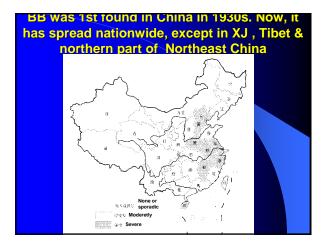
Genetics and Improvement of Resistance to Bacterial Blight in Hybrid Rice







A. Improvement of BB R in hybrid rice in China

In early 1970s, the national program "Rice breeding for high yield, good quality, & R to diseases" was established, BB R hes been rapidly improved.

1. Three-line comb. with BB R registered at national or provincial level (1973~2006)^a

Period	Total	Re	sistant	R percentage (%)	
1973~198	6	87	31	35.6 (ind.)	
		43	26	60.0 (jap.)	
1996~200	5	169	18	10.7 (ind.)	
2006		6	4	66.7 (jap. South)	
		64	5	7.8 (jap. North)	

^a Combinations with an annual acreage of more than 6.667 ha²

Comb. with high yield, good quality , R to BB or more dis.

- * Before 1980s, Weiyou 64, Weiyou 6, & Shanyou 6 had reached an annual area of 1.333 M ha².
- * Up to 2005, II you 084, Shanyou 77, Guofeng 1.
- * Recently, II you 1511, Yixang 2408, & sup. H.R Zhongzheyou 1 (area reached 0.067 M ha²) exhibiting R to BB & BL.
- Jap. H. Youyou , Jiayou & Xiouyou 5 exhibiting multiple- R to diseases & insects.

Period	Total	Resistant	R perc. (%
1994~2000	32	17	53.1
2001~2006	21	6	28.6

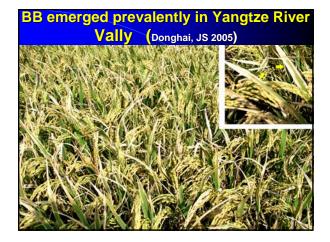
Comb. with high yield, good quaity & R to BB or more dis.

*After 2000, Peiza-shanqing, Peiza-maoxuan, Peiliangyou-teqing, & Yunguang 8.

*Up to 2006, Liangyou- peijiu, accumulated area reached 4.681 M ha²(2005), Peiza-shuangqi, & jap. 70 you 9.

* In 2007, 2 Sup. rice comb. Fengliangyou 4, Xinliangyou 6380 & Peiza 35, Xinliangyou 6, Xinliangyou 98 with HR-MR to BB & BL.



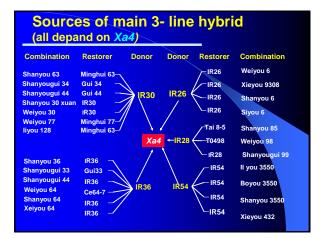


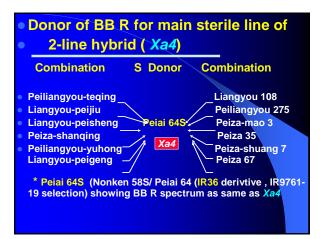
B. Discussion of the actual & potential damage situation

Resurgence of BB after 20 years of "quietness" appeared danger from the dis. in China

1. Reduced rice variation for BB R

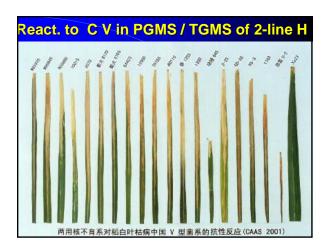
Studied on pedigree of 287 BB R cultivars & donors, inheritance of 100 ones, and tested genitic allelism of 52 cultivars, indicated that gene Xa4 was mainly used in indica rice breeding.





