HGW=100 grain weight; SEM= Standard Error of Mean

NERICA varieties have a yield advantage over their *O. glaberrima* and *O. sativa* parents, either through superior weed competitiveness, drought tolerance, and pest or disease resistance or simply through higher yielding potentials. ST 12 on the other hand, from the Stocked rice collections of Togo field and Nagoya University, is the donor for *Gn1a* and *WFP* alleles. Advanced lines of this WISH carries *WFP* alleles responsible for increase in primary branching

Other Information:

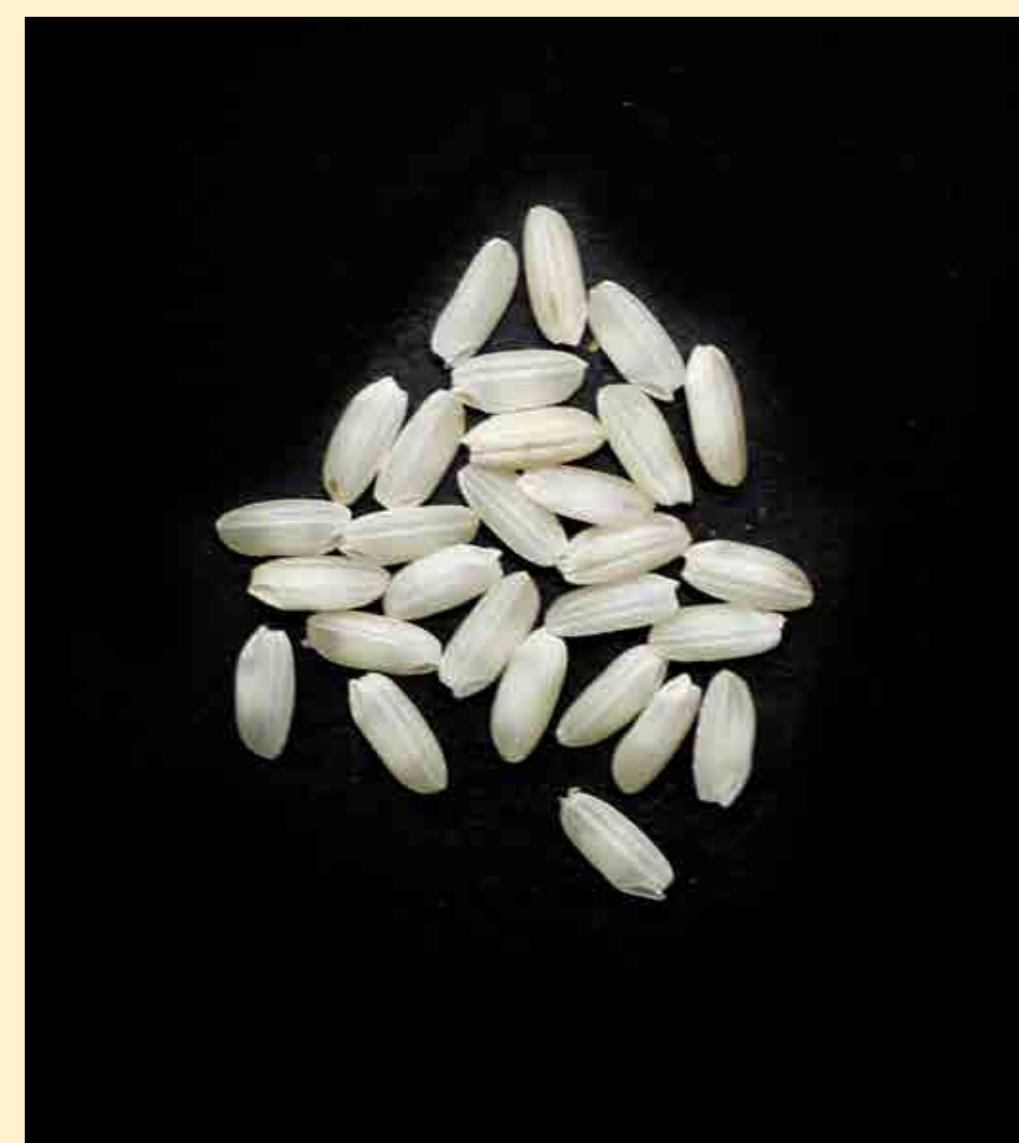
Generation: BC<sub>3</sub>F<sub>4</sub>  
IR Designations:

IR 124686-7-6-4-7	IR 124684-1-4-8	IR 124686-4-1-5	IR 124686-5-9-8
IR 124684-3-1-2	WISH 14:6-5-9-1	IR 124686-10-2-5	IR 124686-10-2-1
WISH 14:6-2-3-1	IR 124686-15-4-5	WISH 14:6-5-9-12	
IR 124686-2-5-1	IR 124686-15-4-7	WISH 14:6-5-9-6	





# NERICA 6 x ST12 (*Gn1a* + *WFP*)



A. Agronomic Data of Advanced WISH Yield Lines

Line	DTH	PH	TN	PL	PB	SB	FG	UFG	TNG	HGW
	Average Data $\pm$ SEM	Average Data $\pm$ SEM	Average Data $\pm$ SEM	Average Data $\pm$ SEM	Average Data $\pm$ SEM	Average Data $\pm$ SEM	Average Data $\pm$ SEM	Average Data $\pm$ SEM	Average Data $\pm$ SEM	Average Data $\pm$ SEM
NERICA 6	73 $\pm$	132 $\pm$ 3.83	10 $\pm$ 1.41	25.93 $\pm$ 0.16	14 $\pm$ 0.40	43 $\pm$ 4.30	150 $\pm$ 12.42	40.46 $\pm$ 2.28	271 $\pm$ 10.75	2.44 $\pm$ 0.07
ST12	72 $\pm$	128.9 $\pm$ 3.21	11 $\pm$ 1.63	24.03 $\pm$ 0.39	20 $\pm$ 0.86	59 $\pm$ 5.44	173.26 $\pm$ 14.79	72.67 $\pm$ 7.17	391 $\pm$ 29.16	2.6 $\pm$ 0.05
WISH 14:23-12-6-1-3	68 $\pm$	129.1 $\pm$ 2.35	5 $\pm$ 0.32	25.6 $\pm$ 0.64	13 $\pm$ 0.75	34 $\pm$ 4.11	154.73 $\pm$ 10.70	33.4 $\pm$ 3.96	519 $\pm$ 28.07	3.16 $\pm$ 0.07
WISH 14:23-12-7-1-5	70 $\pm$	122.7 $\pm$ 1.50	5 $\pm$ 0.24	25.40 $\pm$ 0.61	14 $\pm$ 0.32	47 $\pm$ 3.97	183.59 $\pm$ 15.38	39.2 $\pm$ 3.10	668 $\pm$ 43.23	2.44 $\pm$ 0.09
WISH 14:23-17-3-1-4	69 $\pm$	138.5 $\pm$ 2.14	6 $\pm$ 0.20	28.83 $\pm$ 0.40	13 $\pm$ 0.37	49 $\pm$ 2.42	208.6 $\pm$ 17.79	28.33 $\pm$ 3.32	711 $\pm$ 46.02	2.64 $\pm$ 0.02
WISH 14:23-17-9-2-3	68 $\pm$	122.5 $\pm$ 2.79	7 $\pm$ 0.68	24.83 $\pm$ 0.26	146 $\pm$ 0.40	43 $\pm$ 1.69	179.53 $\pm$ 8.54	37.86 $\pm$ 3.01	653 $\pm$ 33.26	2.28 $\pm$ 0.05
WISH 14:23-17-9-6-5	71 $\pm$	125 $\pm$ 1.34	6 $\pm$ 0.20	27.13 $\pm$ 0.70	13 $\pm$ 0.37	37 $\pm$ 2.41	164.93 $\pm$ 10.60	23.39 $\pm$ 3.07	565 $\pm$ 30.42	2.9 $\pm$ 0.06

DTH= Days to 50% Heading ; PH=Plant Height; TN=Tiller Number; PL= Panicle Length; PB=Primary Branches; SB=Secondary Branches; FG= Filled Grains; UFG=Unfilled Grains; TNG= Total Number of Grains; HGW=100 grain weight; SEM= Standard Error of Mean

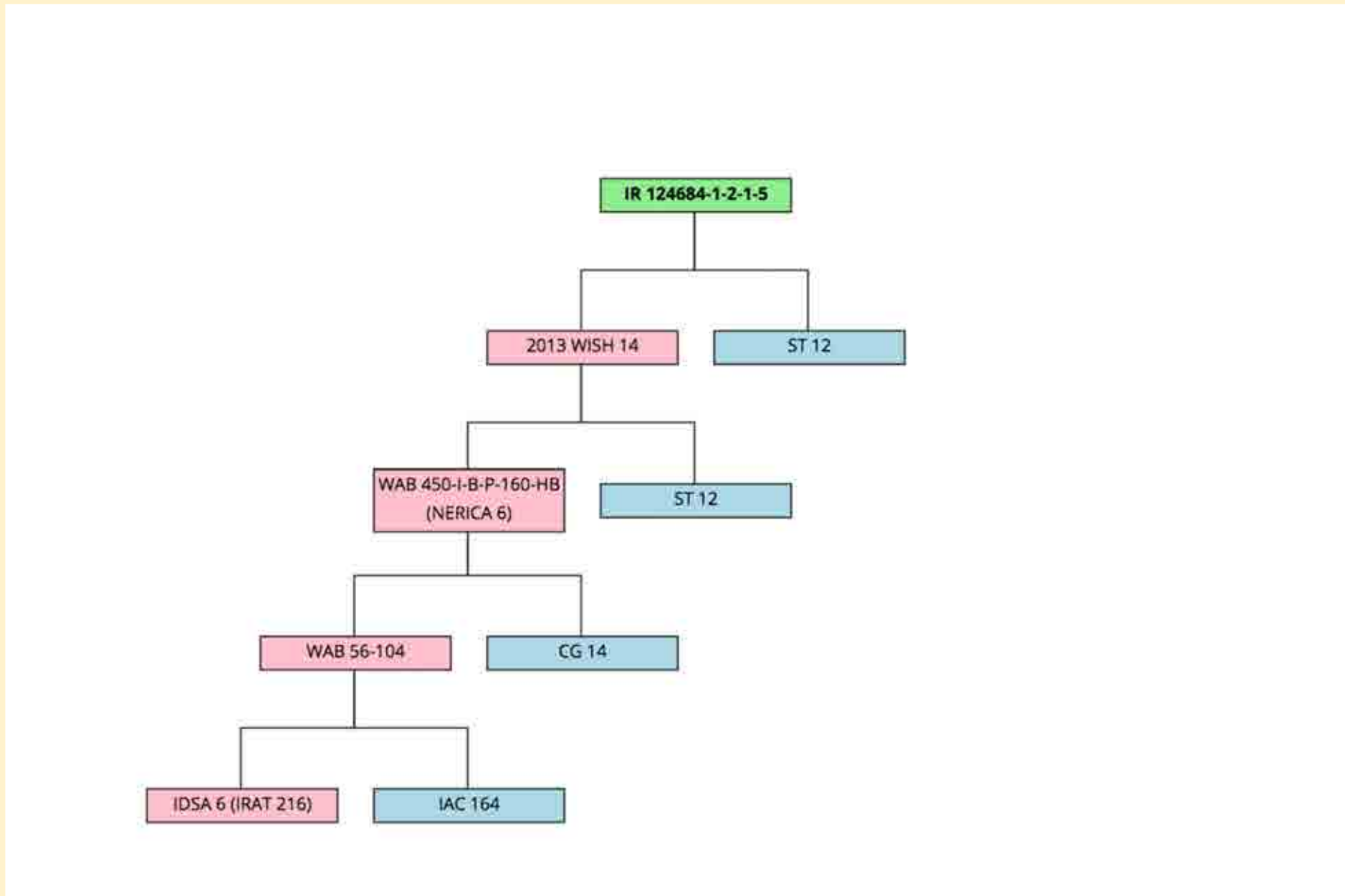
NERICA varieties have a yield advantage over their *O. glaberrima* and *O. sativa* parents, either through superior weed competitiveness, drought tolerance, and pest or disease resistance or simply through higher yielding potentials. ST 12 on the other hand, from the Stocked rice collections of Togo field and Nagoya University, is the donor for *Gn1a* and *WFP* alleles. Advanced lines of this WISH carries *Gn1a* alleles responsible for increase in grain number and *WFP* alleles responsible for increase in primary branching.

Other Information:

Generation: BC<sub>3</sub>F<sub>4</sub>

IR Designations:

IR 124686-12-6-1-3   IR 124684-2-1-5   IR 124686-7-7-6   IR 124686-5-3-1  
IR 124686-12-7-1-5   IR 124684-2-1-7   IR 124686-7-7-7  
IR 124686-17-3-1-4   IR 124684-2-1-9   IR 124686-11-3-3  
IR 124686-17-9-2-3   IR 124684-3-1-2   IR 124686-11-3-10  
IR 124686-17-9-6-5   IR 124684-4-10-9   IR 124686-11-3-11





# WAB56-104 x ST6 (*Gn1a*)



A. Agronomic Data of Advanced WISH Yield Lines

Line	DTH	PH	TN	PL	PB	SB	FG	UFG	TNG	HGW
	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM
ST6	83±	119.3±1.50	11±0.73	26.06±0.42	18±0.63	68±1.81	200.2±15.97	82.93±12.76	449±43.75	2.62±0.04
WAB56-104	76±	114.2±3.88	14±1.57	25.3±0.44	14±0.58	39±4.61	119.73±9.05	68.13±9.25	306±21.60	2.36±0.02
WISH 21:7-10-2-2-3-5	77±	122.4±1.95	7±1.02	26.6±0.68	12±0.32	36±1.84	115.4±13.57	55.4±12.87	512±25.90	3.08±0.06
WISH 21:7-13-5-1-5	75±	98.8±2.48	7±0.24	25.63±0.70	13±0.40	37±1.76	120.53±12.83	54.06±9.77	524±31.82	2.62±0.02
WISH 21:7-13-6-1-7	78±	102.6±2.91	8±0.37	24.93±0.29	12±0.37	38±2.06	135.73±10.53	46.46±6.73	547±26.27	2.66±0.04
WISH 21:7-14-7-1-7	77±	135.3±4.54	9±0.49	26.76±0.83	16±0.51	45±2.84	182.53±9.74	40.46±5.98	669±31.93	2.86±0.04
WISH 21:7-14-8-1-7	75±	122.5±2.32	9±1.16	24.73±0.83	15±0.58	31±2.71	146.13±13.07	32.8±1.71	537±34.83	2.12±0.05

DTH= Days to 50% Heading ; PH=Plant Height; TN=Tiller Number; PL= Panicle Length; PB=Primary Branches; SB=Secondary Branches; FG= Filled Grains; UFG=Unfilled Grains; TNG= Total Number of Grains; HGW=100 grain weight; SEM= Standard Error of Mean

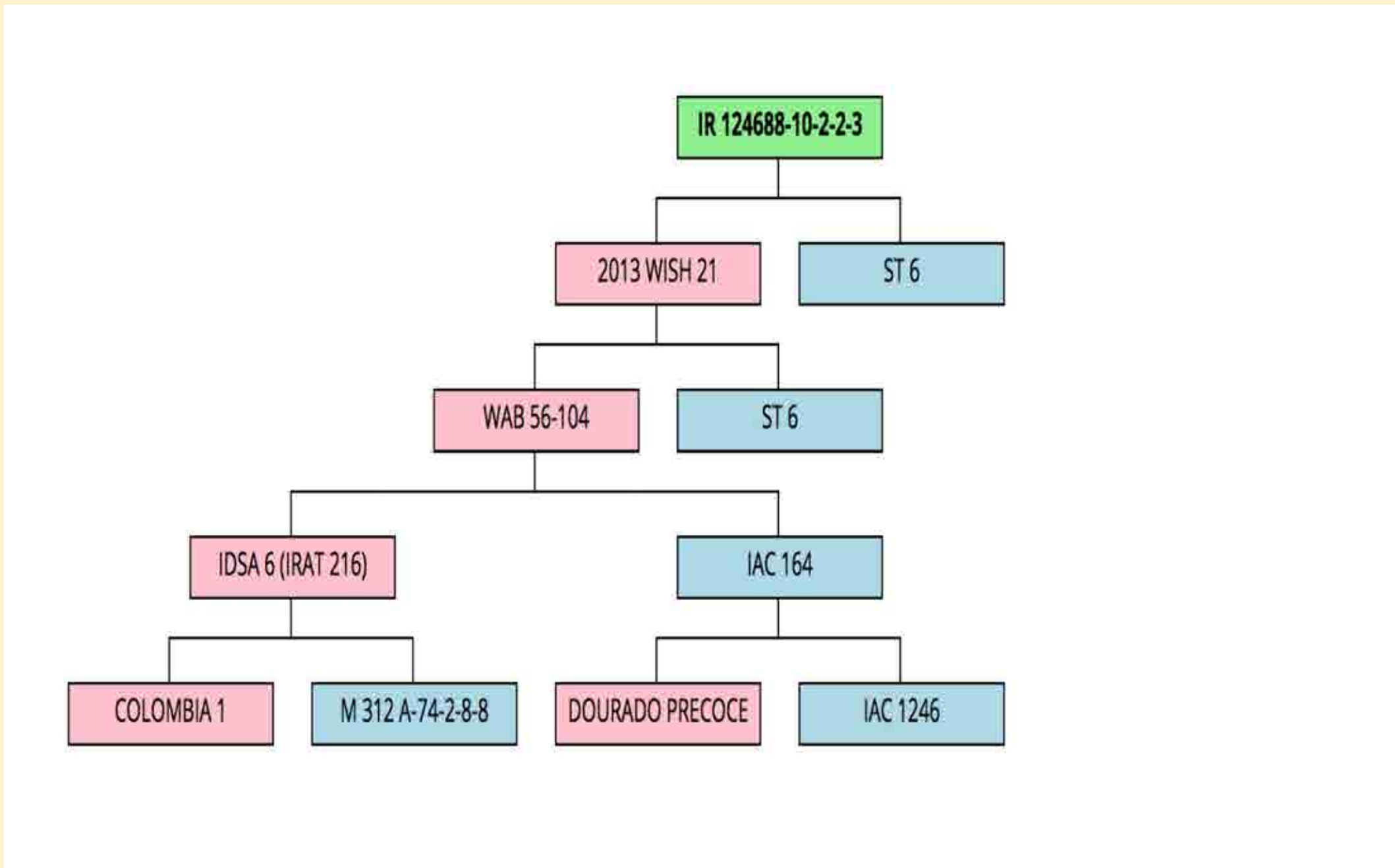
WAB56-104 is an improved upland line developed by AfricaRice, with important agronomic traits such as high yield and short growth duration. ST6 on the other hand, from the stocked rice collections of Togo field in Nagoya University, is the donor for *Gn1a* and *WFP* alleles. Advanced lines of this WISH carries *Gn1a* alleles responsible for increase in grain number.

## Other Information:

Generation: BC<sub>3</sub>F<sub>5</sub>

IR Designations:

- IR 124688-10-2-2-3
- IR 124688-13-5-1-5
- IR 124688-13-6-1-7
- IR 124688-14-7-1-7
- IR 124688-14-8-1-7





# WAB56-104x ST12 (*Gn1a*)



A. Agronomic Data of Advanced WISH Yield Lines

Line	DTH	PH	TN	PL	PB	SB	FG	UFG	TNG	HGW
	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM
ST12	75 ±	128.9 ± 3.21	11 ± 1.63	24.03 ± 0.39	20 ± 0.83	59 ± 5.41	173.67 ± 14.79	72.67 ± 7.17	391 ± 29.18	2.6 ± 0.05
WAB56-104	76 ±	114.2 ± 3.88	14 ± 1.57	25.3 ± 0.44	14 ± 0.48	37 ± 4.54	119.73 ± 9.05	68.13 ± 9.25	324 ± 29.02	2.36 ± 0.02
WISH 22:1-3-1-1-5	77 ±	116.3 ± 1.10	6 ± 0.73	21.8 ± 0.66	12 ± 0.52	29 ± 2.24	111.73 ± 9.53	38.13 ± 5.93	450 ± 30.15	2.9 ± 0.15
WISH 22:1-4-1-1-3	77 ±	113.7 ± 2.12	8 ± 0.87	22 ± 0.41	13 ± 0.39	28 ± 4.10	128 ± 18.49	32 ± 4.38	480 ± 61.06	2.86 ± 0.07
WISH 22:1-4-1-6-7	78 ±	118.1 ± 2.22	8 ± 0.40	23.73 ± 0.47	11 ± 0.29	44 ± 1.22	155.33 ± 3.58	40.33 ± 6.16	587 ± 18.62	3.06 ± 0.19
WISH 22:3-15-9-1-5	79 ±	103.5 ± 2.89	8 ± 0.60	23.43 ± 0.66	14 ± 0.71	40 ± 5.89	105.33 ± 8.43	67.07 ± 10.79	517 ± 34.02	2.42 ± 0.07
WISH 22:3-2-4-1-8	80 ±	128 ± 3.51	8 ± 0.32	26.93 ± 0.52	16 ± 0.55	67 ± 5.49	246.67 ± 13.84	58.67 ± 10.55	916 ± 57.00	2.36 ± 0.05

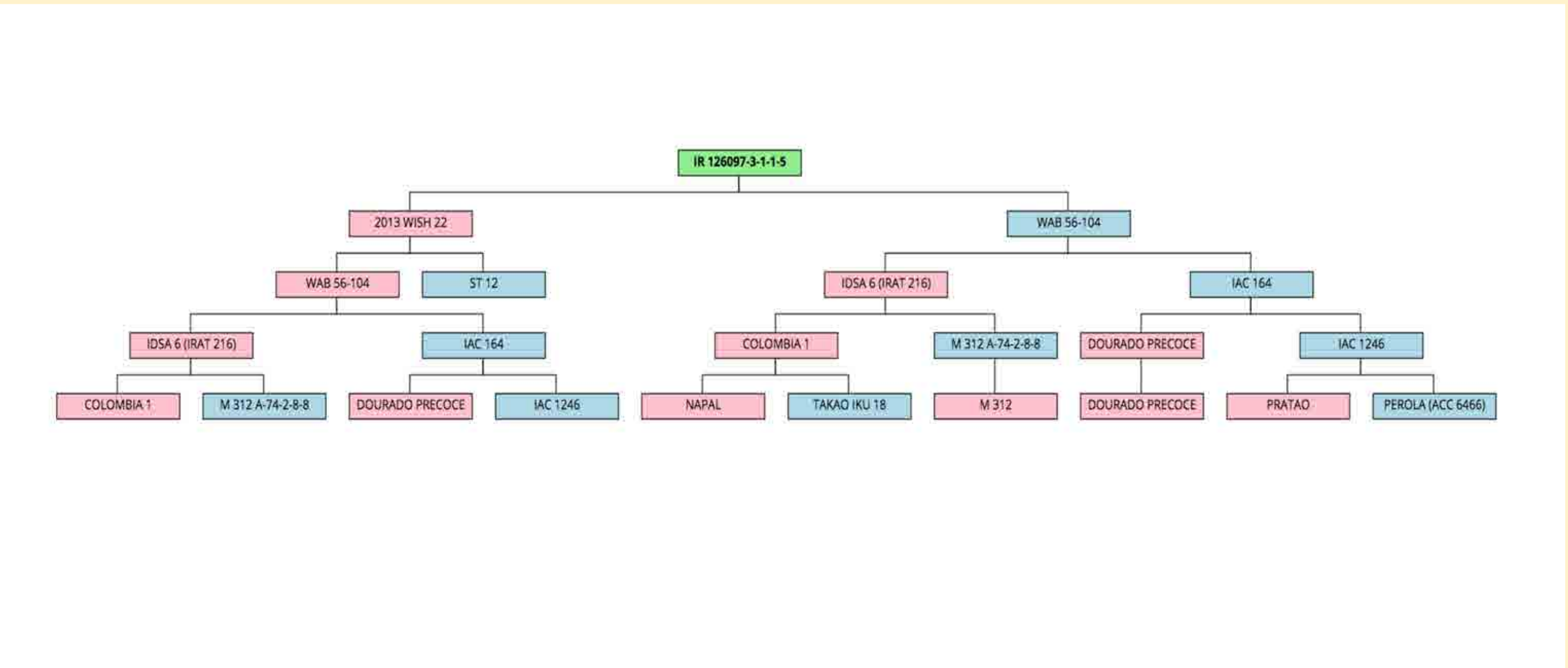
DTH= Days to 50% Heading ; PH=Plant Height; TN=Tiller Number; PL= Panicle Length; PB=Primary Branches; SB=Secondary Branches; FG= Filled Grains; UFG=Unfilled Grains; TNG= Total Number of Grains; HGW=100 grain weight; SEM= Standard Error of Mean

WAB56-104 is an improved upland line developed by AfricaRice, with important agronomic traits such as high yield and short growth duration. ST12 on the other hand, from the stocked rice collections of Togo field in Nagoya University, is the donor for *Gn1a* and *WFP* alleles. Advanced lines of this WISH carries *Gn1a* alleles responsible for increase in grain number.

## Other Information:

Generation: BC<sub>3</sub>F<sub>5</sub>  
 IR Designations:

- IR 126097-3-1-1-5
- IR 126097-4-1-1-3
- IR 126097-4-1-6-7
- IR 124690-2-4-1-8
- IR 124690-15-9-1-5





# WAB56-104 x ST12 (*WFP*)



A. Agronomic Data of Advanced WISH Yield Lines

Line	DTH	PH	TN	PL	PB	SB	FG	UFG	TNG	HGW
	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM
ST12	75±	128.9±3.21	11±1.63	24.03±0.39	20±0.86	59±5.44	173.26±14.79	72.66±7.17	391±29.16	2.6±0.05
WAB56-104	76±	114.2±3.88	14±1.57	25.3±	14±0.58	39±4.61	119.73±9.05	68.13±9.25	324±29.03	2.36±0.02
WISH 22:3-17-2-1-5	83±	136±2.92	8±1.24	22.63±	25±0.68	63±3.44	181.13±13.76	124.53±11.87	917±2.57±	2.88±0.09
WISH 22:3-3-10-3-3	73±	107±5.01	5±1.00	20.08±	19±0.88	20±2.91	37.89±7.95	134.72±9.61	401±51.87	2.7±0.08
WISH 22:3-8-3-1-5	78±	125.6±4.63	8±0.97	21.95±	21±0.68	16±1.86	114.26±5.62	56.26±7.41	480±45.97	2.8±0.05
WISH 22:5-1-6-1-4	79±	137.4±3.78	5±0.40	29.23±	25±0.49	45±5.16	188.53±11.15	70.46±5.50	777±42.38	2.7±0.08
WISH 22:5-3-3-1-2	78±	120±2.19	4±0.25	25±0.44	26±1.50	48±5.05	194.83±10.41	62.91±9.54	773±34.03	2.57±0.11

DTH= Days to 50% Heading ; PH=Plant Height; TN=Tiller Number; PL= Panicle Length; PB=Primary Branches; SB=Secondary Branches; FG= Filled Grains; UFG=Unfilled Grains; TNG= Total Number of Grains; HGW=100 grain weight; SEM= Standard Error of Mean

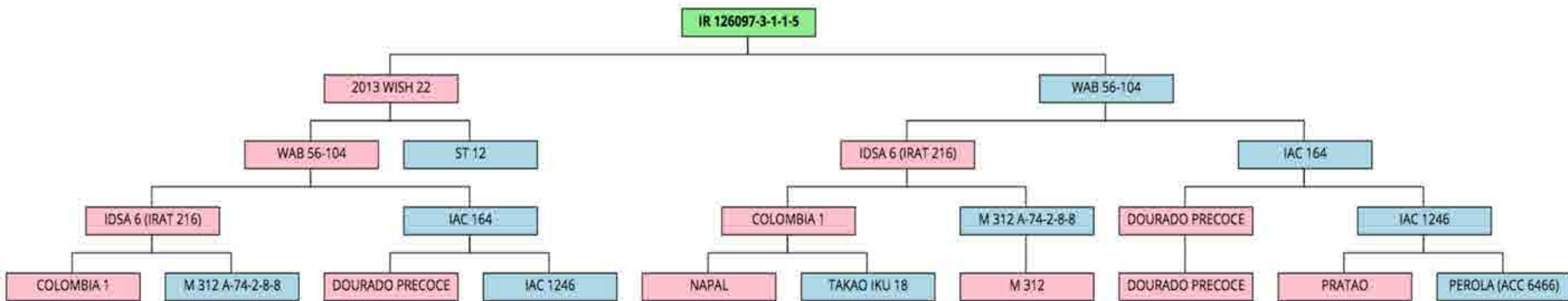
WAB56-104 is an improved upland line developed by AfricaRice, with important agronomic traits such as high yield and short growth duration. ST12 on the other hand, from the stocked rice collections of Togo field in Nagoya University, is the donor for *Gn1a* and *WFP* alleles. Advanced lines of this WISH carries *WFP* alleles responsible for increase in primary branching.

## Other Information:

Generation: BC<sub>3</sub>F<sub>5</sub>

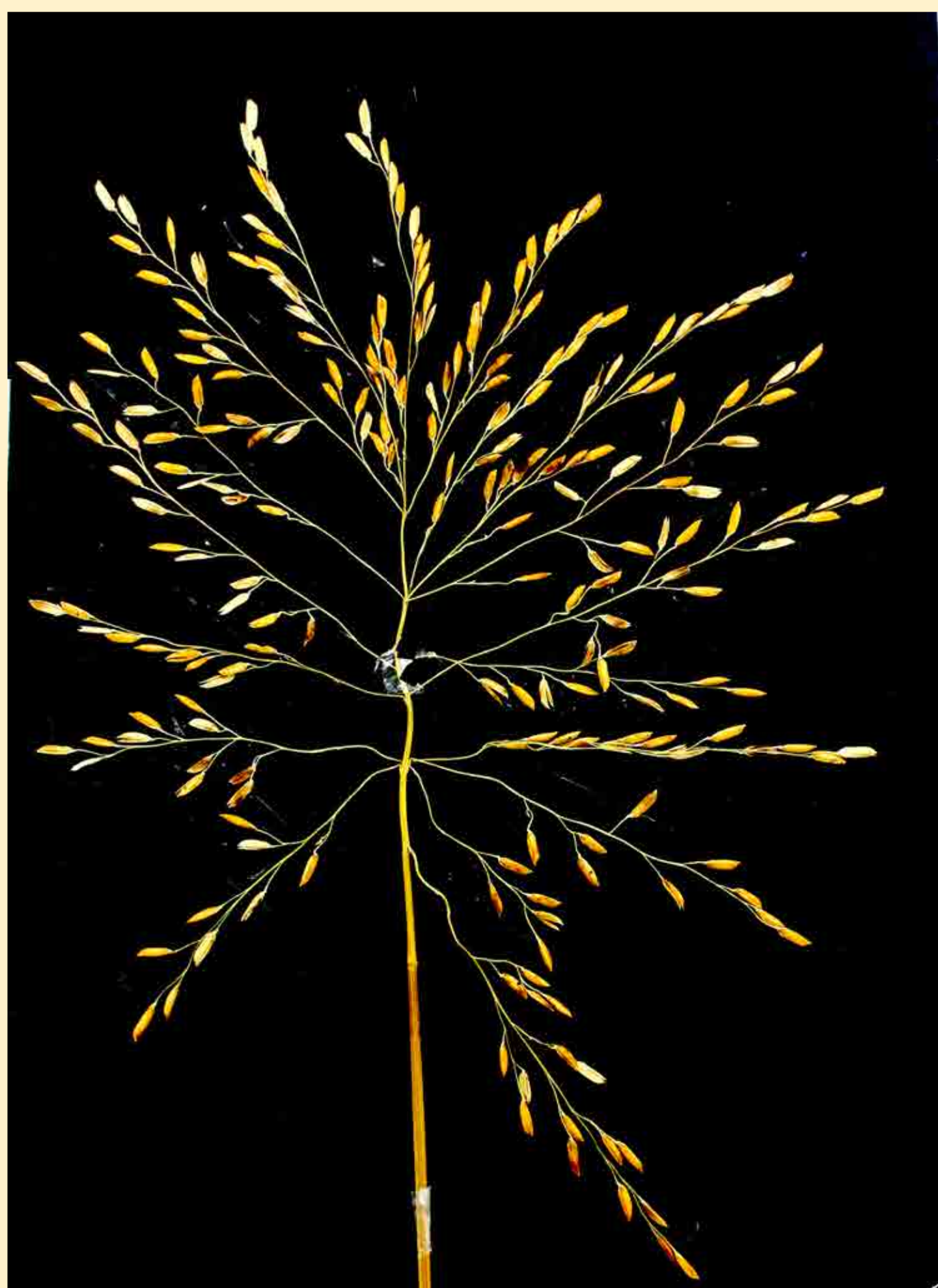
IR Designations:

- IR 124690-3-10-3-3
- IR 124690-8-3-1-5
- IR 124690-17-2-1-5
- IR 124691-1-6-1-4
- IR 124691-3-3-1-2





# WAB56-104x ST12 (*Gn1a*+*WFP*)



A. Agronomic Data of Advanced WISH Yield Lines

Line	DTH	PH	TN	PL	PB	SB	FG	UFG	TNG	HGW
	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM
ST12	75±	128.9±3.21	11±1.63	24.03±0.39	20±0.29	59±5.44	173.26±14.79	72.66±7.17	391±29.16	2.6±0.05
WAB56-104	76±	114.2±3.88	14±1.57	25.3±0.44	14±0.58	39±4.61	119.73±9.05	68.13±9.25	324±29.03	2.36±0.02
WISH 22:3-20-7-1-5	76±	124.1±3.38	5±0.32	24.23±0.29	25±0.71	52±5.94	174.66±7.69	84.13±10.07	776.4±34.99	2.26±0.07
WISH 22:5-6-1-3-7	80±	121.3±2.09	6±0.40	20.63±0.69	26±1.16	74±6.07	198.6±22.21	146.86±14.90	1036.4±92.72	2.7±0.07
WISH 22:5-8-12-3-4	75±	135.7±4.69	5±0.32	24±0.71	28±0.87	61±6.07	91.8±16.25	165.26±17.57	716.4±53.40	2.52±0.11
WISH 22:5-8-12-6-9	75±	142±3.15	6±0.51	25.83±0.46	26±0.58	58±2.10	107.33±17.91	155.86±16.64	789.6±40.69	3.04±0.07
WISH 22:5-8-8-11-2	79±	118.2±1.45	5±0.51	22.43±0.46	23±0.40	50±1.50	80.13±11.70	136.8±9.17	605.2±40.58	2.48±0.10

DTH= Days to 50% Heading ; PH=Plant Height; TN=Tiller Number; PL= Panicle Length; PB=Primary Branches; SB=Secondary Branches; FG= Filled Grains; UFG=Unfilled Grains; TNG= Total Number of Grains; HGW=100 grain weight; SEM= Standard Error of Mean

WAB56-104 is an improved upland line developed by AfricaRice, with important agronomic traits such as high yield and short growth duration. ST 12 on the other hand, from the Stocked rice collections of Togo field and Nagoya Universit, is the donor for *Gn1a* and *WFP* alleles. Advanced lines of this WISH carries *Gn1a* alleles responsible for increase in grain number and *WFP* alleles responsible for increase in primary branching.

