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OMICS International conferenceseries.com
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Brisbane, Australia July 14-15, 2016

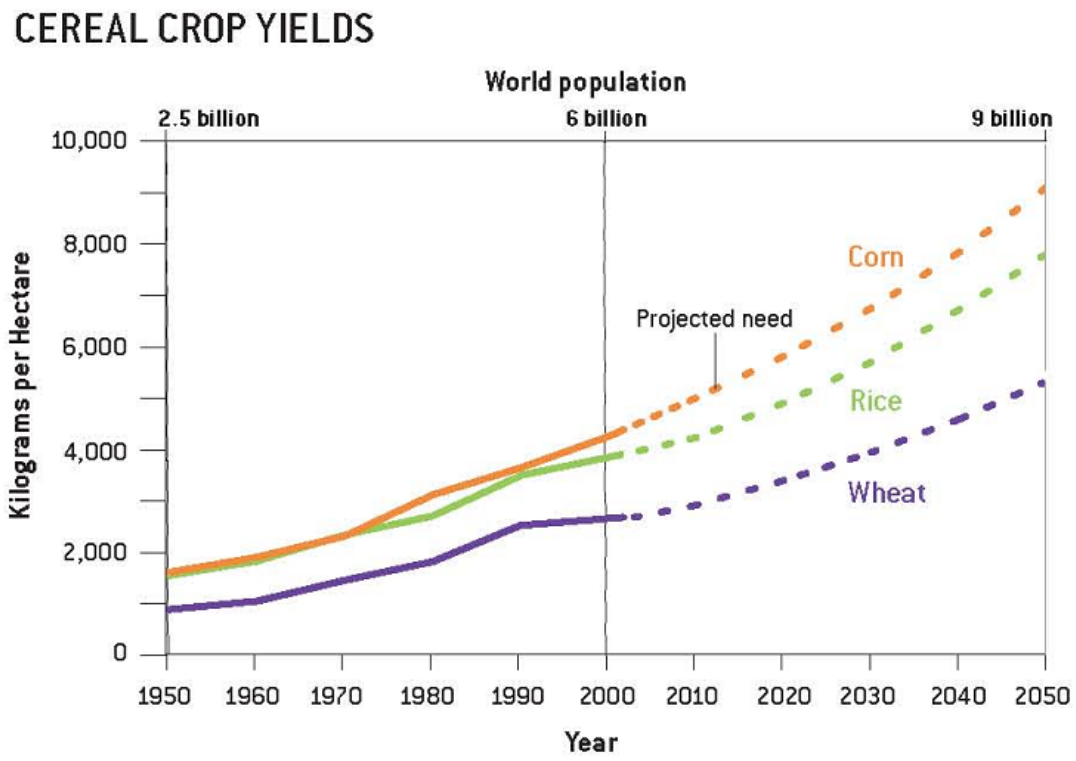
Harnessing the hidden genetic diversity for improving multiple abiotic stress tolerance in rice

Jianlong Xu

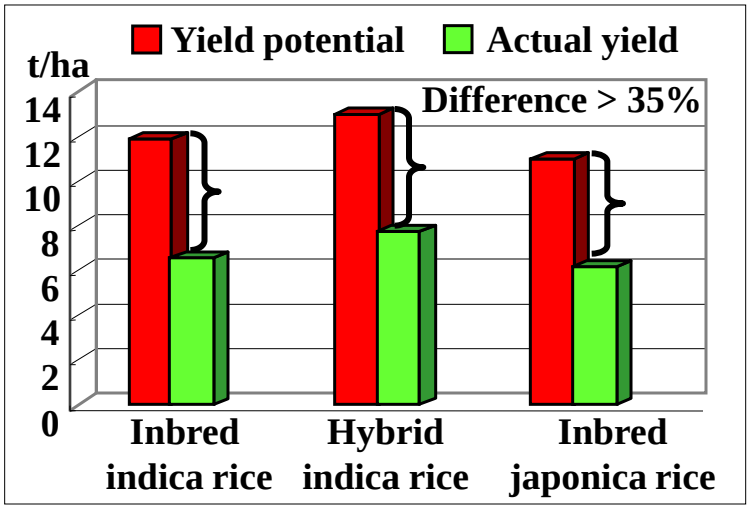
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Actual yield in farmer field is much lower than theoretical yield due to various biotic and abiotic stresses. Future breeding will focus on: improving yield potential or improving biotic and abiotic stress tolerances based on existing yield level.

Improving yield potential



Filling yield gaps



Goff and Salmeron 2004 Scientific American 291(2) 42-49

Besides biotic stresses such as diseases and insects, drought, salinity, extreme low or high temperature, etc. are most important abiotic stresses affecting rice yield.

In the past, less efforts have been taken in rice breeding for stress tolerance. So there is slow advance in stress tolerance breeding compared with other traits.



Drought



Salinity



High temperature

Stress tolerances are quantitatively inherited and very complex. So far, a wide range of segregating populations derived from bi-parental crosses have been used for QTL mapping, and many important QTLs have been identified and cloned in rice. Contrastly, slow progresses have been made so far in MAS-based breeding for complex traits, mainly due to the following two aspects.

(1) Populations derived from bi-parents can't identify favorable alleles for the target trait. Thus we have no idea about which favorable alleles for use in molecular breeding.

(2) QTLs are largely dependent on genetic background. So QTL detected in mapping population is most probably unsuitable use in breeding population due to separation of mapping and breeding populations.

Germplasm holds a large of genetic variation for improving agricultural crops. Although backcross is effective to improve simple qualitative traits, but very few successful improvement of quantitative traits.

Here we demonstrate a new strategy to establish breeding populations for integration of QTL mapping and simultaneous improvement for multiple complex traits in rice.





Recurrent parent: Huang-Hua-Zhan (HHZ)



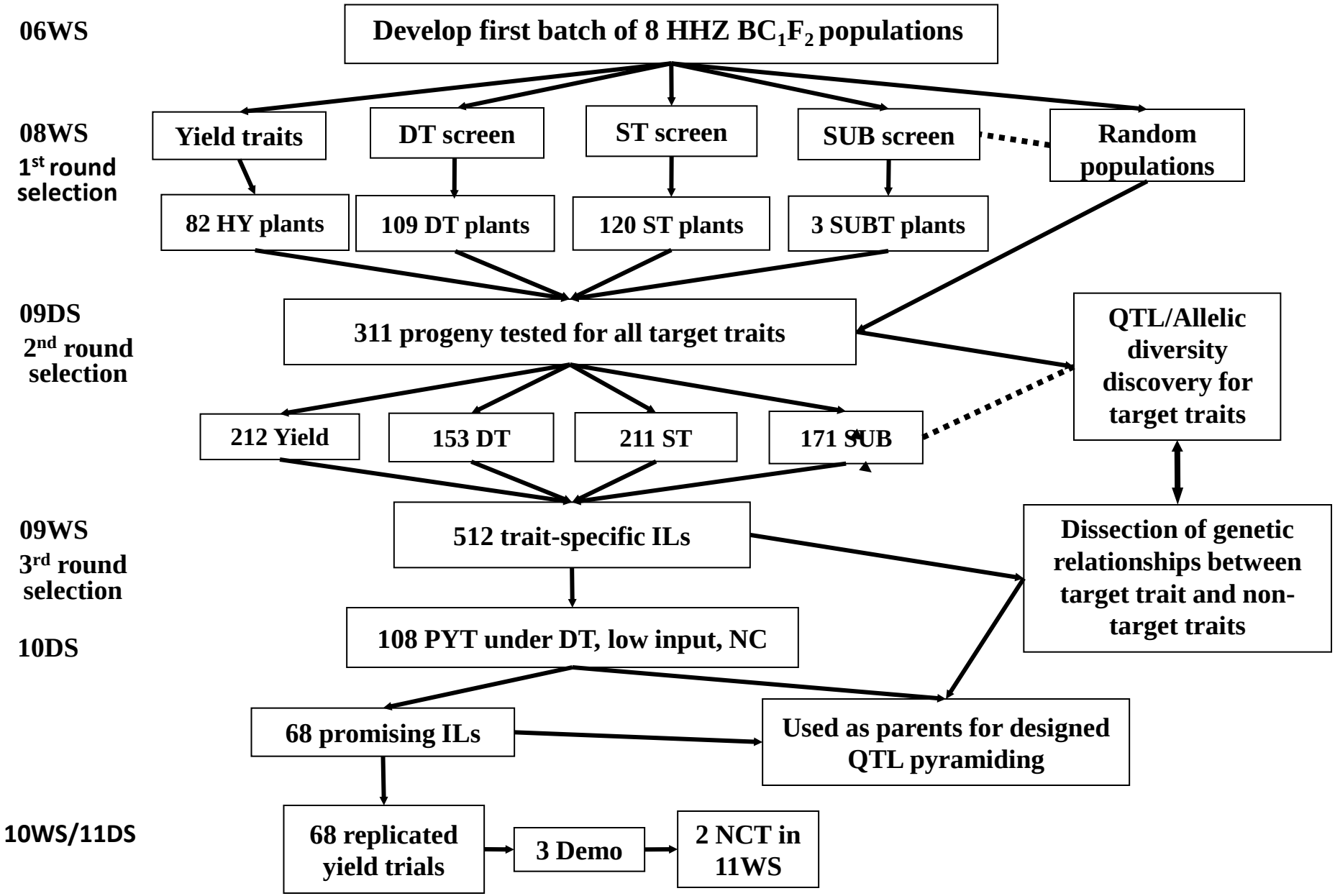
Huang-Hua-Zhan （HHZ）

- High yield, high grain quality and wide adaptation
- Registered by more than 8 provinces in China
- Extension area up to 5 million hectare in China

Two batches of 16 populations with the recurrent parent, Huang-Hua-Zhan (HHZ) and 16 donors from 9 different countries

