Identification, Mapping, Isolation of the Genes Resisting to Bacterial Blight and Breeding Application in Rice

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Abstract

Bacterial blight, caused by Xanthomonas oryzae pv. oryzae, Xoo, is the most devastating plant bacterial disease in Asia. Exploration, identification and utilization of new resistant germplasms to rice breeding are the effective pathway to control the disease. Mapping and cloning the resistant genes makes MAS (marker-assisted selection) and transgenic technology play a great role in breeding program for disease resistance and let people have a profound insight on molecular mechanism of resistance to bacterial blight. In this paper, mapping, cloning and application of the genes resisting to bacterial blight were summarized, and also some suggestions were put forward to relieve the damaging extent caused by bacterial blight via utilizing disease resistant breeding program.

Keywords
Rice bacterial blight; Gene mapping; Gene isolation; Disease resistance breeding

Background

Bacterial blight caused by Xanthomonas oryzae pv. oryzae, Xoo, is the vascular bundle disease, and it has three common kinds: leaf blight type, wilting type and withering type. Bacterial blight broke out in many rice producing regions, such as Asia (China, Korea, India, Philippines), America, North America and Australia since it was first found in Fukuoka of Japan in the 1890s. Except for Sinkiang and Gansu, bacterial blight occurred in many areas of China, especially in places near the sea, the river, the upland and easy waterlogged areas. Generally, the yield reduced 10%-30%, seriously more than 50%, and even 100% caused by this disease (Mew, 1987). Studying on genetics of resistance to bacterial blight was first carried out by Japan and IRRI, subsequently, followed by Sri Lanka, India, China and so on. Since the identification of strains Xoo used were different in different countries, scientists found that it was difficult to distinguish the resistance genes. In order to compare the identified genes, the identical differential standard was set up (Ogawa, 1993). Since the bacterial races vary continually influenced by the artificial and natural selection of genes resistance to bacterial blight, it is critical to explore and identify the new resistant resources to control the changeful races.

I Identification of Resistance Genes to Rice Bacterial Blight

It is a long-term competitive evolutionary process between the pathogenicity of pathogenic bacteria and resistant hosts, the pathogenic bacteria will vary under stress of the resistant hosts, and the resistant hosts will react to the varied pathogenic bacteria in turn. One of the effective approaches to control the invasion of pathogenic bacteria of bacterial blight is exploring new resistant resources. As usual, the outstanding resources may be found in local varieties, wild rice varieties and artificial mutational materials. To date, 31 genes have been identified, which were located on 10 chromosomes except for Chr9 and Chr10 (Figure 1). The 6 cloned genes were identified to be resistant genes, 9 were unidentified genes, and there were 3 resistant genes from artificial mutation materials and 6 from local varieties (Nakai et al., 1998; Taura et al., 1991; Taura et al., 1992; Lee et al., 2003).
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1.1 Unidentified genes
Mutagenesis has played a great role in enriching the resistant resources of bacterial blight and the researchers have obtained a series of new genes which were in different resistance levels and resistance specurms. So far, 9 genes, from mutagenesis and local varieties have not been identified, listed in table 1.

1.2 Identified genes
Chromosome 1: *Xa29(t), xa34(t)*, deriving from B5, a transgenic line of *Oryza officinalis* and BG1222, a variety from Sri Lanka, respectively. *Xa29(t)* was located on chromosome 1 within a 1.3 cM region flanked by RFLP markers C904 and R596. *xa34(t)* was defined to an interval which spans approximately 204 kb equal to 0.4 cM between the markers RM10927 and BGID25, and cosegregated with indel markers BGID34 and BGID36. Gene prediction results showed that there were no homologous proteins with the known resistance genes, indicating that a new mechanism might be performed by *xa34(t)* (Tan et al., 2004; Chen et al., 2011).