## Other Information:

Generation: BC<sub>3</sub>F<sub>5</sub>

IR Designations:

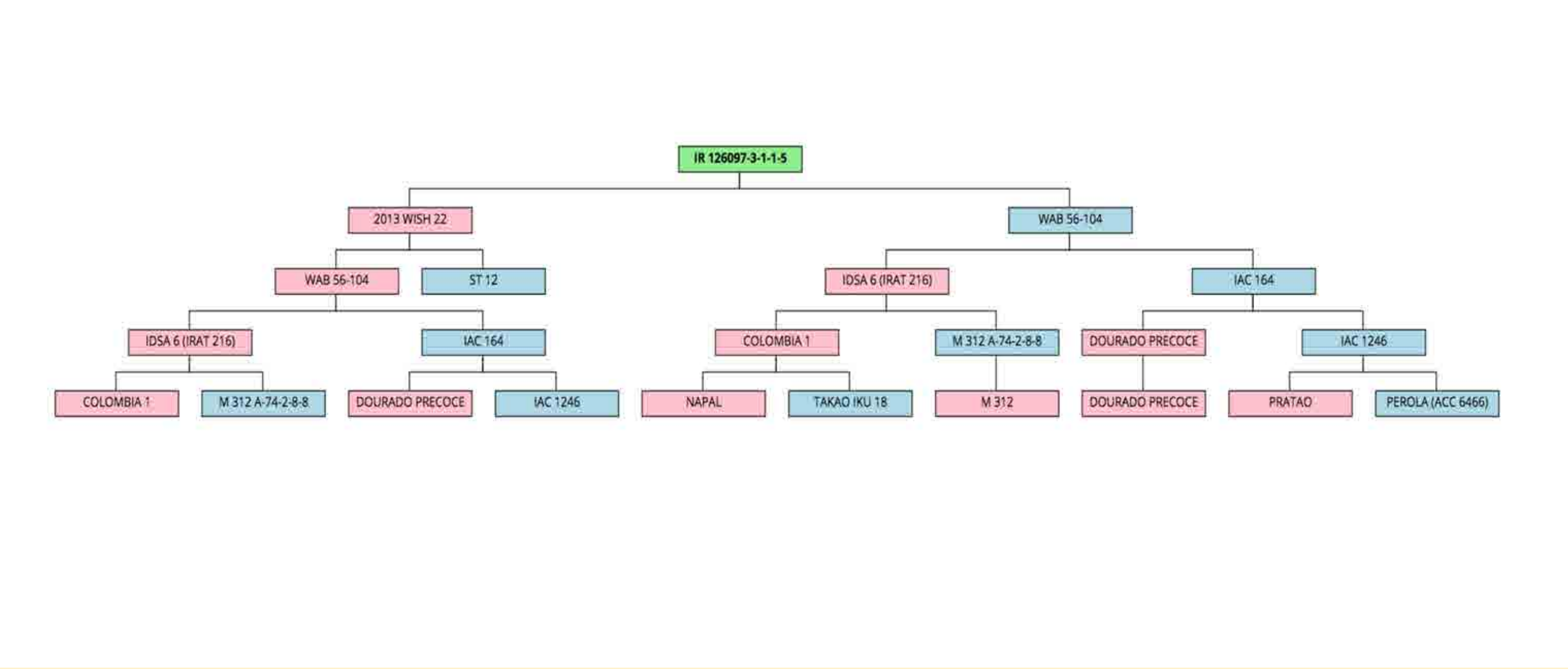
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IR 124691-6-1-3-7

IR 124691-8-8-11-2

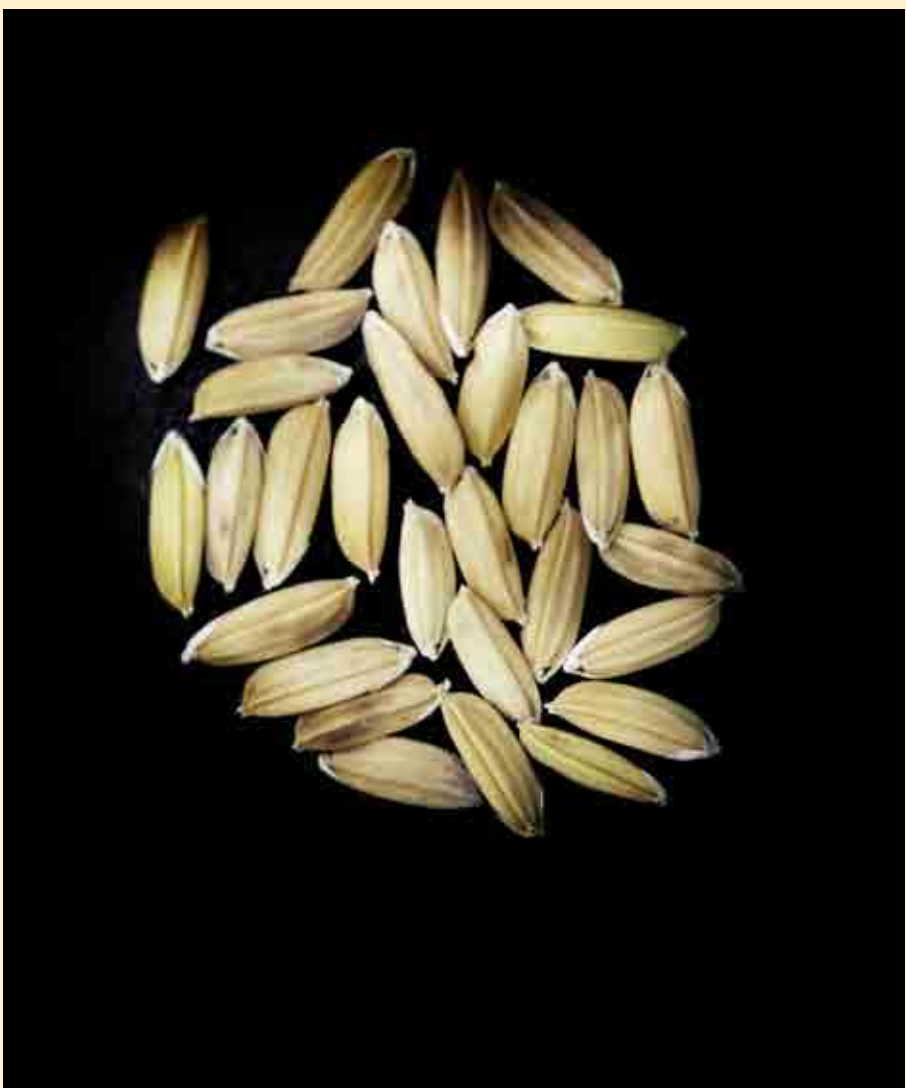
IR 124691-8-12-3-4

IR 124691-8-12-6-9





# WAB56-50 x ST12 (*Gn1a*)



A. Agronomic Data of Advanced WISH Yield Lines

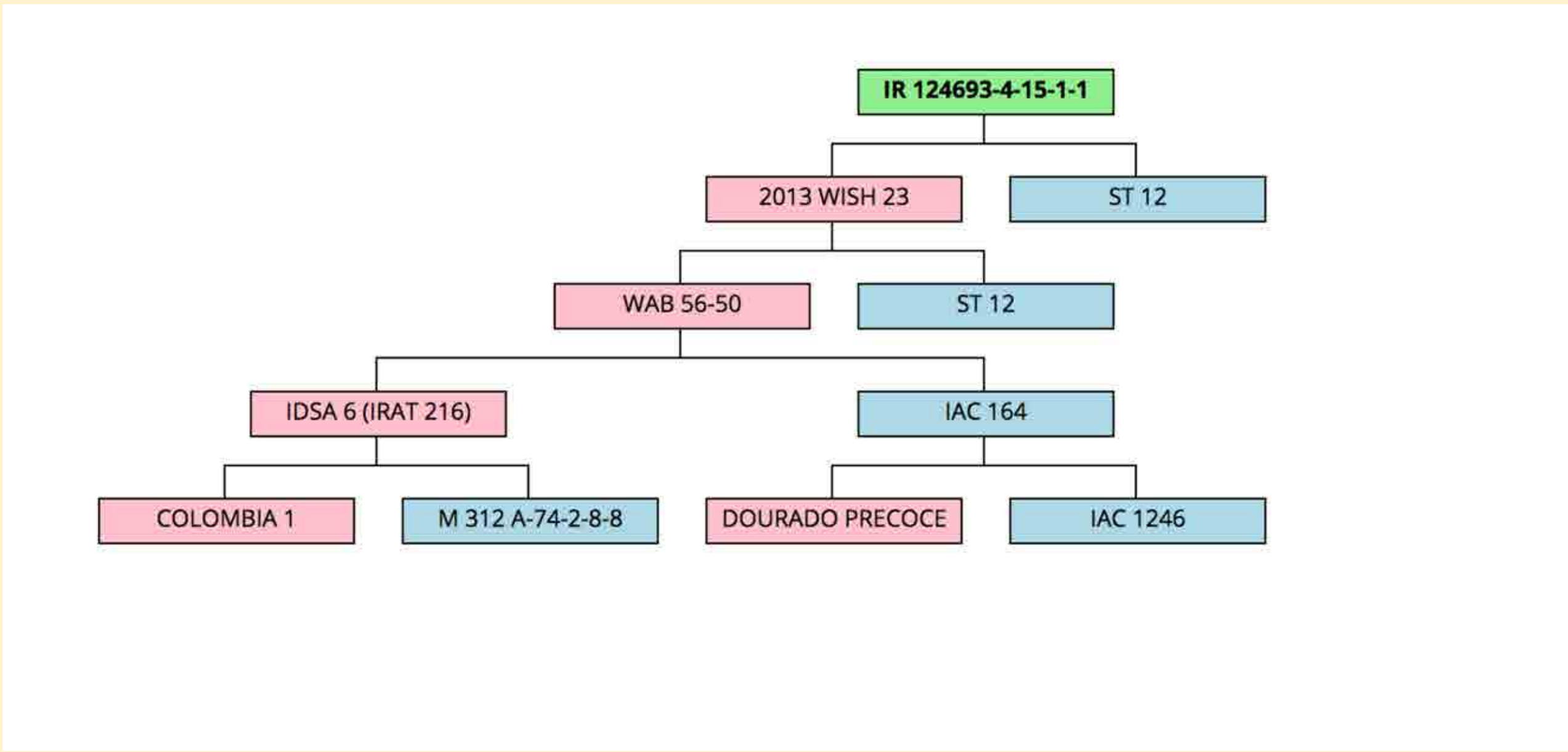
Line	DTH	PH	TN	PL	PB	SB	FG	UFG	TNG	HGW
	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM
ST12	75±	128.9±3.21	11±1.63	24.03±0.39	20±0.86	59±5.44	173.26±14.79	72.66±7.17	391±29.16	2.6±0.05
WAB56-50	78±	129.8±2.37	14±1.21	24.33±0.66	13±0.37	27±2.84	101.13±3.01	55.73±2.11	268±6.52	2.3±0.04
WISH 23:1-7-4-15-1-1	78±	123.4±3.91	6±0.66	24.37±0.30	12±0.32	27±1.00	116.53±5.10	26.13±1.99	428±19.51	3.3±0.03
WISH 23:1-7-4-16-1-4	79±	119.3±2.73	6±0.81	22.2±0.89	12±0.55	28±3.01	107.76±11.59	36.16±2.53	408±24.43	3.5±0.08

DTH= Days to 50% Heading ; PH=Plant Height; TN=Tiller Number; PL= Panicle Length; PB=Primary Branches; SB=Secondary Branches; FG= Filled Grains; UFG=Unfilled Grains; TNG= Total Number of Grains; HGW=100 grain weight; SEM= Standard Error of Mean

WAB56-50 is also an improved upland line developed by AfricaRice, with important agronomic traits such as high yield and short growth duration. ST12 on the other hand, from the stocked rice collections of Togo field in Nagoya University, is the donor for *Gn1a* and *WFP* alleles. Advanced lines of this WISH carries *Gn1a* alleles responsible for increase in grain number.

## Other Information:

Generation: BC<sub>3</sub>F<sub>5</sub>  
IR Designations:  
IR 124693-4-15-1-1  
IR 124693-4-16-1-4





# WAB56-50 x ST12 (*WFP*)



A. Agronomic Data of Advanced WISH Yield Lines

Line	DTH	PH	TN	PL	PB	SB	FG	UFG	TNG	HGW
	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM
ST12	75 ±	128.9 ±3.21	11 ± 1.63	24.03 ± 0.39	20 ± 0.86	59 ± 5.44	173.26 ± 14.79	72.66 ± 7.17	391 ± 29.16	2.6 ± 0.05
WAB56-50	78 ±	129.8 ±2.37	14 ± 1.21	24.33 ± 0.66	13 ± 0.37	27 ± 2.84	101.13 ± 3.01	55.73 ± 2.11	268 ± 6.52	2.3 ± 0.04
WISH 23:1-12-3-2-3-2	79 ±	123.6 ±2.50	5 ± 0.24	22.47 ± 0.58	20 ± 0.58	30 ± 4.55	147.7 ± 16.56	44.4 ± 4.19	545 ± 77.26	3.4 ± 0.11
WISH 23:1-12-6-20-1-3	77 ±	111 ± 2.63	5 ± 0.32	20.5 ± 0.62	14 ± 1.17	24 ± 2.54	118.26 ± 5.64	37.8 ± 6.36	468 ± 30.04	2.8 ± 0.09
WISH 23:1-12-6-3-2-5	78 ±	122.1 ± 3.41	6 ± 0.75	25.3 ± 0.49	19 ± 0.60	33 ± 2.06	142.86 ± 9.38	49.93 ± 4.28	578 ± 25.51	3.2 ± 0.04
WISH 23:1-12-6-3-2-7	77 ±	127.7 ± 2.22	7 ± 0.84	24.83 ± 0.58	19 ± 0.40	34 ± 2.55	133.53 ± 4.32	62.4 ± 2.42	587 ± 7.17	3.1 ± 0.14
WISH 23:1-4-4-16-2-3	76 ±	130.2 ± 2.71	5 ± 0.20	23.71 ± 0.68	20 ± 0.73	35 ± 2.54	139.3 ± 3.80	56.23 ± 8.38	504 ± 41.33	3.2 ± 0.05

DTH= Days to 50% Heading ; PH=Plant Height; TN=Tiller Number; PL= Panicle Length; PB=Primary Branches; SB=Secondary Branches; FG= Filled Grains; UFG=Unfilled Grains; TNG= Total Number of Grains; HGW=100 grain weight; SEM= Standard Error of Mean

WAB56-50 is also an improved upland line developed by AfricaRice, with important agronomic traits such as high yield and short growth duration. ST12 on the other hand, from the stocked rice collections of Togo field in Nagoya University, is the donor for *Gn1a* and *WFP* alleles. Advanced lines of this WISH carries *WFP* alleles responsible for increase in primary branching.

Other Information:

**Generation:** BC<sub>3</sub>F<sub>5</sub>

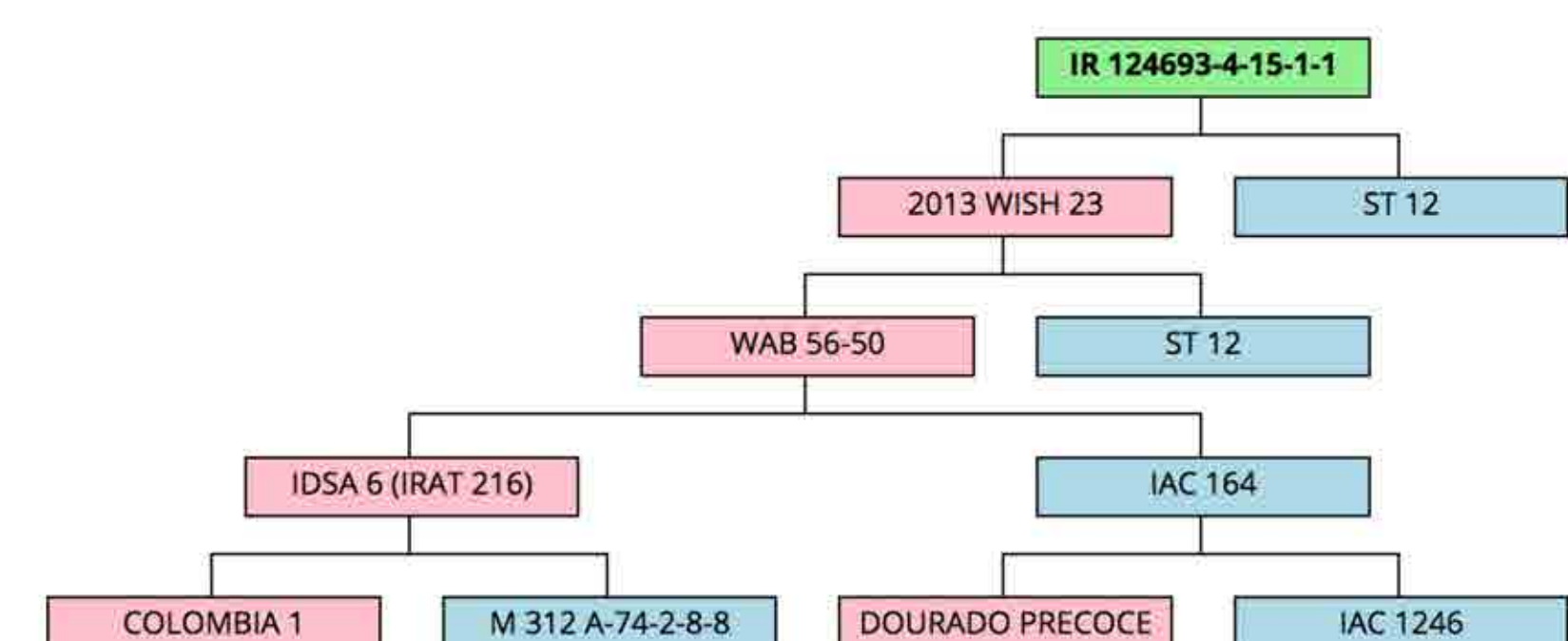
**IR Designations:**

IR 126096-4-16-2-3

IR 124694-6-3-2-5

IR 124694-6-3-2-7

IR 124694-6-20-1-3





# WAB56-50 x ST12 (*Gn1a* + *WFP*)



A. Agronomic Data of Advanced WISH Yield Lines

Line	DTH	PH	TN	PL	PB	SB	FG	UFG	TNG	HGW
	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM
ST12	75±	128.9±3.21	11±1.63	24.03±0.39	20±0.86	59±5.44	173.26±14.79	72.66±7.17	391±29.16	2.6±0.05
WAB56-50	78±	129.8±2.37	14±1.21	24.33±0.66	13±0.37	27±2.84	101.13±3.01	55.73±2.11	268±6.52	2.3±0.04
WISH 23:1-12-10-20-1-5	77±	126.5±2.13	6±0.58	22.7±0.49	20±0.51	35±3.44	161.73±9.53	47.6±10.90	629±31.68	3.38±0.08
WISH 23:1-12-10-20-2-7	78±	130.3±1.56	6±0.49	24.03±0.42	16±0.75	29±3.54	138.66±10.93	23.2±3.13	486±40.67	3.12±0.06
WISH 23:1-12-10-20-3-10	79±	121.7±2.34	5±0.24	24.06±0.27	17±0.58	37±4.85	137.46±15.50	63.13±6.66	601±53.16	2.84±0.10
WISH 23:1-12-3-2-12-5	78±	128.4±3.45	5±0.45	22.45±1.11	20±0.75	43±3.53	138.86±6.02	105±14.53	687±70.68	3.56±0.05
WISH 23:1-12-3-2-12-8	80±	126.62±5.96	7±1.35	22.87±1.29	17±1.22	38±5.95	138.75±11.92	67.75±12.24	620±62.41	3.32±0.08

DTH= Days to 50% Heading ; PH=Plant Height; TN=Tiller Number; PL= Panicle Length; PB=Primary Branches; SB=Secondary Branches; FG= Filled Grains; UFG=Unfilled Grains; TNG= Total Number of Grains; HGW=100 grain weight; SEM= Standard Error of Mean

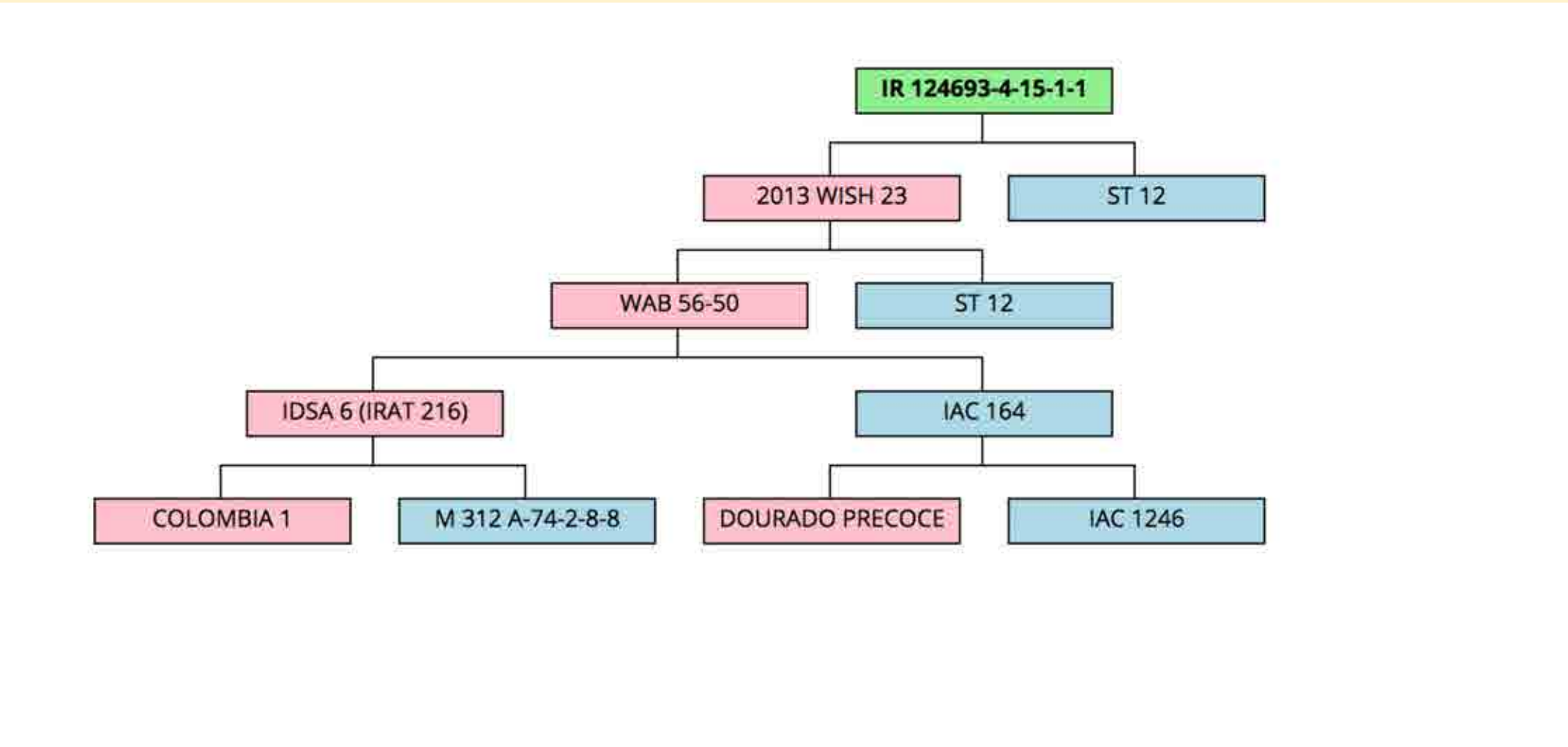
WAB56-50 is also an improved upland line developed by AfricaRice, with important agronomic traits such as high yield and short growth duration. ST12 on the other hand, from the stocked rice collections of Togo field in Nagoya University, is the donor for *Gn1a* and *WFP* alleles. Advanced lines of this WISH carries *Gn1a* + *WFP* alleles responsible for increase in grain number and primary branching.

## Other Information:

Generation: BC<sub>3</sub>F<sub>5</sub>

IR Designations:

- IR 124694-3-2-12-5
- IR 124694-3-2-12-8
- IR 124694-3-2-3-2
- IR 124694-10-20-1-5
- IR 124694-10-20-2-7
- IR 124694-10-20-3-10





# WAB56-50 x ST6 (*Gn1a*)



A. Agronomic Data of Advanced WISH Yield Lines

Line	DTH	PH	TN	PL	PB	SB	FG	UFG	TNG	HGW
	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM
ST6	83±	119.3±1.50	11±0.73	26.1±0.42	18±0.63	68±1.81	200.2±15.97	82.93±12.76	449±43.75	2.62±0.04
WAB56-50	78±	129.8±2.37	14±1.21	24.33±0.66	13±0.37	27±2.84	101.13±3.01	55.73±2.11	268±6.52	2.3±0.04
WISH 24:3-14-4-1-3	77±	110.5±1.51	7±0.24	22±0.67	12±0.51	24±0.95	97.27±5.43	34.8±2.71	396±18.69	2.88±0.07
WISH 24:3-20-10-1-4	80±	107±1.25	8±0.45	23.5±0.26	12±0.49	26±2.40	113.53±6.18	33.26±5.81	440±27.65	3.12±0.12
WISH 24:3-7-3-1-1	79±	121.25±2.11	6±0.25	24.96±0.39	13±0.71	36±1.66	145.34±11.51	27.16±4.32	517±32.60	3.27±0.10
WISH 24:40-8-5-1-5	80±	114.1±3.70	8±1.03	25±0.54	15±0.20	34±1.53	127.2±6.33	42.46±2.67	509±21.50	3.14±0.14
WISH 24:40-8-5-2-6	79±	111±2.10	6±0.75	24.83±0.64	13±0.71	33±4.07	137.13±15.67	30±1.77	501±48.08	3.14±0.10

DTH= Days to 50% Heading ; PH=Plant Height; TN=Tiller Number; PL= Panicle Length; PB=Primary Branches; SB=Secondary Branches; FG= Filled Grains; UFG=Unfilled Grains; TNG= Total Number of Grains; HGW=100 grain weight; SEM= Standard Error of Mean

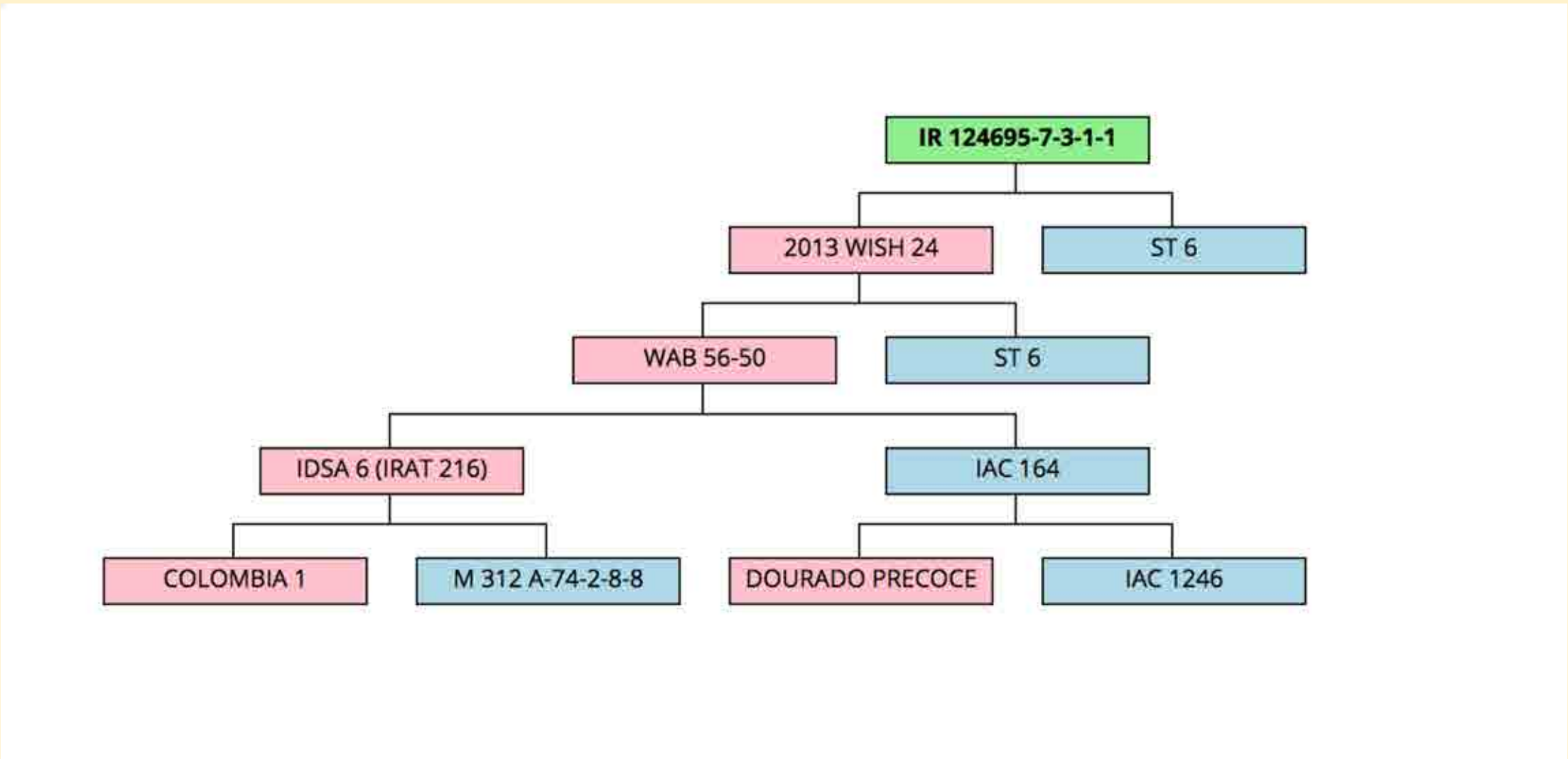
WAB56-50 is also an improved upland line developed by AfricaRice, with important agronomic traits such as high yield and short growth duration. ST6 on the other hand, from the stocked rice collections of Togo field in Nagoya University, is the donor for *Gn1a* and *WFP* alleles. Advanced lines of this WISH carries *Gn1a* alleles responsible for increase in grain number.

## Other Information:

Generation: BC<sub>3</sub>F<sub>5</sub>

IR Designations:

- IR 124695-7-3-1-1
- IR 124695-14-4-1-3
- IR 124695-20-10-1-4
- IR 124697-8-5-1-5
- IR 124697-8-5-2-6





# WAB56-50 x ST6 (*WFP*)



A. Agronomic Data of Advanced WISH Yield Lines

Line	DTH	PH	TN	PL	PB	SB	FG	UFG	TNG	HGW
	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM
ST6	83±	119.3±1.50	11±0.73	26.07±0.42	18±0.63	68±1.81	200.2±15.97	82.93±12.76	449±43.75	2.62±0.04
WAB56-50	78±	129.8±2.37	14±1.21	24.33±0.66	13±0.37	27±2.84	101.13±3.01	55.73±2.11	268±6.52	2.3±0.04
WISH 24:13-10-4-1-4	77±	134.5±6.89	6±0.24	24.9±0.48	14±0.37	64±27.16	119.53±11.00	59.2±3.48	505±58.17	3.14±0.19
WISH 24:5-5-10-1-2	77±	116.8±3.62	6±0.86	24.47±0.41	13±0.24	31±1.50	124.14±5.09	79.93±44.19	612±139.38	3.34±0.22
WISH 24:5-8-4-1-1	80±	111.1±1.71	5±0.49	26.28±0.91	16±0.51	30±3.89	111.63±16.54	61.60±3.90	477±39.14	2.84±0.15
WISH 24:5-8-5-1-3	79±	109.3±3.46	7±1.08	23.57±0.45	14±0.60	34±1.34	109.97±4.30	59.07±6.57	475±41.39	2.82±0.13

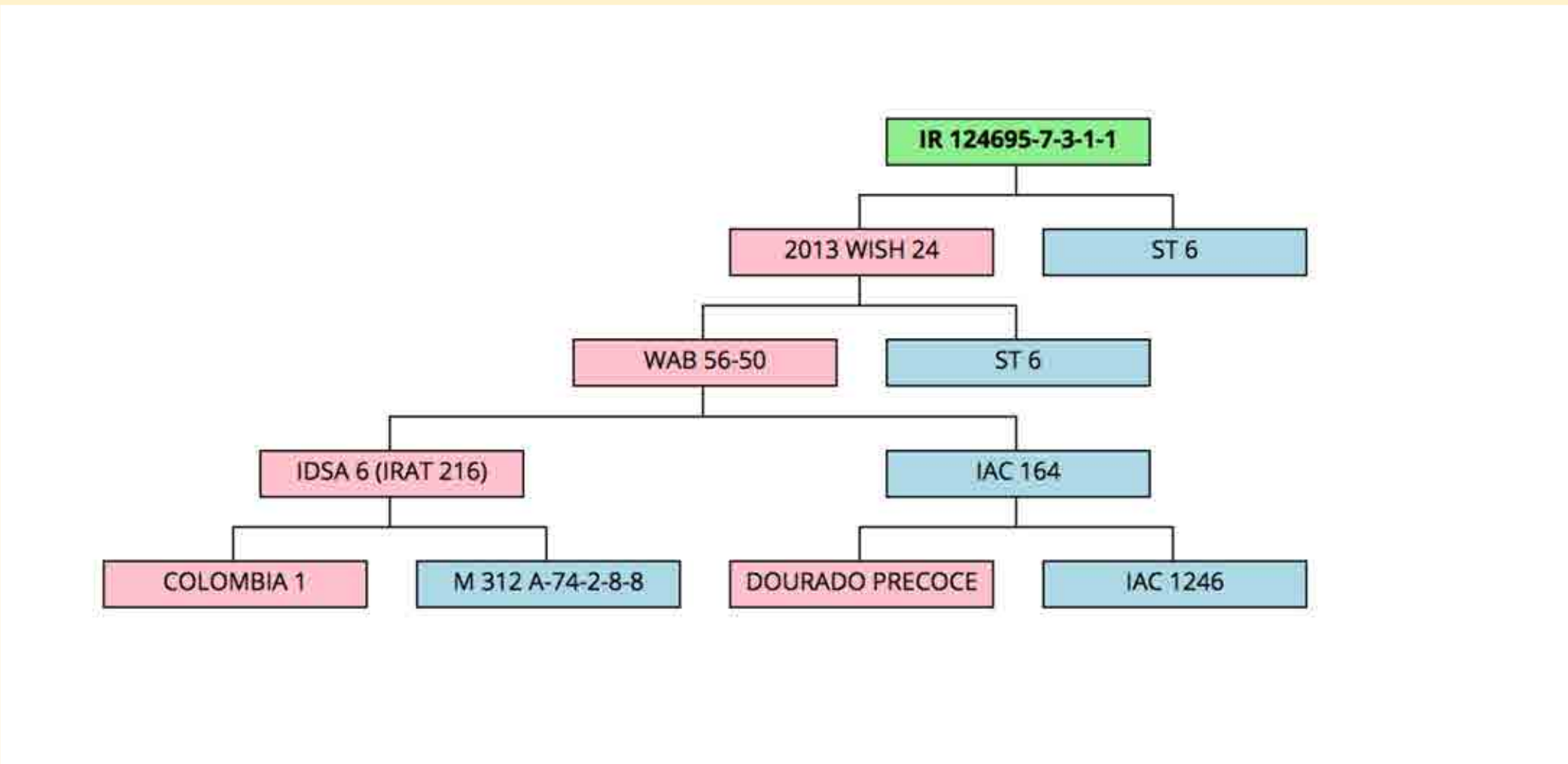
DTH= Days to 50% Heading ; PH=Plant Height; TN=Tiller Number; PL= Panicle Length; PB=Primary Branches; SB=Secondary Branches; FG= Filled Grains; UFG=Unfilled Grains; TNG= Total Number of Grains; HGW=100 grain weight; SEM= Standard Error of Mean

WAB56-50 is also an improved upland line developed by AfricaRice, with important agronomic traits such as high yield and short growth duration. ST6 on the other hand, from the stocked rice collections of Togo field in Nagoya University, is the donor for *Gn1a* and *WFP* alleles. Advanced lines of this WISH carries *WFP* alleles responsible for increase in primary branching.