Batch	Pop.	Donor	Country of origin	Gen.(10 DS)
1	HHZ5	OM1723	Vietnam (I)	BC1F5
1	HHZ8	Phalguna	India (I)	BC1F5
1	HHZ9	IR50	IRRI (I)	BC1F5
1	HHZ11	IR64	IRRI (I)	BC1F5
1	HHZ12	Teqing	China (I)	BC1F5
1	HHZ15	PSB Rc66	Philippines (I)	BC1F5
1	HHZ17	CDR22	India (I)	BC1F5
1	HHZ19	PSB Rc28	Philippines (I)	BC1F5
2	HHZ1	Yue-Xiang-Zhan	China (I)	BC1F4
2	HHZ2	Khazar	Iran (J)	BC1F4
2	HHZ3	OM1706	Vietnam (I)	BC1F4
2	HHZ6	IRAT352	CIAT (upland)	BC1F4
2	HHZ10	Zhong 413	China (I)	BC1F4
2	HHZ14	R644	China (I)	BC1F4
2	HHZ16	IR58025B	IRRI (I)	BC1F4
2	HHZ18	Bg304	Sri Lanka (I)	BC1F4

The Introgression Breeding Procedure for Batch 1



Population	Selection	Seed generation	Target trait		No of selected lines	Total no of lines of each trait	No. of lines of each generation	No. of lines of each population
HHZ5	1st selection（08WS）	BC1F3	Yield		11		47	161
			DT		21			
			ST		15			
	2nd selection（09DS）	BC1F4	yield	yield－yield	21	36	114	
				DT－yield	6			
				ST－yield	9			
			DT	yield－DT	6	51		
				DT－DT	27			
				ST－DT	18			
			ST	yield－ST	6	27		
				DT－ST	0			
				ST－ST	21			
HHZ8	1st selection（08WS）	BC1F3	Yield		9		37	93
			DT		13			
			ST		15			
	2nd selection（09DS）	BC1F4	yield	yield－yield	3	15	56	
				DT－yield	0			
				ST－yield	12			
			DT	yield－DT	12	15		
				DT－DT	0			
				ST－DT	3			
			ST	yield－ST	0	26		
				DT－ST	12			
				ST－ST	14			



HHZ background ILs grown in wet season at IRRI

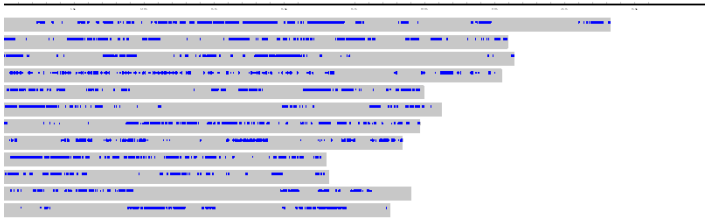
Parental genome sequencing information (clean data)

	Base number (G)	Genome equivalent (x)
CDR22	8.4	19.6
HHZ	14.6	33.9
IR50	7.7	17.8
IR64	6.9	16.1
OM1723	5.9	13.7
Phalguna	6.9	16.0
PSBRc28	9.3	21.6
PSBRc66	7.7	18.0
Teqing	17.4	40.5
Average	9.4	21.9

Sequencing (2-3x) of the 497 HHZ ILs resulted in 3782 bins based on 400 K SNPs across the rice genome.

Distribution of 400 K SNPs based on sequence data of the 9 parents

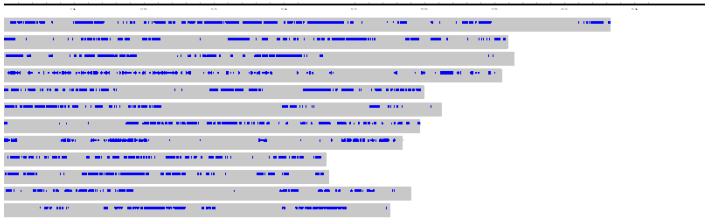
HHZ 5



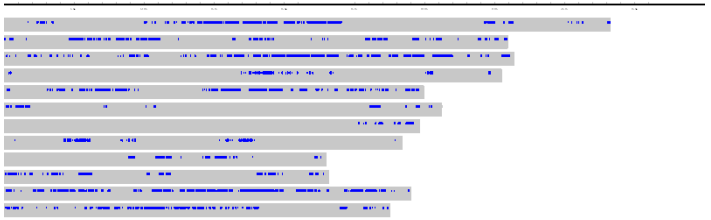
HHZ 12



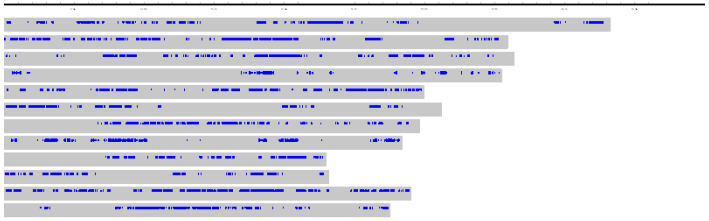
HHZ 8



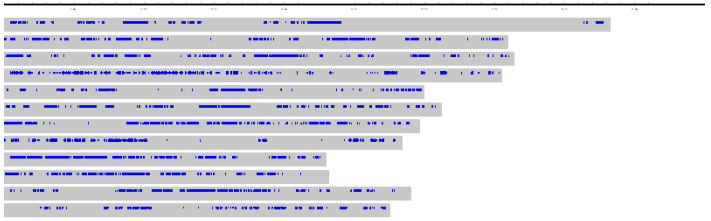
HHZ 15



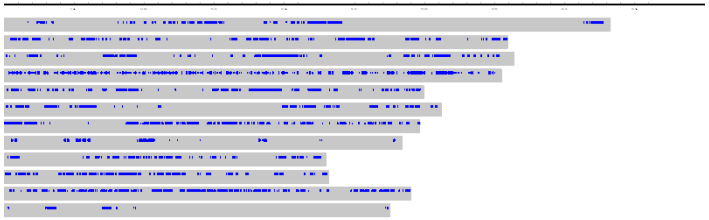
HHZ 9



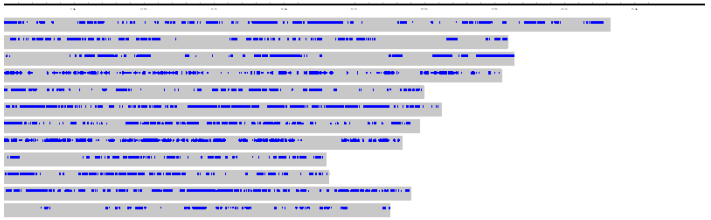
HHZ 17

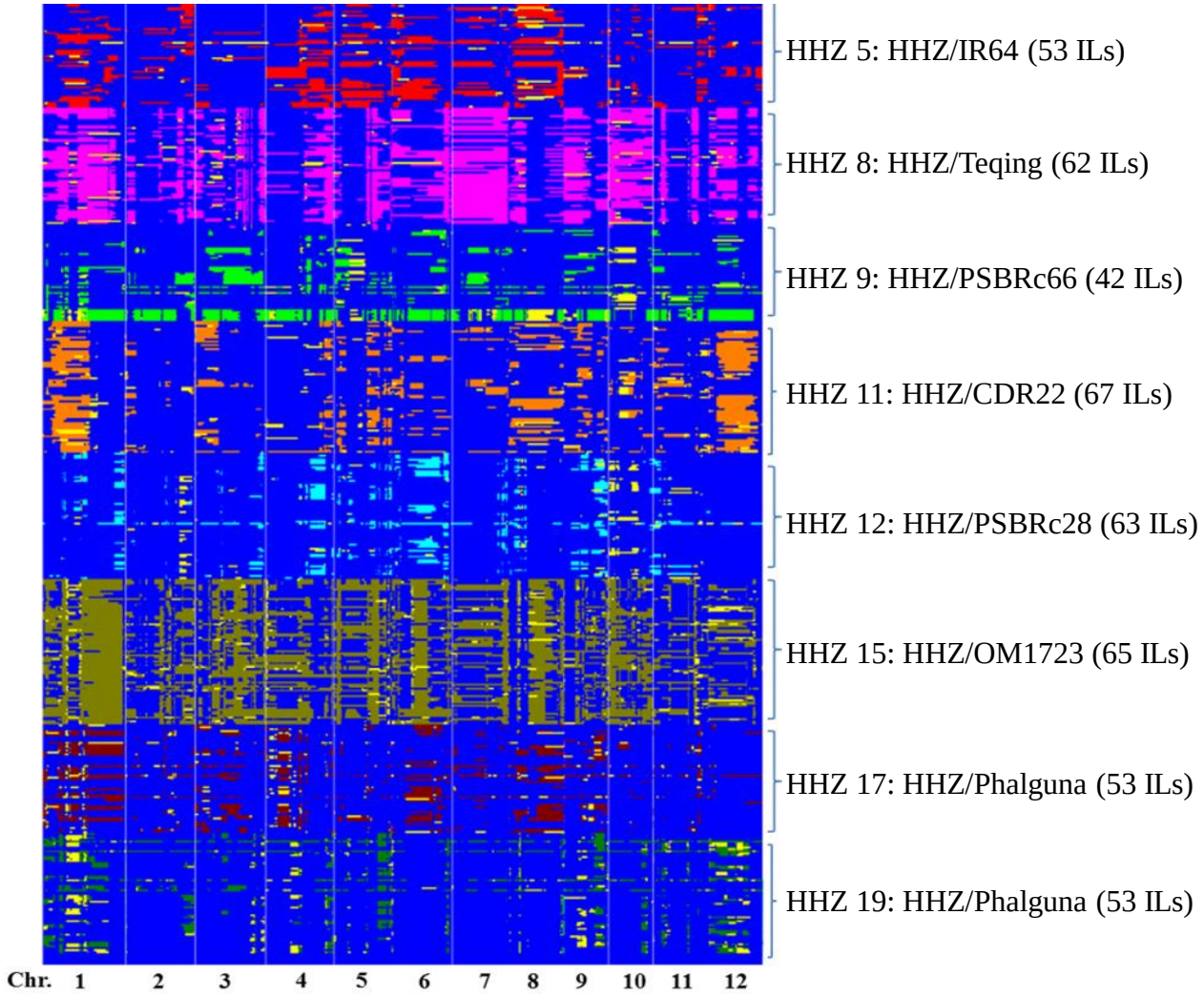


HHZ 11



HHZ 19





Graphical genotype. Blue for HHZ, yellow for heterozygote , and other 8 colors for corresponding donors

Using selected ILs to identify QTL for target trait

Principle of QTL detection

Compared with the expected ratio in the random population (60 individuals as a check), a significant deviation (excess or deficiency) of donor allele frequency at single loci in the selected IL population implies a positive selection favoring the donor allele (in excess), or negative selection against the donor allele (in deficiency). So, significant deviation loci are considered as QTL affecting the selected traits.