Chromosome 2: *xa24*, a new recessive gene in DV86 was identified by Mir and Khush and confirmed by Khush and Angeles. Wu et al (2008) found that *xa24* was resisted to the Philippine *Xoo* races 4, 6, 10 and Chinese *Xoo* strains Zhe173, JL691, and KS-1-21, and was mapped on chromosome 2 within a 0.14 cM region, and an approximately 71 kb in length between RM14222 and RM14226.

Figure 1: Approximate positions of the genes resisting to bacterial blight on chromosome
Note: S: Short arm; C: Centromere; L: Long arm; Thin line: Marker; Black ellipse and rectangle: Gene
Table 1 Unidentified resistance genes to bacterial blight

<table>
<thead>
<tr>
<th>Name of gene</th>
<th>Dominance or recessive</th>
<th>Donor</th>
<th>Identifying race</th>
<th>Reference</th>
</tr>
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<tbody>
<tr>
<td>xa15</td>
<td>-</td>
<td>M41</td>
<td>T7174, T7147,</td>
<td>Nakai et al., 1998</td>
</tr>
<tr>
<td></td>
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<td></td>
<td>T7133, H75373</td>
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<tr>
<td>Xa16</td>
<td>+</td>
<td>Tetep</td>
<td>Japanese race V</td>
<td>Ogawa et al., 1993</td>
</tr>
<tr>
<td>Xa17</td>
<td>+</td>
<td>Asominori</td>
<td>Japanese race II</td>
<td>Ogawa et al., 1993</td>
</tr>
<tr>
<td>Xa18</td>
<td>+</td>
<td>Toyonishiki,</td>
<td>H8584</td>
<td>Ogawa et al., 1993</td>
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<td></td>
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<td>Milyang 23, H8584</td>
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<tr>
<td>xa19</td>
<td>-</td>
<td>XM5</td>
<td>Philippines races</td>
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</tr>
<tr>
<td>xa20</td>
<td>-</td>
<td>XM6</td>
<td>Philippines races</td>
<td>Taura et al., 1992</td>
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<tr>
<td>xa26(t)</td>
<td>-</td>
<td>Nep Bha Bong To</td>
<td>PXO112</td>
<td>Lee et al., 2003</td>
</tr>
<tr>
<td>Xa27(t)</td>
<td>+</td>
<td>Arai Raj</td>
<td>PXO86, PXO112</td>
<td>Lee et al., 2003</td>
</tr>
<tr>
<td>xa28(t)</td>
<td>-</td>
<td>Lota Sail</td>
<td>PXO86, PXO112</td>
<td>Lee et al., 2003</td>
</tr>
</tbody>
</table>

Note: +: Dominance; -: Recessive

Chromosome 3: Xa11, resistance to Japanese Xoo races IB, II, IIIA and V, was mapped on the short arm of chromosome 3 with a genetic distance 2.0 cM and 1.0 cM from the marker RM347 and KUX11, respectively (Goto et al., 2009).

Chromosome 4: up to now, seven genes included Xa1, Xa2, Xa12, Xa14, Xa25(t), Xa30(t) and Xa31(t) have been positioned on this chromosome. Except Xa25(t), other six genes distributed on the followed six clones: OSINBa0008M17, OSINBa0093O08, OSINBa0058K23, OSINB0008SC12, OSINBa0053k19 and OSINBa0060EO8. Xa1 and Xa12 are close linkage, Xa2 is located between HZR950-5 and HRZ970-4, Xa30(t) between LOC- Os4g53060 (0.2 cM) and LOC-Os4g53120 (0.1 cM), Xa31(t) between C600 (0.1 cM) and G235 (0.1 cM), Xa14 between HZR970-8 and HZR998-1, Xa25(t) between RM6784 and RM1153, covering 19 clones containing the above six clones (Ku et al., 2008; Wang et al., 2009; Bao et al., 2010; Yoshimura et al., 1998; He et al., 2006; Gao et al., 2005).