## Other Information:

Generation: BC<sub>3</sub>F<sub>5</sub>  
IR Designations:

- IR 126095-5-10-1-2
- IR 126095-8-4-1-1
- IR 126095-8-5-1-3
- IR 124696-10-4-1-4





# WAB56-50 x ST6 (*Gn1a*+*WFP*)



A. Agronomic Data of Advanced WISH Yield Lines

Line	DTH	PH	TN	PL	PB	SB	FG	UFG	TNG	HGW
	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM
ST6	83±	119.3±1.50	10.8±0.73	26.06±0.42	18±0.63	68±1.81	200.2±15.97	82.93±12.76	449±43.75	2.62±0.04
WAB56-50	78±	129.8±2.37	13.6±1.21	24.33±0.66	13±0.37	27±2.84	101.13±3.01	55.73±2.11	268±6.52	2.3±0.04
WISH 24:13-1-10-11-3	78±	109.7±3.78	6.2±1.11	24.5±0.45	24±8.98	44±3.39	133.26±13.27	73.6±2.08	621±36.74	2.74±0.07
WISH 24:13-1-10-3-6	80±	111.3±2.11	5.4±0.51	24.36±0.29	15±0.77	44±3.06	129.43±11.60	94.43±10.08	618±28.08	3.12±0.08
WISH 24:13-1-10-4-7	79±	108.4±1.73	6.4±0.75	22.26±1.52	16±0.60	39±4.97	124.2±12.77	67.4±10.63	575±50.10	2.76±0.13
WISH 24:13-1-10-9-3	79±	118.4±2.36	6.8±0.80	25.27±0.50	15±0.40	47±2.88	144.53±7.16	74.6±6.29	657±32.47	2.82±0.04

DTH= Days to 50% Heading ; PH=Plant Height; TN=Tiller Number; PL= Panicle Length; PB=Primary Branches; SB=Secondary Branches; FG= Filled Grains; UFG=Unfilled Grains; TNG= Total Number of Grains; HGW=100 grain weight; SEM= Standard Error of Mean

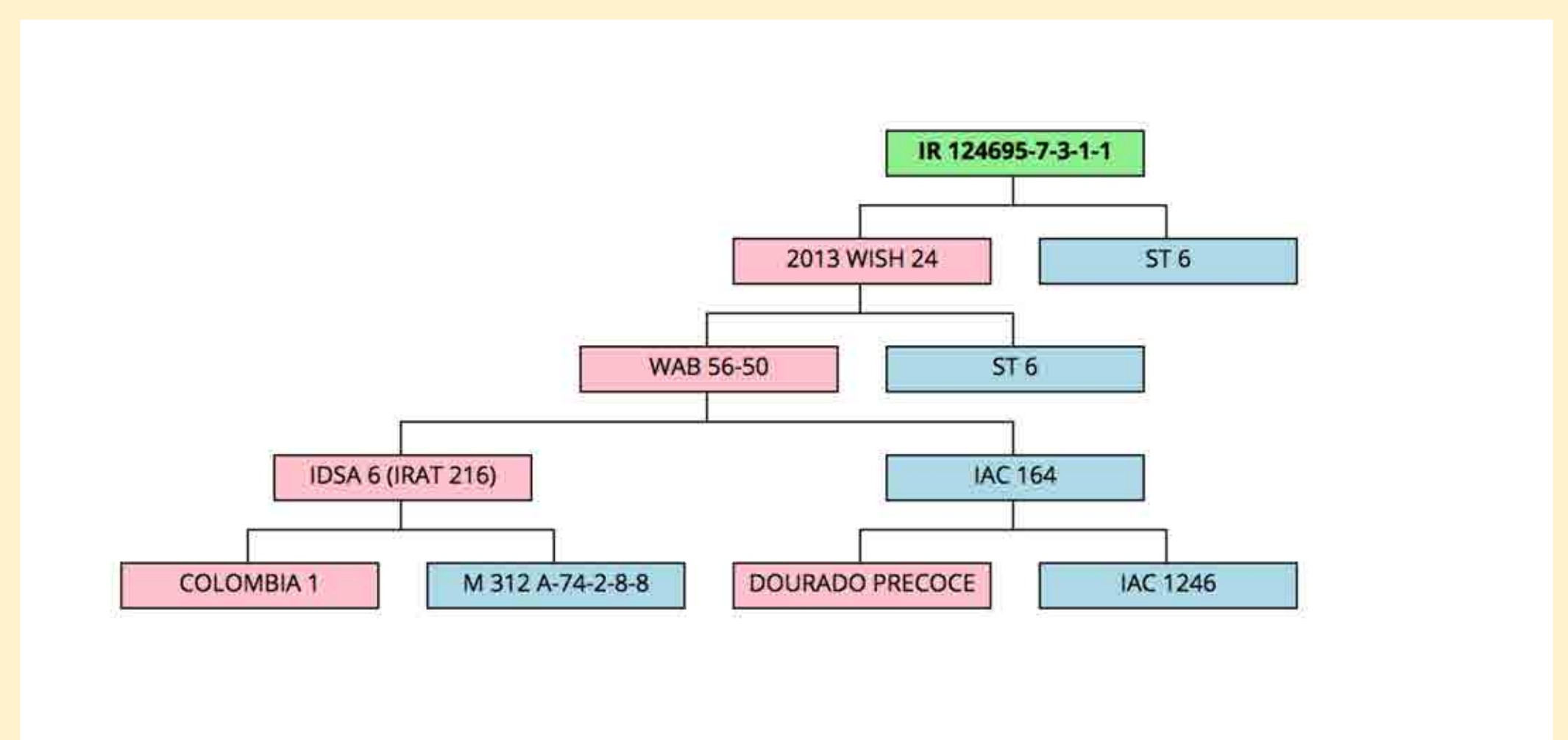
WAB56-50 is also an improved upland line developed by AfricaRice, with important agronomic traits such as high yield and short growth duration. ST6 on the other hand, from the stocked rice collections of Togo field in Nagoya University, is the donor for *Gn1a* and *WFP* alleles. Advanced lines of this WISH carries *Gn1a* and *WFP* alleles responsible for increase in grain number. And primary branching.

Other Information:

**Generation:** BC<sub>3</sub>F<sub>5</sub>

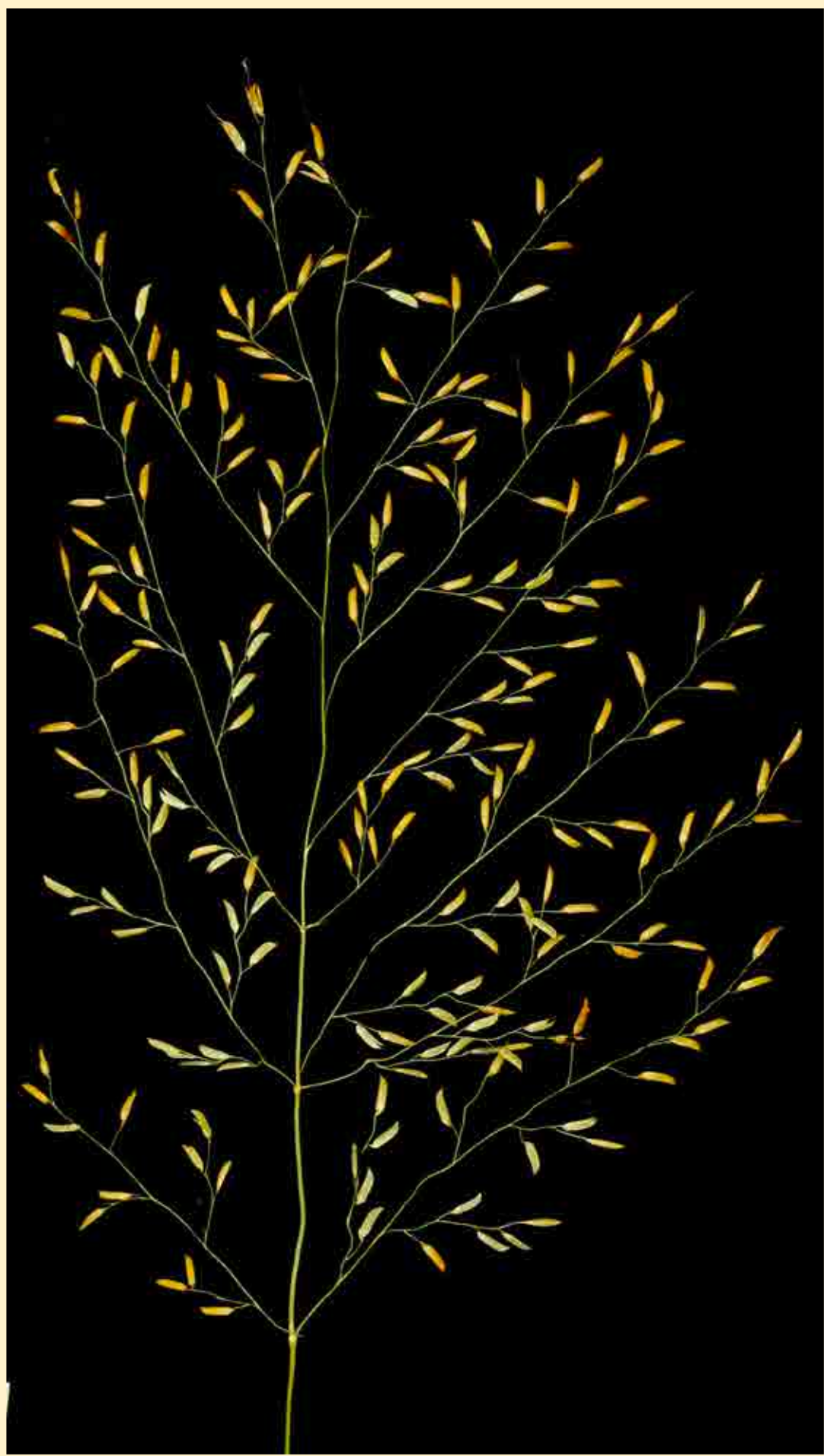
**IR Designations:**

IR 124696-1-10-2-2      IR 124696-1-10-11-3  
 IR 124696-1-10-3-4      IR 124696-1-10-9-3  
 IR 124696-1-10-3-6  
 IR 124696-1-10-4-7





# Basmati x ST12 (*WFP*)



A. Agronomic Data of Advanced WISH Yield Lines

Line	DTH	PH	TN	PL	PB	SB	FG	UFG	TNG	HGW
	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM
Basmati	97 ±	194.2 ± 2.85	18 ± 2.23	34.33 ± 0.32	11 ± 0.32	22 ± 1.20	131.13 ± 4.70	29.4 ± 3.02	481.6 ± 12.46	2.34 ± 0.05
ST12	75 ±	111.6 ± 3.03	11.4 ± 0.51	23.76 ± 0.72	19 ± 1.86	68 ± 7.57	187.53 ± 15.71	149.06 ± 59.56	779.4 ± 36.66	2.6 ± 0.05
WISH 28:2-1-5-9-4-10	86 ±	145.7 ± 3.07	13 ± 1.29	27.56 ± 0.96	13 ± 0.55	40 ± 2.01	142.06 ± 9.79	24.93 ± 6.16	501 ± 18.26	2.22 ± 0.02
WISH 28:2-1-6-1-2-6	86 ±	138.4 ± 4.00	12 ± 0.32	22.5 ± 0.69	12 ± 0.32	40 ± 1.71	113.26 ± 5.78	43.66 ± 9.35	470.8 ± 38.18	2.5 ± 0.05
WISH 28:2-2-1-1-1-4	85 ±	142 ± 1.94	19 ± 1.78	24.03 ± 2.00	10 ± 0.68	35 ± 1.25	129.26 ± 4.86	42.73 ± 2.53	516 ± 12.18	2.52 ± 0.05
WISH 28:2-2-11-1-1-7	86 ±	131.7 ± 2.52	13 ± 1.59	25.6 ± 0.42	13 ± 0.68	28 ± 3.32	116.86 ± 6.32	18.39 ± 3.97	405.8 ± 25.47	2.18 ± 0.04
WISH 28:2-2-11-1-4-8	84 ±	131.1 ± 2.47	14 ± 1.66	23.26 ± 0.57	11 ± 0.37	31 ± 1.44	169.53 ± 71.27	33.8 ± 1.25	610 ± 214.51	2.32 ± 0.06
WISH 28:2-2-11-1-8-9	88 ±	125.8 ± 2.01	14 ± 1.39	23.4 ± 0.44	11 ± 0.40	24 ± 1.36	102.53 ± 6.12	192.23 ± 173.89	883 ± 519.53	2.24 ± 0.07
WISH 28:2-2-12-22-3-9	88 ±	119.4 ± 3.64	13 ± 1.00	24.13 ± 0.59	12 ± 0.58	25 ± 0.81	109.46 ± 2.92	30.13 ± 3.01	418.8 ± 8.05	2.34 ± 0.04
WISH 28:2-2-12-4-10-7	87 ±	133 ± 4.12	15 ± 3.19	22.76 ± 0.43	12 ± 0.40	36 ± 2.92	110.6 ± 9.01	25 ± 5.30	406.8 ± 37.42	2.34 ± 0.04
WISH 28:2-2-17-4-5-10	86 ±	109.8 ± 3.84	13 ± 1.16	21.93 ± 0.46	11 ± 0.45	35 ± 1.12	104.33 ± 6.08	27.8 ± 4.98	396.4 ± 16.39	2.28 ± 0.07
WISH 28:2-2-3-1-1-5	84 ±	120.4 ± 4.84	16 ± 1.34	23.36 ± 0.86	12 ± 0.24	30 ± 1.74	130.06 ± 6.48	20.06 ± 4.57	450.4 ± 28.13	2.2 ± 0.07
WISH 28:2-2-6-1-6-6	87 ±	111.5 ± 5.37	18 ± 1.87	20.83 ± 0.86	10 ± 0.40	25 ± 1.44	113.26 ± 3.51	29.13 ± 6.50	427.2 ± 21.86	2.02 ± 0.04

DTH= Days to 50% Heading ; PH=Plant Height; TN=Tiller Number; PL= Panicle Length; PB=Primary Branches; SB=Secondary Branches; FG= Filled Grains; UFG=Unfilled Grains; TNG= Total Number of Grains; HGW=100 grain weight; SEM= Standard Error of Mean

Basmati rice has a unique position in the rice world due to its fragrance, aroma, grain morphology, quality and other desirable traits. Various basmati rice varieties have quantitative, distinct features, better plant type and superior characteristics with good growth habit in comparison with other varieties. ST12 on the other hand, from the stocked rice collections of Togo field in Nagoya University, is the donor for *Gn1a* and *WFP* alleles. Advanced lines of this WISH carries *WFP* alleles responsible for increase in primary branching.

Other Information:

Generation:  $BC_3F_6$

IR Designations:

IR 124714-1-18-1-1-3

IR 124714-2-1-1-1-4

IR 124714-2-3-1-1-5

IR 124714-2-6-1-6-7

IR 124714-2-11-1-1-7

IR 124714-2-11-1-4-8

IR 124714-2-11-1-8-9

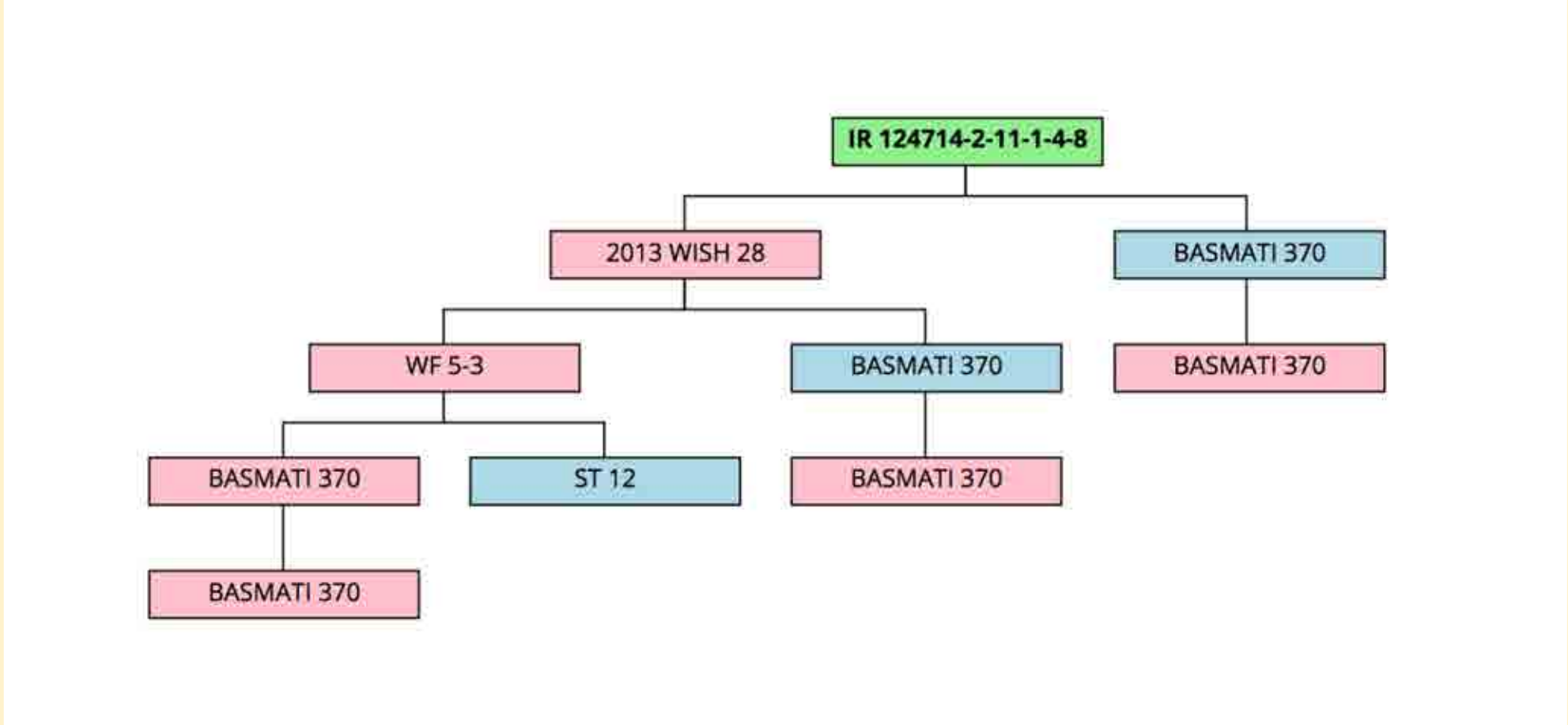
IR 124714-1-5-9-4-10

IR 124714-2-12-4-10-7

IR 124714-1-6-1-2-6

IR 124714-2-17-4-5-10

IR 124714-2-12-22-3-9





# IR64 x ST12 (*Gn1a*)



A. Agronomic Data of Advanced WISH Yield Lines

Line	DTH	PH	TN	PL	PB	SB	FG	UFG	TNG	HGW
	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM
IR64	98 ±	94 ±2.5	18 ±1.30	24.8 ±0.77	11 ±0.24	28 ±0.37	46.6 ±4.48	42.13 ±4.77	266 ±17.41	2.72 ±0.04
ST12	75 ±	111.6 ±3.03	11 ±0.51	23.76 ±0.72	20 ±1.86	68 ±7.57	187.53 ±15.71	149.06 ±59.56	779 ±36.66	2.6 ±0.05
WISH 31:1-2-17-2-1-11	87 ±	80.2 ±1.31	18 ±1.87	24.2 ±0.23	8 ±0.24	20 ±0.58	86.4 ±3.60	18.33 ±3.49	314 ±16.12	2.74 ±0.04
WISH 31:1-2-17-2-1-8	87 ±	83.3 ±0.68	18 ±2.35	26.36 ±0.40	9 ±0.37	23 ±0.97	94.33 ±5.83	15 ±2.65	328 ±17.91	2.82 ±0.04
WISH 31:1-2-17-3-1-4	90 ±	78.8 ±1.52	17 ±1.08	24 ±0.30	8 ±0.20	21 ±0.93	73.63 ±11.86	19.66 ±2.65	272 ±38.39	2.92 ±0.04
WISH 31:1-2-17-3-1-7	86 ±	82 ±0.94	21 ±3.04	25.5 ±0.21	9 ±0.24	25 ±1.20	106.46 ±5.51	13.39 ±1.59	360 ±12.27	2.74 ±0.02
WISH 31:1-2-18-9-1-1	82 ±	78.2 ±1.55	16 ±3.04	24.13 ±0.30	8 ± 0.20	22 ±1.91	86.86 ±7.33	25.46 ±1.71	337 ±20.74	2.54 ±0.05
WISH 31:1-2-18-9-1-10	83 ±	80.6 ±1.18	20 ±2.60	23.53 ±0.31	8 ±0.24	22 ±1.66	76.93 ±4.04	27.93 ±2.88	315 ±19.87	2.46 ±0.02
WISH 31:1-2-6-6-1-2	88 ±	82.2 ±3.85	26 ±2.60	23.76 ±0.38	9 ±0.24	21 ±1.30	76 ±1.22	25.86 ±2.09	306 ±7.24	2.66 ±0.02
WISH 31:1-2-6-6-1-5	83 ±	78.8 ±2.24	19 ±1.33	22.73 ±0.27	8 ±0.20	16 ±0.86	69.4 ±2.54	18.06 ±2.30	262 ±12.18	2.7 ±0.03
WISH 31:1-3-7-9-1-6	90 ±	82.4 ±0.48	26 ±1.77	25.16 ±0.22	9 ±0.24	25 ±0.98	87.6 ±4.84	43.46 ±6.20	393 ±20.76	2.5 ±0.03
WISH 31:1-3-7-9-1-9	87 ±	83.1 ±1.73	22 ±0.51	24.66 ±0.15	8 ±0.24	21 ±0.93	69.46 ±5.02	44.06 ±1.21	341 ±12.17	2.6 ±0.04

DTH= Days to 50% Heading ; PH=Plant Height; TN=Tiller Number; PL= Panicle Length; PB=Primary Branches; SB=Secondary Branches; FG= Filled Grains; UFG=Unfilled Grains; TNG= Total Number of Grains; HGW=100 grain weight; SEM= Standard Error of Mean

IR64 is an indica rice variety and has been accepted as a high-quality and high-yielding variety in many countries. ST 12 on the other hand, from the Stocked rice collections of Togo field and Nagoya University, is the donor for *Gn1a* and *WFP* alleles. Advanced lines of this WISH carries *Gn1a* alleles responsible for increase in grain number.

Other Information:

Generation: BC<sub>3</sub>F<sub>6</sub>  
IR Designations:

IR 124715-2-6-6-1-2

IR 124715-2-6-6-1-5

IR 124715-2-17-2-1-11

IR 124715-2-17-3-1-4

IR 124715-3-7-9-1-6

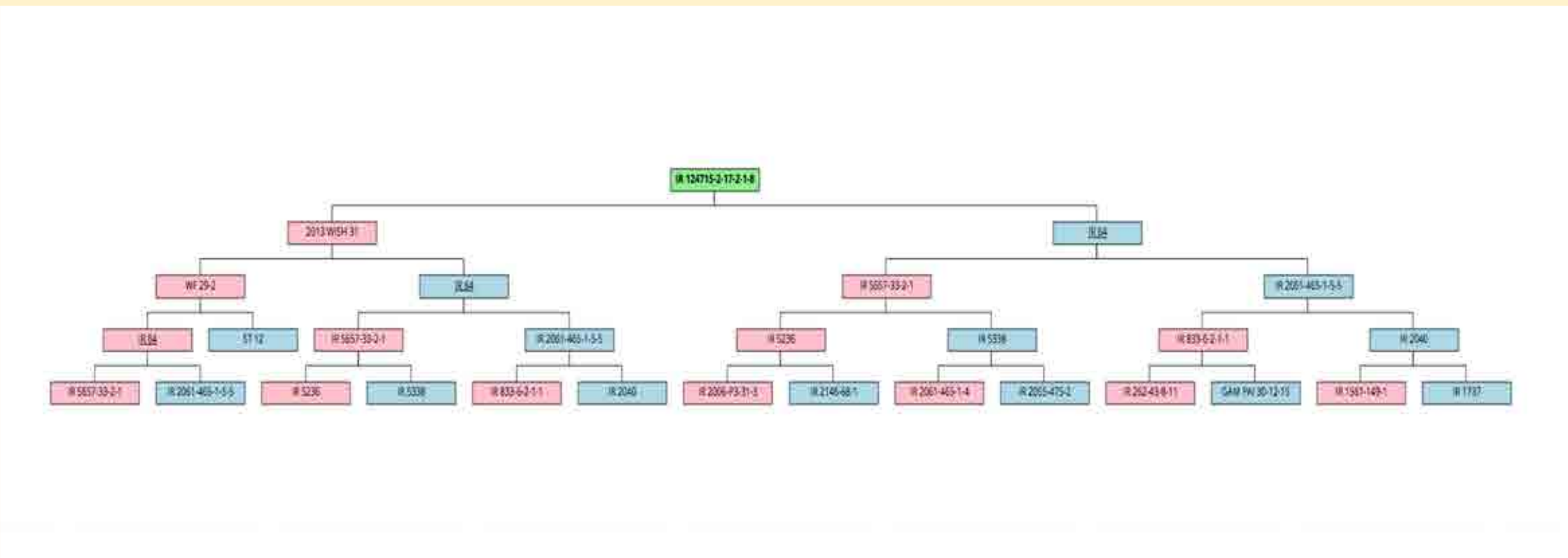
IR 124715-3-7-9-1-9

IR 124715-2-18-9-1-10

IR 124715-2-17-2-1-8

IR 124715-2-18-9-1-1

IR 124715-2-17-3-1-7





# IR64 x ST6 (*Gn1a*)



A. Agronomic Data of Advanced WISH Yield Lines

Line	DTH	PH	TN	PL	PB	SB	FG	UFG	TNG	HGW
	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM
IR64	98±	94±2.50	18±1.30	24.8±0.77	11±0.21	28±0.37	86.60±4.48	42.13±4.77	266.2±17.41	2.72±0.04
ST6	83±	119.3±1.50	10.8±0.73	26.06±0.42	26±0.45	58±4.72	200.20±15.97	82.93±12.76	890.6±28.82	2.62±0.04
WISH 32:2-4-13-1-1-1	86±	75.5±1.58	8.4±0.81	20.1±0.52	7±	16±0.97	54.06±4.22	22.46±10.25	229.6±20.42	2.84±0.09
WISH 32:2-4-13-2-1-2	89±	84±0.57	18±2.07	24.666±0.55	9±0.32	23±0.93	99.8±6.95	16.86±1.82	350±20.66	2.7±0.03
WISH 32:2-4-13-3-1-3	87±	90.4±1.63	17.2±2.11	25.866±0.38	7±0.24	19±2.32	87.53±10.91	16.06±1.55	298.6±46.89	2.92±0.05
WISH 32:2-4-29-1-1-4	86±	83.5±1.47	20.6±1.75	23.834±0.44	8±0.20	21±0.66	82.19±2.86	11.8±0.87	282±10.22	2.82±0.04
WISH 32:2-4-29-2-1-5	89±	84.4±2.23	19.4±1.75	24.3±0.21	9±0.32	15±0.71	73.07±4.08	16.59±0.96	269±13.91	2.7±0.08

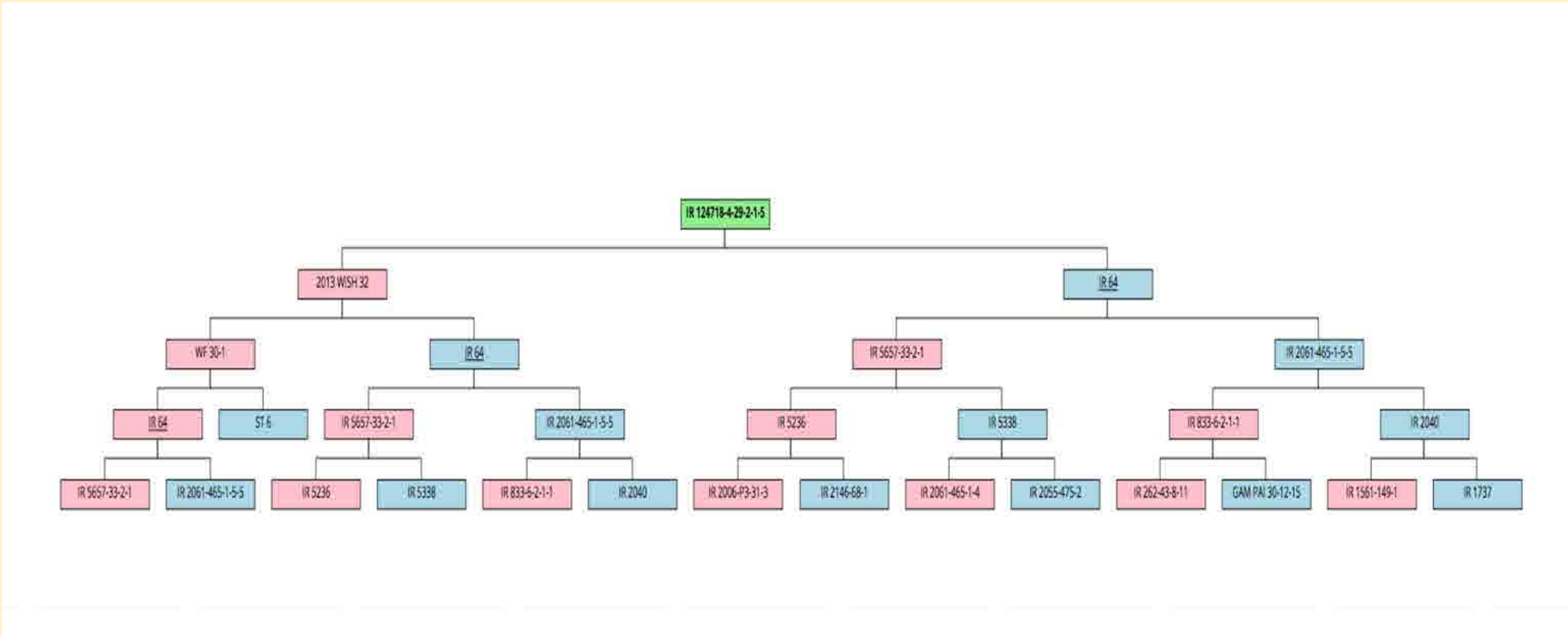
DTH= Days to 50% Heading ; PH=Plant Height; TN=Tiller Number; PL= Panicle Length; PB=Primary Branches; SB=Secondary Branches; FG= Filled Grains; UFG=Unfilled Grains; TNG= Total Number of Grains; HGW=100 grain weight; SEM= Standard Error of Mean

IR64 is an indica rice variety and has been accepted as a high-quality and high-yielding variety in many countries. ST 6 on the other hand, from the Stocked rice collections of Togo field and Nagoya University, is the donor for *Gn1a* and *WFP* alleles. Advanced lines of this WISH carries *Gn1a* alleles responsible for increase in grain number.