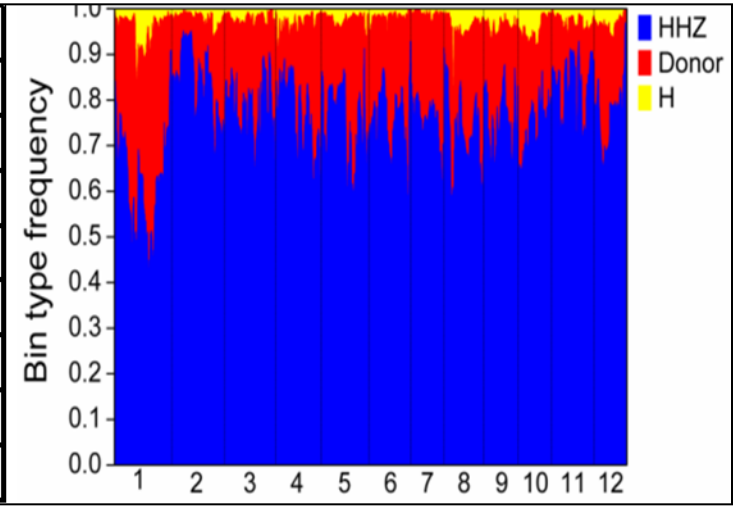
Gene action at putative QTL

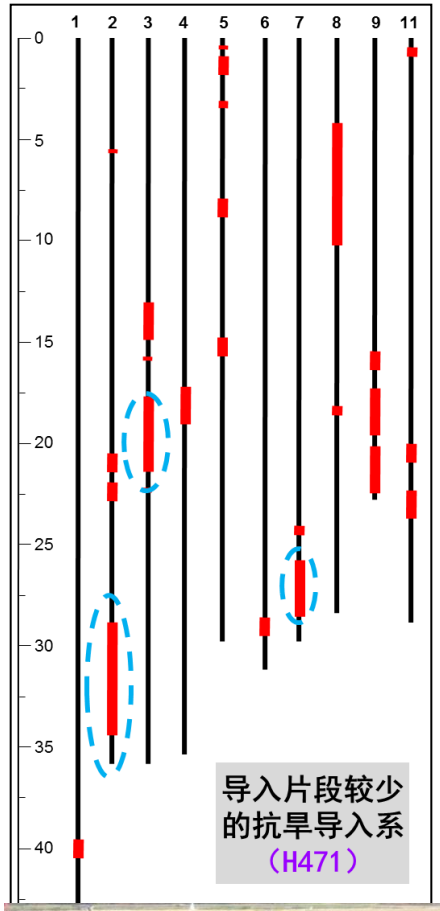
- **Excess of the donor homozygote → additive gene action**
- **Excess of the heterozygote → overdominance gene action**
- **Excess of both the donor homozygote and heterozygote → partial or complete dominance gene action**

Li et al. PMB, 2005, 59:33-52

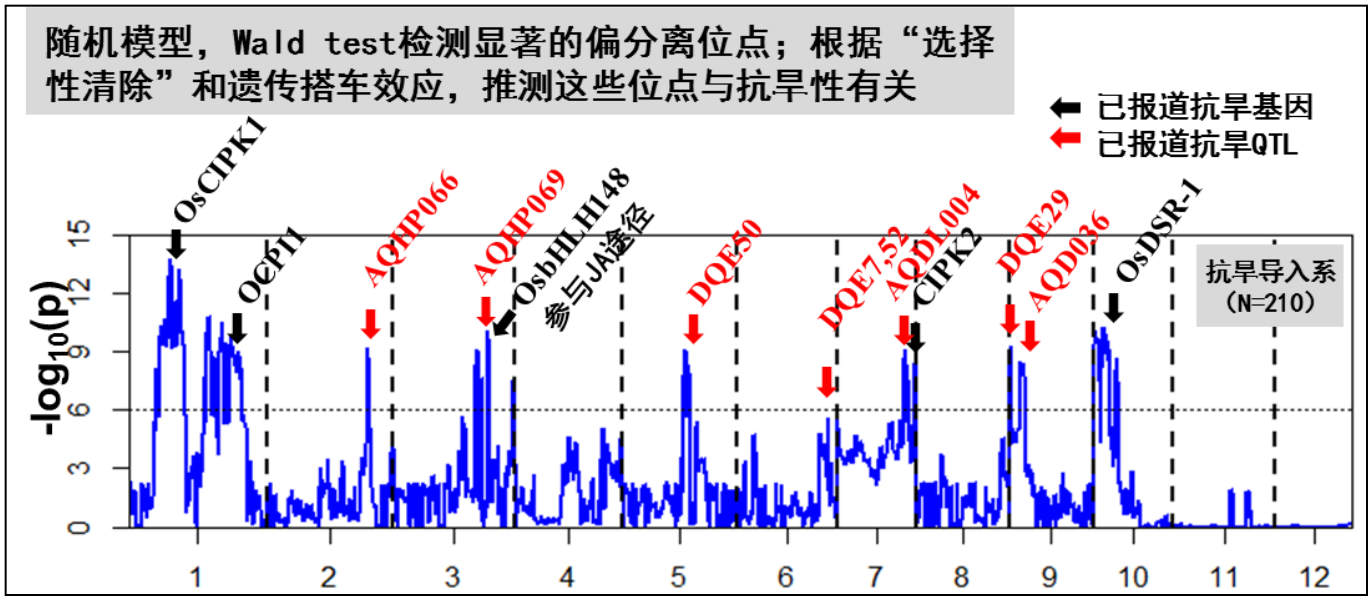
(1) QTL mapping for target trait: DT

群体	抗旱	耐盐	高产
HHZ/IR64	39	33	40
HHZ/Teqing	51	41	43
HHZ/PSBRC66	29	31	32
HHZ/CDR22	50	43	39
HHZ/PSBRC28	43	55	26
HHZ/OM1723	36	53	53
HHZ/Phalguna	35	56	42
HHZ/IR50	56	44	23