Chromosome 5: xa5 was a recessive gene conferring resistance to bacterial blight in whole growth period from DV85, DV86, and DZ78 in Bangladesh, located on the short arm of chromosome 5 within a 0.5 cM region, about 70 kb, flanked by SNPS marker RS7 and SSR marker RM611 (Sidu et al., 1978; Blair et al., 2003). Chromosome 6: three genes, Xa7, Xa27 and xa33(t) were mapped on chromosome 6. Xa7, a dominant gene which did not mediate resistance to bacterial blight until adult-plant stage, mapped to an interval of 0.21 cM between the markers GDSSR02 and RM20593. Xa27, within a 0.052 cM region was flanked by the RFLP markers M964 and M1197 cosegregated with markers M631, M1230 and M449. RGP markers C12560S and S12715 with a genetic interval of 0.9 cM, lied outside of the RFLP markers M964 and M1197. The recombination frequency between marker G1091, and Xa7 was 8.8%, and was 22.1 cM away from marker S12715. However, Xa7 and Xa27 have different resistance spectrums to Xoo races of bacterial blight, confirming that Xa27 was not allelic to Xa7. xa33(t) was close linkage with marker RM20590, which cosegregated with Xa7, however, the resistance characteristics were significant difference between Xa7 and xa33(t) (Sidu et al., 1978; Gu et al., 2004; Korinsak et al., 2009).

Chromosome 7: xa8, a recessive gene from variety PI231129 from American, which conferred resistance or moderately resistance to Xoo races of north India with a genetic distance of 19.9 cM from marker RM214. The closer markers would be developed in future (Sidu et al., 1978; Singh et al.).
Chromosome 8: *xa13*, a fully recessive gene originating from varieties B1J, AC19-1-1, AUS274-1, Chinsurah Boro II and Kalimakri77-5 (Ogawa et al., 1993), which specifically confers resistance to Philippine *Xoo* race 6, was flanked by RFLP marker RP7 and SSR marker SR11 within a 0.84 cM interval (Chu et al., 2006).

Chromosome 11: ten resistant genes, *Xa10*, *Xa23*, *Xa21*, *Xa30(t)*, *Xa3/Xa26*, *Xa22(t)*, *Xa4*, *Xa32(t)*, *Xa35(t)* and *Xa36(t)* have been distributed on chromosome 11. *Xa21*, identified from *Oryza rufipogon*, were mapped on two clones: P045F09 and OJ111-B01 with the genetic position of 84.6~85.7 cM on Chromosome 11, and cosegregated with RFLP and OJ111-B01 with the genetic position of 84.6~85.7 rufipogon chromosome 11.

*Xa35(t)* Chromosome 11: ten resistant genes, (Chu et al., 2006).

RP7 and SSR marker SR11 within a 0.84 cM interval (Philippine 1993), which specifically confers resistance to Chinsurah Boro II and Kalimakri77-5 (Ogawa et al., 2005; Jin et al., 2007). Yoshimura et al., 1995; Gu et al., 2008; Wang et al., respectively (Ronald et al., 1992; Song et al., 1995; Ronald et al., 1992; Song et al., 1995; Yoshimura et al., 1995; Gu et al., 2008; Wang et al., 2005; Jin et al., 2007). *Xa3/Xa26* and *Xa3/Xa26*, was more than 10 cM between the two markers: RM206 and RM224, *Xa30(t)* was more closed to the terminal and centromere than *Xa23* and *Xa3/Xa26*, respectively (Ronald et al., 1992; Song et al., 1995; Yoshimura et al., 1995; Gu et al., 2008; Wang et al., 2005; Jin et al., 2007). *Xa3/Xa26*, *Xa22(t)* and *Xa4* were mapped on sub clone M3H8 flanked by marker RM224 and RM114, with the genetic distance of 0 cM, 0.4 cM and 0.5 cM away RFLP marker R1056, respectively, and its position was 116.2 cM on clone OSJBa004M04 (Yang et al., 2003; Wang et al., 2003). Recently, *Xa32(t)*, *Xa35(t)* and *Xa36(t)* were also placed on the long arm end of chromosome 11, *Xa4* was likely less closed to the end than *Xa36(t)*, because *Xa4* was more 0.2 cM to the terminal marker RM224 than *Xa36(t)*. *Xa35(t)*, cosegregated with marker RM114, was closest to the end of long arm. *Xa32(t)* away the terminal marker RM5926 with the genetic of 2.6 cM may go between *Xa36(t)* and *Xa35(t)*, since *Xa36(t)* was more 1.2 cM to RM5926 than *Xa32(t)* (Zheng et al., 2009; Guo et al., 2010; Miao et al., 2010).