## Other Information:

Generation: BC<sub>3</sub>F<sub>6</sub>  
IR Designations:

- IR 124718-4-13-1-1-1
- IR 124718-4-13-2-1-2
- IR 124718-4-13-3-1-3
- IR 124718-4-29-1-1-4
- IR 124718-4-29-2-1-5





IR64 x ST6 (*WFP*)



### A. Agronomic Data of Advanced WISH Yield Lines

Line	DTH	PH	TN	PL	PB	SB	FG	UFG	TNG	HGW
	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM
IR64	98±	94±2.50	18±1.30	25±0.77	11±0.24	28±0.37	46.6±4.48	42.13±4.77	266±17.41	2.72±0.04
ST6	83±	119.3±1.50	11±0.73	26±0.42	26±0.45	58±4.72	200.2±15.97	82.93±12.76	891±28.82	2.62±0.04
WISH 32:2-4-6-10-1-1	82±	100.9±4.50	24±1.78	24.2±0.14	9±0.37	23±1.22	99.6±7.18	17.46±2.12	351±19.72	2.4±0.03
WISH 32:2-4-6-10-1-2	79±	112±2.22	22±1.89	26.13±0.51	9±0.40	26±1.20	106.66±4.61	23.39±1.17	390±17.04	2.38±0.06
WISH 32:2-4-6-10-1-5	86±	97.9±4.40	16±2.18	25.16±0.40	9±0.24	20±0.75	83.93±2.48	20.93±2.57	314±12.03	2.58±0.02
WISH 32:2-4-6-10-1-6	85±	102.8±1.82	17±2.06	24.33±0.29	9±0.20	23±1.21	96.26±3.14	18.6±1.81	345±13.34	2.38±0.02
WISH 32:2-4-6-2-1-6	87±	81.6±1.50	16±2.84	22.9±0.23	9±0.24	18±0.86	85.13±3.93	17.79±1.19	309±10.72	2.62±0.02
WISH 32:2-4-7-2-1-4	88±	83.1±2.14	13±0.97	21.49±0.30	8±0.24	18±0.81	73.33±2.46	16.13±3.50	268±9.19	2.44±0.04
WISH 32:2-4-9-5-1-5	87±	81.6±0.29	20±2.22	22.26±0.30	8±0.37	12±0.40	65.73±2.55	10.53±1.49	229±8.03	2.72±0.08
WISH 32:2-4-9-5-1-6	86±	80±0.61	17±2.82	22.66±0.19	9±0.37	14±0.24	70.8±1.17	9.2±0.96	240±4.49	2.6±0.03
WISH 32:2-4-9-6-1-5	87±	81.1±0.61	14±1.89	22.53±0.39	8±0.40	12±1.03	63.4±4.99	10.26±0.97	221±17.17	2.56±0.04

DTH= Days to 50% Heading ; PH=Plant Height; TN=Tiller Number; PL= Panicle Length; PB=Primary Branches; SB=Secondary Branches; FG= Filled Grains; UFG=Unfilled Grains; TNG= Total Number of Grains; HGW=100 grain weight; SEM= Standard Error of Mean

IR64 is an indica rice variety and has been accepted as a high-quality and high-yielding variety in many countries. ST 6 on the other hand, from the Stocked rice collections of Togo field and Nagoya University, is the donor for *Gn1a* and *WFP* alleles. Advanced lines of this WISH carries *WFP* alleles responsible for increase in primary branching.

### Other Information:

Generation:  $\text{BC}_3\text{F}_6$

## IR Designations:

IR 124718-4-6-2-1-6      IR 124718-4-7-2-1-4

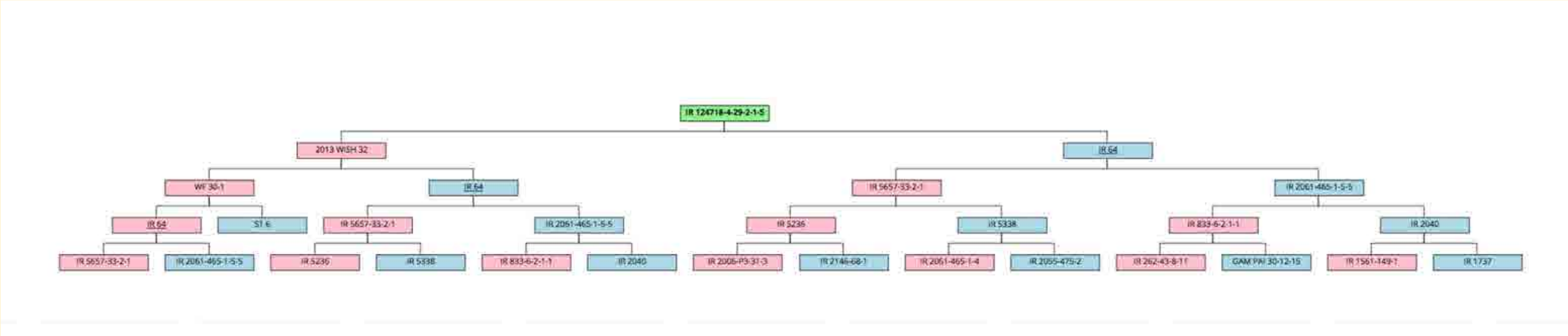
IR 124718-4-6-10-1-1      IR 124718-4-9-5-1-6

IR 124718-4-6-10-1-2      IR 124718-4-9-6-1-5

IR 124718-4-6-10-1-5

IR 124718-4-6-10-1-6

IR 124718-4-9-5-1-5





# IR64 x ST6 (*Gn1a*+*WFP*)



A. Agronomic Data of Advanced WISH Yield Lines

Line	DTH	PH	TN	PL	PB	SB	FG	UFG	TNG	HGW
	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM
IR64	98±	94±2.50	18±1.30	25±0.77	11±0.24	28±0.37	46.6±4.48	42.13±4.77	266±17.41	2.72±0.04
ST6	83±	119.3±1.50	11±0.73	26±0.42	26±0.45	58±4.72	200.2±15.97	82.93±12.76	891±28.82	2.62±0.04
WISH 32:2-4-22-4-1-7	87±	94.3±1.33	15±0.89	24.2±0.16	10±0.40	21±1.17	90.73±4.69	15.59±2.46	319±18.52	2.68±0.02
WISH 32:2-4-22-6-1-9	87±	95.5±2.62	13±1.16	22.2±0.56	10±0.20	29±1.57	83.53±9.16	17.33±3.13	303±28.99	2.62±0.04
WISH 32:2-4-25-1-1-10	88±	82.6±1.74	11±1.67	21.83±0.35	10±0.32	25±1.66	77.93±5.48	14.33±4.06	278±26.51	2.56±0.04
WISH 32:2-4-4-8-2-5	89±	94.2±1.98	13±1.54	24.16±0.63	10±0.20	24±0.87	92.66±4.10	29.4±4.72	366±22.93	2.58±0.04

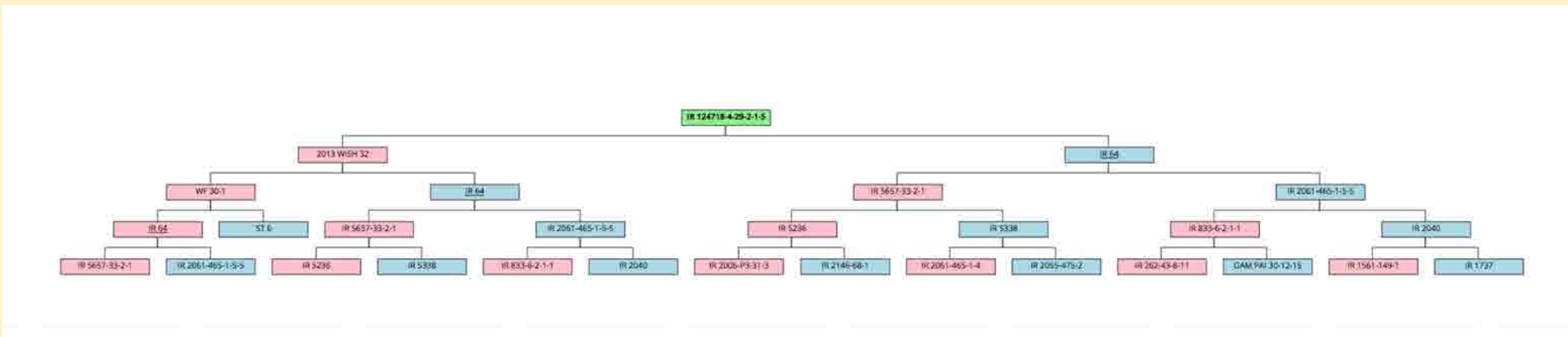
DTH= Days to 50% Heading ; PH=Plant Height; TN=Tiller Number; PL= Panicle Length; PB=Primary Branches; SB=Secondary Branches; FG= Filled Grains; UFG=Unfilled Grains; TNG= Total Number of Grains; HGW=100 grain weight; SEM= Standard Error of Mean

IR64 is an indica rice variety and has been accepted as a high-quality and high-yielding variety in many countries. ST6 on the other hand, from the stocked rice collections of Togo field in Nagoya University, is the donor for *Gn1a* and *WFP* alleles. Advanced lines of this WISH carries *Gn1a* and *WFP* alleles responsible for increase in grain number snd primary branching.

Other Information:

Generation: BC<sub>3</sub>F<sub>6</sub>  
IR Designations:

- IR 124718-4-4-8-2-5
- IR 124718-4-22-4-1-7
- IR 124718-4-22-6-1-9
- IR 124718-4-25-1-1-10





Silewah x ST12 (*Gn1a*)



### A. Agronomic Data of Advanced WISH Yield Lines

Line	DTH	PH	TN	PL	PB	SB	FG	UFG	TNG	HGW
Average Data ± SEM		Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM
Silewah	85 ±	162.2 ±0.97	9.6 ±0.51	27 ±0.69	10 ±0.45	28 ±	98.6 ±1.78	47.4 ±6.58	267 ±17.83	2.7 ±0.08
ST12	75 ±	111.6 ±3.03	11.4 ±0.51	23.76 ±0.72	20 ±1.86	68 ±7.57	187.53 ±15.71	149.06 ±59.56	779 ±36.66	2.6 ±0.05
WISH 60:3-2-1-1-1-1	83±	153±14.00	7±	28.42±0.75	10±1.00	36±1.50	114.33±12.34	115±17.67	688±16.00	2.5±0.40
WISH 60:3-2-1-1-1-3	79±	146.4±3.58	7±0.68	26.83±0.32	9±0.51	35±1.59	142.13±7.81	61.13±15.72	610±40.85	2.56±0.02
WISH 60:3-2-2-1-1-5	80±	148.1±3.73	7±0.68	25.63±0.66	10±0.32	39±1.58	126±3.76	36.86±2.87	489±12.19	2.58±0.05

DTH= Days to 50% Heading ; PH=Plant Height; TN=Tiller Number; PL= Panicle Length; PB=Primary Branches; SB=Secondary Branches; FG= Filled Grains; UFG=Unfilled Grains; TNG= Total Number of Grains; HGW=100 grain weight; SEM= Standard Error of Mean

Silewah is an Indonesian rice variety which was reported to show a high cold resistance. ST 12 on the other hand, from the Stocked rice collections of Togo field and Nagoya University, is the donor for *Gn1a* and *WFP* alleles. Advanced lines of this WISH carries *Gn1a* alleles responsible for increase in grain number.

Other Information:

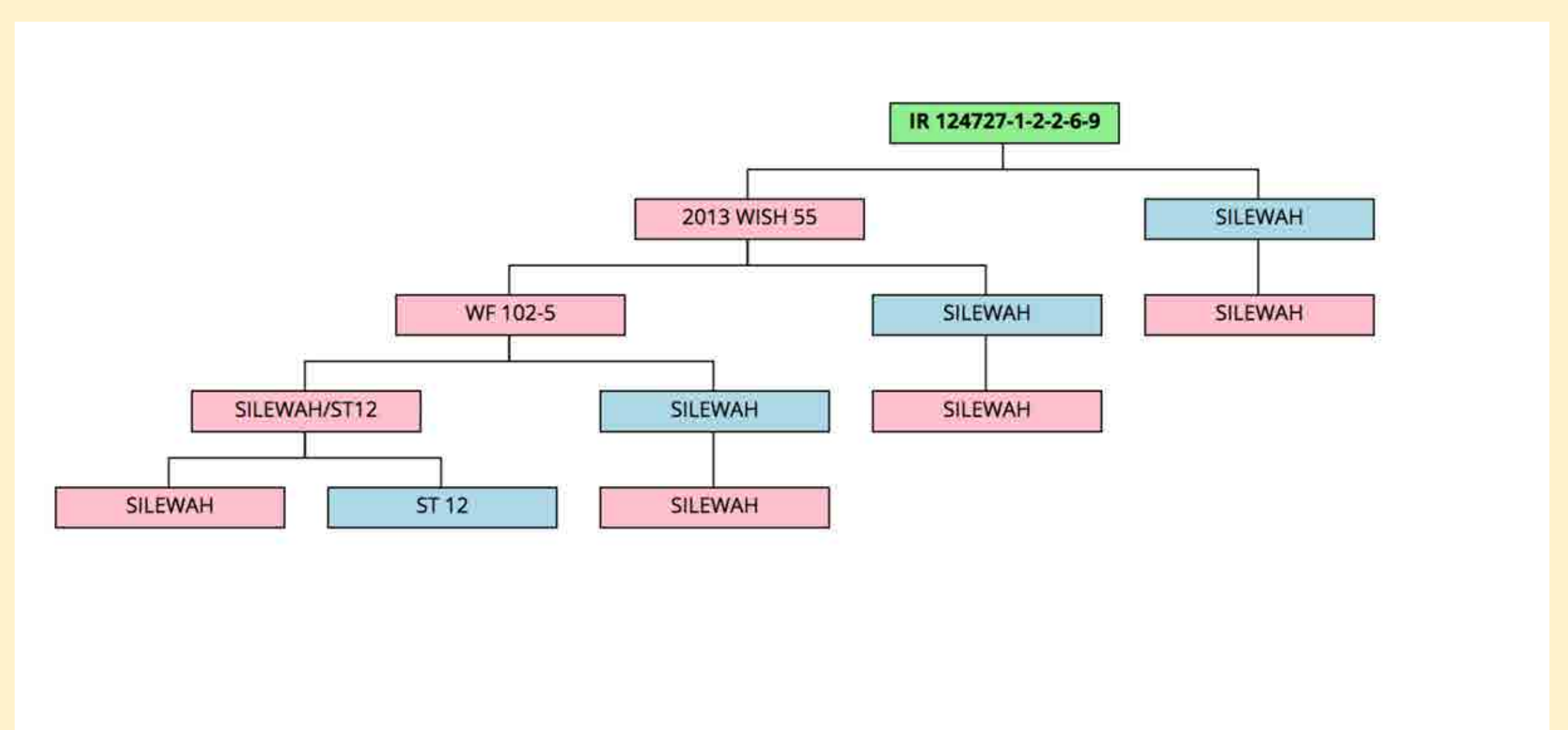
Generation:  $\text{BC}_3\text{F}_6$

## IR Designations:

IR 124729-2-1-1-1-1

IR 124729-2-1-1-1-3

IR 124729-2-1-1-1-5





Silewah x ST12 (*WFP*)



### A. Agronomic Data of Advanced WISH Yield Lines

Line	DTH	PH	TN	PL	PB	SB	FG	UFG	TNG	HGW
	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM
Silewah	85 ±	162.2 ±0.97	9.6 ±0.51	27 ±0.69	10 ±0.45	28 ±	98.6 ±1.78	47.4 ±6.58	267 ±17.83	2.7 ±0.08
ST12	75 ±	111.6 ±3.03	11.4 ±0.51	23.76 ±0.72	20 ±1.86	68 ±7.57	187.53 ±15.71	149.06 ±59.56	779 ±36.66	2.6 ±0.05
WISH 60:2-2-17-1-1-7	77±	150.1±3.07	7±1.10	27.86±0.39	19±0.74	40±2.73	85.06±8.07	107.33±11.18	577±52.24	2.96±0.25
WISH 60:2-2-3-1-1-3	78±	156.3±3.81	4.4±0.24	28.56±0.28	16±0.57	39±4.48	122.13±8.12	48.8±9.06	513±39.31	2.88±0.09
WISH 60:2-2-5-3-1-5	77±	162.2±3.61	5.2±0.49	32.06±0.75	19±0.61	44±2.32	168.93±8.96	73.8±8.81	728±13.62	2.96±0.07
WISH 60:2-3-10-1-1-9	76±	167.2±2.29	5.2±0.20	30±0.80	17±1.40	31±3.15	104.6±8.98	77.46±14.00	546±57.46	2.92±0.13
WISH 60:2-3-11-1-1-11	78±	166.9±3.18	6.6±0.51	32.16±0.66	19±0.83	45±3.60	145.5±8.77	94±11.09	718±47.90	3.02±0.09

DTH= Days to 50% Heading ; PH=Plant Height; TN=Tiller Number; PL= Panicle Length; PB=Primary Branches; SB=Secondary Branches; FG= Filled Grains; UFG=Unfilled Grains; TNG= Total Number of Grains; HGW=100 grain weight; SEM= Standard Error of Mean

Silewah is an Indonesian rice variety which was reported to show a high cold resistance. ST 12 on the other hand, from the Stocked rice collections of Togo field and Nagoya University, is the donor for *Gn1a* and *WFP* alleles. Advanced lines of this WISH carries *WFP* alleles responsible for increase in primary branches.

Other Information:

Generation:  $\text{BC}_3\text{F}_5$

## IR Designations:

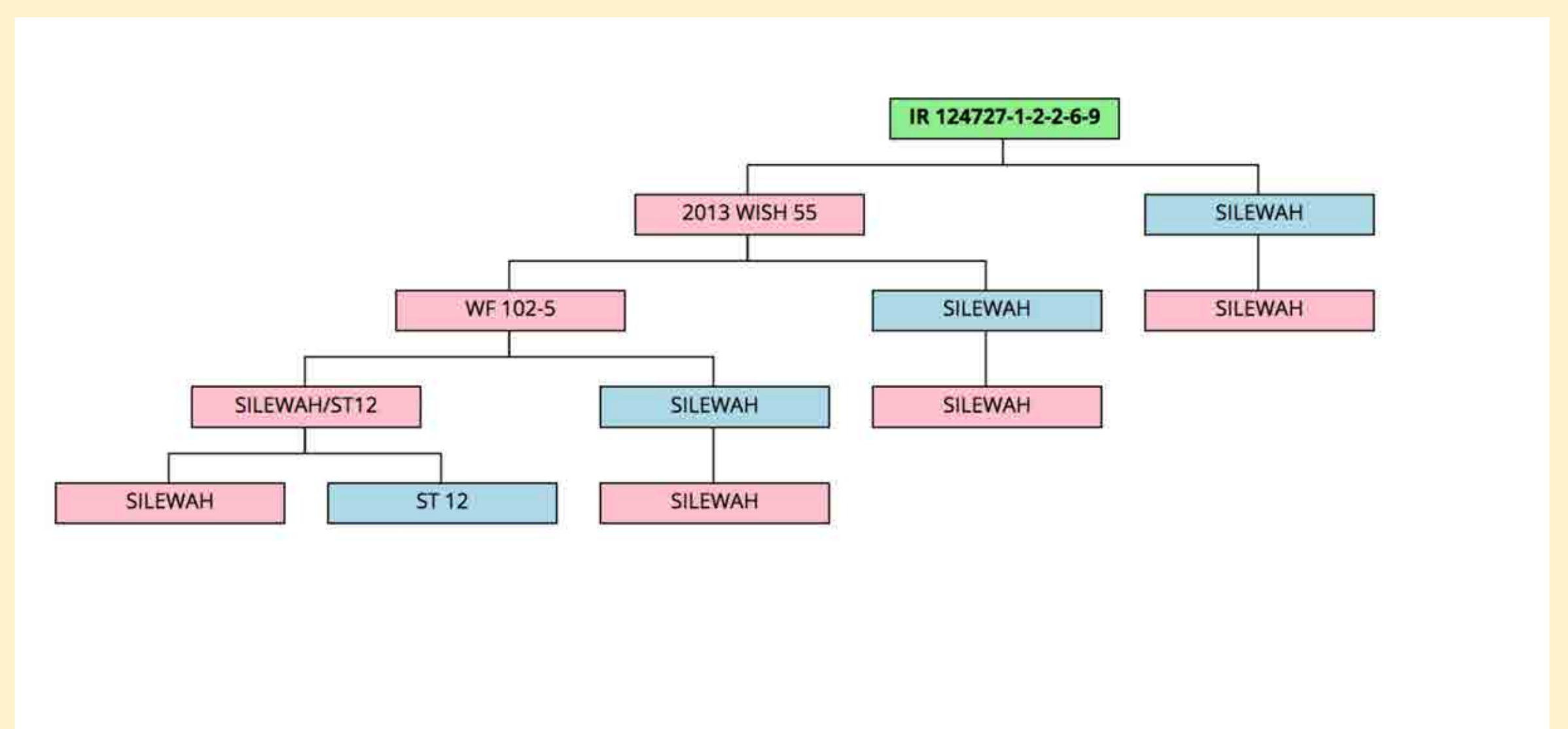
IR 124728-2-3-1-1-3

IR 124728-2-5-3-1-5

IR 124728-2-17-1-1-10

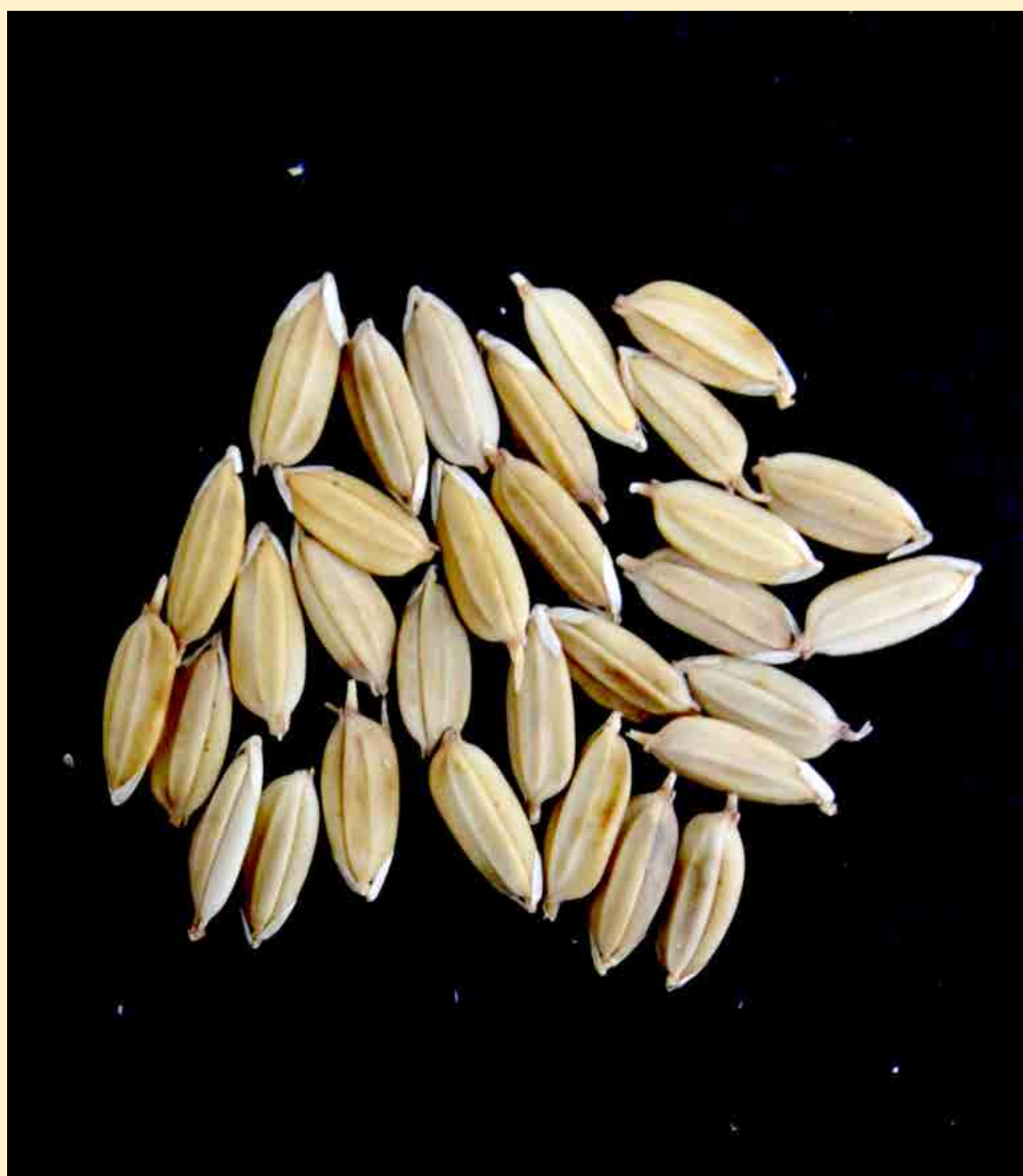
IR 124728-3-10-1-1-9

IR 124728-3-11-1-1-11





# Silewah x ST12 (*Gn1a*+*WFP*)



A. Agronomic Data of Advanced WISH Yield Lines

Line	DTH	PH	TN	PL	PB	SB	FG	UFG	TNG	HGW
	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM
Silewah	85 ±	162.2 ±0.97	9.6 ±0.51	27 ±0.69	10 ±0.45	28 ±	98.6 ±1.78	47.4 ±6.58	267 ±17.83	2.7 ±0.08
ST12	75 ±	111.6 ±3.03	11.4 ±0.51	23.76 ±0.72	20 ±1.86	68 ±7.57	187.53 ±15.71	149.06 ±59.56	779 ±36.66	2.6 ±0.05
WISH 66:2-2-2-1-1-1	80 ±	167.2 ±3.21	7.8 ±0.73	31.53 ±1.15	14 ±0.87	37 ±3.14	167.73 ±14.16	38.73 ±2.61	619 ±45.22	2.9 ±0.06
WISH 66:2-2-2-1-1-2	79 ±	173.3 ±5.31	6.8 ±0.37	30.33 ±0.98	14 ±0.66	37 ±4.27	157.79 ±11.86	57.4 ±12.62	646 ±68.25	2.8 ±0.12
WISH 66:2-2-2-1-1-5	78 ±	179.9 ±2.46	8.2 ±0.86	29.2 ±0.89	13 ±0.20	43 ±1.50	166.26 ±6.13	56.73 ±9.38	669 ±24.67	2.6 ±0.07
WISH 66:2-2-4-1-1-11	79 ±	186.7 ±3.78	7 ±0.55	29.46±0.59	14 ±0.51	40 ±3.50	180.26 ±13.01	52.53 ±12.73	698 ±73.03	2.6 ±0.05
WISH 66:2-2-4-1-1-5	80 ±	180.4 ±2.08	9 ±0.32	30.9 ±0.74	14 ±0.20	56 ±1.07	220.2 ±8.01	62.66 ±8.47	849 ±20.64	2.8 ±0.02

DTH= Days to 50% Heading ; PH=Plant Height; TN=Tiller Number; PL= Panicle Length; PB=Primary Branches; SB=Secondary Branches; FG= Filled Grains; UFG=Unfilled Grains; TNG= Total Number of Grains; HGW=100 grain weight; SEM= Standard Error of Mean

Silewah is an Indonesian rice variety which was reported to show a high cold resistance. ST 12 on the other hand, from the Stocked rice collections of Togo field and Nagoya University, is the donor for *Gn1a* and *WFP* alleles. Advanced lines of this WISH carries *Gn1a* and *WFP* alleles responsible for increase in grain number and primary branches.

## Other Information:

Generation: BC<sub>3</sub>F<sub>6</sub>

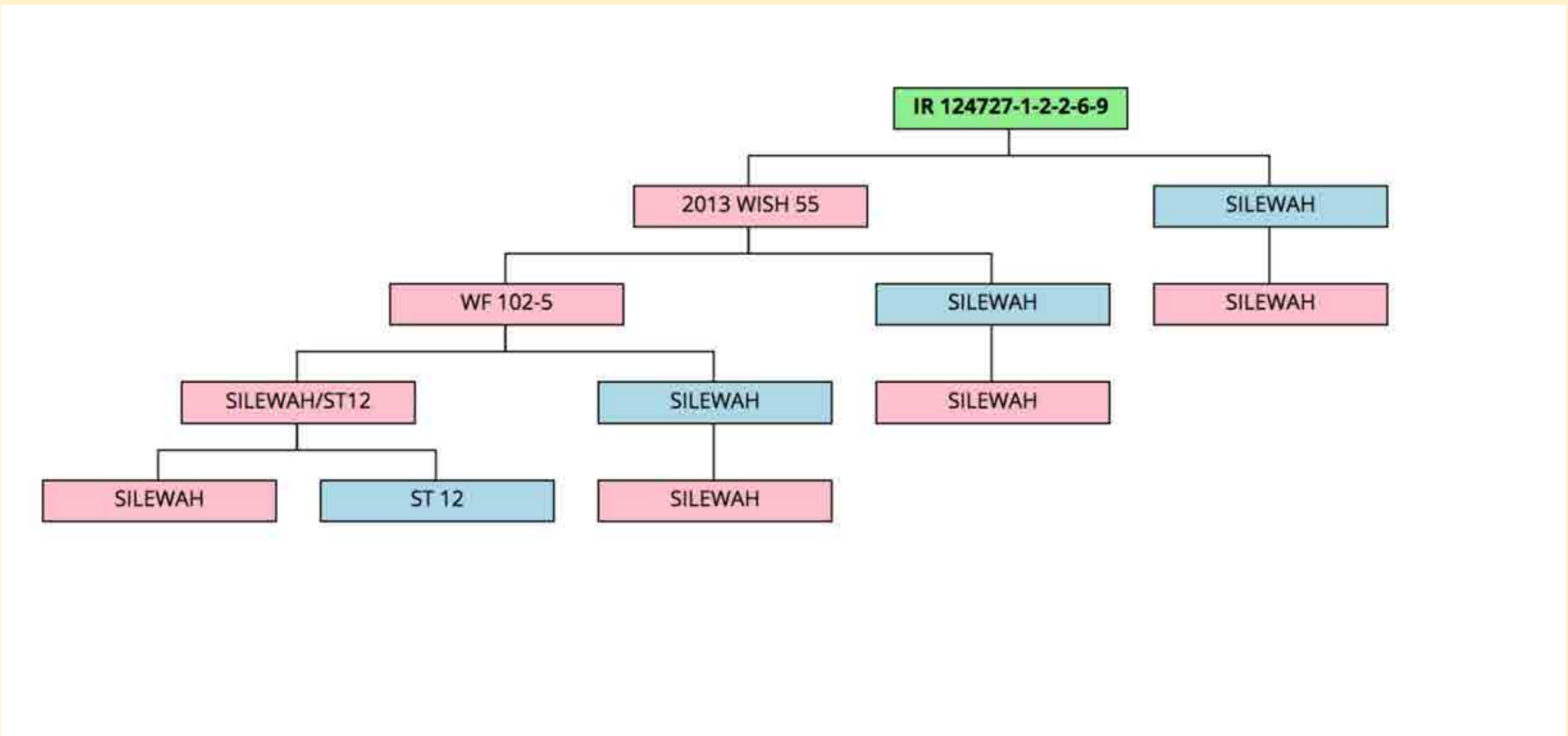
IR Designations:

IR 124727-1-2-2-6-7

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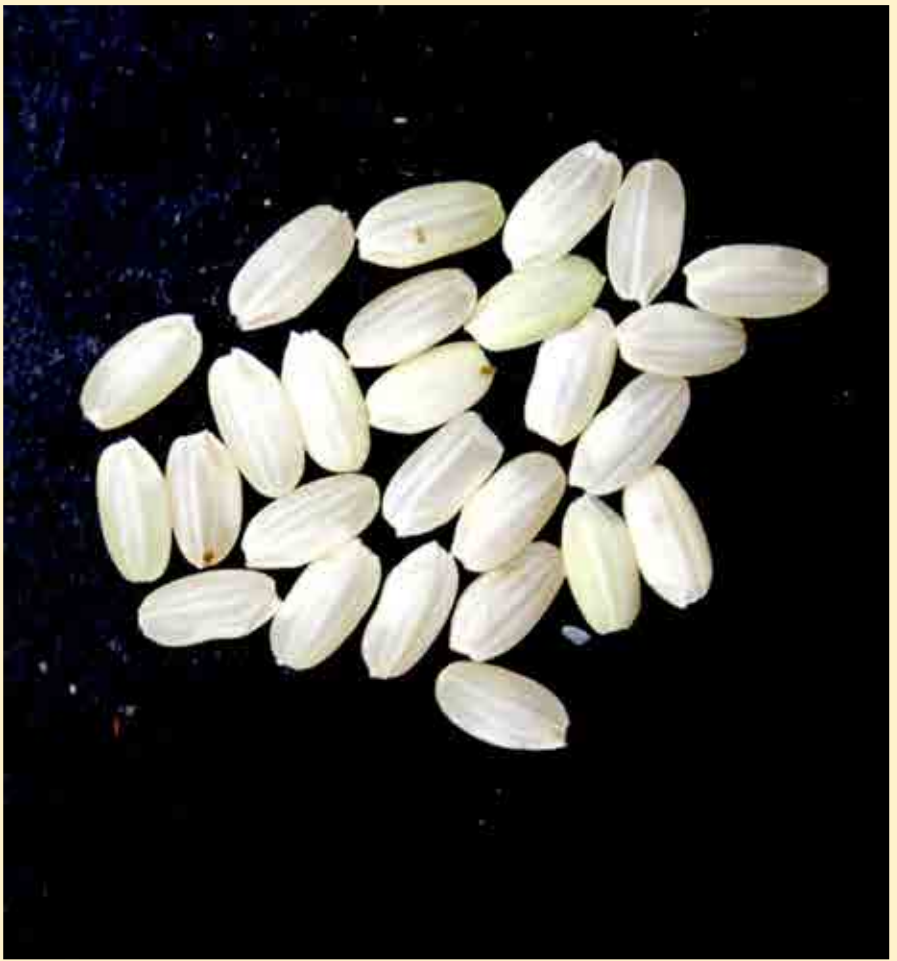
IR 124727-1-2-2-6-9

IR 124727-1-2-2-6-10





# IRAT 109 x ST12 (*Gn1a*)



A. Agronomic Data of Advanced WISH Yield Lines

Line	DTH	PH	TN	PL	PB	SB	FG	UFG	TNG	HGW
	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM
IRAT109	72±	117.5±1.99	7±0.80	22.56±0.49	13±0.51	24±0.66	117±7.99	32.8±3.14	449±24.52	2.86±0.05
ST12	75±	111.6±3.03	11±0.51	23.76±0.72	20±1.86	68±7.57	187.53±15.71	149.06±59.56	779±36.66	2.6±0.05
WISH 42:1-2-2-1-15	73±	97±2.47	6±0.20	20.86±0.21	14±0.68	35±1.47	144.66±6.18	66.2±11.57	813±53.30	3.38±0.02
WISH 42:2-1-2-1-1	71±	85.8±1.39	6±0.93	18.43±0.23	11±0.20	26±1.54	99.8±5.89	42.53±9.72	767±37.57	3.04±0.10
WISH 42:2-1-20-1-18	70±	98.6±2.62	12±0.68	19.4±0.24	12±0.58	30±1.25	104.13±11.03	51±7.57	765±21.36	2.96±0.09
WISH 42:2-1-20-2-1-9	72±	87.2±0.97	8±0.49	19.21±0.24	12±0.20	20±1.10	216.06±33.28	37.26±1.64	684±26.47	3.02±0.07
WISH 42:2-1-3-1-6-5	71±	82.67±0.88	7±0.88	17.11±0.20	10±0.33	16±1.73	270.44±5.86	23.55±3.45	803±23.59	2.96±0.09
WISH 42:2-1-4-1-1-7	70±	73±	5±	17.33±	9±	14±	279±	13.33±	892±	3.3±

DTH= Days to 50% Heading ; PH=Plant Height; TN=Tiller Number; PL= Panicle Length; PB=Primary Branches; SB=Secondary Branches; FG= Filled Grains; UFG=Unfilled Grains; TNG= Total Number of Grains; HGW=100 grain weight; SEM= Standard Error of Mean

IRAT109 is a tropical japonica rice variety which is know for its drought tolerant trait. ST 12 on the other hand, from the Stocked rice collections of Togo field and Nagoya University, is the donor for *Gn1a* and *WFP* alleles. Advanced lines of this WISH carries *Gn1a* alleles responsible for increase in grain number.