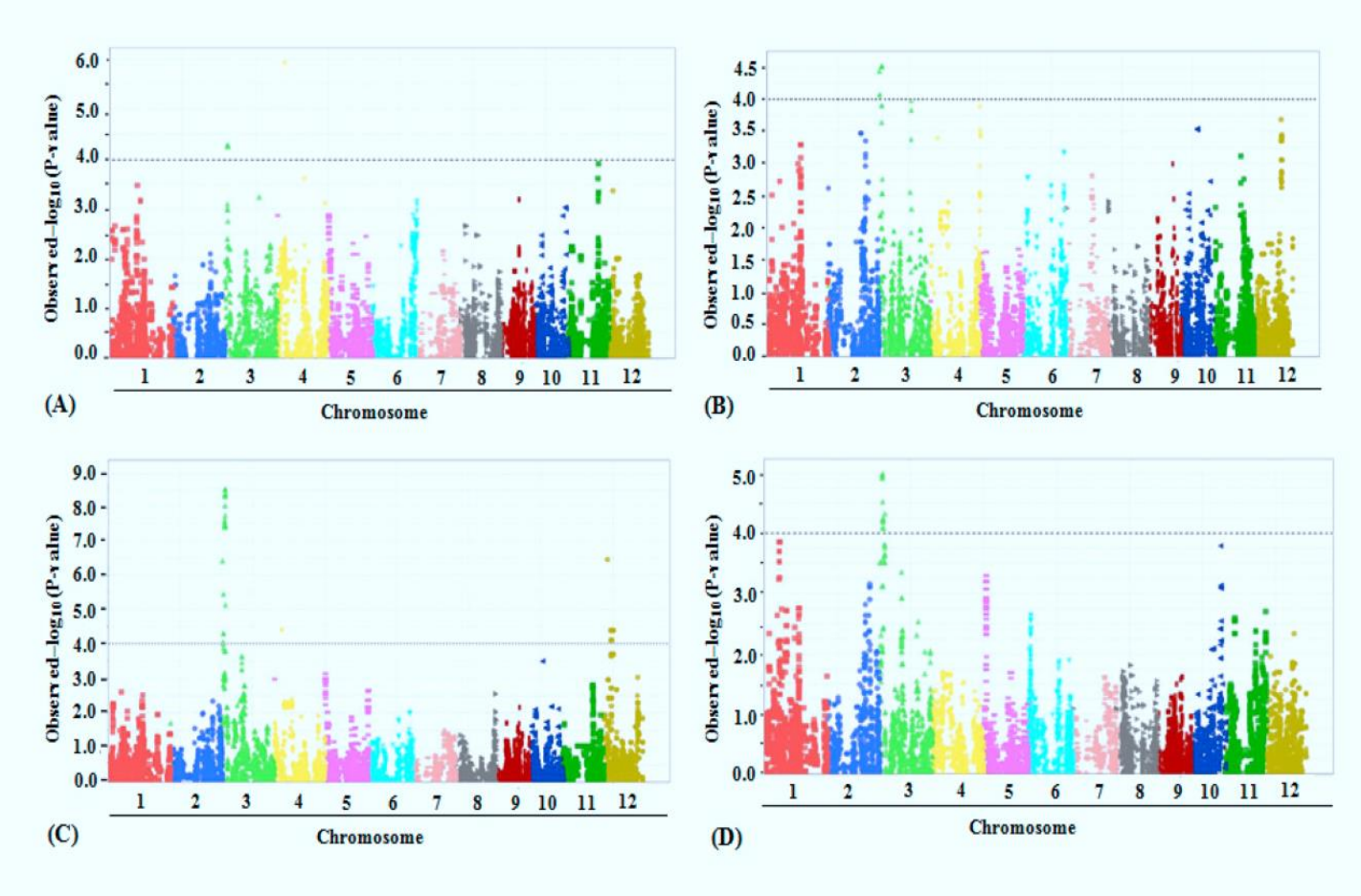


随机模型，Wald test检测显著的偏分离位点；根据“选择性清除”和遗传搭车效应，推测这些位点与抗旱性有关





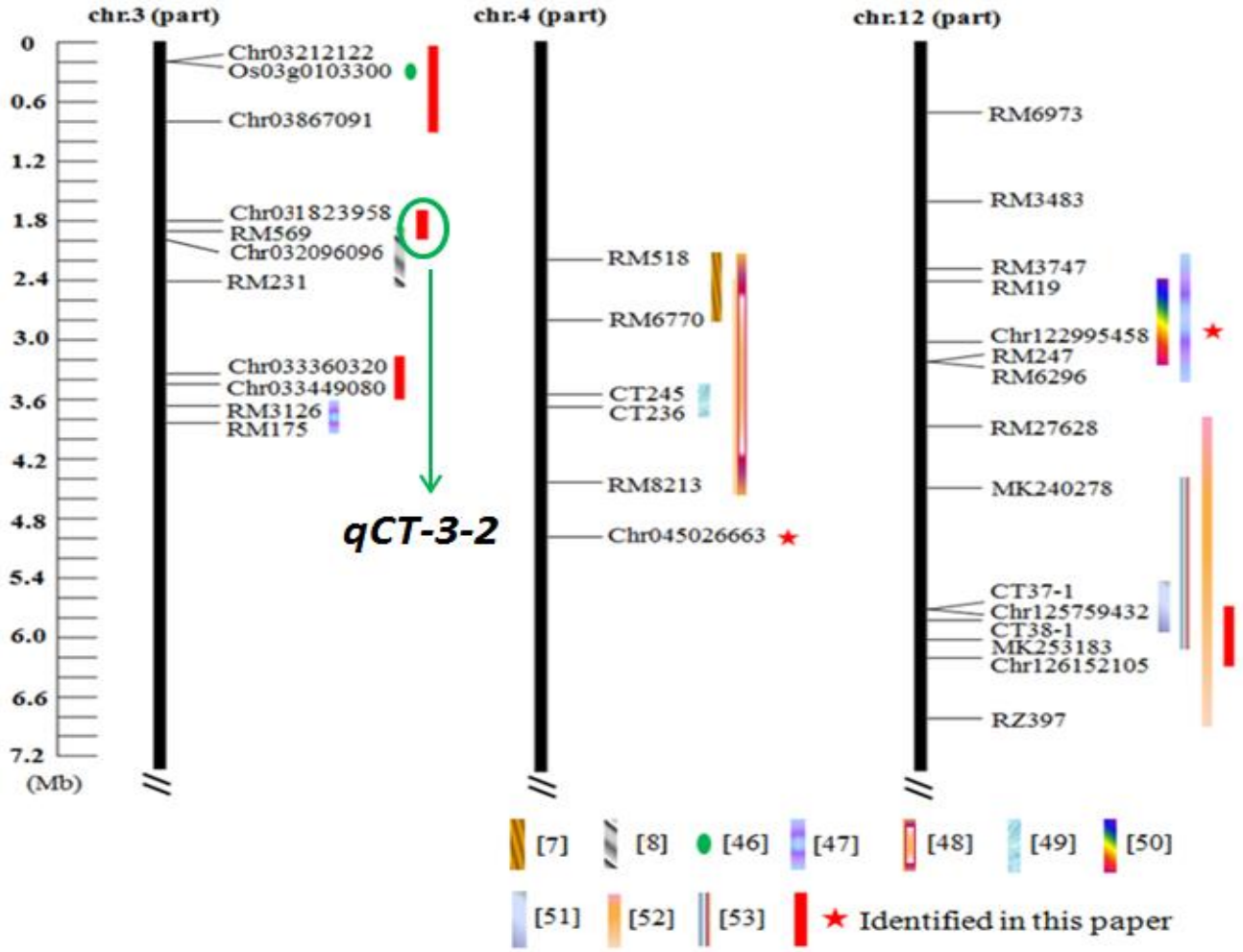
(2) QTL mapping for non-target trait: CT at booting stage



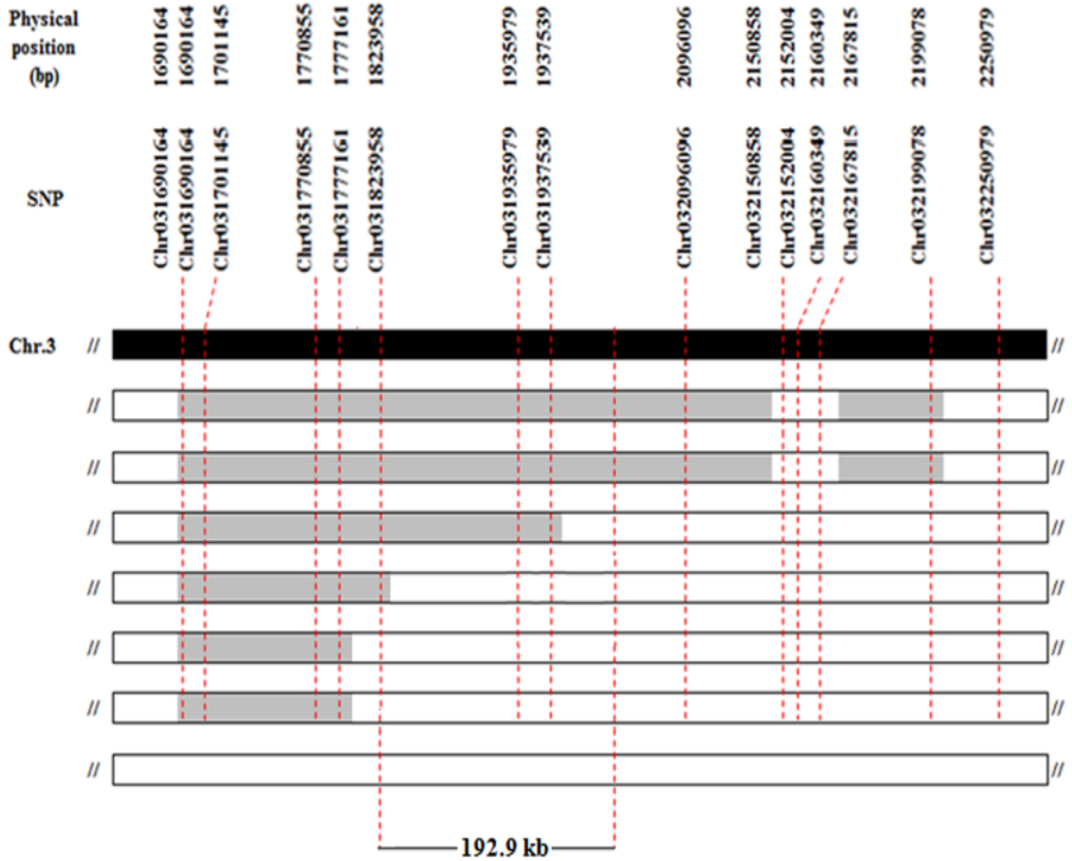
Manhattan plot for association mapping of CT in different sites

QTL for CT at booting stage detected by GWAS

Env.	QTL	Chr.	SNP at	Posi. (bp)	*P* value	贡献率 (%)
YX2013	*qCT-3-1*	3	Chr03212122	212122	3.62E-05	4.1
YX2013	***qCT-3-2***	**3**	**Chr031934364**	**1934364**	**3.00E-05**	**4.4**
XD2013	***qCT-3-2***	**3**	**Chr031935593**	**1935593**	**5.30E-05**	**4.2**
XD2013	*qCT-4*	4	Chr045026663	5026663	1.14E-06	6.7
SM2014	*qCT-3-3*	3	Chr033449080	3449080	4.72E-05	4.2
SM2014	***qCT-3-2***	**3**	**Chr031934364**	**1934364**	**1.03E-05**	**5.6**
XD2014	*qCT-3-1*	3	Chr03266205	266205	3.96E-07	6.7
XD2014	***qCT-3-2***	**3**	**Chr032108411**	**2108411**	**3.33E-09**	**9.5**
XD2014	*qCT-4*	4	Chr045026663	5026663	3.83E-05	5.1
XD2014	*qCT-12-1*	12	Chr122995458	2995458	3.64E-07	8.5
XD2014	*qCT-12-2*	12	Chr125804934	5804934	3.64E-07	4.2



Comparison of CT QTLs detected in ILs with those previously identified



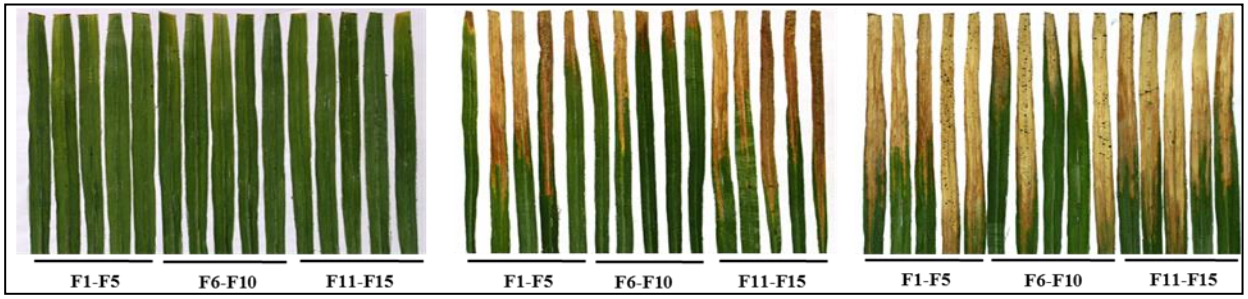
Line	Donor parent	RGP (%)	Ripening rate (%)
M166	Phalguna	95.8	9.1±0.2 A
M157	Phalguna	97.4	17.8±1.2 A
M158	Phalguna	97.3	15.3±0.9 A
M116	Phalguna	99.2	67.9±4.7 B
M557	PSBRC28	99.3	68.7±5.2 B
M543	PSBRC28	99.8	73.1±3.6 B
HHZ	-	-	64.5±4.2 B

Fine-mapping of *qCT3-2* using 8 recombination ILs in the confidence interval identified by 400,000 SNPs. White bar stands for HHZ, grey for donors. The HHZ allele at the QTL increased CT at booting stage.