Chromosome 12: *xa32(t)*, stemed from a new germplasm which was generated from the cross of the somatic cell of *Oryza meyeriana* originating from the hybrids Xishuangbanna, Yunnan, wild type and cultivared rice, was 1.7 cM away from marker RM20A (Ruan et al., 2008). *Xa25(t)*, which confered specially resistance to PXO339 at the whole period identified from Minghu63, was located within a 9.5 cM region between NBS109 (a homologous sequences of resistance gene) and RFLP marker G1314 (Chen et al., 2002).

1.3 Unnamed genes

Two new germplasms, SH5 and SH76, which stemed from the somatic hybridization of japonica rice 8411 and *Oryza meyeriana*, were proved to be resistant to bacterial blight and likely to be a new gene or a new linked group (Huang et al., 2008).

2 The clone resistance genes to bacterial blight

Cloning resistant genes is the premise of knowing clearly the molecular mechanism of host resistance to bacterial blight. Bacterial blight is the mode system for studying diseases caused by pathogenic bacteria on monocotyledonous hosts. So far, 6 genes have been cloned, and two of them are recessive genes, *xa5* and *xa13*, the others are dominant genes, *Xa21*, *Xa1*, *Xa3/Xa26 and Xa27*. The cloned genes are classified two categories according to their functions: expressive resistance, the expression or not of the genes plays great role in resisting to bacterial blight (*xa13* and *Xa27*); interactive resistance, the hosts’ expression products can interact with the proteins expressed by pathogenic bacteria (*xa5*, *Xa21*, *Xa1* and *Xa3/Xa26*).

Interestingly, the genes possessing similar functions disciplinary distribute on chromosome. *xa5*, *xa13* and *Xa27* lie on chromosome 5, 8 and 6, respectively, and only two other genes, *Xa7* and *xa33(t)* exist on chromosome 6. However, the chromosome with *Xa21*, *Xa1* and *Xa3/Xa26* exist many other resistant genes, and these genes belong to gene cluster distribution.

2.1 Expressive resistance

*xa13* is a recessive gene which confers high specially
resistance to Xoo PXO99, containing five exons and encoding a protein of 307 amino acids which targets to the plasma membrane. *xa13* is a promoter-mutation resistant gene, and the expression of *Xa13* is the basis of pathogenic bacteria infecting to rice. The low expression of *Xa13* as a result of promoter-mutation restrains pathogen infection leads to abnormal development of pollen grains and reduction of setting percentage because of its function involved in pollen development (Chu et al., 2006). In contrast to *xa13*, the expression of *Xa27* makes a contribution to restraining invasion of pathogen bacteria.

*Xa27* and *avrXa27* are the first cloned pair of resistance gene corresponding to a virulence gene from rice and *Xoo*. *Xa27* is an intronless gene and encodes protein of 113 amino acids. *Xa27* with its allelic gene encodes the protein with identical sequence and expresses only in the vicinity of tissue infected by bacteria harbouring *avrXa27*, indicating that *Xa27* works as an local defense instead of system defense. More interestingly, the intergression lines of *Xa27* can mediate resistance to compatible strains of *Xoo*. The experiment of promoter displacement makes clear that the diverse expression is attributed to the different promoter-driven in resistant and susceptible plants (Gu et al., 2005).