## Other Information:

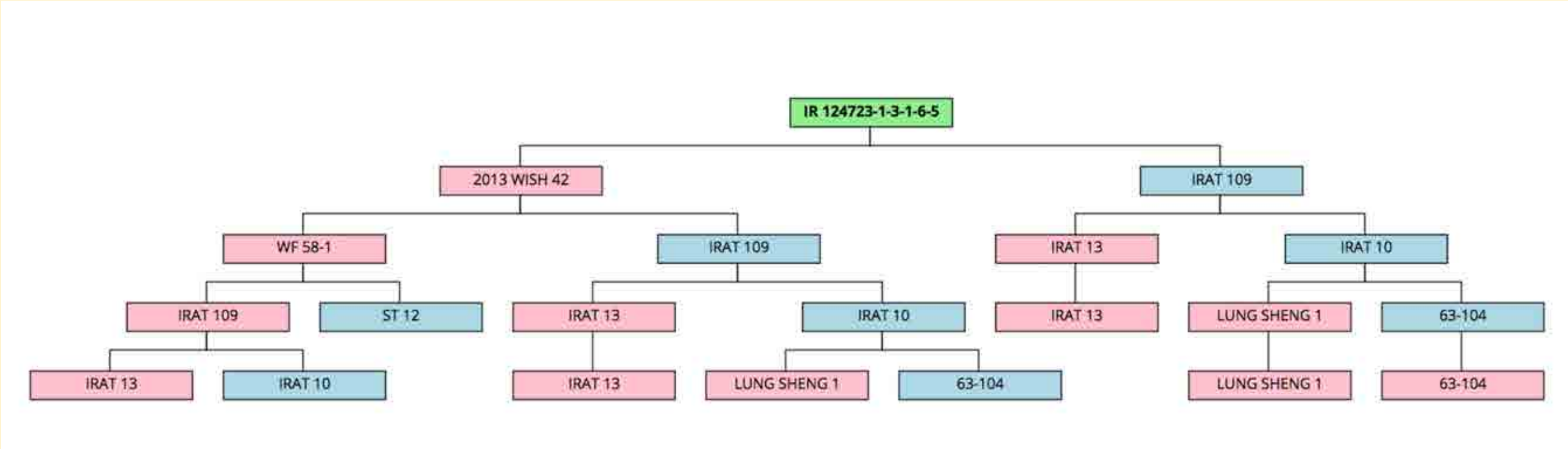
Generation: BC<sub>3</sub>F<sub>6</sub>

IR Designations:

IR 124723-1-3-1-6-5

IR 124723-1-4-1-1-7

IR 124723-1-20-2-1-9





# IRAT 109 x ST12 (*WFP*)



A. Agronomic Data of Advanced WISH Yield Lines

Line	DTH	PH	TN	PL	PB	SB	FG	UFG	TNG	HGW
	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM
IRAT109	72 ±	117.5 ± 1.99	7 ± 0.80	22.56 ± 0.49	13 ± 0.51	24 ± 0.66	117 ± 7.99	32.8 ± 3.14	449 ± 24.52	2.8 ± 0.05
ST12	75 ±	111.6 ± 3.03	11 ± 0.51	23.76 ± 0.72	20 ± 1.86	68 ± 7.57	187.53 ± 15.71	149.06 ± 59.56	779 ± 36.66	2.6 ± 0.05
WISH 42:1-2-6-1-3	73 ±	93.6 ± 1.63	4 ± 0.37	20 ± 0.28	18 ± 0.84	28 ± 2.63	103.83 ± 4.21	67.4 ± 4.27	581 ± 62.79	3.5 ± 0.06
WISH 42:1-2-7-1-1-2	70 ±	102.75 ± 2.46	4 ± 0.71	21.45 ± 0.36	18 ± 0.41	37 ± 2.39	132.16 ± 11.08	76.5 ± 10.04	626 ± 35.56	3.5 ± 0.05

DTH= Days to 50% Heading ; PH=Plant Height; TN=Tiller Number; PL= Panicle Length; PB=Primary Branches; SB=Secondary Branches; FG= Filled Grains; UFG=Unfilled Grains; TNG= Total Number of Grains; HGW=100 grain weight; SEM= Standard Error of Mean

IRAT109 is a tropical japonica rice variety which is know for its drought tolerant trait. ST 12 on the other hand, from the Stocked rice collections of Togo field and Nagoya University, is the donor for *Gn1a* and *WFP* alleles. Advanced lines of this WISH carries *WFP* alleles responsible for increase in primary branches.

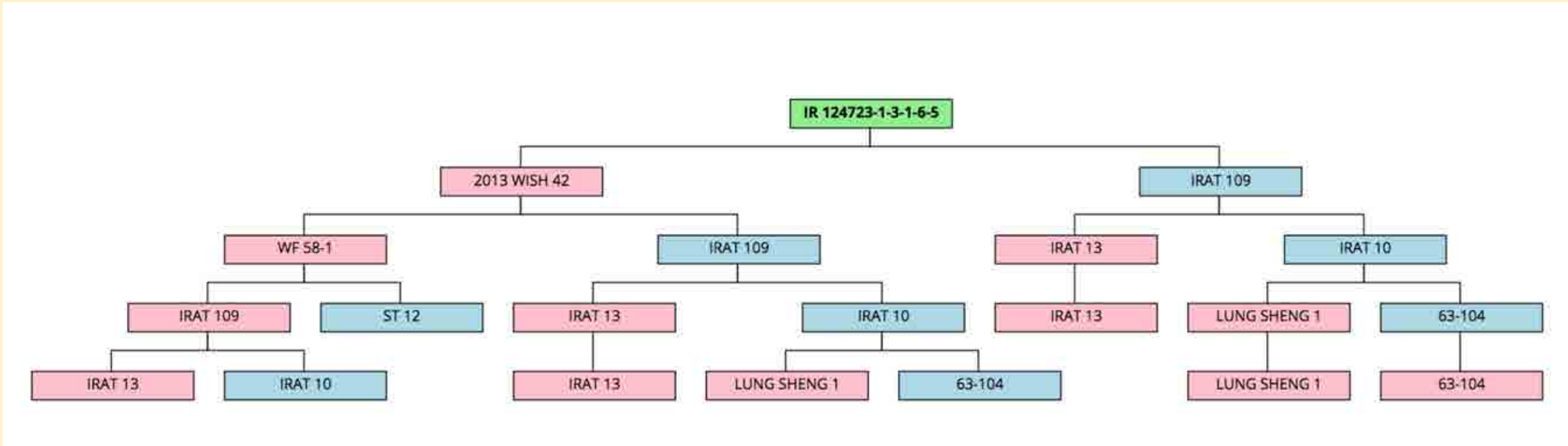
## Other Information:

Generation: BC<sub>3</sub>F<sub>6</sub>

IR Designations:

IR 124722-2-7-1-1-2

IR 124722-2-6-1-3





# IRAT 109 x ST12 (*Gn1a*+*WFP*)



A. Agronomic Data of Advanced WISH Yield Lines

Line	DTH	PH	TN	PL	PB	SB	FG	UFG	TNG	HGW
	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM
IRAT109	72 ±	117.5 ±1.99	7 ±0.80	22.56 ±0.49	13 ±0.51	24 ±0.66	117 ±7.99	32.8 ±3.14	450 ±24.52	2.86 ±0.05
ST12	75 ±	111.6 ±3.03	11 ±0.51	23.76 ±0.72	20 ±1.86	68 ±7.57	187.53 ±15.71	149.06 ±59.56	779 ±36.66	2.6 ±0.05
WISH 42:2-1-13-10-4-3	69 ±	92.6 ±4.41	6 ±0.81	18.2 ±0.14	16 ±0.95	40 ±3.17	120.8 ±6.79	114.66 ±8.09	706 ±37.58	2.88 ±0.04
WISH 42:2-1-18-10-8-1	68 ±	95.2 ±1.39	4 ±0.45	18.9 ±0.16	18 ±0.51	43 ±1.63	130.96 ±8.78	126.1 ±11.72	715 ±69.31	2.88 ±0.07
WISH 42:2-1-19-10-1-4	74 ±	99.6 ±2.54	4 ±0.55	18.56 ±0.37	14 ±0.32	47 ±3.83	105.73 ±7.42	117.8 ±10.88	671 ±40.87	2.76 ±0.05
WISH 42:2-1-9-10-1-9	73 ±	100.2 ±2.58	6 ±0.24	18.5 ±0.14	15 ±0.51	40 ±2.06	123.26 ±7.26	109.2 ±9.68	679 ±32.79	2.88 ±0.06
WISH 42:2-5-10-1-1-2	72 ±	89.4 ±2.77	5 ±1.03	19.1 ±0.23	15 ±0.40	38 ±3.12	108.66 ±7.91	119.76 ± 6.96	589 ±47.50	2.92 ±0.07
WISH 42:2-5-10-1-1-3	70 ±	95.5 ±4.73	5 ±1.03	18.7 ±0.36	15 ±1.03	30 ±2.17	115.99 ±17.41	110.5 ±15.62	680 ±42.72	2.875 ±0.09
WISH 42:2-5-5-1-1-3	69 ±	96.6 ±3.75	5 ±0.80	18.5 ±0.34	21 ±0.51	50 ±2.14	143.86 ±6.58	145.56 ± 7.62	842 ±42.72	2.74 ±0.06

DTH= Days to 50% Heading ; PH=Plant Height; TN=Tiller Number; PL= Panicle Length; PB=Primary Branches; SB=Secondary Branches; FG= Filled Grains; UFG=Unfilled Grains; TNG= Total Number of Grains; HGW=100 grain weight; SEM= Standard Error of Mean

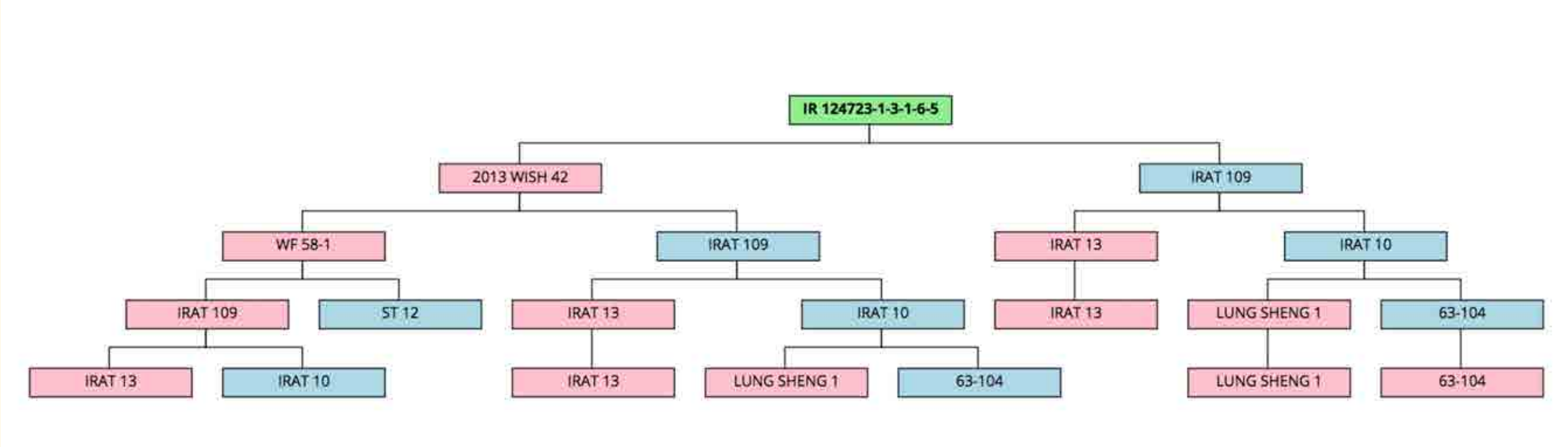
IRAT109 is a tropical japonica rice variety which is know for its drought tolerant trait. ST 12 on the other hand, from the Stocked rice collections of Togo field and Nagoya University, is the donor for *Gn1a* and *WFP* alleles. Advanced lines of this WISH carries *Gn1a* and *WFP* alleles responsible for increase in grain number and primary branches.

Other Information:

Generation: BC<sub>3</sub>F<sub>6</sub>

IR Designations:

- IR 124723-5-5-1-1-3
- IR 124723-5-10-1-1-2
- IR 124723-1-2-1-1
- IR 124723-5-10-1-1-3
- IR 124723-1-9-10-1-9
- IR 124723-1-13-10-4-3
- IR 124723-1-19-10-1-5
- IR 124723-1-18-10-8-1





# Kinandang Patong x ST12 (*Gn1a*)



A. Agronomic Data of Advanced WISH Yield Lines

Line	DTH	PH	TN	PL	PB	SB	FG	UFG	TNG	HGW
	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM
Kinandang patong	80±	108.1±1.62	8±0.93	23.36±0.39	15±0.60	38±0.73	210±12.98	69±10.70	737±35.34	3.28±0.07
ST12	75±	111.6±3.03	11±0.51	23.76±0.72	20±1.86	68±7.57	187.53±15.71	149.06±59.56	779±36.66	2.6±0.05
WISH 77:4-2-6-1-1-1-1	78±	158.4±4.50	6±0.66	22.96±0.94	15±0.89	49±4.08	215.46±19.37	62.13±7.59	832±69.56	2.64±0.07
WISH 77:4-2-6-1-1-11-1	79±	144.4±2.72	6±0.37	16.7±0.39	14±0.97	43±3.73	257.2±20.03	36.73±8.55	882±77.83	2.4±0.03
WISH 77:4-2-6-2-1-1-1	80±	154.66±0.93	8±0.88	18.16±0.44	16±0.33	75±2.33	249.78±18.36	111.66±13.86	1084±48.94	2.13±0.15
WISH 77:4-2-6-4-1-7-8	81±	143.1±2.35	8±0.63	17.23±0.35	14±0.49	40±1.24	230.59±8.80	64.73±9.85	886±26.59	2.18±0.04
WISH 77:4-2-7-1-1-1-1	80±	142±2.66	6±0.87	16.36±0.71	12±0.58	34±5.16	156.66±17.57	36±11.82	578±75.21	2.02±0.07

DTH= Days to 50% Heading ; PH=Plant Height; TN=Tiller Number; PL= Panicle Length; PB=Primary Branches; SB=Secondary Branches; FG= Filled Grains; UFG=Unfilled Grains; TNG= Total Number of Grains; HGW=100 grain weight; SEM= Standard Error of Mean

Kinandang Patong is a drought tolerant tropical japonica rice variety from the Philippines. Its main characteristic is that the roots grow deep and straight downwards, delving into parched soil for water. ST 12 on the other hand, from the Stocked rice collections of Togo field and Nagoya University, is the donor for *Gn1a* and *WFP* alleles. Advanced lines of this WISH carries *Gn1a* alleles responsible for increase in grain number.

## Other Information:

Generation: BC<sub>3</sub>F<sub>7</sub>

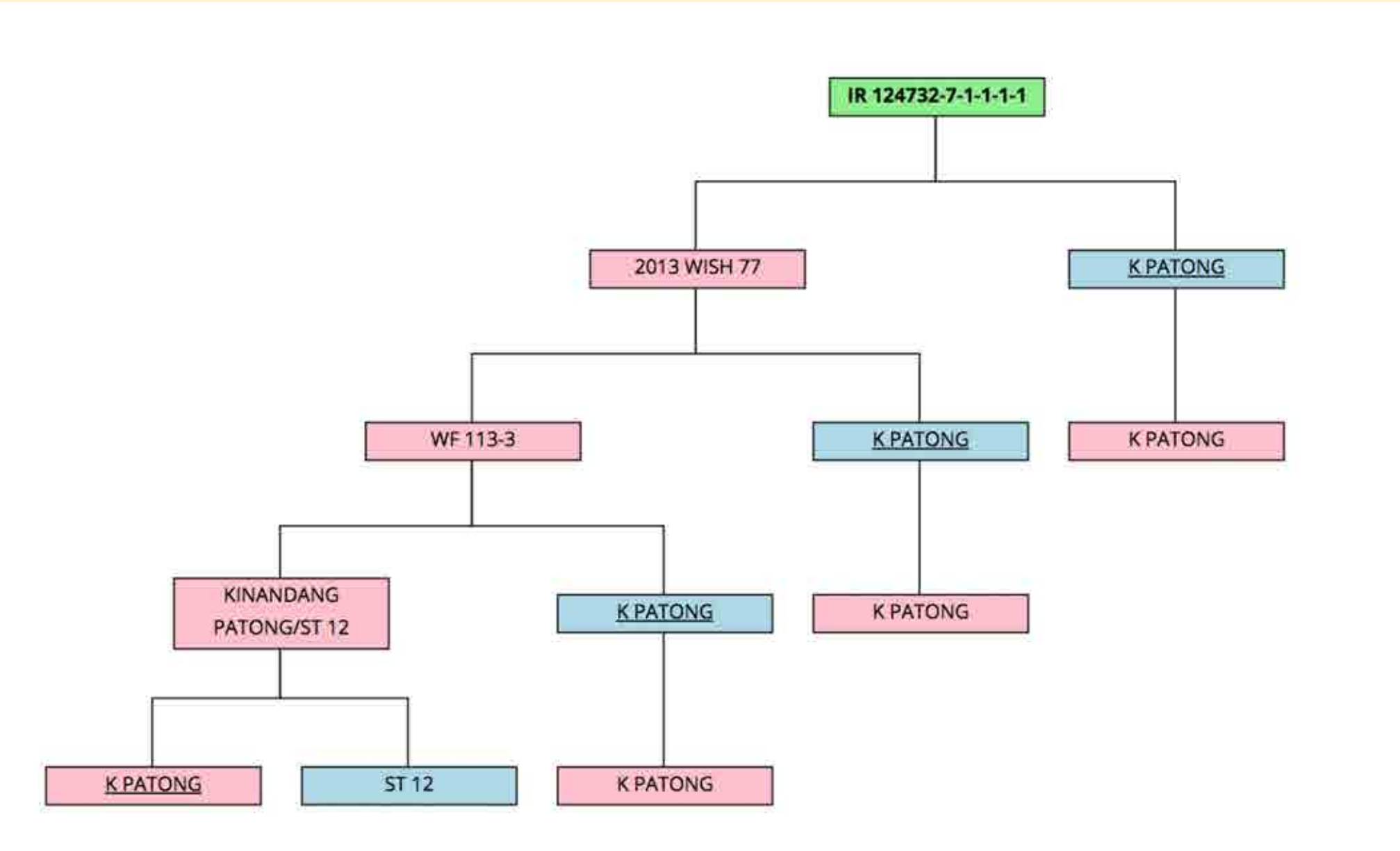
IR Designations:

IR 124732-6-3-1-2-6      IR 124732-6-1-1-1-1

IR 124732-6-4-1-7-8      IR 124732-6-2-1-1-1

IR 124732-6-1-1-11-1

IR 124732-7-1-1-1-1





# Kinandang Patong x ST12 (*WFP*)



A. Agronomic Data of Advanced WISH Yield Lines

Line	DTH	PH	TN	PL	PB	SB	FG	UFG	TNG	HGW
	Average Data $\pm$ SEM	Average Data $\pm$ SEM	Average Data $\pm$ SEM	Average Data $\pm$ SEM	Average Data $\pm$ SEM	Average Data $\pm$ SEM	Average Data $\pm$ SEM	Average Data $\pm$ SEM	Average Data $\pm$ SEM	Average Data $\pm$ SEM
Kinandang patong	80 $\pm$	108.1 $\pm$ 1.62	8 $\pm$ 0.93	23.36 $\pm$ 0.39	15 $\pm$ 0.60	38 $\pm$ 0.73	210 $\pm$ 12.98	69 $\pm$ 10.70	737 $\pm$ 35.34	3.28 $\pm$ 0.07
ST12	75 $\pm$	111.6 $\pm$ 3.03	11 $\pm$ 0.51	23.76 $\pm$ 0.72	20 $\pm$ 1.86	68 $\pm$ 7.57	187.53 $\pm$ 15.71	149.06 $\pm$ 59.56	779 $\pm$ 36.66	2.6 $\pm$ 0.05
WISH 72:1-1-7-10-1-6-1	82 $\pm$	120.5 $\pm$ 1.26	4.2 $\pm$ 0.20	19.86 $\pm$ 0.40	20 $\pm$ 0.49	87 $\pm$ 5.33	322.53 $\pm$ 26.16	156.66 $\pm$ 16.78	1438 $\pm$ 86.23	2.12 $\pm$ 0.05
WISH 72:1-1-7-14-1-6-1	80 $\pm$	121.4 $\pm$ 0.76	5.8 $\pm$ 0.20	18.75 $\pm$ 0.30	16 $\pm$ 0.81	70 $\pm$ 3.44	220 $\pm$ 21.04	141.76 $\pm$ 9.65	995 $\pm$ 30.57	2.2 $\pm$ 0.03
WISH 72:1-1-7-16-1-4-1	79 $\pm$	134.2 $\pm$ 4.09	8 $\pm$ 0.45	18.1 $\pm$ 0.49	13 $\pm$ 0.58	62 $\pm$ 4.66	264.13 $\pm$ 20.55	37.33 $\pm$ 4.19	904 $\pm$ 70.38	2.26 $\pm$ 0.04
WISH 72:1-1-7-2-7-3-2	78 $\pm$	132.3 $\pm$ 16.60	7 $\pm$ 1.53	19.78 $\pm$ 0.46	20 $\pm$ 1.00	95 $\pm$ 2.91	433.66 $\pm$ 35.29	98.66 $\pm$ 16.26	1597 $\pm$ 65.45	2.13 $\pm$ 0.12
WISH 72:1-1-7-4-2-1-4	80 $\pm$	127.3 $\pm$ 1.72	6.6 $\pm$ 0.68	19.9 $\pm$ 0.45	20 $\pm$ 1.21	85 $\pm$ 7.86	377.4 $\pm$ 40.47	73.47 $\pm$ 15.77	1353 $\pm$ 151.20	2.3 $\pm$ 0.05

DTH= Days to 50% Heading ; PH=Plant Height; TN=Tiller Number; PL= Panicle Length; PB=Primary Branches; SB=Secondary Branches; FG= Filled Grains; UFG=Unfilled Grains; TNG= Total Number of Grains; HGW=100 grain weight; SEM= Standard Error of Mean

Kinandang Patong is a drought tolerant tropical japonica rice variety from the Philippines. Its main characteristic is that the roots grow deep and straight downwards, delving into parched soil for water. ST 12 on the other hand, from the Stocked rice collections of Togo field and Nagoya University, is the donor for *Gn1a* and *WFP* alleles. Advanced lines of this WISH carries *WFP* alleles responsible for increase in primary branches.

Other Information:

**Generation:** BC<sub>3</sub>F<sub>7</sub>

**IR Designations:**

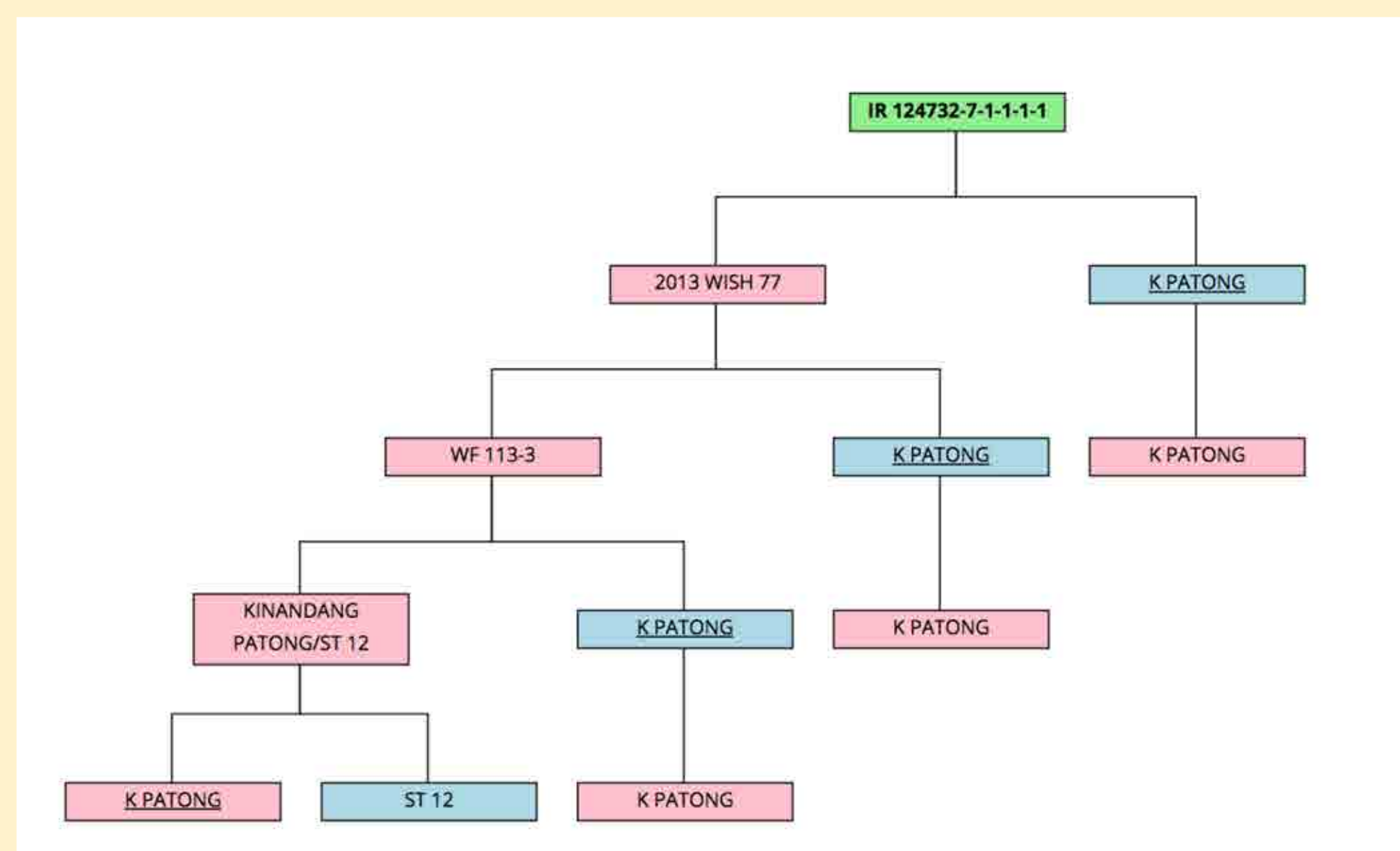
IR 124731-7-2-7-3-2

IR 124731-7-4-2-1-4

IR 124731-7-10-1-6-1

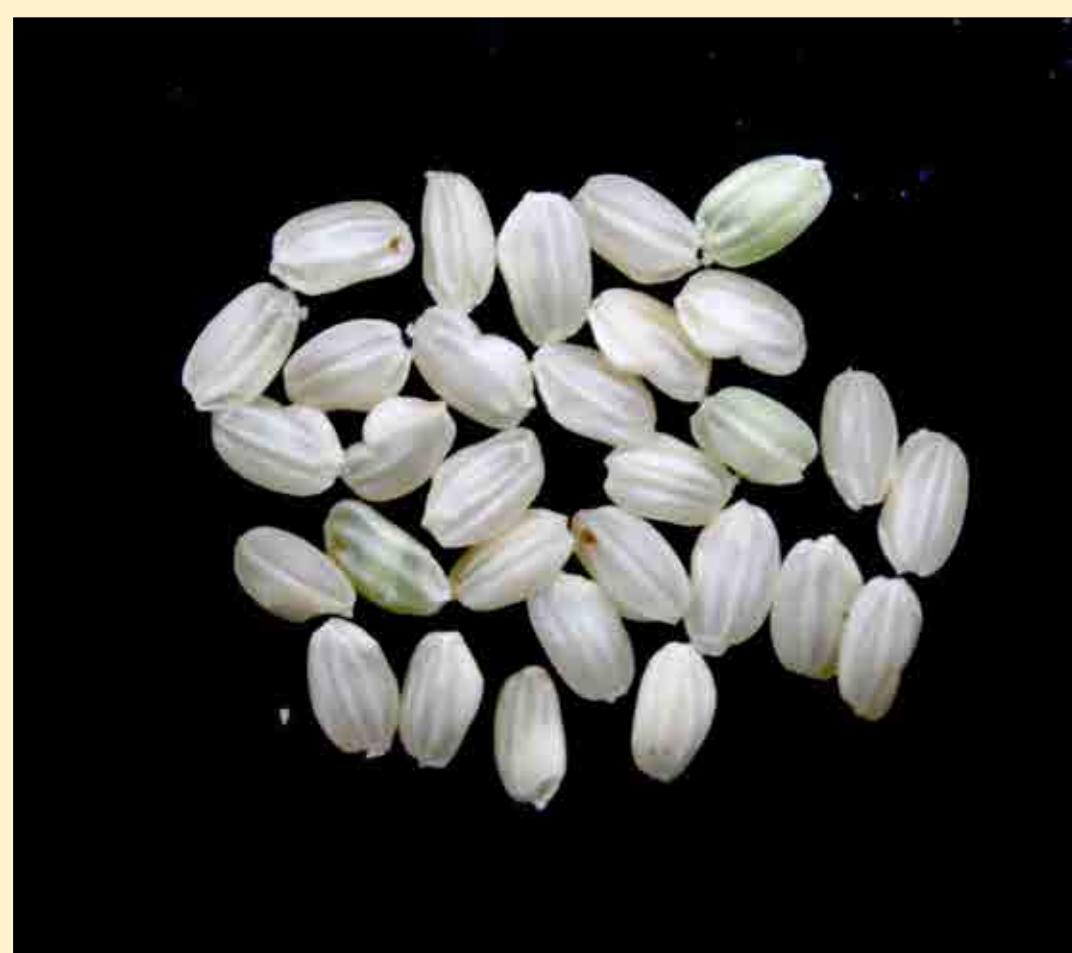
IR 124731-7-14-1-6-1

IR 124731-7-16-1-4-1





# Kinandang Patong x ST6 (*Gn1a*)



A. Agronomic Data of Advanced WISH Yield Lines

Line	DTH	PH	TN	PL	PB	SB	FG	UFG	TNG	HGW
	Average Data $\pm$ SEM	Average Data $\pm$ SEM	Average Data $\pm$ SEM	Average Data $\pm$ SEM	Average Data $\pm$ SEM	Average Data $\pm$ SEM	Average Data $\pm$ SEM	Average Data $\pm$ SEM	Average Data $\pm$ SEM	Average Data $\pm$ SEM
Kinandang patong	80 $\pm$	108.1 $\pm$ 1.62	8 $\pm$ 0.93	23.36 $\pm$ 0.39	15 $\pm$ 0.60	38 $\pm$ 0.73	210 $\pm$ 12.98	69 $\pm$ 10.70	737 $\pm$ 35.34	3.28 $\pm$ 0.07
ST6	83 $\pm$	119.3 $\pm$ 1.50	11 $\pm$ 0.73	26.06 $\pm$ 0.42	26 $\pm$ 0.45	58 $\pm$ 4.72	200.2 $\pm$ 15.97	82.93 $\pm$ 12.76	890 $\pm$ 28.82	2.62 $\pm$ 0.04
WISH 82:5-1-4-10-1-1	79 $\pm$	145.1 $\pm$ 1.86	7 $\pm$ 0.51	19.23 $\pm$ 0.43	16 $\pm$ 0.20	62 $\pm$ 2.11	235.66 $\pm$ 18.40	71.46 $\pm$ 7.75	921 $\pm$ 53.20	2.44 $\pm$ 0.04
WISH 82:5-1-4-8-1-4-2	79 $\pm$	148.7 $\pm$ 3.51	4 $\pm$ 0.40	19.3 $\pm$ 0.49	14 $\pm$ 0.58	57 $\pm$ 2.34	193.06 $\pm$ 21.26	75.4 $\pm$ 13.60	805 $\pm$ 78.21	2.44 $\pm$ 0.08
WISH 82:5-1-4-8-2-7-4	80 $\pm$	143.7 $\pm$ 4.67	6 $\pm$ 0.24	19.59 $\pm$ 0.36	14 $\pm$ 0.75	55 $\pm$ 2.84	224.59 $\pm$ 16.26	77.8 $\pm$ 2.82	907 $\pm$ 33.80	2.46 $\pm$ 0.09
WISH 82:5-1-4-9-1-9	81 $\pm$	147 $\pm$ 2.27	6 $\pm$ 0.49	21.1 $\pm$ 0.47	13 $\pm$ 0.20	50 $\pm$ 1.66	195.46 $\pm$ 6.79	53.66 $\pm$ 6.69	747 $\pm$ 33.80	2.45 $\pm$ 0.04
WISH 82:5-1-4-9-2-2	80 $\pm$	149.8 $\pm$ 2.66	7 $\pm$ 0.32	21.66 $\pm$ 0.27	14 $\pm$ 0.40	50 $\pm$ 2.99	232.13 $\pm$ 9.75	36.4 $\pm$ 9.07	806 $\pm$ 45.61	2.46 $\pm$ 0.07

DTH= Days to 50% Heading ; PH=Plant Height; TN=Tiller Number; PL= Panicle Length; PB=Primary Branches; SB=Secondary Branches; FG= Filled Grains; UFG=Unfilled Grains; TNG= Total Number of Grains; HGW=100 grain weight; SEM= Standard Error of Mean

Kinandang Patong is a drought tolerant tropical japonica rice variety from the Philippines. Its main characteristic is that the roots grow deep and straight downwards, delving into parched soil for water. ST 6 on the other hand, from the Stocked rice collections of Togo field and Nagoya University, is the donor for *Gn1a* and *WFP* alleles. Advanced lines of this WISH carries *Gn1a* alleles responsible for increase in grain number.