Zhu et al. PLoS ONE, 2015,10(12)

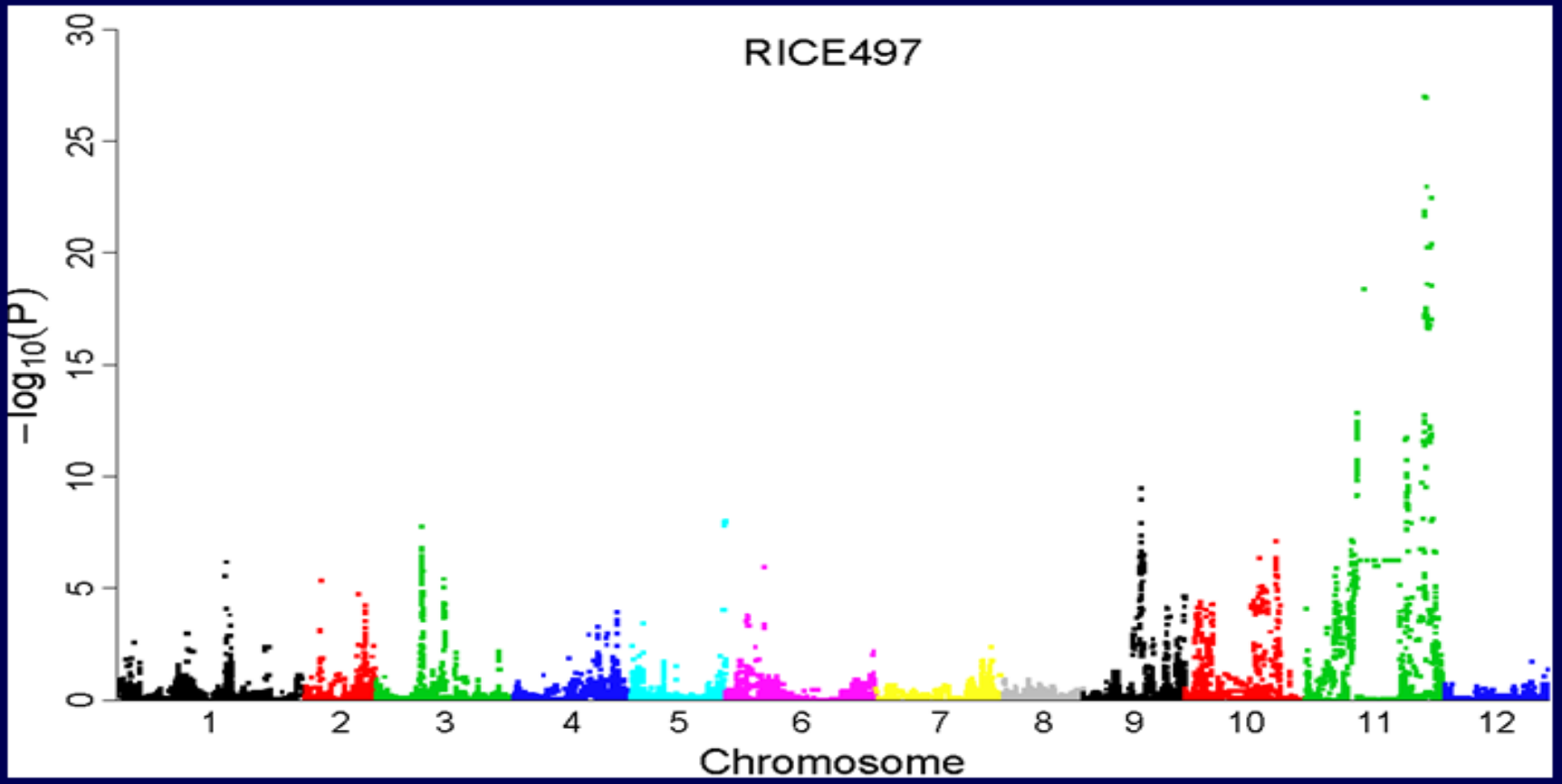
(3) QTL mapping for non-target trait: BBR

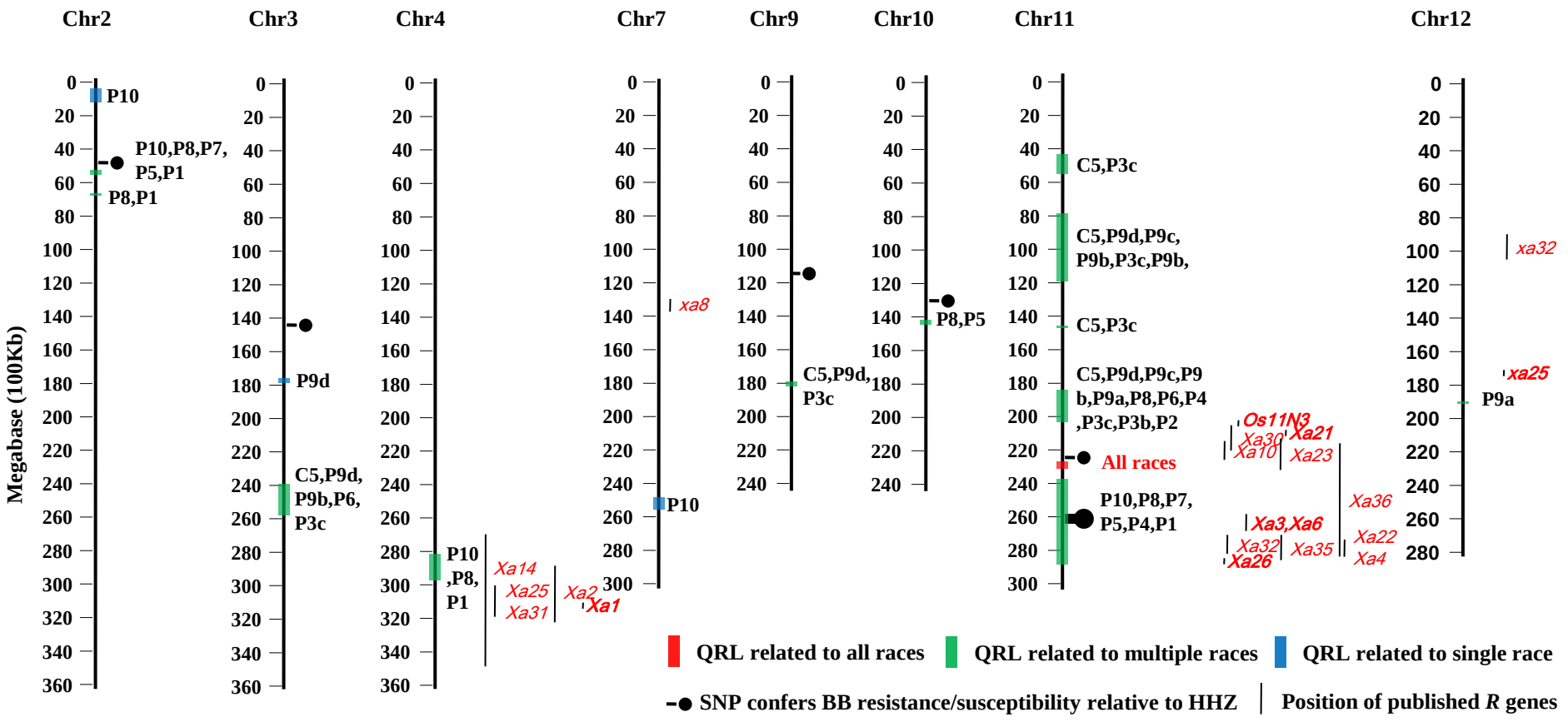
	PXO 61	PXO 86	PXO 79	PXO 340	PXO 71	PXO 112	PXO 99	PXO 145	PXO 280	PXO 339	PXO 341	PXO 347	PXO 349	PXO 363	Mean
HHZ	9.8	21.2	13.1	25.7	10.4	2.4	29.6	5.0	8.6	28.8	8.4	26.6	15.2	24.6	16.4
PSBRC66	6.4	18.5	16.4	21.4	11.6	0.7	13.0	2.6	8.8	4.1	7.0	12.0	3.4	17.3	10.2
HHZ15-SAL13-Y2	0.2	0.2	0.2	0.2	0.2	0.2	0.2	0.2	0.2	0.2	0.2	0.2	0.2	0.2	0.2
HHZ15-SAL-13-Y3	0.2	0.2	0.2	0.2	0.2	0.2	0.2	0.2	0.2	0.2	0.2	0.2	0.2	0.2	0.2
HHZ15-DT7-SAL1	0.2	0.2	0.2	0.2	0.2	0.2	0.2	0.2	0.2	0.2	0.2	0.2	0.2	0.2	0.2
HHZ15-DT7-SAL3	0.2	0.2	0.2	0.2	0.2	0.2	0.2	0.2	0.2	0.2	0.2	0.2	0.2	0.2	0.2
HHZ15-DT7-SAL6	0.2	0.2	0.2	0.2	9.3	0.2	0.2	0.2	0.2	0.2	0.2	0.2	0.2	0.2	0.9
PSBRC28	2.8	20.3	21.6	24.0	11.2	3.9	22.4	4.7	9.2	26.0	8.5	23.7	22.9	21.9	15.9
HHZ19-SAL-14-Y3	0.2	0.2	0.2	0.2	0.2	0.2	0.2	0.2	0.2	0.2	0.2	0.2	0.2	0.2	0.2
HHZ19-DT8-SAL2	0.2	0.2	0.2	0.2	0.2	0.2	0.2	0.2	0.2	0.2	0.2	0.2	0.2	0.2	0.2
HHZ19-SAL12-SAL4	0.2	0.7	0.9	0.5	0.2	0.2	0.2	0.2	0.4	0.2	0.3	0.9	0.2	0.2	0.4
HHZ19-SAL14-SAL4	0.2	1.0	0.6	0.3	0.2	0.2	0.2	0.2	0.3	0.2	0.7	0.2	0.2	0.2	0.3
HHZ19-SAL15-SAL2	0.2	3.8	2.2	0.6	0.4	0.4	0.8	0.5	0.3	0.3	0.3	0.6	0.4	0.4	0.8