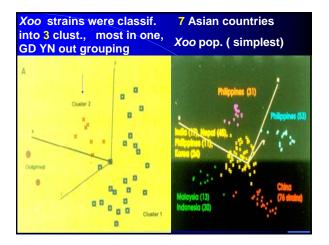
A new BB strain (C patho. V) virulent to *Xa4*

- * Such genetic uniformity must make rice vulnerable to dis. epidemics, which often results in shifts of virulence in Xoo popul.
 As early as in 1985, WU & XU first found a
- new BB strain (patho. V) in GD, was virulent to IR26 (*Xa4*). It made a warning, the host cult. carrying R gene *Xa4* had been cultivated extensively for the last 15 years



2. Xoo genetic popul. in China

- * Genetic popul. struct. of Xoo (1984-2000), showed very simply, most strains were grouped in clusters 1 or 2, only str. from GD & YN were distinct from the others.
- * As expected, YN Xoo popul. contained some new patho., 9 & 8 out of the 14 races are virulent to cultivars carrying Xa4 & Xa21, respectively (Ji et al., 2003).
- * In GD, another new strain is virulent to Xa1, 2, 3, 4, 10, 11, 14, 21, xa8, & xa13, except xa5, Xa7 & Xa23 tested (Zeng, 2005,2007).



C. Approaches to improve BB R in breeding hybrid rice

- 1. Broaden genetic basis of BB R
- Up to 2006, 30 BB R genes were ident. 18 mapped.
- Tightly linked PCR-based markers of Xa4, Xa7, Xa21, Xa23, xa5, & xa13 were identified; Xa1, xa5, xa13, Xa21, Xa26 (Minghui 63) & Xa27
- (O. minuta) were cloned.

2. Alternate BB R genes

- * In early 1980s, Zhu et al. developed TD series lines (carrying Xa7) , which were used to develop indica restorers Kanghuei 63, 98, & D205
- * Using these restorers, BB R comb., Kangyou 63, 98, II You 205, & Fengyou 205 were developed & popularized in BB epidemic fields in JS, ZJ, AH, YUN, JX, HEN, HUB, & HUN 9 Provinces. The accumulated area of 2.50 M ha² had reached (Ding 2005).

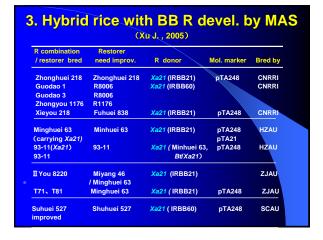
Xoo patho, distribution in China

- A smart use of R genes should be based on information of host-patho. interaction .
- * Patho. I I dominate in Northern China (jap.)
- * Patho. IV, II, V in Southern China (ind.) * Patho. IV, II, V (spread. threshold value approach. 20%. in Yangtze Valley (ind. Jap.)
- * Available broad-spect. R genes, Xa23 (O. rufipogon), Xa22, Xa21, Xa7, & xa5 can be used to overcome the dependence of limited genetic sources.

Country	Race (str.)	R gene attacked	Effective R gene	
Bangladesh	12 (74)	Xa1, 2, 3, 4, 7, 10, 11, xa5, xa8	Xa3, 12, Pyra.	
India	5 (58)	Xa1, 2, 3, 4, 10, 11, 12, xa5	Pyramiding line	
Nepal	16 (45)	Xa1, 2, 3, 4, 10, 11, 12, xa5	xa5 , Xa7, Pyra.	
Myanmar	7 (27)	Xa1, 2, 4, 10, 11, xa5	Xa7, Pyra.	
Tailand	5 (35)	Xa1, 2, 10, 11, xa5	Xa 4, 7, Pyra.	
Indonesia	8 (78)	Xa1, 2, 3, 10, 11, xa8	xa5 , Xa7 <mark>, Pyra</mark> .	
Philippines	5 (61)	Xa1, 2, 4, & 11	xa5 , Xa7, 12	
Malaysia	2 (11)	Xa1, 2, 10, 11, xa8	Xa4, 7, 12 & xa5	
China (sou)	6 (24)	Xa1 2 3 4 10 11 12 va8	va5 ¥a7 *22 22	

Attacked & offective BB P genes in Asian





D. Problems to be addressed in the future

- * The R new comb. released gradually reduce since later 90s, the questions are :
- a) were the comb. not screened prior to their release?
- b) the BB R breeding is still one of the main objectives?
- * Thus, we are faced with two challenges:
- a) how to deal with the changing pathogen?
- b) design & develop durable R

Conclusion

- * Composed of tradititional and molecular methods should bring a new era to the BB R in hybrid rice breeding program.
- * Gene pyramiding, or rotation, where genes are effective (spatial & temporal deployment) * Adopting "horizontal R".
- Pathogen : identify tester strains for screening breeding lines for different regions
- Collaborative researches should be strengthened further. (Intern. breeding, pathol. entomol.)