Other Information:

**Generation:** BC<sub>3</sub>F<sub>7</sub>

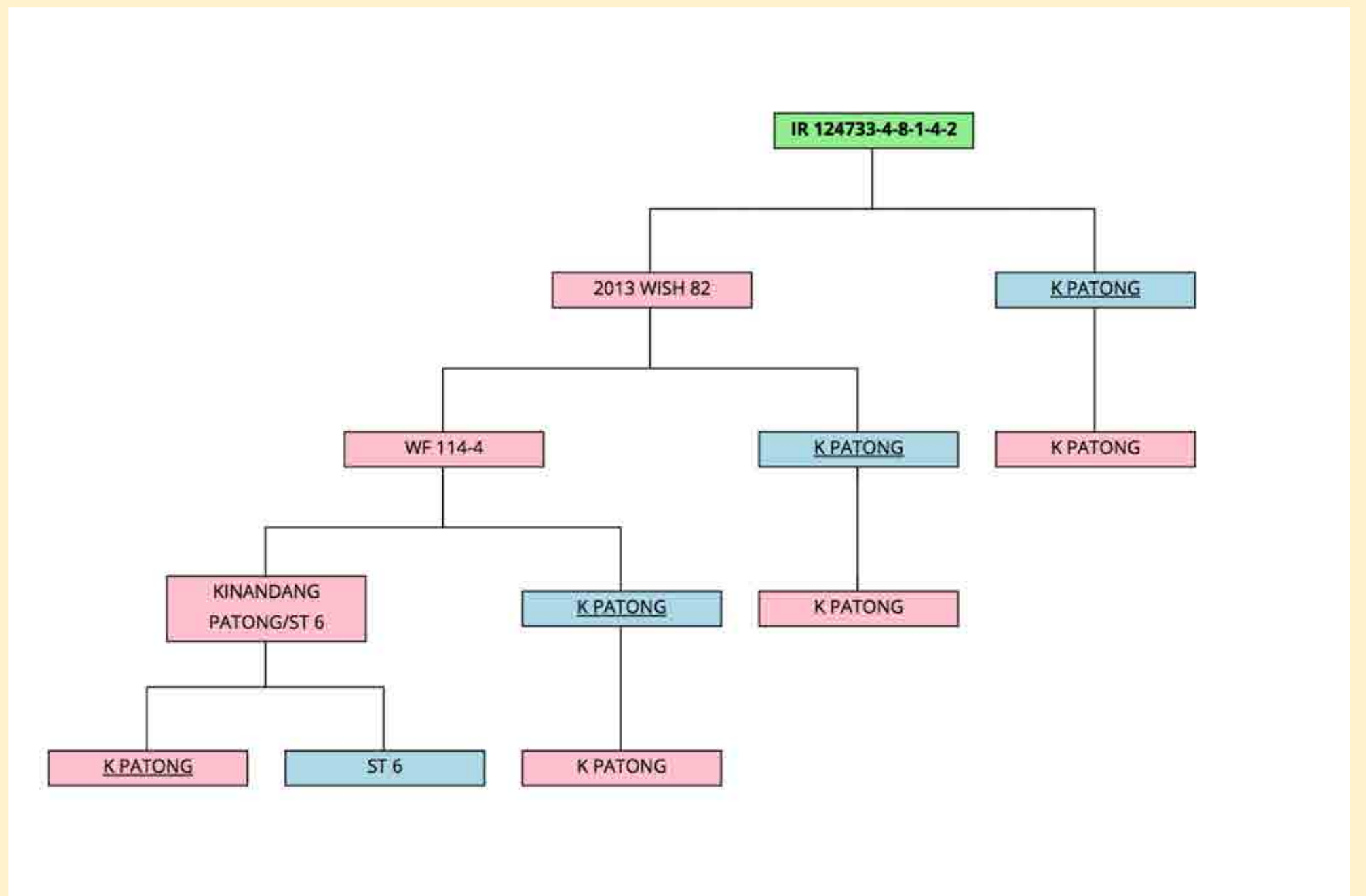
**IR Designations:**

IR 124733-4-8-1-4-2

IR 124733-4-8-2-7-4

IR 124733-4-9-1-9-1

IR 124733-4-9-2-2





## Kinandang Patong x ST6 (*WFP*)



### A. Agronomic Data of Advanced WISH Yield Lines

Line	DTH	PH	TN	PL	PB	SB	FG	UFG	TNG	HGW
	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM
Kinandang patong	80 ±	108.1 ±1.62	8 ±0.93	23.36 ±0.39	15 ±0.60	38 ±0.73	210 ±12.98	69 ±10.70	737 ±35.34	3.28 ±0.07
ST6	83 ±	119.3 ±1.50	10 ±0.73	26.06 ±0.42	26 ±0.45	58 ±4.72	200.2 ±15.97	82.93 ±12.76	891 ±28.82	2.62 ±0.04
WISH 88:1-3-5-3-1-8-3	80±	98.8±1.59	8±0.58	19.09±0.14	21±0.98	62±3.35	262.66±11.80	60.6±6.97	970±46.32	1.92±0.02
WISH 88:1-3-5-3-2-9-4	81±	96.9±1.16	7±0.49	20.29±0.53	23±1.03	62±4.15	276.6±18.29	72.16±6.25	901±86.52	2.08±0.09
WISH 88:1-3-5-3-4-6-5	79±	98.2±1.49	7±1.16	18.83±0.62	21±1.20	74±5.59	281.39±40.18	76.13±11.60	1073±154.39	2.06±0.04
WISH 88:1-3-5-4-1-1-2	79±	96.7±1.15	9±1.16	18.83±0.64	23±1.83	71±3.96	241.4±12.28	90.8±10.58	997±48.94	1.98±0.07

DTH= Days to 50% Heading ; PH=Plant Height; TN=Tiller Number; PL= Panicle Length; PB=Primary Branches; SB=Secondary Branches; FG= Filled Grains; UFG=Unfilled Grains; TNG= Total Number of Grains; HGW=100 grain weight; SEM= Standard Error of Mean

Kinandang Patong is a drought tolerant tropical japonica rice variety from the Philippines. Its main characteristic is that the roots grow deep and straight downwards, delving into parched soil for water. ST 6 on the other hand, from the Stocked rice collections of Togo field and Nagoya University, is the donor for *Gn1a* and *WFP* alleles. Advanced lines of this WISH carries *WFP* alleles responsible for increase in primary branches.

Other Information:

Generation:  $\text{BC}_3\text{F}_7$

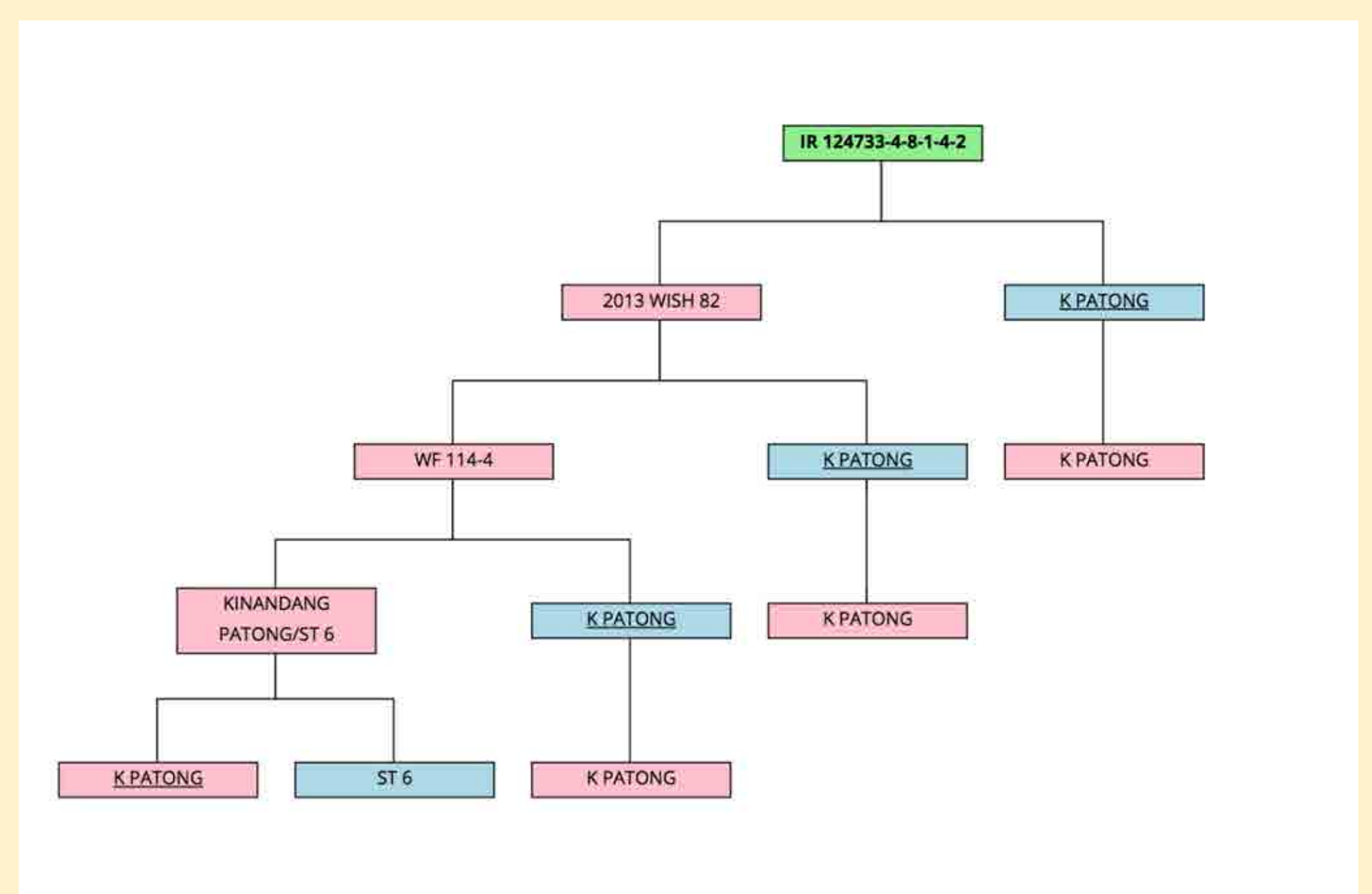
## IR Designations:

IR 124734-5-3-1-8-5

IR 124734-5-3-4-6-5

IR 124734-5-3-2-9-4

IR 124734-5-4-1-1-2





# Kinandang Patong x ST6 (*Gn1a*+*WFP*)



A. Agronomic Data of Advanced WISH Yield Lines

Line	DTH	PH	TN	PL	PB	SB	FG	UFG	TNG	HGW
	Average Data $\pm$ SEM	Average Data $\pm$ SEM	Average Data $\pm$ SEM	Average Data $\pm$ SEM	Average Data $\pm$ SEM	Average Data $\pm$ SEM	Average Data $\pm$ SEM	Average Data $\pm$ SEM	Average Data $\pm$ SEM	Average Data $\pm$ SEM
Kinandang patong	80 $\pm$	108.1 $\pm$ 1.62	8 $\pm$ 0.93	23.36 $\pm$ 0.39	15 $\pm$ 0.60	38 $\pm$ 0.73	210 $\pm$ 12.98	69 $\pm$ 10.70	737 $\pm$ 35.34	3.28 $\pm$ 0.07
ST6	83 $\pm$	119.3 $\pm$ 1.50	10 $\pm$ 0.73	26.06 $\pm$ 0.42	26 $\pm$ 0.45	58 $\pm$ 4.72	200.2 $\pm$ 15.97	82.93 $\pm$ 12.76	891 $\pm$ 28.82	2.62 $\pm$ 0.04
WISH 96:1-1-4-1-10-1-3	77 $\pm$	171.3 $\pm$ 3.84	10 $\pm$ 0.49	29 $\pm$ 0.55	17 $\pm$ 0.51	52 $\pm$ 2.93	184.39 $\pm$ 13.00	77.06 $\pm$ 13.04	784 $\pm$ 54.17	2.96 $\pm$ 0.10
WISH 96:1-1-4-14-10-2	82 $\pm$	184.9 $\pm$ 2.55	10 $\pm$ 0.55	31 $\pm$ 0.32	17 $\pm$ 0.40	49 $\pm$ 2.48	182.06 $\pm$ 14.92	94.53 $\pm$ 8.55	829 $\pm$ 27.21	2.94 $\pm$ 0.02
WISH 96:1-1-4-2-9-1-1	82 $\pm$	172.66 $\pm$ 2.59	11 $\pm$ 2.52	30 $\pm$ 0.58	15 $\pm$ 0.33	41 $\pm$ 5.69	186.67 $\pm$ 13.46	53.67 $\pm$ 11.13	721 $\pm$ 37.58	3.1 $\pm$ 0.10
WISH 96:1-1-4-6-10-4-5	80 $\pm$	165.3 $\pm$ 5.14	6 $\pm$ 0.73	28.2 $\pm$ 0.58	16 $\pm$ 0.51	42 $\pm$ 1.17	131.87 $\pm$ 5.56	94.4 $\pm$ 5.83	680 $\pm$ 24.31	3.08 $\pm$ 0.20

DTH= Days to 50% Heading ; PH=Plant Height; TN=Tiller Number; PL= Panicle Length; PB=Primary Branches; SB=Secondary Branches; FG= Filled Grains; UFG=Unfilled Grains; TNG= Total Number of Grains; HGW=100 grain weight; SEM= Standard Error of Mean

Kinandang Patong is a drought tolerant tropical japonica rice variety from the Philippines. Its main characteristic is that the roots grow deep and straight downwards, delving into parched soil for water. ST 6 on the other hand, from the Stocked rice collections of Togo field and Nagoya University, is the donor for *Gn1a* and *WFP* alleles. Advanced lines of this WISH carries *Gn1a* and *WFP* alleles responsible for increase in grain number and primary branches.

## Other Information:

**Generation:** BC<sub>3</sub>F<sub>7</sub>

**IR Designations:**

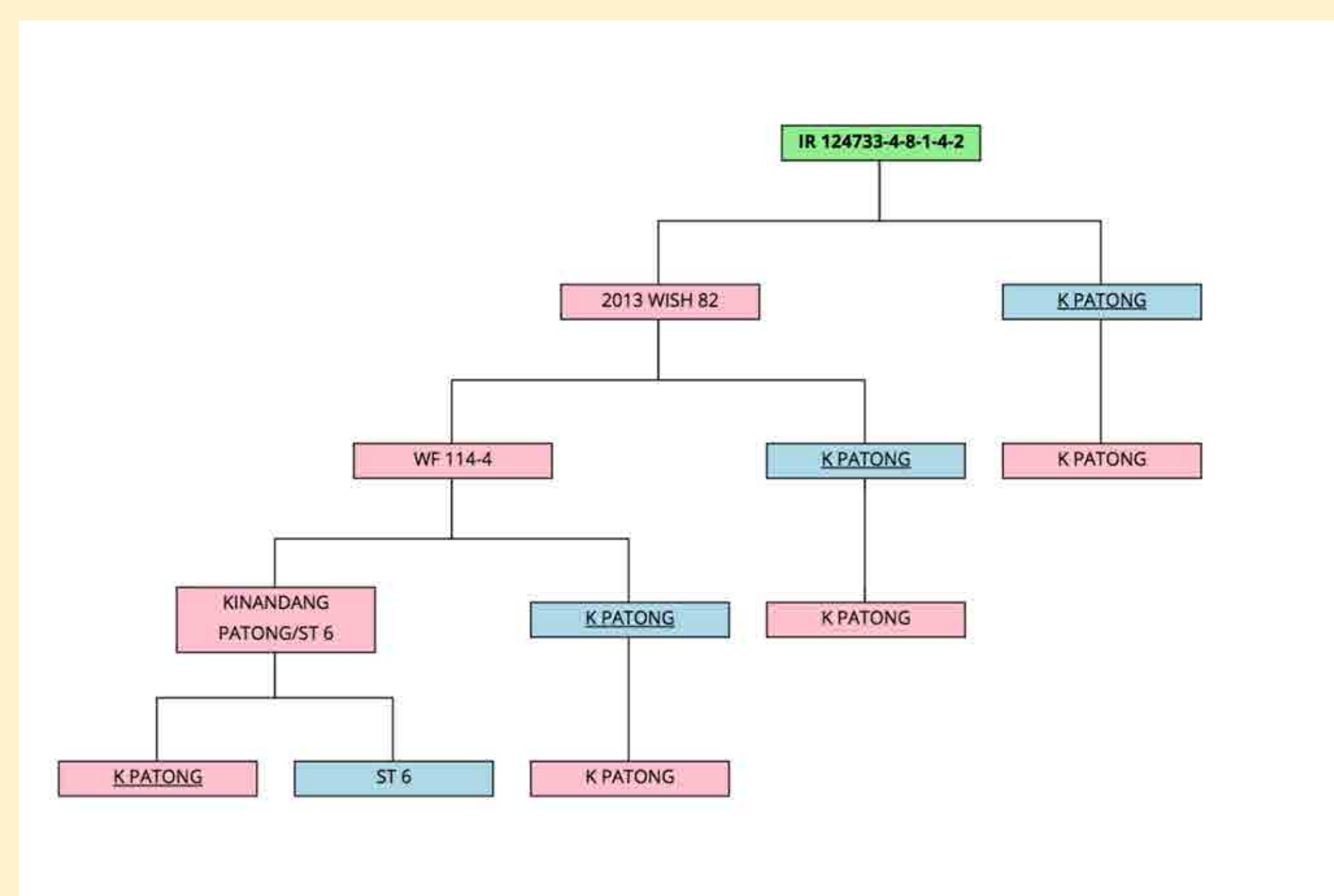
IR 124734-5-6-1-1-4

IR 124734-5-3-2-3-1

IR 124734-5-1-1-12-1

IR 124734-5-3-2-1-1

IR 124735-4-1-10-1-3





# Azucena x ST12 (*Gn1a*)



A. Agronomic Data of Advanced WISH Yield Lines

Line	DTH	PH	TN	PL	PB	SB	FG	UFG	TNG	HGW
	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM
Azucena	90 ±	164.7 ±1.38	10 ±0.58	29.27 ±1.02	13 ±0.51	33 ±1.66	130.2 ±1.28	49 ±7.36	273 ±11.13	2.72 ±0.04
ST12	75 ±	111.6 ±3.03	11 ±0.51	23.76 ±0.72	20 ±1.86	68 ±7.57	187.53 ±15.71	149.06 ±59.56	779 ±36.66	2.6 ±0.05
WISH 96:1-1-4-1-10-1-3	86 ±	171.3 ±3.84	10 ±0.49	29 ±0.55	17 ±0.51	53 ±2.93	184.39 ±13.00	77.06 ±13.04	784 ±54.17	2.96 ±0.10
WISH 96:1-1-4-14-10-2	84 ±	184.9 ±2.55	10 ±0.55	31 ±0.32	17 ±0.40	49 ±2.48	182.066 ±14.92	94.53 ±8.55	829 ±27.21	2.94 ±0.02
WISH 96:1-1-4-2-9-1-1	88 ±	172.6 ±2.59	11 ±2.52	30 ±0.58	15 ±0.33	41 ±5.69	186.66 ±13.46	53.67 ±11.13	721 ±37.58	3.1 ±0.10
WISH 96:1-1-4-6-10-4-5	88 ±	165.3 ±5.14	7 ±0.73	28.2 ±0.58	16 ±0.51	42 ±5.69	131.86 ±5.56	94.4 ±5.83	679 ±24.31	2.6 ±0.20

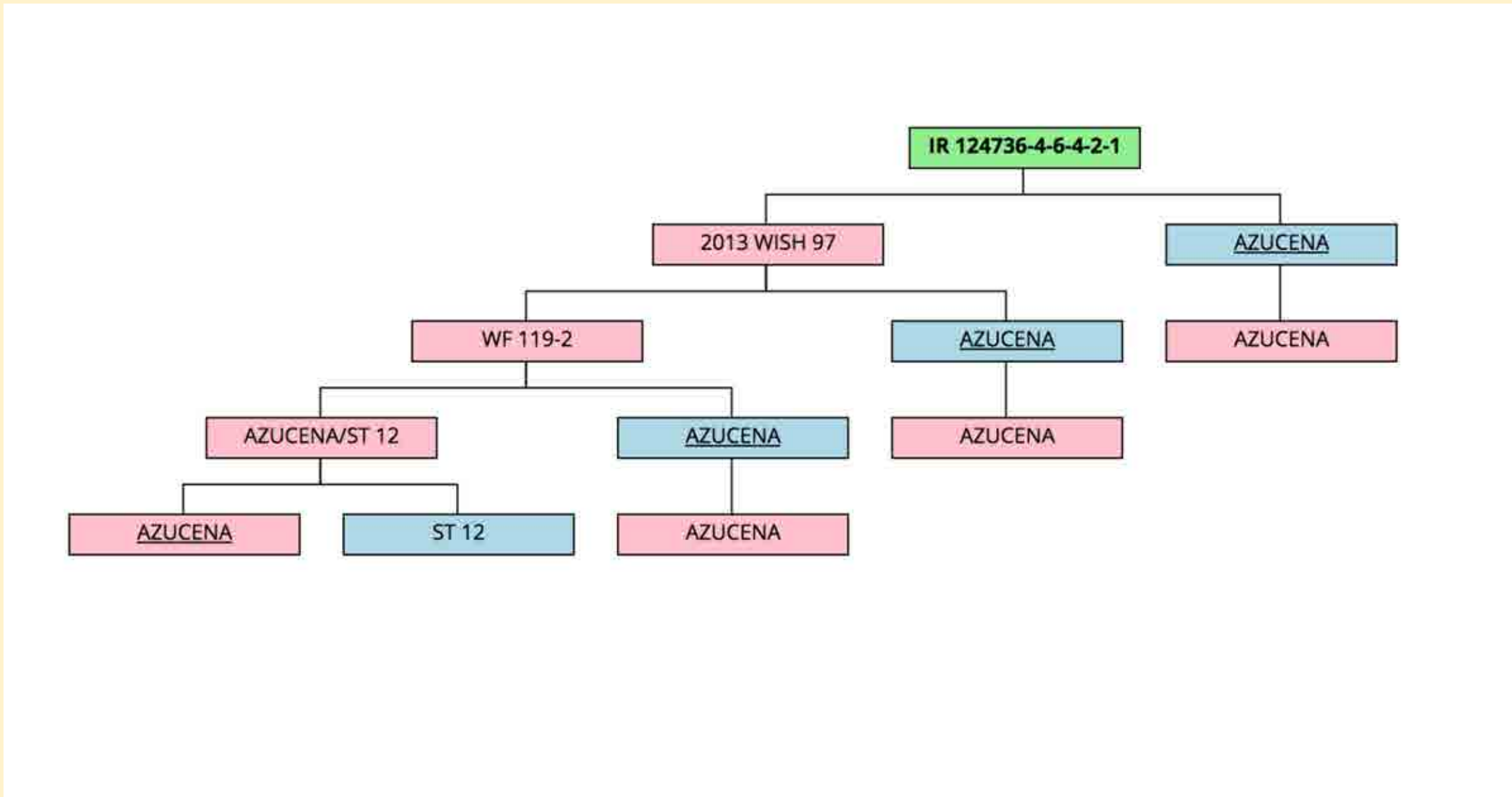
DTH= Days to 50% Heading ; PH=Plant Height; TN=Tiller Number; PL= Panicle Length; PB=Primary Branches; SB=Secondary Branches; FG= Filled Grains; UFG=Unfilled Grains; TNG= Total Number of Grains; HGW=100 grain weight; SEM= Standard Error of Mean

Azucena is an upland rice adapted to non-irrigated fields. ST 12 on the other hand, from the Stocked rice collections of Togo field and Nagoya University, is the donor for *Gn1a* and *WFP* alleles. Advanced lines of this WISH carries *Gn1a* alleles responsible for increase in grain number.

## Other Information:

Generation: BC<sub>3</sub>F<sub>7</sub>  
IR Designations:

- IR 124735-4-6-10-4-5
- IR 124735-4-14-10-2-1
- IR 124735-4-2-9-1-1
- IR 124735-4-22-10-9-1
- IR 124735-4-1-10-1-3





# Azucena x ST12 (*WFP*)



A. Agronomic Data of Advanced WISH Yield Lines

Line	DTH	PH	TN	PL	PB	SB	FG	UFG	TNG	HGW
	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM
Azucena	90	164.7 ±1.38	10 ±0.58	29.27 ±1.02	13 ±0.51	33 ±1.66	130.2 ±1.28	49 ±7.36	273 ±11.13	2.72 ±0.04
ST12	75	111.6 ±3.03	11 ±0.51	23.76 ±0.72	20 ±1.86	68 ±7.57	187.53 ±15.71	149.06 ±59.56	770 ±36.66	2.6 ±0.05
WISH 97:1-1-4-16-1-1-1	87	148.66 ±2.89	8 ±2.33	25 ±1.53	14 ±2.52	29 ±11.68	88.22 ±20.39	61.88 ±17.45	450 ±105.41	2.5 ±0.10
WISH 97:1-1-4-19-1-1-8	89	165.1 ±2.96	7 ±0.60	30.4 ±0.68	16 ±0.37	39 ±3.22	144.4 ±12.72	46.86 ±10.73	574 ±56.86	2.62 ±0.07
WISH 97:1-1-4-26-1-1-10	87	151.3 ±3.06	9 ±1.44	28 ±1.14	13 ±0.51	30 ±4.47	108.93 ±19.86	64.13 ±4.48	519 ±60.95	2.52 ±0.06
WISH 97:1-1-4-3-1-10-5	87	153.16 ±2.05	11 ±0.33	25.33 ±0.67	13 ±0.58	27 ±3.84	70.27 ±8.65	70.94 ±13.56	384 ±80.31	2.36 ±0.12
WISH 97:1-1-4-6-4-2-1	88	182 ±1.82	10 ±1.17	31.8 ±0.49	17 ±0.32	61 ±5.00	173.4 ±16.39	134.40 ±18.59	923 ±86.72	2.78 ±0.09
WISH 97:1-1-4-6-5-2-7	86	152.8 ±1.36	9 ±0.71	25.2 ±0.49	12 ±0.49	30 ±2.89	71.93 ±12.36	56.86 ±7.96	386 ±43.27	2.39±0.12

DTH= Days to 50% Heading ; PH=Plant Height; TN=Tiller Number; PL= Panicle Length; PB=Primary Branches; SB=Secondary Branches; FG= Filled Grains; UFG=Unfilled Grains; TNG= Total Number of Grains; HGW=100 grain weight; SEM= Standard Error of Mean

Azucena is an upland rice adapted to nonirrigated fields. ST 12 on the other hand, from the Stocked rice collections of Togo field and Nagoya University, is the donor for *Gn1a* and *WFP* alleles. Advanced lines of this WISH carries *WFP* alleles responsible for increase in primary branches.

## Other Information:

Generation: BC<sub>4</sub>F<sub>6</sub>

IR Designations:

IR 124736-4-3-1-10-5

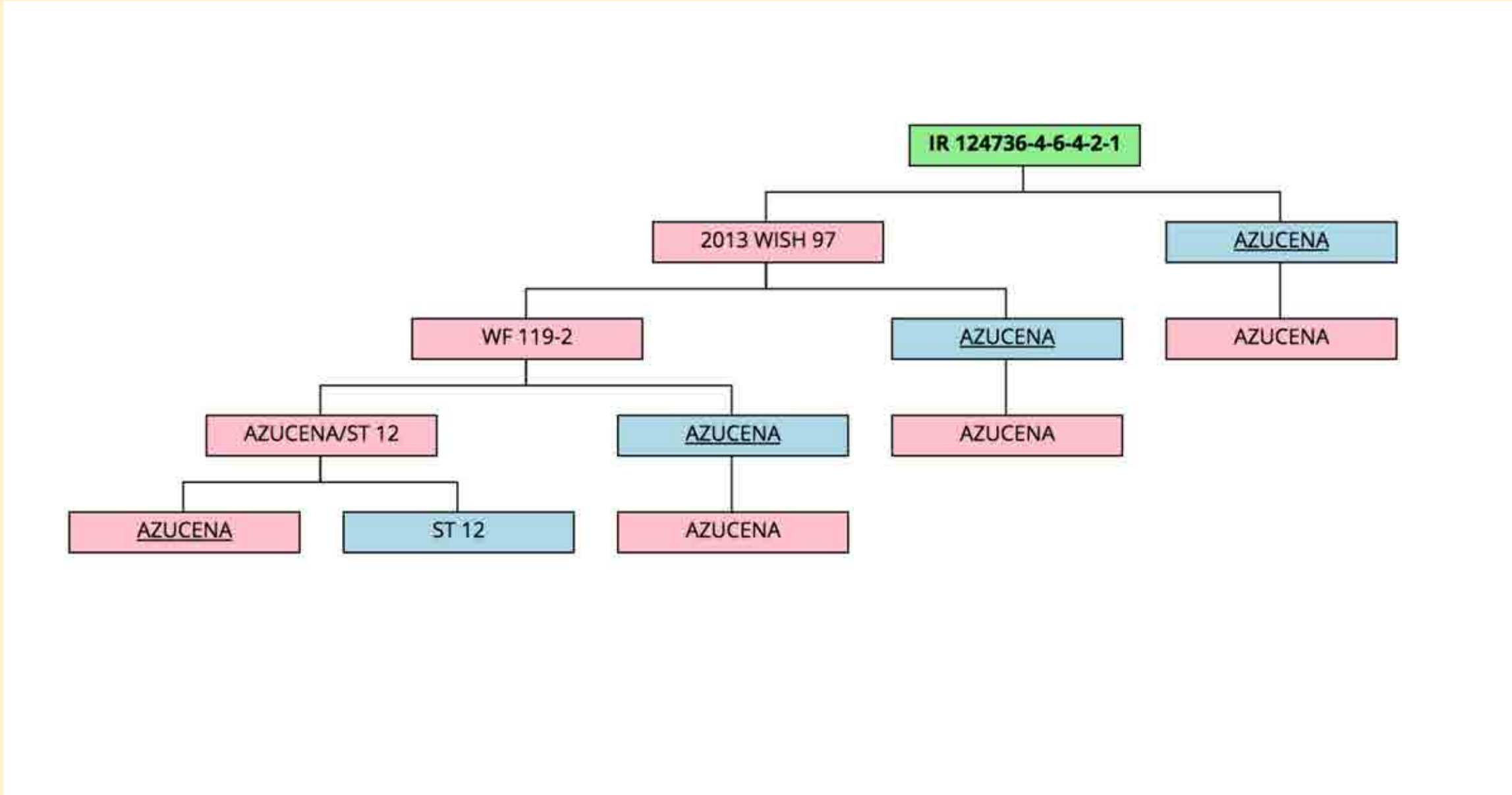
IR 124736-4-6-5-2-7

IR 124736-4-19-1-1-8

IR 124736-4-26-1-1-10

IR 124736-4-6-4-2-1

IR 124736-4-16-1-1-1





# Azucena x ST6 (*Gn1a*)



A. Agronomic Data of Advanced WISH Yield Lines

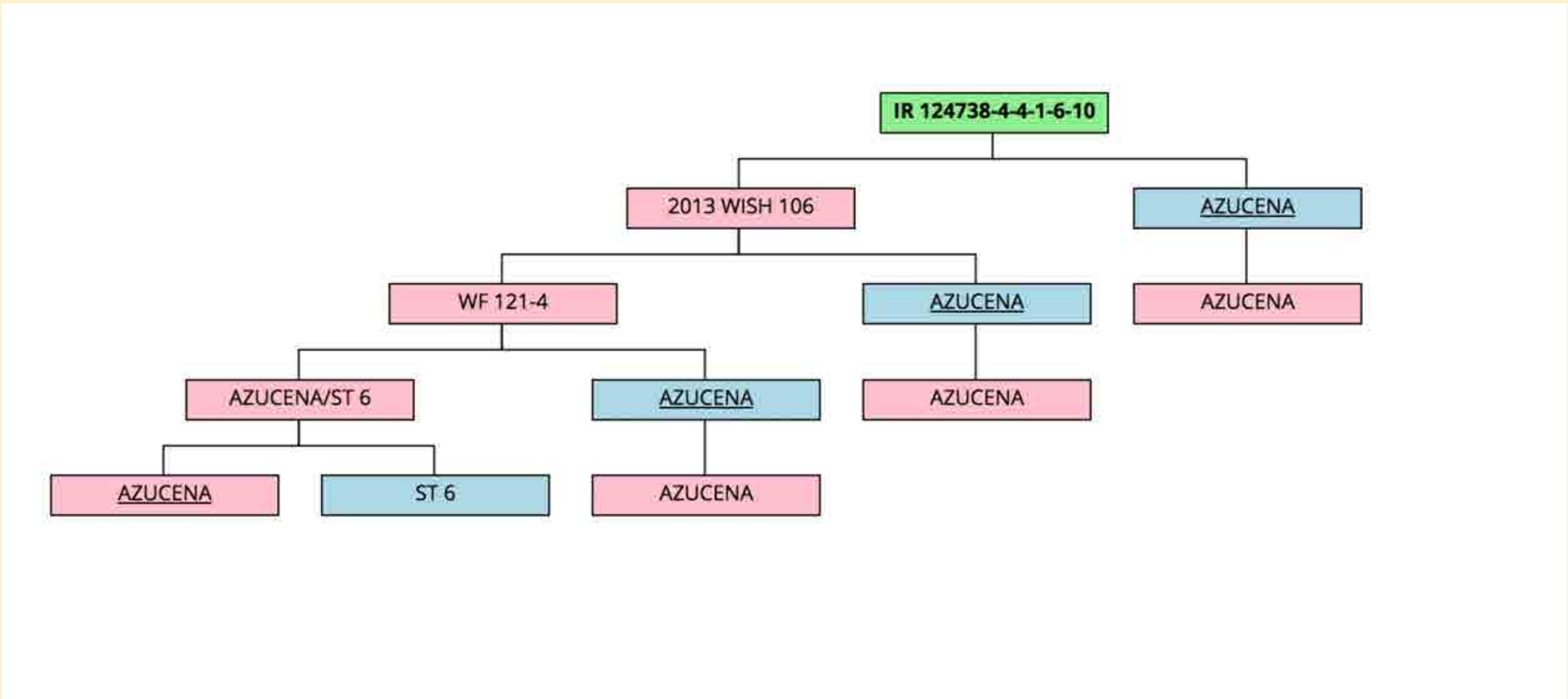
Line	DTH	PH	TN	PL	PB	SB	FG	UFG	TNG	HGW
	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM	Average Data ± SEM
Azucena	90±	164.7± 1.38	10± 0.58	29.27± 1.02	13± 0.51	33± 1.66	130.2± 1.28	49± 7.36	273± 11.13	2.72± 0.04
ST6	83±	119.3± 1.50	11± 0.73	26.06± 0.42	26± 0.45	58± 4.72	200.2± 15.97	82.93± 12.76	891± 28.82	2.62± 0.04
WISH 106:2-2-4-2-1-14-1	85±	164± 0.46	16± 1.50	31.20± 0.79	16± 0.41	49± 1.60	206.5± 8.01	19.33± 1.93	678± 27.94	3± 0.07
WISH 106:2-2-4-2-1-16-1	87±	167.81.50	11± 0.77	33.3± 0.64	19± 0.49	53± 2.73	223.53± 11.37	56.8± 12.14	841± 38.07	2.98± 0.06
WISH 106:2-2-4-21-1-5-12	88±	165± 2.08	14± 0.68	30.88± 0.50	18± 0.68	46± 2.60	217.6± 13.98	34.66± 3.60	756± 37.60	3± 0.03
WISH 106:2-2-4-3-1-10-8	86±	149.3± 3.27	5± 0.68	27.39± 1.04	13± 0.37	27± 2.52	57.06± 13.35	61.46± 10.66	354± 42.39	2.48± 0.17
WISH 106:2-2-4-4-1-6-10	86±	176.8± 3.93	11± 0.80	31.6± 0.67	18± 0.49	46± 1.98	167.73± 10.29	87.6± 9.29	766± 28.94	2.78± 0.09

DTH= Days to 50% Heading ; PH=Plant Height; TN=Tiller Number; PL= Panicle Length; PB=Primary Branches; SB=Secondary Branches; FG= Filled Grains; UFG=Unfilled Grains; TNG= Total Number of Grains; HGW=100 grain weight; SEM= Standard Error of Mean

Azucena is an upland rice adapted to non-irrigated fields. ST 6 on the other hand, from the Stocked rice collections of Togo field and Nagoya University, is the donor for *Gn1a* and *WFP* alleles. Advanced lines of this WISH carries *Gn1a* alleles responsible for increase in grain number.