R to all races R to partial races S to all races

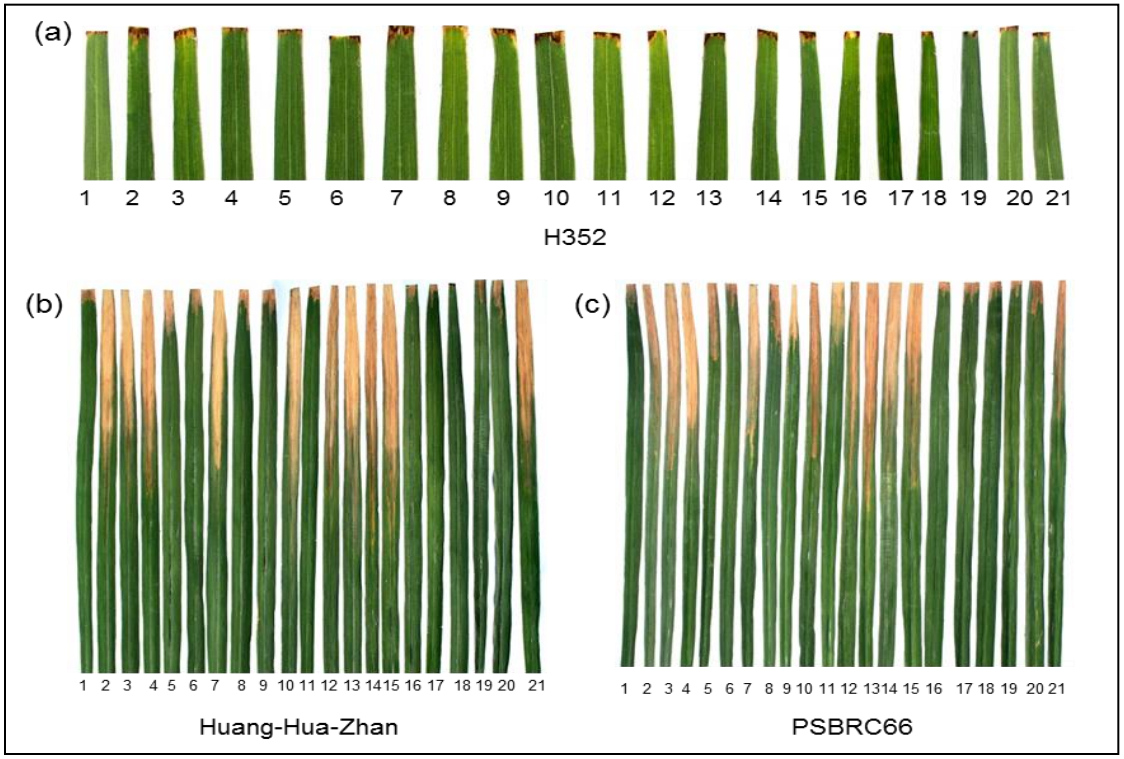
GWAS mapping of BBR using the 497 HHZ ILs and SNPs (race P2 as an example）

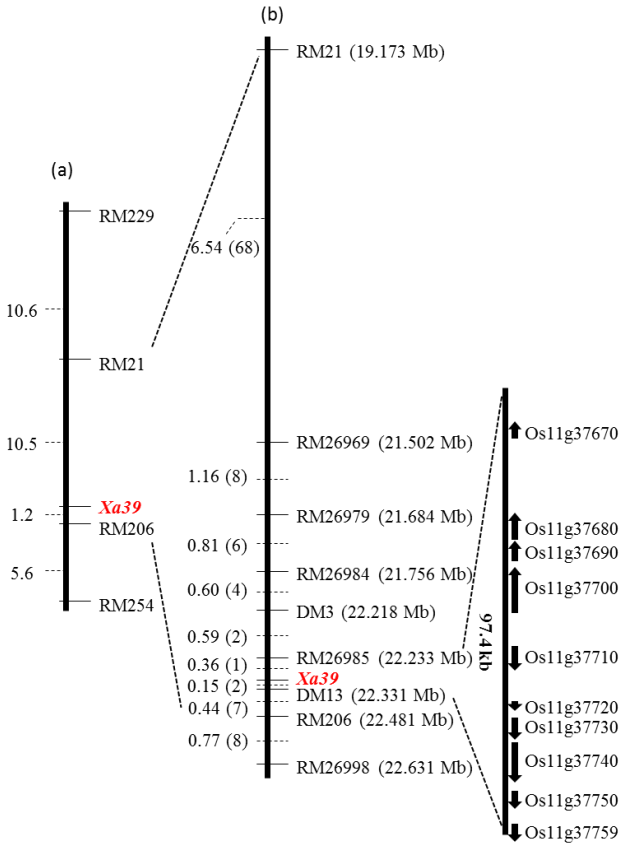


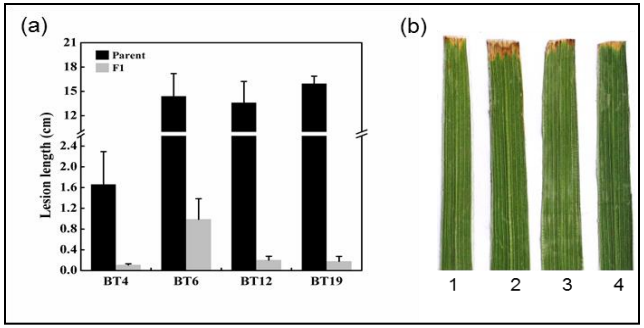


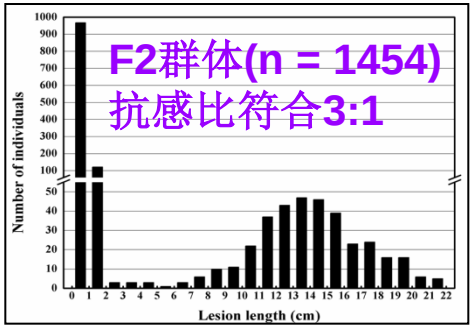
16 QRLs for BBR identified on chromosomes 2-4, 7, 9-12. Most (12/16) loci are resistant to multiple races. QTLs on chromosome 11 showed resistance to all races.

Fine-mapping of the new BBR locus, *Xa39*









***Xa39* was fine-mapped in the region of 94.7 kb *between* RM26985-DM13**

Zhang et al. Plant Pathology, 2015

Characteristics of introgression and selection of different target traits

The numbers of selected BC_1F_2 and BC_1F_3 plants from two rounds of selection for yield, DT and seedling ST from 8 HHZ (the recipient) BC_1 populations

	Donor		BC_1F_2				BC_1F_3[1]			
Population	Name	Origin	Yield	DT	ST	Total	Yield	DT	ST	Total
HHZ5	OM1723	Vietnam	11	21	15	47	26(12)	22(17)	28(11)	76
HHZ8	Phalguna	India	9	13	15	37	15(5)	15(5)	26(8)	56
HHZ9	IR50	Philippines	5	15	15	35	18(6)	13(5)	30(9)	61
HHZ11	IR64	Philippines	11	10	15	36	26(12)	7(2)	24(7)	57
HHZ12	Teqing	China	31	15	15	61	21(13)	18(8)	27(8)	66
HHZ15	PSBRc66	Philippines	8	7	15	30	21(7)	3(1)	21(3)	45
HHZ17	CDR22	India	16	12	15	43	15(11)	18(6)	35(12)	68
HHZ19	PSBRc28	Philippines	9	16	15	40	21(7)	9(3)	37(15)	67
Total			100	109	120	311	163(73)	105(47)	228(73)	496

[1] The numbers in parenthesis are those BC_1F_3 plants selected from the second round of selection.