## Other Information:

Generation: BC<sub>3</sub>F<sub>7</sub>  
IR Designations:  
IR 124738-4-2-1-16-1  
IR 124734-5-5-1-9  
IR 124696-10-6-1-3  
IR 124709-2-8-1-1  
IR 124710-4-5-4-1





Azucena x ST6 (*WFP*)



### A. Agronomic Data of Advanced WISH Yield Lines

Line	DTH	PH	TN	PL	PB	SB	FG	UFG	TNG	HGW
	Average Data $\pm$ SEM	Average Data $\pm$ SEM	Average Data $\pm$ SEM	Average Data $\pm$ SEM	Average Data $\pm$ SEM	Average Data $\pm$ SEM	Average Data $\pm$ SEM	Average Data $\pm$ SEM	Average Data $\pm$ SEM	Average Data $\pm$ SEM
Azucena	90 $\pm$	164.7 $\pm$ 1.38	10 $\pm$ 0.58	29.27 $\pm$ 1.02	13 $\pm$ 0.51	33 $\pm$ 1.66	130.2 $\pm$ 1.28	49 $\pm$ 7.36	273 $\pm$ 11.13	2.72 $\pm$ 0.04
ST6	83 $\pm$	119.3 $\pm$ 1.50	11 $\pm$ 0.73	26.06 $\pm$ 0.42	26 $\pm$ 0.45	58 $\pm$ 4.72	200.2 $\pm$ 15.97	82.93 $\pm$ 12.76	891 $\pm$ 28.82	2.62 $\pm$ 0.04
WISH 102:2-5-2-11-6-10-6	89 $\pm$	169.2 $\pm$ 2.59	7 $\pm$ 0.58	29.5 $\pm$ 0.68	17 $\pm$ 0.55	39 $\pm$ 3.38	179.8 $\pm$ 15.35	42 $\pm$ 12.23	665 $\pm$ 38.62	2.92 $\pm$ 0.05
WISH 102:2-5-2-11-7-1-1	89 $\pm$	159.5 $\pm$ 1.02	7 $\pm$ 0.48	30.37 $\pm$ 0.43	16 $\pm$	46 $\pm$ 4.05	179.66 $\pm$ 16.81	47.58 $\pm$ 8.73	682 $\pm$ 32.39	2.7 $\pm$ 0.14
WISH 102:2-5-2-3-8-8-1	87 $\pm$	154 $\pm$ 1.46	9 $\pm$ 1.16	28.13 $\pm$ 0.88	15 $\pm$ 0.77	30 $\pm$ 2.20	115.66 $\pm$ 19.24	66.06 $\pm$ 14.03	545 $\pm$ 36.67	2.52 $\pm$ 0.14
WISH 102:2-5-2-7-1-9-2	87 $\pm$	150.2 $\pm$ 2.21	10 $\pm$ 0.97	23.9 $\pm$ 0.70	13 $\pm$ 0.51	29 $\pm$ 2.85	72.06 $\pm$ 7.63	70.13 $\pm$ 10.52	427 $\pm$ 30.35	2.42 $\pm$ 0.06
WISH 102:2-5-2-7-2-2-4	85 $\pm$	154.7 $\pm$ 4.19	12 $\pm$ 1.16	24.84 $\pm$ 0.78	14 $\pm$ 0.68	30 $\pm$ 3.89	90.2 $\pm$ 4.84	66.13 $\pm$ 13.45	433 $\pm$ 49.19	2.42 $\pm$ 0.06

DTH= Days to 50% Heading ; PH=Plant Height; TN=Tiller Number; PL= Panicle Length; PB=Primary Branches; SB=Secondary Branches; FG= Filled Grains; UFG=Unfilled Grains; TNG= Total Number of Grains; HGW=100 grain weight; SEM= Standard Error of Mean

Azucena is an upland rice adapted to non-irrigated fields. ST 6 on the other hand, from the Stocked rice collections of Togo field and Nagoya University, is the donor for *Gn1a* and *WFP* alleles. Advanced lines of this WISH carries *WFP* alleles responsible for increase in primary branches.

Other Information:

Generation:  $\text{BC}_3\text{F}_7$

## IR Designations:

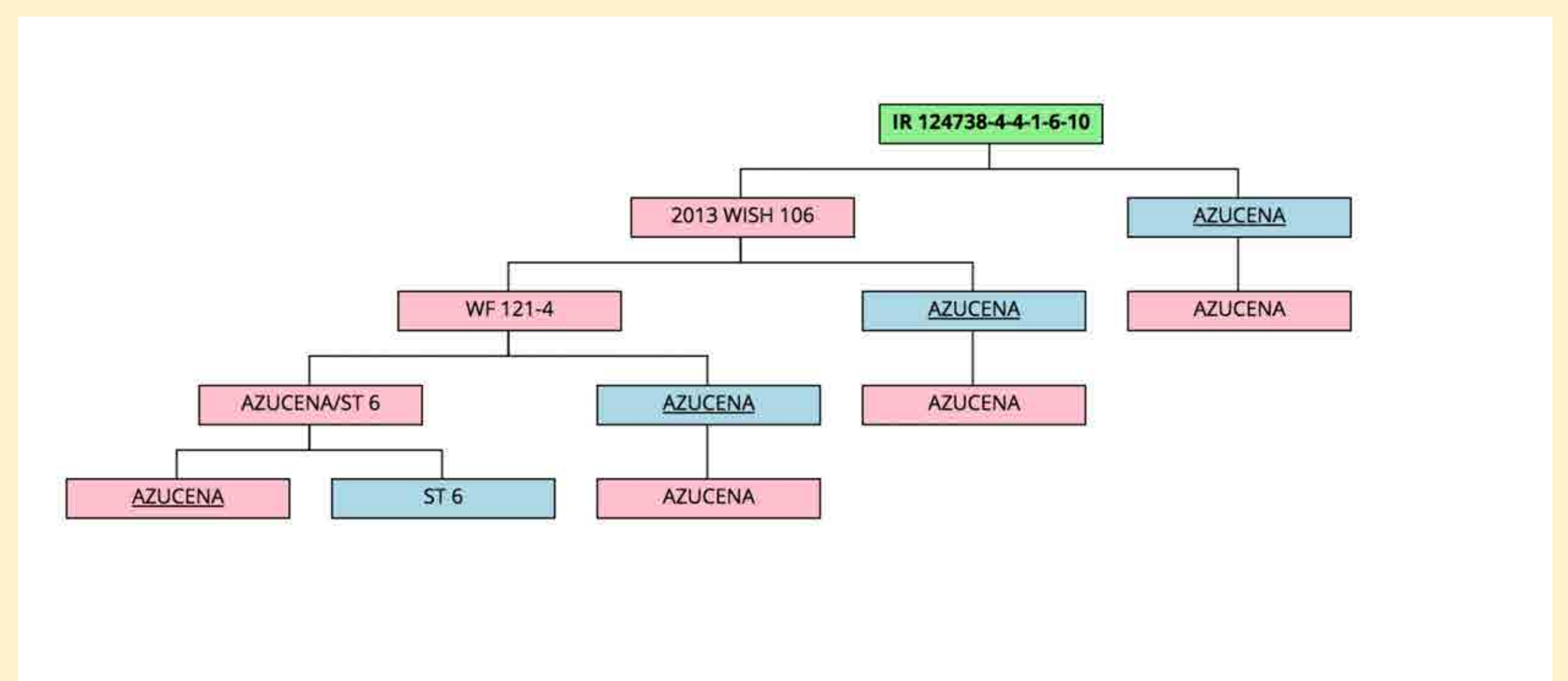
IR 124737-2-11-6-10-6

IR 124737-2-3-8-8-1

IR 124737-2-11-7-1-1

IR 124738-4-3-1-10-8

IR 124738-4-4-1-6-10





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# **Wonder Rice Initiative for Food Security and Health(WISH) Developed Blast Resistant Lines**

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Kinandang Patong x Sensho (*pi21*)

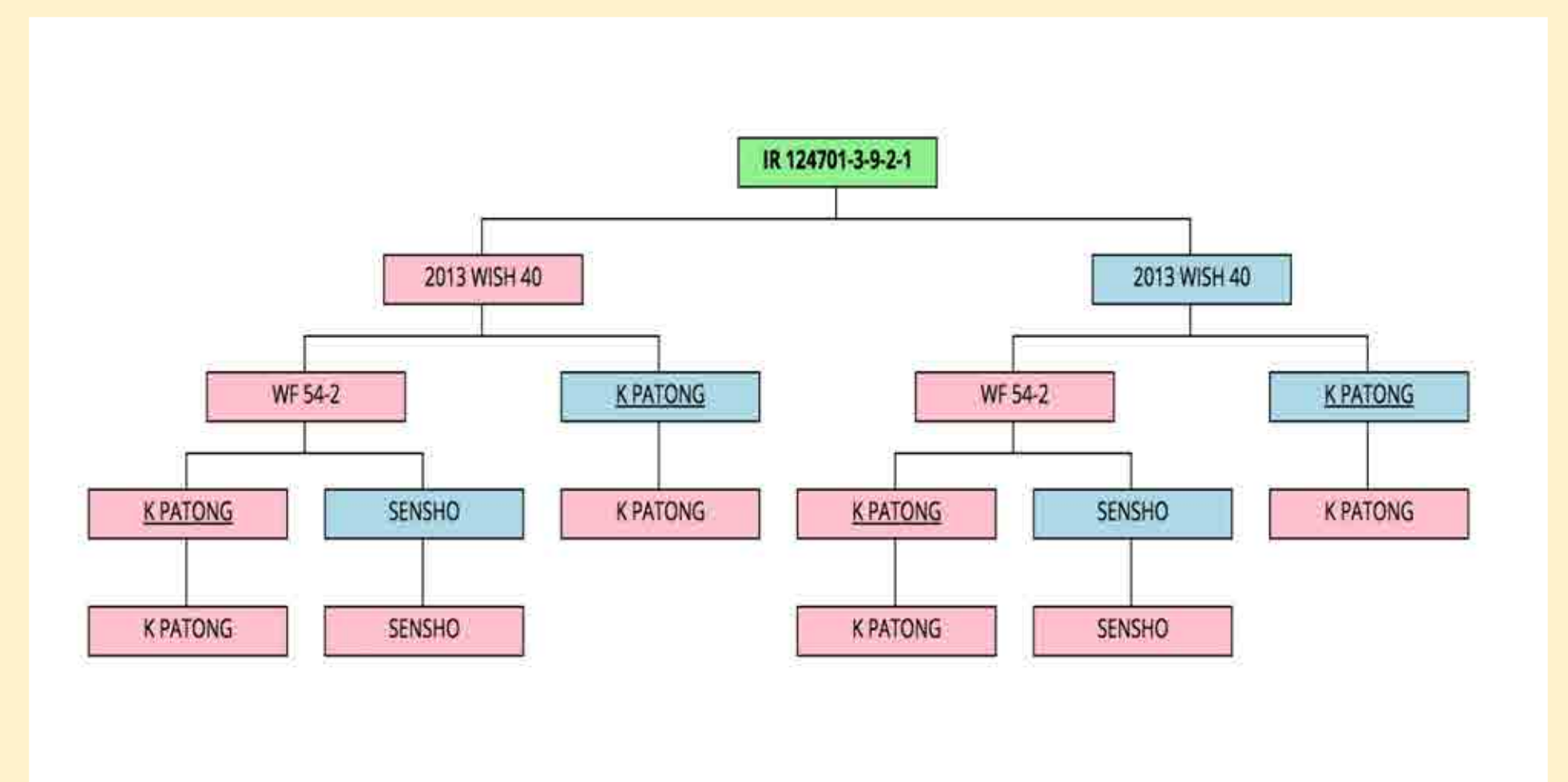


### A. Agronomic data of advanced WISH blast resistant lines

Line	Background	Generation	DTH	Plant Height	Tiller No.	Panicle Length	No. of PB	Total Grain Number	Fertility %
Kinandang Patong	Recurrent Parent		80	155.25	5.30	23.22	14.50	839.33	77.17
Sensho	Donor		61	107.92	8.00	21.67	6.50	264.83	87.83
WISH 40:1-3-3-9-2-1	Kinandang Patong	BC4F4	81	152.92	5.67	23.86	13.50	845.00	82.67
WISH 40:1-3-16-11-11-	Kinandang Patong	BC4F4	79	151.25	5.67	22.32	14.00	937.83	76.67
WISH 40:1-3-18-7-1-1	Kinandang Patong	BC4F4	80	158.50	4.83	20.97	14.50	839.50	82.00
WISH 40:1-3-7-7-2-1	Kinandang Patong	BC4F4	80	141.08*	6.33	22.45	14.67	930.17	82.17
WISH 40:1-3-18-1-9-1	Kinandang Patong	BC4F4	79	141.83	4.67	22.64	14.50	968.83	79.50

**B. Reaction of advanced WISH lines to natural blast infection in the field based on IRRI SES scores. Diseased leaf area (DLA) scores are provided for each line**

Line name	Initial reading		Phenotype (based on SES score)	Final reading		Phenotype (based on SES score)
	Average scores			Average scores		
	SES score	% DLA		SES score	% DLA	
LTH	5.3	33.5	MR	ND	ND	S
CO39	7.1	60	S	8.2	80	S
IR65482-4-136-2-2 ( <i>Pr40</i> )	1.4	1	R	1.6	1	R
Sensho	1.1	2	R	1.5	2	R
KP	0	0	R	0.5	0	R
WISH 40-1-3-16-11	0	0	R	0.5	0	R
WISH 40-1-3-3-9	0	0	R	0	0	R
WISH 40-1-3-7-7	0	0	R	0	0	R



Other Information:

IR Designation:

IR 124701-3-9-2-1  
IR 124701-16-11-11-1  
IR 124701-18-7-1-1

KP is an established upland cultivar which has been reported to exhibit weak resistance to a both upland and lowland isolates of blast. Sensho on the other hand, is an upland rice cultivar that shares the recessive allele of Owarihatamochi, is the donor for Pi21 allele. Advanced lines of this WISH carries *Pi21* alleles responsible for blast resistance.



# IRAT 109 x Sensho (*pi21*)



A. Agronomic data of advanced WISH blast resistant lines

Line	Background	Generation	DTH	Plant Height	Tiller No.	Panicle Length	No. of PB	Total Grain Number	Fertility %
IRAT109	Recurrent Parent		72	116.83	6.50	22.39	13.33	438.50	76.80
Sensho	Donor		61	107.92	8.00	21.67	6.50	264.83	87.83
WISH 44:5-1-14-3-2-1	IRAT109	BC4F4	69	142.75	5.83	25.14	11.67	457.33	87.85
WISH 44:5-1-18-4-4-1	IRAT109	BC4F4	69	139.17	6.67	24.17	12.67	435.33	91.53
WISH 44:5-1-22-2-4-1	IRAT109	BC4F4	71	144.33	7.17	24.61	14.17	490.50	89.30
WISH 44:5-1-8-2-2-1	IRAT109	BC4F4	71	120.75	6.67	23.78	12.00	407.83	87.78
WISH 44:5-1--9-6-2-1	IRAT109	BC4F4	72	110.67	5.83	21.06	13.17	393.33	81.80

B. Reaction of advanced WISH lines to natural blast infection in the field based on IRRI SES scores. Diseased leaf area (DLA) scores are provided for each line

Line name	Initial reading Average scores		Phenotype (based on SES score)	Final reading Average scores		Phenotype (based on SES score)
	SES score	% DLA		SES score	% DLA	
LTH	5.3	33.5	MR	ND	ND	S
CO39	7.1	60	S	8.2	80	S
IR65482-4-136-2-2 ( <i>Pi40</i> )	1.4	1	R	1.6	1	R
Sensho	1.1	2	R	1.5	2	R
IRAT 109	0	0	R	0	0	R
WISH 44:5-1-14-3	0	0	R	0	0	R
WISH 44:5-1-18-4	0	0	R	0	0	R
WISH 44:5-1-22-2	0	0	R	0	0	R
WISH 44:5-1-8-2	0	0	R	0	0	R
WISH 44:5-1-9-6	0	0	R	0	0	R

R=resistant, MR=moderately resistant, S=susceptible, ND=no data obtained because all plants died  
*Pi40*=resistant control, LTH and CO39=susceptible control

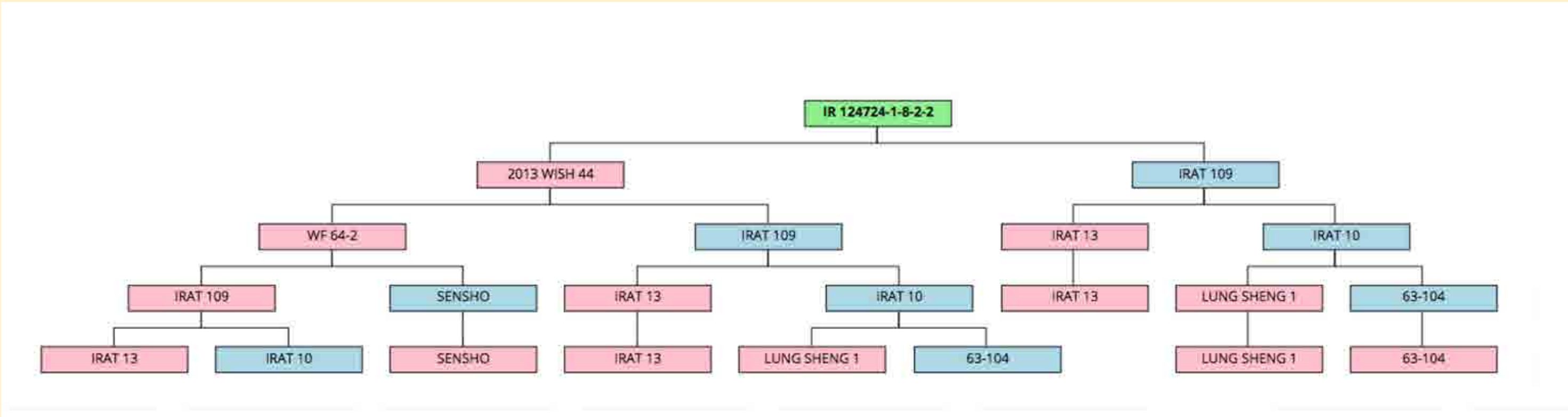
Other Information:

IR Designation:

IR 124724-1-8-2-2-1

IR 124724-1-9-6-2-1

IRAT109 is a tropical japonica rice variety which is know for its drought tolerant trait. Sensho on the other hand, is an upland rice cultivar that shares the recessive allele of Owarihatamochi, is the donor for Pi21 allele. Advanced lines of this WISH carries *Pi21* alleles responsible for blast resistance.





# IRBB4/5/12/21x Sensho (*pi21*)



A. Agronomic data of advanced WISH blast resistant lines

Line	Background	Generation	DTH	Plant Height	Tiller No.	Panicle Length	No. of PB	Total Grain Number	Fertility %
IRBB	Recurrent Parent		80	111.08	15.17	27.89	12.67	587.50	84.92
Sensho	Donor		61	107.92	8.00	21.67	6.50	264.83	87.83
WISH 48:1-3-1-1-3-1	IRBB	BC4F4	79	104.00	13.83	26.36	12.17	513.83	84.68
WISH 48:1-3-2-1-1-1	IRBB	BC4F4	80	114.33	10.00	28.14	11.17	682.50	77.55
WISH 48:1-3-18-1-1-1	IRBB	BC4F4	79	107.00	10.50	27.84	10.00	542.83	88.35
WISH 48:1-3-20-1-4-1	IRBB	BC4F4	81	120.42	11.17	27.61	11.50	789.17	60.53
WISH 48:1-3-21-1-1-1	IRBB	BC4F4	82	115.42	9.17	28.36	12.83	611.33	65.65

B. Reaction of advanced WISH lines to natural blast infection in the field based on IRRI SES scores. Diseased leaf area (DLA) scores are provided for each line

Line name	Initial reading		Phenotype (based on SES score)	Final reading		Phenotype (based on SES score)
	Average scores			Average scores		
	SES score	% DLA		SES score	% DLA	
LTH	5.3	33.5	MR	ND	ND	S
CO39	7.1	60	S	8.2	80	S
IR65482-4-136-2-2 ( <i>Pi40</i> )	1.4	1	R	1.6	1	R
Sensho	1.1	2	R	1.5	2	R
IRBB	4	5	MR	5	15	MR
WISH 48:1-3-1-1	2	1	R	2	1	R
WISH 48:1-3-18-1	2	3	R	3.5	5	R
WISH 48:1-3-2-1	1	1	R	1	1	R
WISH 48:1-3-20-1	3	3	R	1	1	R
WISH 48:1-3-21-1	1	1	R	2	1	R

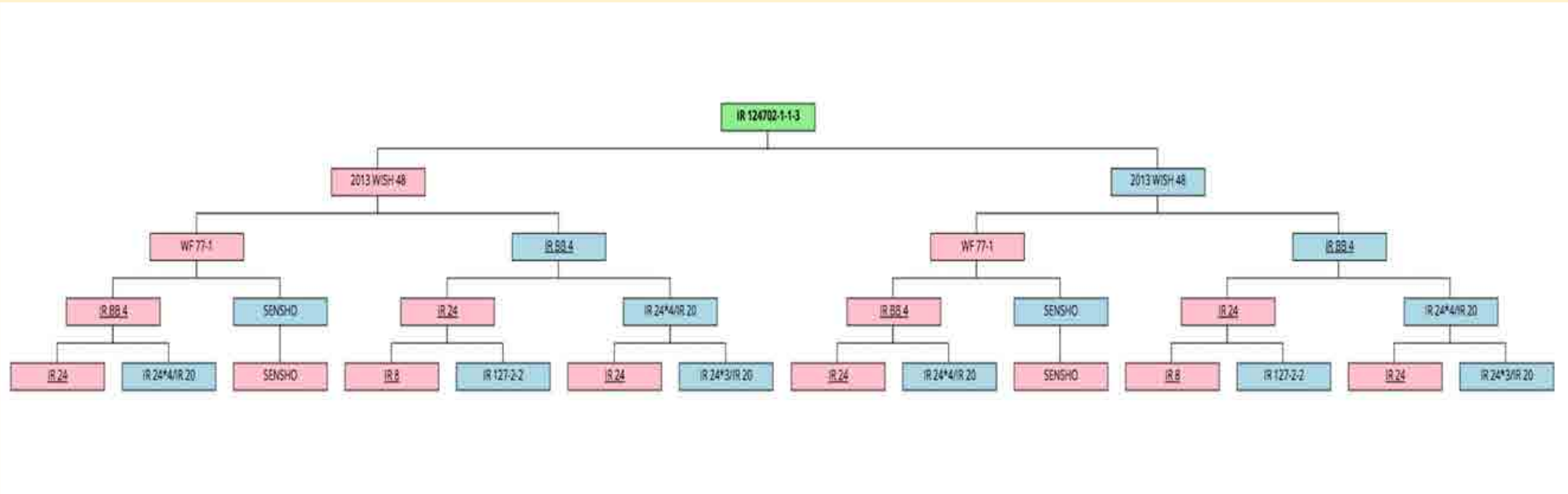
R=resistant, MR=moderately resistant, S=susceptible, ND=no data obtained because all plants died  
*Pi40*=resistant control, LTH and CO39=susceptible control

Other Information:

IR Designation:

- IR 124702-1-1-3-1
- IR 124702-2-1-1-1
- IR 124702-18-1-1-1
- IR 124702-20-1-4-1
- IR 124702-21-1-1-1

IRBB, also an *indica* variety, is a pyramiding line bred to express the *Xa4*, *xa5*, *xa13* and *Xa21* genes for bacterial blight resistance Sensho on the other hand, is an upland rice cultivar that shares the recessive allele of Owarihatamochi, is the donor for *Pi21* allele. Advanced lines of this WISH carries *Pi21* alleles responsible for blast resistance.





# IR63307-4B-13-2 x Sensho (*pi21*)



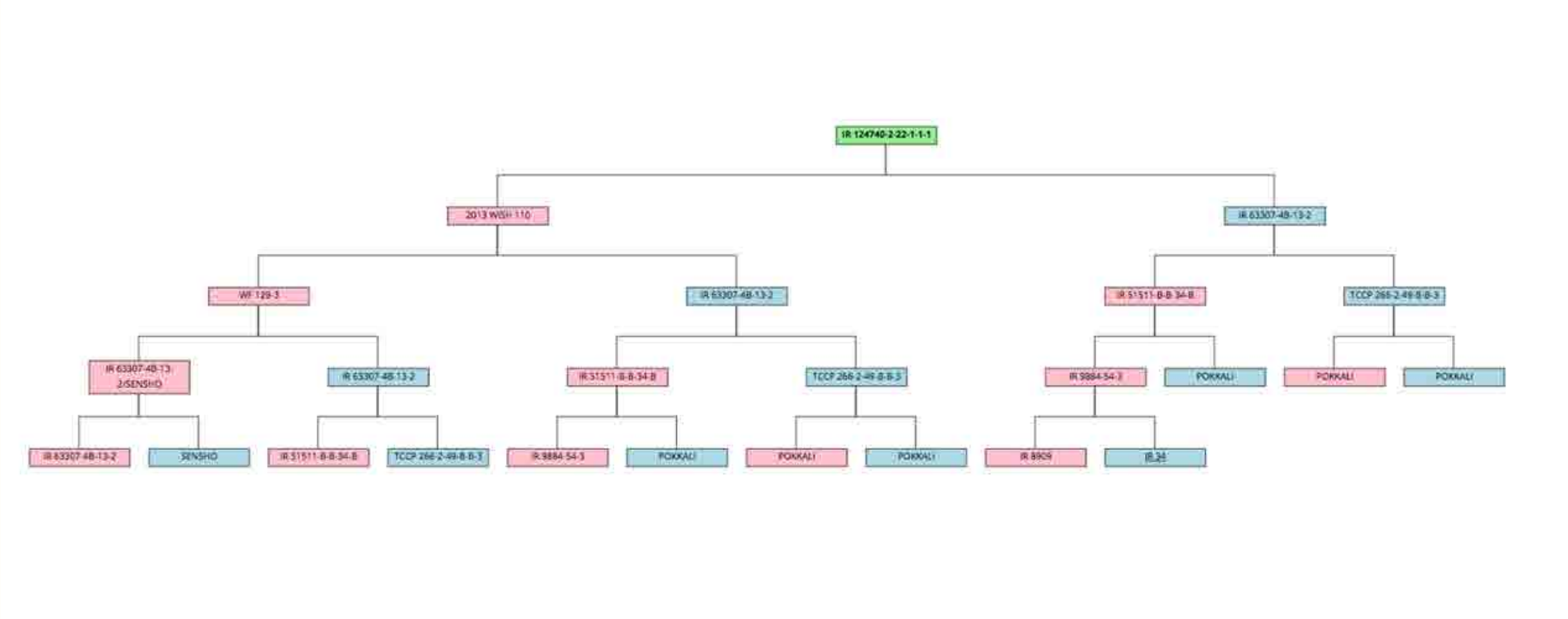
### A. Agronomic data of advanced WISH blast resistant lines

Line	Background	Generation	DTH	Plant Height	Tiller No.	Panicle Length	No. of PB	Total Grain Number	Fertility %
IR63307	Recurrent Parent		80	121.67	14.67	28.86	11.33	495.67	68.12
Sensho	Donor		61	107.92	8.00	21.67	6.50	264.83	87.83
WISH 110:2-5-2-22-1-1	IR63307	BC <sub>5</sub> F <sub>5</sub>	79	122.00	12.33	28.22	12.33	573.67	72.73
WISH 110:1-1-11-5-4-1	IR63307	BC <sub>5</sub> F <sub>5</sub>	78	148.92	8.83	29.08	12.67	622.17*	78.39
WISH 110:1-1-11-12-1-	IR63307	BC <sub>5</sub> F <sub>5</sub>	78	132.42	13.17	30.42	12.00	513.67	80.05
WISH 110:2-5-2-1-1-3-	IR63307	BC <sub>5</sub> F <sub>5</sub>	80	157.58	15.33	32.67*	12.67	636.00	80.15
WISH 110:2-5-2-12-1-4	IR63307	BC <sub>5</sub> F <sub>5</sub>	81	118.33	15.67	27.19	11.67	533.33	67.95

### B. Reaction of advanced WISH lines to natural blast infection in the field based on IRRI SES scores. Diseased leaf area (DLA) scores are provided for each line

Line name	Initial reading		Phenotype (based on SES score)	Final reading		Phenotype (based on SES score)
	Average scores			Average scores		
	SES score	% DLA		SES score	% DLA	
LTH	5.3	33.5	MR	ND	ND	S
CO39	7.1	60	S	8.2	80	S
IR65482-4-136-2-2 ( <i>Pi40</i> )	1.4	1	R	1.6	1	R
Sensho	1.1	2	R	1.5	2	R
IR63307	0.5	1	R	0.5	1	R
WISH 110:1-1-11-12-1	1	1	R	1	1	R
WISH 110:1-1-11-5-4	2	1	R	0.5	1	R
WISH 110:2-5-2-1-1	1	1	R	0.5	1	R
WISH 110:2-5-2-12-1	0	0	R	0.5	1	R
WISH 110:2-5-2-22-1	0.5	1	R	0.5	1	R

R=resistant, MR=moderately resistant, S=susceptible, ND=no data obtained because all plants died  
*Pi40*=resistant control, LTH and CO39=susceptible control



### Other Information:

#### IR Designation:

- IR 124739-11-5-4-1-1
- IR 124739-11-12-1-1-1
- IR 124740-2-1-1-3-1
- IR 124740-2-12-1-4-1
- IR 124740-2-22-1-1-1

IR63307 is an *indica* variety that has been released in the Philippines as a cultivar for its tolerance to saline soils. Sensho on the other hand, is an upland rice cultivar that shares the recessive allele of Owarihatamochi, is the donor for Pi21 allele. Advanced lines of this WISH carries *Pi21* alleles responsible for blast resistance.

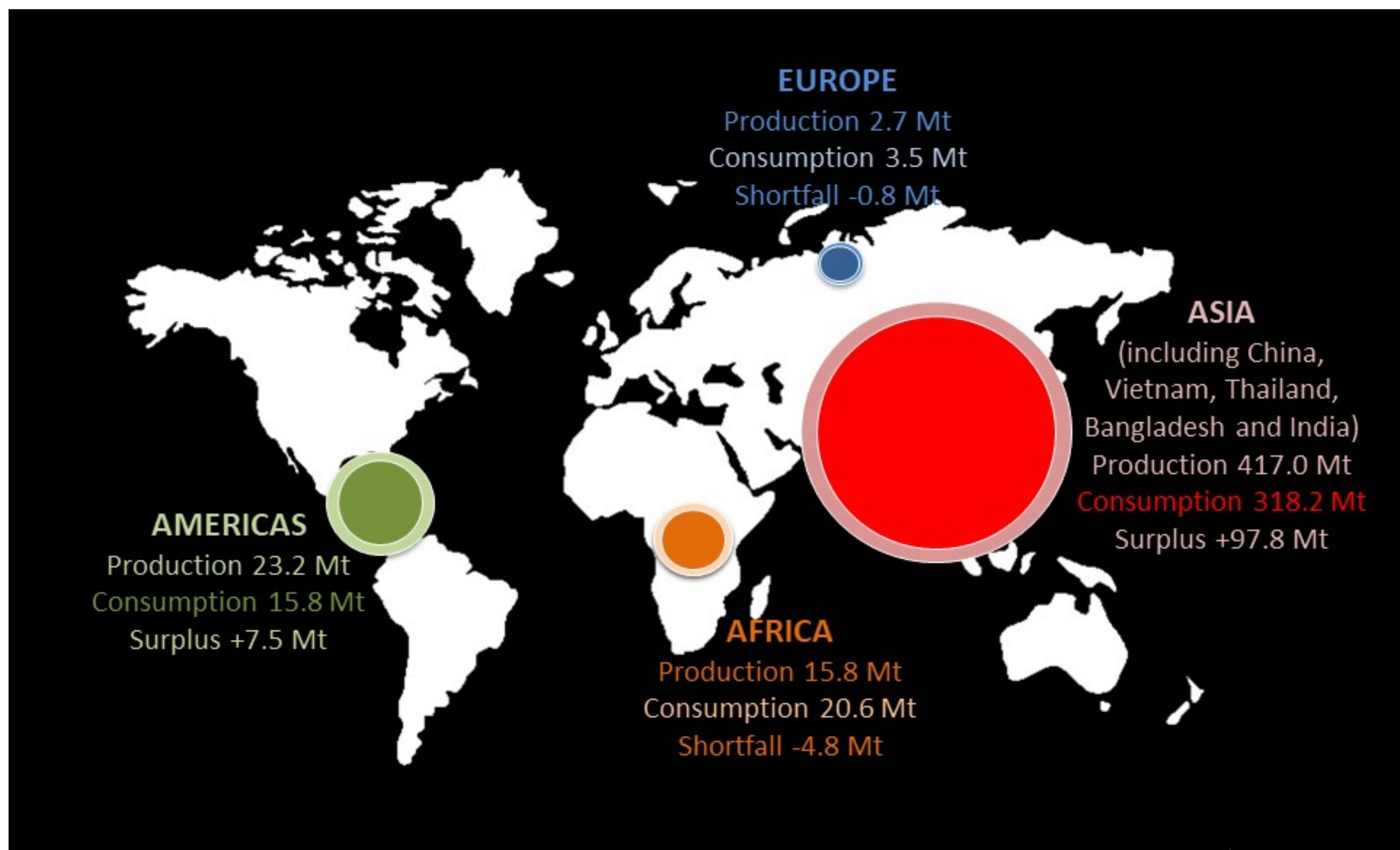


## Precision breeding strategy to increase the yield and improve disease resistance in rice varieties under the WISH Project

Hunger remains the world's number one health risk, killing more people than malaria, AIDS and tuberculosis combined. Everyday more than 25,000 people die because of food shortage and these include 14,000 children under the age of 5. In 2016, FAO reported an increased in the estimated number of malnourished people from 777 million in 2015 to 815 million in 2016. Although several initiatives had been put into place by various organizations and governments to address the issue of malnutrition and food shortage, the reality of the daunting challenges ahead could very possibly undermine the progress made under such initiatives.

By 2050, the world population is projected to surpass the 9 billion mark, bringing once again, the issue of food security in the forefront of priorities for governments across the globe. In sub-Saharan Africa, and Southeast and Western Asia where food security has visibly worsened because of civil conflicts, erratic weather patterns brought about by climate change will severely compound food shortage.

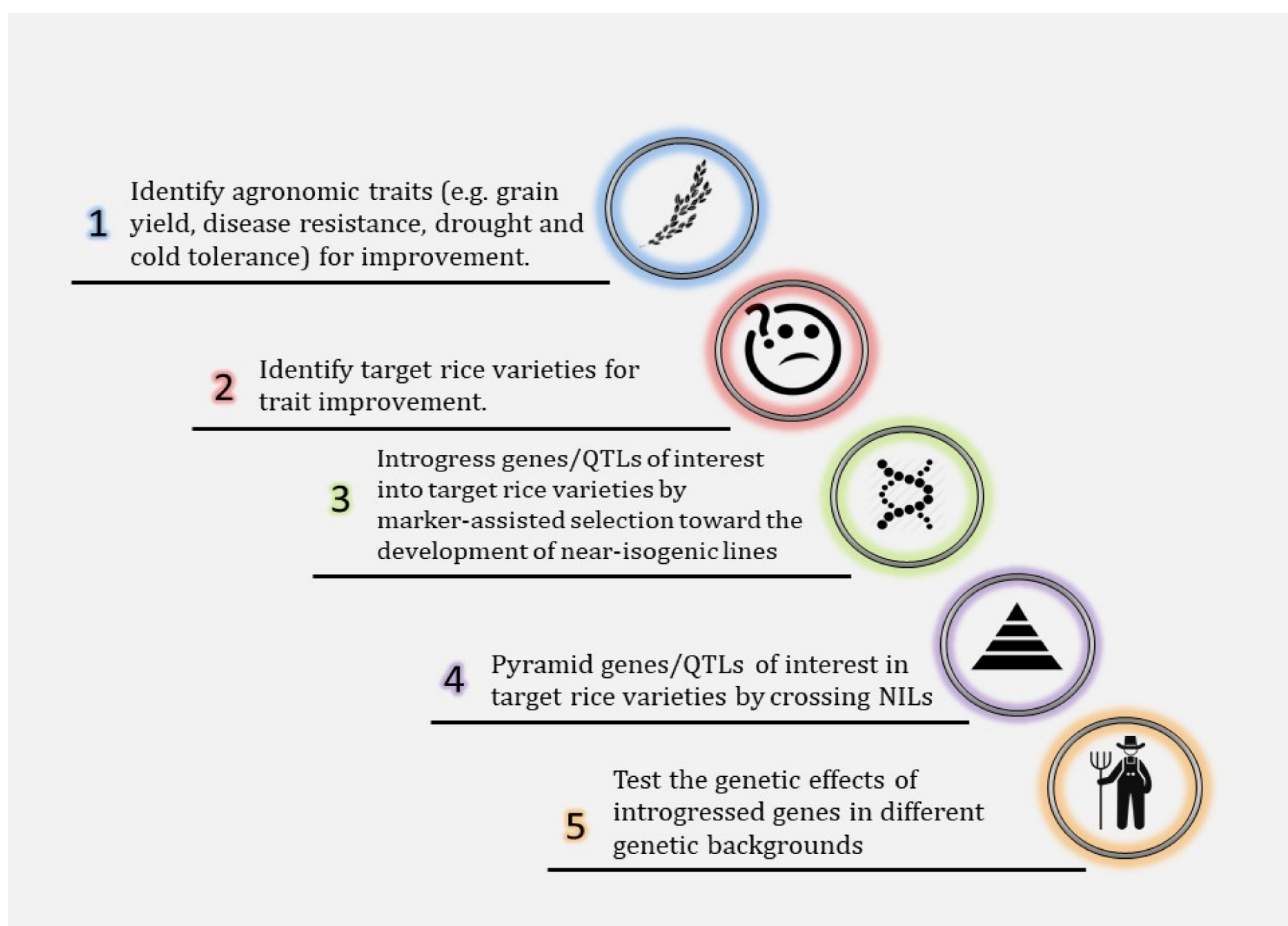
Rice is the staple food for 3.5 billion people across the world. Although the crop is already cultivated in more than 100 countries worldwide, more than 90% of rice is still produced and consumed in Asia (Fig 1). In Africa, rice is quickly becoming a staple food and projections for 2035 indicate that production has to increase by 35 million tons to meet the increasing demands for rice in the region. Given the importance of rice as a staple food, increasing rice productivity will play a critical role in contributing to the world food supply, particularly in Asia and Africa.





The **Wonder Rice Initiative for Food Security and Health (WISH)** Project was built on the premise of increasing rice production in Asia and Africa by conventional means to contribute in food security in both regions. The initiative was spearheaded by Nagoya University in collaboration with Kyushu University in Japan and the International Rice Research Institute in the Philippines, with the full support of the Japan International Cooperation Agency.

Like most successful breeding program, the WISH Project established a breeding strategy based on DNA marker technology that was implemented towards improving rice varieties for yield and abiotic stress resistance (Fig 2). The first component of this approach focused on the identification of agriculturally important traits that will contribute the most towards the improvement of the rice sector. Second is the careful selection of target rice varieties for trait improvement. After establishing the traits and target varieties for improvement, the genes controlling the target agronomic traits were introgressed into the selected rice varieties by marker-assisted selection towards the development of near-isogenic lines (NIL). The NILs were crucial in our efforts to pyramid various genes underlying important agronomic traits into different genetic backgrounds. Finally, field tests to evaluate the performance of each improved variety were conducted under various rice ecosystems of target regions in Africa as well as in Asia.



**Fig 2. Breeding strategy implemented under the WISH project.**

#### *Identification of target traits for improvement*

The WISH project aims to produce high yielding rice varieties for Asia and Africa by improving two traits that are directly related to yield namely (1) grain number and (2) number of primary branches per panicle. *GRAIN NUMBER 1a* (*Gn1a*) gene is a negative regulator of grain number that was identified on chromosome 1 of the *indica* rice cultivar, Habataki.



*Gn1a* increases grain number by reducing the expression of *OsCKX2*, an enzyme that degrades cytokinin. Preliminary analysis showed that introgression of *Gn1a* increased grain yield in rice cv. Koshihikari by 21% (Ashikari et al., 2005).

*WEALTHY FARMER'S PANICLE* (*WFP*), on the other hand, is a positive regulator of grain number identified on chromosome 8 of ST-12, a temperate *japonica* variety. *WFP* encodes a *SQUAMOSA PROMOTER BINDING PROTEIN-LIKE 14* (*OsSPL14*) and controls shoot branching in the vegetative stage and panicle branching in the reproductive stage. *WFP* introgression can almost double the number of primary branches per panicle, resulting in a significant increase in yield. (Miura et al., 2010). Both *Gn1a* and *WFP* were isolated in our laboratory in Nagoya University in Japan.

Another trait that we sought to improve was blast resistance. Blast caused by the fungus *Magnaporthe grisea* is one of the most destructive pathogens of rice worldwide (Dean et al., 2005). A blast-infected plant would exhibit disease lesions on stems, leaves, nodes, and panicles. Economic losses due to blast have been estimated to equal yields that can feed 60 million people (Scheuermann et al., 2012). In Africa, the region's relatively high humidity has caused the widespread occurrence of the disease, resulting in severe yield losses. Surveys in Burkina Faso recorded yield losses of 17-599 kg/ha (1-22% of production) in the rainfed lowlands and 134-867 kg/ha (4.2-45.3% of production) in irrigated systems (Séré et al., 2008) due to blast. Also, yield losses of up to 100% because of blast have been reported in Gambia (Jobe et al., 2002).

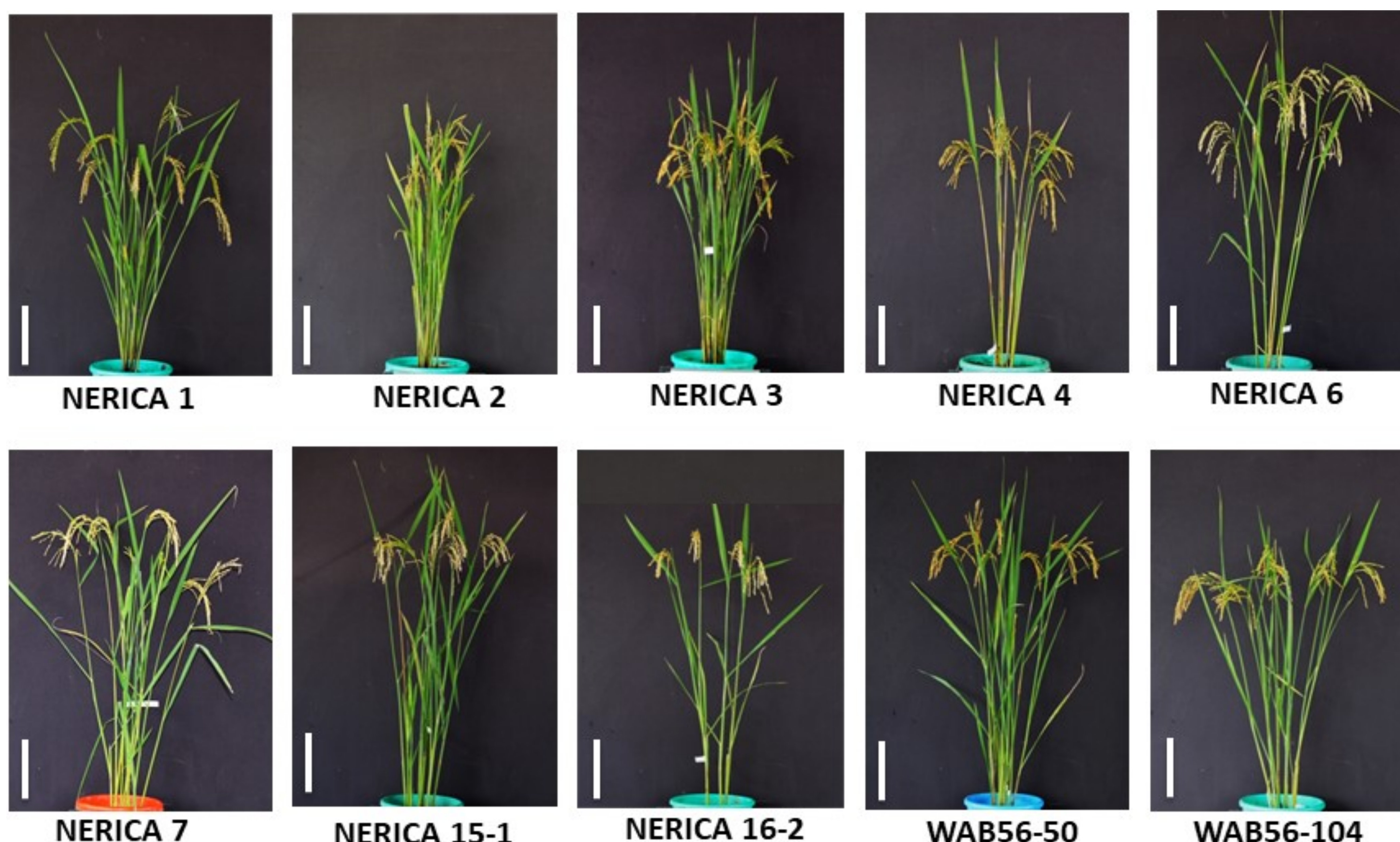
Breeding blast resistant varieties is an effective way to help farmers control the disease, especially in resource-poor farmers' fields (Séré et al., 2007). The quantitative blast resistance gene, *pi21*, was isolated from the *japonica* rice cultivar, Owarihatamochi (Fukuoka et al., 2001). The *pi21* has field resistance and functions by allowing the development of sporulating lesions in the plants but suppressing lesion expansion and spore formation, thereby slowing the spread of the disease (Fukuoka et al., 2009). While complete resistance often fails to overcome new compatible blast races (Kiyosawa 1982), genes conferring field resistance such as *pi21* are considered to be durable, especially under exposure to new blast races. Under the WISH breeding program, the *japonica* rice cultivar Sensho, having the resistant *pi21* allele, was used as a donor to improve blast resistance in our target rice varieties.

### ***Identification of target rice varieties for improvement***

Consideration of the environmental conditions and the needs of the end-users are two primary criteria for the success of conventional breeding programs targeting any particular trait. Professional breeders, who are often not actual farmers, tend to focus on yield and disease resistance, and place in lower priority the basic preferences of the rice farmers for particular traits such as grain color, shape and taste; crop maturation; and ease of harvesting and storage. When improvement of a rice variety does not match the farmers' requirements, the variety will most likely not be adopted. To lessen the risk of non-acceptability of newly developed varieties by farmers, breeding programs have started to involve close collaborations with farmers, consumers and end-users in a strategy known as participatory plant breeding (PPB). Although the term PBB has been used in many cases, it always focuses on individual environments and end-users' needs, making it easier for the farmers to adopt whatever variety the breeders develop (Ceccarelli and Grando, 2009).

Under the WISH project, our priority was to improve existing rice varieties, rather than to develop new ones. The selection of the varieties to improve was based on the preference of farmers for particular traits as well as on the availability of varieties with inherent adaptation to various environmental stresses.



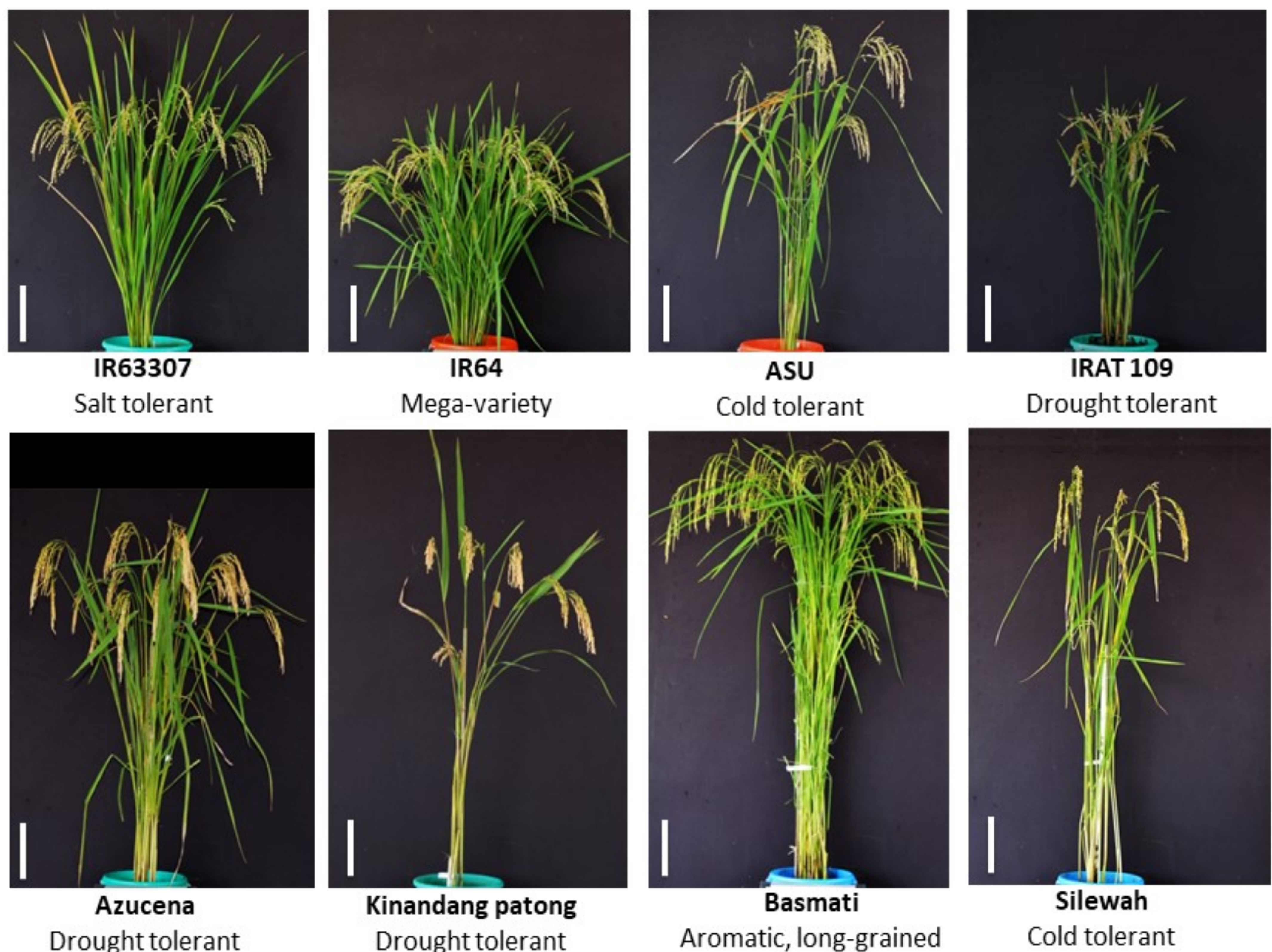


**Fig 3. NERICA lines that were selected for improvement under the WISH Project. bar=10cm**

Because the WISH project is geared towards contributing in the general improvement of the rice sector in Africa, we included several NERICA varieties in our breeding program (Fig 3). The NERICAs or New Rice for Africa varieties were originally derived from crosses between *O. sativa* and *O. glaberrima*. These varieties were developed at the Africa Rice Center (WARDA) in the 1990s to rescue millions of poor rice farmers in sub-Saharan Africa (SSA). NERICAs have the combined high yield performance and short growth cycle of the Asian cultivated rice *O. sativa*, and the natural resistance to harsh environments of *O. glaberrima*. Initially, 18 NERICA varieties were generated, with NERICAs 1 to 11 being developed by crossing the released variety CG 14 (*O. glaberrima*) with WAB56-104 (*O. sativa*). NERICA 12 to 18 were developed by crossing the same *O. glaberrima* parent (CG14) with two different *O. sativa* parent namely WAB56-50 and WAB181-18. These NERICA lines have many advantages including high yield, short growth duration, early vigor which contributes to weed competitiveness, good cooking and eating qualities that are acceptable to local consumers, and high protein content. Due to these advantages, the NERICA varieties have been adopted in many countries, summing up to 200,000 hectares across Africa in 2006 (Somado, Guei, and Keya, 2008). In Côte d'Ivoire, the introduction of NERICAs had a big impact on female farmers, increasing yields in women's fields up to 741 kg/ha (Diagne 2006). Guinea also shows a relatively high level of NERICA adoption, using the short-duration NERICA varieties to complement long-duration traditional varieties (Barry et al., 2008).

Aside from the NERICAs, we also targeted to improve varieties that have inherent adaptation to various abiotic stresses including drought, cold and salinity (Fig 4). The complexity of abiotic stress stress tolerance has limited the extensive elucidation of the molecular mechanism underlying such traits. For example, drought resistance is regulated by numerous small-effect loci and is highly affected by the interaction between these loci and the environment (Hu and Xiong, 2014). Since there is no single gene or QTL that can confer drought tolerance to a variety, it was more strategic to improve the existing drought tolerant varieties than to transfer multiple genes controlling the trait into a target variety. Our selection of varieties with tolerance to various abiotic stresses are already locally grown by farmers in target regions and therefore are suitable as breeding materials.





**Fig 4. Examples of Asian rice varieties that were selected for improvement under the WISH Project. bar=10cm**

#### *Introgression of target traits into target rice varieties by marker-assisted selection*

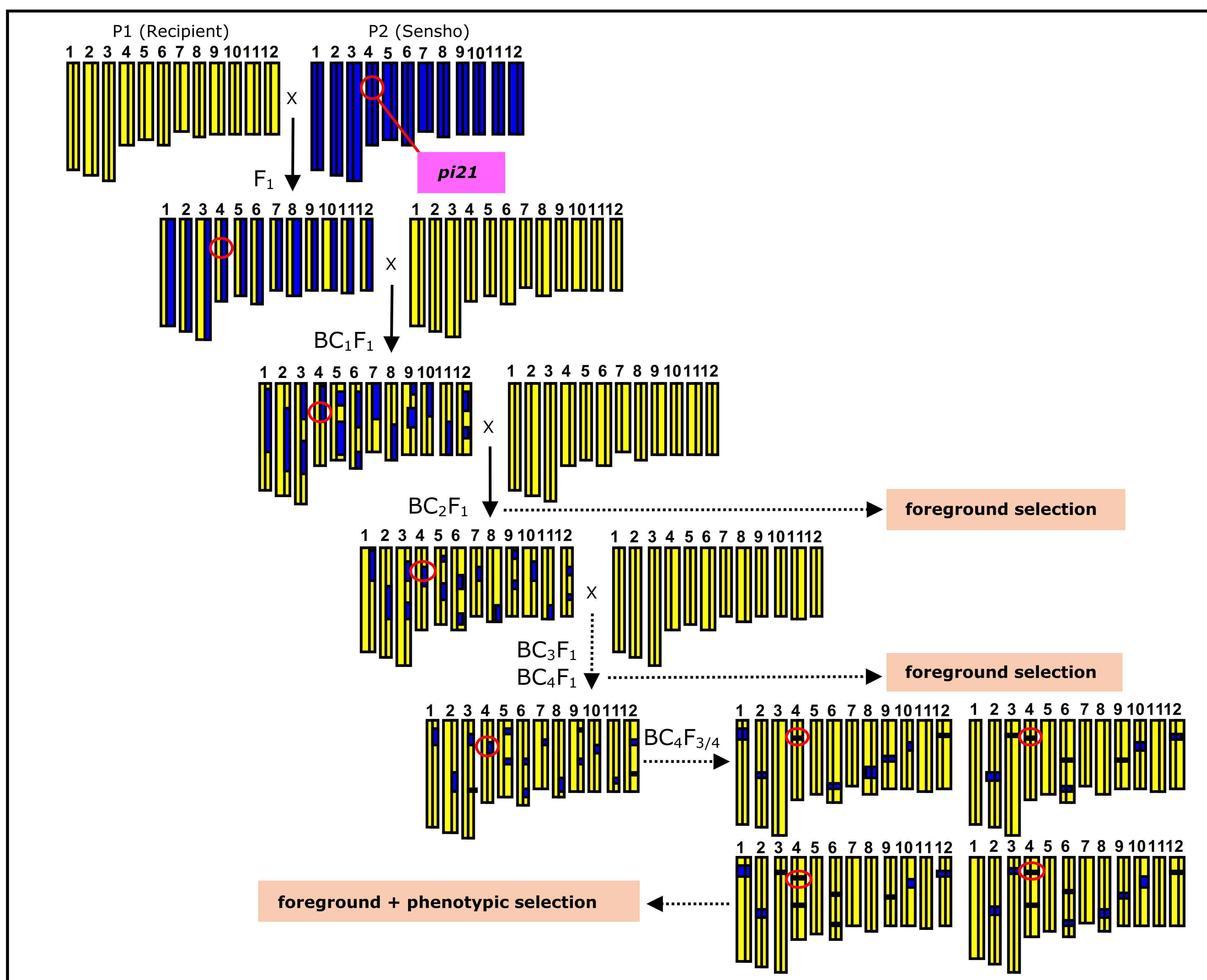
The advent of molecular marker technology in the late 1980s significantly changed the landscape for crop breeding. Development of molecular markers such as restriction fragment length polymorphism, amplified fragment length polymorphism, expressed sequence tags, simple sequence repeats and most recently, single nucleotide polymorphism have made mapping of genetic loci controlling complex traits possible. To date, thousands of genes/QTLs controlling traits of agricultural importance have been identified and some of them, cloned including *Gn1a* and *WFP* ([www.gramene.org](http://www.gramene.org)). Because mapping capitalizes on the linkage between a genetic marker and a gene, markers that have been identified as tightly linked to a gene controlling a trait of interest can be used to indirectly select for a specific phenotype. This approach is known as marker-assisted selection or MAS.

As a breeding tool, MAS offers several advantages compared to conventional breeding. First, it is generally simpler than phenotypic screening and hence can save time, resources, and effort (Collard and Mackill et al., 2008). Second, MAS can be carried out during the early growth stages of the plant, enabling early selection and exclusion of undesirable plant genotypes (Collard and Mackill et al., 2008). In rice for example, selection for a trait related to the panicles has to wait until the later reproductive stage of the plant when the phenotype is already visible. In cases where materials have to be crossed, this kind of visual selection could be too late. With MAS, materials carrying the trait of interest can be selected even before transplanting and those without the target genes can be immediately discarded.



Third, single plants can be selected from plant families by the application of MAS because it clarifies the individual genotypes of plants. MAS can distinguish between plants with a homozygous or heterozygous genotype, whereas for conventional phenotypic selection, this is almost impossible by (Collard and Mackill et al., 2008). Lastly, it helps in identifying the true identity of materials and contributes to early discovery of contamination due to the sheer number of breeding lines to be managed.

Under the WISH project, genes controlling grain number (*Gn1a*) and number of primary branches per panicle (*WFP*), as well as blast resistance (*pi21*) were introgressed into the target varieties by marker-assisted backcrossing (Fig 5). Target varieties that are being improved for grain number and number of primary branches per panicle were backcrossed to the recurrent parent 3 times before subjecting the breeding lines to generation advance via selfing. Ideally, backcrossing 3 times to the recurrent parents would allow the recovery of more than 93% of genetic background of the target variety. Generation advance via selfing would fix heterozygous fragments in the genetic background of the recurrent parent although the proportion of fixation would be more random.



**Fig 5. Backcrossing scheme for the marker-assisted backcrossing approach used to transfer *Gn1a*, *WFP* and *pi21* to WISH target varieties.**



Nevertheless, this would also increase the recovery of the original genetic composition of the recurrent parent. Target varieties that are being improved for blast resistance were backcrossed 4 times before advancing via self-fertilization. Breeding for disease resistance have been reported to be commonly accompanied by linkage drags which results in the reduction in the fitness of a cultivar due the co-introduction of deleterious genes with the genes of interest. The *pi21* has been reported to be linked with genes that are associated with poor eating quality (Fukuoka, 2009). The higher number of backcrosses not only allows the recovery of a higher proportion of the recurrent genome but also helps in dissecting linkage drags using molecular markers that are closely linked to *pi21*.

Marker-assisted selection for *Gn1a*, *WFP* and *pi21* was carried out starting from the BC<sub>1</sub>F<sub>1</sub> generation. The list of markers used to monitor the introgression of the target genes in the target varieties at various stages of development are presented in Table 1 and Table 2. Phenotypic selection was also carried out in the field to make sure that the materials that were selected for backcrossing or generation advance are similar in gross morphology as the recurrent parent.

The combined backcrossing and generation advance for each target variety under the WISH project was geared towards the development of NILs. Ultimately, it is also the objective of this project to pyramid target genes for yield as well as for blast resistance into a single genetic background.

**Table 1. List of SSR markers that were used to monitor the introgression of *Gn1a* and *WFP* from the donor to the target rice varieties. An indel marker was used to monitor the introgression of *pi21* in target rice varieties. The check mark indicates the applicability of the marker for monitoring the transfer of each of the target genes into target rice varieties.**

Recurrent parent	Gn1a (5269-5274 kb)				WFP (25274-25279)			pi21
	downstream			upstream	downstream		upstream	
	RM3233 5055 kb	RM3425 5116 kb	RM3360 5236 kb	RM10319 5363 kb	RM23667 24563 kb	RM3452 24777 kb	RM5493 26145 kb	
NERICA 1	✓	☒	✓	☒	☒	✓	✓	✓
NERICA 3	✓	✓	✓	✓	✓	✓	✓	-
NERICA 4	☒	✓	✓	✓	✓	✓	☒	-
NERICA 6	☒	✓	✓	✓	✓	✓	✓	✓
NERICA 7	✓	✓	✓	✓	✓	✓	✓	-
NERICA 15-1	✓	✓	✓	✓	✓	✓	✓	-
NERICA 16-2	✓	✓	✓	✓	✓	✓	✓	-
WAB 56-50	☒	☒	✓	✓	✓	✓	✓	-
WAB 56-104	☒	☒	✓	✓	✓	✓	✓	-
IR6604	✓	✓	✓	✓	✓	✓	✓	-
IR64	✓	✓	☒	✓	✓	✓	✓	-
Azucena	✓	✓	✓	☒	☒	✓	✓	✓
Kinandang Patong	✓	✓	✓	☒	☒	✓	✓	✓
IRAT 109	✓	✓	✓	✓	✓	✓	✓	✓
ASU	✓	✓	✓	✓	☒	✓	✓	-
Silewah	✓	✓	✓	✓	☒	✓	✓	-
Basmati	✓	✓	✓	✓	✓	✓	✓	✓



## Testing of the performance of improved rice varieties in target regions

Many rice varieties with improved yield have been developed and released in the last couple of decades. The International Rice Research Institute (IRRI) alone has released more than a thousand of IRRI-bred and improved rice varieties in 78 countries since its establishment in 1960 ([www.irri.org](http://www.irri.org)). Some of these varieties became “successful” in that they were accepted by local farmers and consequently disseminated at a larger scale. However, this has not always been the case. While breeders tend to focus on specific target traits, farmers may have other criteria in adopting a variety for cultivation.

Under the WISH project, regionally preferred varieties were chosen for improvement to lessen the negative factors that may contribute to the non-acceptability of the improved varieties by farmers.

Products of initial crosses were backcrossed 3 times and then selfed at least 6-7 times to recover as much of the genetic constitution of the recurrent parent as possible. Ideally, such lines would have the phenotype of the recurrent parent with the addition of the improved target trait. However, genetic exchanges between the donor and the recurrent parent during intercrossing are very likely to affect the expression of other traits aside from the target character for improvement. Thus, it is critical to have the local farmers check and select the improved varieties for their actual performance in the field. In addition, complex traits such as yield, is largely affected by differences in temperature, light intensity, humidity, soil nutrition, water component and irrigation management. Differences in the performance of WISH lines under different target areas can therefore be expected.

**Table 2. Sequence of markers used in monitoring the introgression of *Gn1a*, *WFP* and *pi21* in target rice varieties.**

Marker Name	Primer Sequence		Target QTL/gene	QTL/Gene donor	Remarks
	Forward primer	Reverse primer			
RM8146	AGCAGCGCCAGTGTGAGAACC	CCATTCTGCTTCGAGGATGAAACC	Gn1	ST6/ST12	upstream marker
RM5423	TCCCACTTGCAGACGTAGGTAGG	CACTGATCTGATGCAACTGTTTGG	Gn1	ST6/ST12	upstream marker
RM3425	CAGCAGCAAGAACCCTAGAAATCC	CTCGTGATCAACCGACAAAGC	Gn1	ST6/ST12	upstream marker
RM10314	CATGCATACTTTGTGCCTTGTC	GCACGTGCTCCTACATTGATGC	Gn1	ST6/ST12	upstream marker
RM3360	ACTTACACAAGGCCGGGAAAGG	TGGTAGTGGTAACTCTACTCCGATGG	Gn1	ST6/ST12	upstream marker
RM10310	TGCAGTAATATGCTGTGCTGATCG	AAGCTAGCTCGATTGGTCAACG	Gn1	ST6/ST12	upstream marker
RM3233	GAAATTCGAAATGGAGGGAGAGC	GGTGAGTAAACAGTGGTGGTGAGC	Gn1	ST6/ST12	upstream marker
RM10319	TCTAACACAGAACTCCCGAAGATCC	CGATCAGGAGCGTTACATATTTGG	Gn1	ST6/ST12	downstream marker
RM10326	AGCCGGGCATACAGTCTTTCTCC	TCATGGCGTGTGGCACTAGC	Gn1	ST6/ST12	downstream marker
RM10346	GCTTGATCTGCCCTTGTTCTTGG	AACTCGAGCGGCCTTCTCAGC	Gn1	ST6/ST12	downstream marker
RM3452	TGGAATTGGTCTCTCCAACTCC	CAGTATGTGTTGGTGGTCAAGC	WFP	ST6/ST12	upstream marker
RM23367	CCAGTGTGCGACACTAATCTTCC	ACGAACATAGCGCCAAATCTCC	WFP	ST6/ST12	upstream marker
RM23408	CCATCTCAACTCCTTCGTTTACTGC	TCGACTGTTTGCTTGAATAGGC	WFP	ST6/ST12	upstream marker
RM3634	TTTCCGGTCTCTCGCTAAGTTGC	AACCTCGTCATCGGCCTGTAAGC	WFP	ST6/ST12	upstream marker
RM5493	GCGGTAACAAACCAACCAACC	AAAGCAGGACACAGTCACACAGG	WFP	ST6/ST12	downstream marker
pi21	GATCCTCATCGTCGACGTCTGGC	AGGGTACGGCACCAGCTTG	pi21	Sensho	

Thus, it is critical to have the local farmers check and select the improved varieties for their actual performance in the field. In addition, complex traits such as yield, is largely affected by differences in temperature, light intensity, humidity, soil nutrition, water component and irrigation management. Differences in the performance of WISH lines under different target areas can therefore be expected. Similarly, local performance testing is a very important part of breeding for improved disease resistance. Field screening in Africa of varieties with resistance to Asian blast pathogens demonstrates the existence of different blast pathotypes between these two continents (Séré et al., 2007). Hence, WISH lines that show resistance to blast in the Philippines can be susceptible to African pathotypes when tested in targeted regions in Africa. Conversely, lines representing negative results in the Philippines may be resistant to blast pathogens in Africa, since most of the genomic background is derived from African locally preferred varieties.



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