The mean grain yield (g/plant) performances of BC_1F_5 ILs from different selection schemes (SS) under the normal condition during the 2012 dryseason at IRRI

Selection Scheme (9)	N1	The normal condition				
		Mean±SD	High yield ILs		Low yield ILs	
			N2	Mean±SD	N3	Mean±SD
YY	72	24.8±5.5	**11**	34.8±2.3a	15	18.1±1.3
DY	33	23.8±5.1	5	31.6±1.8b	7	17.1±3.0
SY	57	23.5±5.6	10	32.1±2.4ab	15	17.1±2.7
YD	59	24.3±4.9	7	32.2±2.1ab	11	16.9±2.5
DD	24	24.8±5.2	7 (**28%**)	31.4±3.1b	6	18.9±0.7
SD	20	24.0±4.2	3	31.3±1.7b	3	18.2±1.2
YS	21	24.4±5.2	3	31.9±1.9b	3	16.4±4.3
DS	151(**30%**)	24.3±5.4	26	31.6±2.5b	27	16.3±2.9
SS	54	25.5±5.1	15 (**28%**)	30.9±1.5b	10	17.3±1.6
Mean	496	24.4	**87 (30%)**	32	**97 (37%)**	15.4
HHZ (CK)		24.6				

The mean grain yield (g/plant) performances of BC_1F_5 ILs from different selection schemes (SS) under drought stress condition during the 2012 dryseason at IRRI

496 ILs suffered an mean yield loss by 51%, while HHZ by 61%, a medium stress level.

Selection scheme	N1	Under drought				
		Mean±SD	High yield ILs		Low yield ILs	
			N2	Mean±SD	N3	Mean±SD
YY	72	11.7±3.2b	43	13.6±2.0	8	5.8±2.0
DY	33	11.3±3.9b	19	13.7±2.9	5	5.7±2.1
SY	57	11.1±3.0b	32	13.0±1.9	7	6.0±1.5
YD	59	13.1±3.3a	46(**78%**)	14.4±2.6	2	6.9±0.8
DD	24	11.7±3.5b	17 (**71%**)	13.6±2.3	5	6.5±1.4
SD	20	12.0±2.7ab	11	13.8±2.1	0	-
YS	21	13.1±3.1a	19(**90%**)	13.6±2.9	0	-
DS	151	11.6±3.5b	94	13.6±2.1	23	6.1±2.0
SS	54	11.9±3.1ab	35	13.7±2.0	8	7.0±0.5
Mean	496	11.8	**316 (45%)**	13.7	**58 (34%)**	6.2
HHZ (CK)		9.4c				

The mean grain yield (g/plant) performances of BC_1F_5 ILs from different selection schemes (SS) under salt stress condition during the 2012 dryseason at IRRI

496 ILs suffered an mean yield loss by 29%, while HHZ by 32%, a medium stress level.

Selection scheme	N1	Salinity				
		Mean±SD	High yield ILs		Low yield ILs	
			N2	Mean±SD	N3	Mean±SD
YY	72	17.9±4.2ab	23	22.6	10	11.5
DY	33	16.0±4.3cd	6	22.4	12	11.6
SY	57	16.9±4.4bcd	14	21.9	14	10.7
YD	59	**18.8**±4.6a	25 (**42%**)	23.2	8	12.1
DD	24	15.7±4.4d	7	21.4	10	11.6
SD	20	15.5±3.7d	3	21.5	6	11.4
YS	21	**18.2**±5.5ab	10 (**47%**)	22.6	6	11.5
DS	151	16.7±4.7c	35	23.6	38	11.2
SS	54	**18.2**±5.1ab	14	24.5	7	10.6
Mean	496	17.2	137 (**37%**)	23	111 (**32%**)	11.3
HHZ (CK)		16.7c				

Yield performances of the 14 best performing lines under the normal condition in the 2012 dryseason at IRRI

Top 14 high yielding lines				
Order	**Lines [1]**	**Normal**	**Drought**	**Salinity**
1	HHZ17-D1-S2 **(DS)**	**38.6****	**12.1***	**21.8***
2	HHZ11-Y10-Y2 **(YY)**	**37.6****	**12.9****	**22.3***
3	HHZ5-D8-D1	**37.3****	**10.9***	12.5*
4	HHZ19-S7-Y3	**37.2****	**10.8***	17.1
5	HHZ17-Y16-Y3 **(YY)**	**36.8****	**11.0***	10.7*
6	HHZ11-Y11-Y2 **(YY)**	**36.7****	9.4	12.5*
7	*HHZ5-Y1-Y1* **(YY)**	**36.2****	10.5	**27.9****
8	*HHZ17-D4-S3* **(DS)**	**36.1****	**19.1*****	**20.7***
9	HHZ5-Y2-Y1 **(YY)**	**36.0****	**13.8***	**21.0***
10	HHZ17-D4-S1 **(DS)**	**35.8****	**14.9***	16.1
11	HHZ12-D1-S3 **(DS)**	**35.3****	**11.0***	19.2
12	*HHZ5-Y2-Y2* **(YY)**	**35.1****	**13.1****	**26.8****
13	HHZ8-Y1-D3 (YD)	**33.9***	**15.6****	**22.7***
14	HHZ17-Y13-D1 (YD)	**33.3***	**15.0****	**20.5***
CK1	HHZ (the recipient)	24.6	9.4	16.7
CK2	PSB Rc82 (irrigated)	**30.9**	9.9	16.9
CK3	NSIC Rc222 (irrigated)	**33.7**	12.2	15.2
CK4	NSIC Rc192(rainfed)	21.0	11.1	-
CK5	NSIC Rc184 (salinity)			21.0
CK6	IR 74371-70-1-1 (drought)	15.8	9.1	12.8

6 YY, 4 DS, 2 YD, indicating that number of the best yield performing lines under the normal condition was associated with selection under either the normal or drought conditions.

Yield performances of the 14 best performing lines under the drought condition in the 2012 dryseason at IRRI

Top 14 drought tolerant lines				
Order	**Lines**	**Drought**	**Normal**	**Salinity**
1	HHZ19-D12-Y2	**23.2*****	16.5*	18.0
2	HHZ5-Y4-S2 (**YS**)	**21.8*****	**29.0***	17.6
3	***HHZ8-Y2-D1*** **(YD)**	**21.3*****	28.6	**26.9****
4	HHZ19-D14-S2 **(DS)**	**20.8*****	14.7*	10.8*
5	HHZ8-Y3-D1 **(YD)**	**20.0*****	**29.6***	19.5
6	HHZ17-D8-S1 **(DS)**	**19.6*****	22.7	18.2
7	HHZ5-Y4-D2 **(YD)**	**19.6*****	27.4	19.1
8	HHZ17-S1-Y1	**19.5*****	**32.9***	**20.5***
9	HHZ5-Y8-Y2	**19.4*****	23.5	16.7
10	HHZ5-Y3-S2 (**YS**)	**19.3*****	**29.7***	17.9
11	HHZ11-D10-S4 **(DS)**	**19.3*****	25.1	18.9
12	***HHZ17-D4-S3*** **(DS)**	**19.1****	**36.1****	**20.7***
13	HHZ17-D8-S2 **(DS)**	**19.0****	26.7	**23.7***
14	***HHZ5-S14-S2***	**18.4****	28.1	**34.4****
CK1	HHZ (the recipient)	9.4	24.6	16.7
CK2	PSB Rc82 (irrigated)	9.9	30.9	16.9
CK3	NSIC Rc222 (irrigated)	**12.2**	33.7	15.2
CK4	NSIC Rc192(rainfed)	**11.1**	21.0	-
CK5	NSIC Rc184 (salinity)			21.0
CK6	IR 74371-70-1-1 (drought)	9.1	15.8	12.8

5 DS,
3 YD,
2 YS,
indicating that the number of best DT lines was associated with selection under either the drought or normal conditions.

Yield performances of the 14 best performing lines under the salt condition in the 2012 dryseason at IRRI

Top 14 salt tolerant lines				
Order	**Lines**	**Salinity**	**Normal**	**Drought**
1	***HHZ5-S14-S2*** **(SS)**	**34.4****	28.1	**18.4****
2	HHZ8-D10-S3 **(DS)**	**32.7****	22.2	**15.1****
3	HHZ5-S11-S2 **(SS)**	**32.1****	26.7	6.6*
4	HHZ5-Y3-S1	**29.3****	29.0	**13.8****
5	HHZ12-Y4-D3 **(YD)**	**29.2****	26.8	**17.8****
6	HHZ19-Y2-S1	**29.1****	17.9*	**12.6****
7	HHZ5-Y4-D3 **(YD)**	**28.4****	27.5	**18.0****
8	HHZ11-D10-S3 **(DS)**	**28.0****	18.7*	**13.8****
9	HHZ5-Y4-Y1	**28.0****	28.1	**14.2****
10	***HHZ5-Y1-Y1***	**27.9****	**36.2****	10.5
11	HHZ17-S7-S2 **(SS)**	**27.6****	**29.9***	**12.9****
12	HHZ11-Y10-D3 **(YD)**	**27.0****	**31.7***	**13.4****
13	***HHZ8-Y2-D1*** **(YD)**	**26.9****	28.6	**21.3*****
14	***HHZ5-Y2-Y2***	**26.8****	**35.1****	**13.1****
CK1	HHZ (the recipient)	16.7	24.6	9.4
CK2	PSB Rc82 (irrigated)	16.9	30.9	9.9
CK3	NSIC Rc222 (irrigated)	15.2	33.7	12.2
CK4	NSIC Rc192(rainfed)	-	21.0	11.1
CK5	NSIC Rc184 (salinity)	**21.0**		
CK6	IR 74371-70-1-1 (drought)	12.8	15.8	9.1

4 YD, 3 YY, 3 SS, indicating that the number of best ST lines was not associated with selection under salt

After one more round of progeny testing and two more seasons of preliminary yield trials across four testing conditions (normal, drought, salinity and submergence), many BC_1F_5 ILs were nominated to the national coordinated yield trials (NCYTs) of different ecosystems in Philippines, Pakistan, Mozambique and India between 2011-2015.

Six released varieties nominated in the National Cooperative Yield Trials (NCYT) of different countries

Pedigree	Country	Year	Target environments/category	Name or the likely year to be released
HHZ5-S8-D3-SU1	Philippines	2012	Rainfed lowland & Aromatic	GSR 5A
HHZ5-S14-S2-Y2	Philippines	2012	Rainfed lowland	GSR 5
HHZ8-S6-S3-Y2	Philippines	2012	Rainfed lowland	GSR 8
HHZ12-D10-S1-D1	Philippines	2012	Rainfed lowland & Aromatic	GSR 12
HHZ5-S10-D3-Y2	Pakistan	2015	Irrigated	NIBGE-I-GSR
HHZ5-S12-D3-Y2	Pakistan	2015	Irrigated	NIBGE-II-GSR

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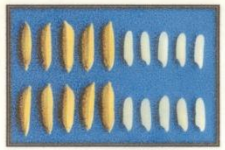
CERTIFICATE OF REGISTRATION

is hereby awarded to

'Katihan 4'
(Oryza sativa L.)

having been approved for Luzon, Visayas and Mindanao areas under

Registry No. NSIC 2014 Rc29



developed by the **International Rice Research Institute**
Los Baños, Laguna

Given this 28th day of November 2014 at the National Seed Industry Council, Bureau of Plant Industry, National Seed Quality Control Services Bldg., Visayas Avenue, Diliman, Quezon City, Philippines.

PAZ J. BENAVIDEZ II
Assistant Secretary for Regulations,
OIC-Director, BPI & Executive Director, NSIC

Republic of the Philippines
Department of Agriculture
BUREAU OF PLANT INDUSTRY
NATIONAL SEED INDUSTRY COUNCIL

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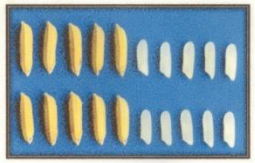
CERTIFICATE OF REGISTRATION

is hereby awarded to

'Salinas 19'
(Oryza sativa L.)

having been approved for Luzon, Visayas and Mindanao areas under

Registry No. NSIC 2014 Rc390



developed by the **International Rice Research Institute**
Los Baños, Laguna

Given this 28th day of November 2014 at the National Seed Industry Council, Bureau of Plant Industry, National Seed Quality Control Services Bldg., Visayas Avenue, Diliman, Quezon City, Philippines.

PAZ J. BENAVIDEZ II
Assistant Secretary for Regulations,
OIC-Director, BPI & Executive Director, NSIC

Republic of the Philippines
Department of Agriculture
BUREAU OF PLANT INDUSTRY
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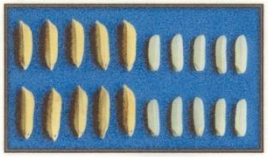
CERTIFICATE OF REGISTRATION

is hereby awarded to

'Salinas 20'
(Oryza sativa L.)

having been approved for Luzon, Visayas and Mindanao areas under

Registry No. NSIC 2014 Rc392



developed by the **International Rice Research Institute**
Los Baños, Laguna

Given this 28th day of November 2014 at the National Seed Industry Council, Bureau of Plant Industry, National Seed Quality Control Services Bldg., Visayas Avenue, Diliman, Quezon City, Philippines.

PAZ J. BENAVIDEZ II
Assistant Secretary for Regulations,
OIC-Director, BPI & Executive Director, NSIC

Twenty-four promising HHZ ILs nominated in the National Cooperative Yield Trials (NCYT) of different countries

Pedigree	Country	Year	Target environments/category	Year to be released
HHZ17-D6-S3-D1	India	2014	Irrigated & rainfed lowland	2016
HHZ11-Y6-Y1-Y1	India	2014	Directed seeded rice	2016
HHZ5-S9-Y3-Y1	India	2014	Directed seeded rice	2016
HHZ5-S10-D1-D1	India	2014	Alkaline & Inland Saline	2016
HHZ12-S2-Y3-Y2	Mozambique	2014	PVS-irrigated	2016
HHZ12-Y4-D1-Y1	Mozambique	2014	PVS-irrigated	2016
HHZ5-S12-D3-Y2	Mozambique	2014	PVS-irrigated	2016
HHZ5-S14-S2-Y1	Mozambique	2014	PVS-irrigated	2016
HHZ5-S14-S2-Y2	Mozambique	2014	PVS-irrigated	2016
HHZ5-S8-D2-S1	Mozambique	2014	PVS-irrigated	2016
HHZ5-Y3-Y1-D1	Mozambique	2014	PVS-irrigated	2016
HHZ8-S14-S3-Y2	Mozambique	2014	PVS-irrigated	2016
HHZ8-S6-S3-S1	Mozambique	2014	PVS-irrigated	2016
HHZ8-S6-S3-Y1	Mozambique	2014	PVS-irrigated	2016
HHZ8-S6-S3-Y2	Mozambique	2014	PVS-irrigated	2016
HHZ5-D7-Y3-S1	Philippines	2013	Group I irrigated	2015
HHZ8-S6-S3-D1	Philippines	2012	Group II irrigated	2015
HHZ5-S5-Y2-Y1	Philippines	2013	Special Purpose- Aromatic	2015
HHZ12-S2-Y3-Y2	Philippines	2013	Saline	2015
HHZ8-S6-S3-Y2	Philippines	2013	Saline	2015
HHZ12-D10-S1-D1	Philippines	2014	Saline	2016
HHZ15-S13-Y1	Philippines	2013	Upland (WS)	2015
HHZ19-S14-Y1	Philippines	2013	Upland (WS)	2015
HHZ8-S6-S3-Y2	Philippines	2013	Rainfed dry-seeded (WS)	2015


NSIC158
HHZ5-SAL10-DT1-DT1
HHZ8-SAL12-Y2-DT1
HHZ12-DT10-SAL1-DT1

Given the fact that so many promising HHZ lines with good yield potential and greatly improved tolerances to one or more stresses were developed in only 8 breeding populations within 6 years, we were wondering that what might have happened to the genetic compositions of these selected BC progenies.

The mean genotypic and introgression frequencies of selected BC_1 introgression lines from 8 HHZ populations

Pop.	BC_1F_2 [1]					BC_1F_3				
	N	B[2]	H	IF	SD	N	B	H	IF	SD
HHZ5	47	0.330c	0.105	0.383b	0.239	75	0.363bc	0.071	0.400bc	0.245
HHZ8	37	0.159d	0.14	0.229c	0.257	56	0.150f	0.104	0.202e	0.205
HHZ9	35	0.177d	0.074	0.214cd	0.287	62	0.300c	0.04	0.320d	0.362
HHZ11	36	0.166d	0.160	0.245c	0.13	55	0.219ef	0.091	0.264	0.180
HHZ12	43	0.397b	0.077	0.436ab	0.311	48	0.399b	0.042	0.420b	0.366
HHZ15	30	0.448a	0.029	0.463a	0.392	45	0.443a	0.007	0.448a	0.444
HHZ17	43	0.122e	0.109	0.177e	0.158	68	0.169f	0.074	0.202e	0.158
HHZ19	40	0.137de	0.062	0.168e	0.248	68	0.256e	0.036	0.184e	0.268
Mean	**311**	**0.244**	**0.105**	**0.297 (19%)**	**0.252**	**491**	**0.273**	**0.061**	**0.304**	**0.273**

(1) IF appeared to be population-specific.

(2) As compared with the expected genotypic frequencies of random BC_1F_2 population by Chi-square test, the selected BC_1F_2 plants in each population significantly deviated from expected, with excess of the donor homozygous genotype and much reduced frequency of the heterozygote, meaning selection was favorable to homozygous introgression but unfavorable to heterozygous introgression of donor genome.

When the donor introgression was compared among ILs derived from different SSs, the donor introgression in the BC_1F_2 progeny did not differ significantly, except that selection for high yield under the irrigated condition produced significantly higher heterozygosity than those selected under drought or salinity.

For two round selections, most SSs had similar donor IF except that the 33 ILs from DY had significantly lower introgression. And ILs from most SSs had similar levels of heterozygosity except for those from YY and YD, which had significantly higher heterozygosity.

The mean genotypic and introgression frequencies of BC_1 ILs generated by different selection schemes from 8 HHZ populations

BC_1F_2 [1]					BC_1F_3				
SS[2]	N	B[3]	H	IF±SD	SS	N	B	H	IF±SD
Y	82	0.239a	0.121a	0.290±0.068	YY	72	0.265b	0.078a	0.302±0.076
D	109	0.250a	0.097b	0.302±0.063	DY	33	0.137d	0.033b	0.154±0.052
S	120	0.234a	0.087b	0.277±0.056	SY	57	0.217c	0.050b	0.242±0.048
					YD	59	0.260b	0.074a	0.297±0.053
					DD	24	0.260b	0.048b	0.284±0.033
					SD	20	0.301a	0.049b	0.325±0.035
					YS	21	0.248bc	0.047b	0.271±0.048
					DS	151	0.192c	0.041b	0.212±0.046
					SS	54	0.247bc	0.051b	0.273±0.068
Mean	**311**	**0.244**	**0.105**	**0.297±0.062**		**491**	**0.273**	**0.061**	**0.304±0.052**

Conclusion

(1) **Selecting appropriate RP (high yield, high quality, wide adaption) is the key for success for improving complex traits in a BC breeding program, and donors do make differences in breeding efficiency which depends on complementary favorable alleles of donors to RP.**

(2) **Rich “hidden” genetic diversity for complex traits exists in the primary gene pool of rice. Though 8 donors mostly represent elite materials under the irrigated conditions without good tolerances to drought and salinity, transgressive progenies, though fewer, were identified in all other populations. Backcross, intense phenotypic selection combined with molecular marker is an effective way to mine this “hidden” diversity.**

(3) **Responses of the BC progenies to phenotypic selection were quite complex, all selection schemes resulted in significantly more promising DT lines, and strong association exists between high yield and DT.**

(4) Introgression or segregation in BC progenies is population-specific. Dramatically reduced heterozygosity in the BC progenies was associated with selection for DT and ST than selection for yield under the non-stress conditions, hinting selection against stress tolerance first then followed by high yield selection is probably a good strategy for developing green super rice in a relative short period.

(5) Trait specific lLs are suitable materials for identifying genes underlying the target (yield, DT and ST) and non-target (resistances to biotic stresses, quality traits, cold tolerance, etc.) traits, thus realizing integration of gene mapping and breeding via selected introgression line population.

Acknowledgement

Research Team:

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Z.K. Li
Y.M. Gao
B.Y. Fu
Y. Li. Zhou
X.Q. Zhao
T. Q. Zheng

Funding:

Chinese Ministry of Agriculture 948 project
Chinese Ministry of Science &Technology 863 project
The BMGF GSR project



Agricultural Genomics Institute at Shenzhen (AGIS), CAAS

Welcome to Shenzhen!


Thanks !