### 2.2 Interaction resistance

#### 2.2.1 *xa5*

*xa5* consisting of 4 exons and 3 introns, encodes the gamma subunit of eukaryotic transcription factor (TFIIAγ) that contains 106 amino acids. Comparing sequence between resistant and susceptible isolines reveals that an amino acid changes from valine to glutamic acid at position 39, which may result in the resistance of *xa5* and the function of TFIIAγ still keeps. Sequencing TFIIAγ from resistant and susceptible cultivars shows that the amino acid at position 39 highly conserves in resistant varieties and owns two kinds of situations in susceptible varieties: Valine and Leucine (Yer et al., 2004).

#### 2.2.2 *Xa21* and *Xa3/Xa26*

*Xa21* encodes a protein of 1025 amino acids, which contains the extracellular NH2-terminus hydrophobic signal peptide, 23 imperfect copies of LRR, a membrane-spanning helix of hydrophobic stretch and a putative intracellular protein kinase catalytic domain. The extracellular LRR can recognize the proteins produced by avirulence gene of pathogenic bacteria, which may activate intracellular STK to withstand the invasion of pathogenic bacteria (Song et al., 1995). Study has proved that XB3 is necessary for stability of Xa21 protein and Xa21-mi...iod resistance, the content of Xa21 decreases along with the decrease of the content of XB3, so does the resistance (Wang et al., 2006). Further study also indicates that the phosphorylation active site of XB24 catalyzes the phosphorylation of some sites and slents the function of XA21 protein before inoculation. The interaction of AX21 protein of *Xoo* and Xa21 protein makes XB24 absciss from XA21 or the reverse after inoculation so that XA21 protein works. However, the interaction of XB15 and XA21 results in dephosphorylation of XA21 protein and makes plant susceptible after inoculation (Chen et al., 2010).

*Xa3/Xa26* also belongs to LRR-STK, containing 4 members, RKa, RKb, RKc, and RKd. *Xa26* consists of two extrons and one intron with the length of 3 309 bp and 105 bp respectively. The amino acids of 1 103 aa consists of NH2-terminus

Signal peptide of 30 aa in length and the extracellular 26 imperfect copies of LRR, a membrane-spanning domain and a intracellular protein kinase domain (Xiang et al., 2006). *Xa3* and *Xa22(t)*, stemmed from Kogyoku, a Japan variety and Zhachanglong, a Yunnan variety, were located in the same region with *Xa26*. The hybridization test reveals that the bands of IRBB3, Zhachanglong and Minghui63 are identical utilizing RKa of the member of *Xa26* as probe. A series of analyses confirm that *Xa3* and *Xa26* are the same and rename as *Xa3/Xa26*, whether the same of *Xa22(t)* and *Xa26* emains to verify. *Xa3* was attested to possess significant difference on spectrum and resistance in different background, even turn to be a recessive character giving rise to the diversification of its name (*Xa4b, Xa6* and *xa9*). As a whole, *Xa3* works well in japonica rice (Sun et al., 2004).

#### 2.2.3 *Xa1*

*Xa1*, conferred special resistance to Japan Xoo race 1
contains 3 exons separated by 2 introns encoding a 5406 bp ORF flanked by 5′ and 3′ untranslated regions of 112 and 392 bp, the derived sequence of XA1 is composed of NBS and six imperfect LRR with not distinct transmembrane domain. Xa1 is a particular induced gene since its expression only detected in leaves inoculated by compatible, incompatible strains and water rather than intact leaves (Yoshimura et al., 1998).

3 Application of genes resistance to bacterial blight

Improving the resistance to bacterial blight of rice utilizing the broad spectrum genes is a economic environmental and efficient method. The conventional way that makes the cross using donor and recurrent parents and sequentially backcrossing with the recurrent parent along with inoculation until 3 to 4 generation, then selfing and gaining the homozygous plants through inoculation is time-wasting, labor-consuming and difficults in pyramiding recessive genes and several genes together. The improvement of MAS, transgenesis, another culture, which combines with the conventional breeding, gradually breaks the constrains of traditional breeding.

3.1 Single-gene

In the 1980s and 1990s, Xa4 and Xa3 were the major resistance resources used in Indica rice and Japonica rice respectively. Since the loss of resistance, xa5, Xa7, Xa21 and Xa23 were put into practice recently and largely used for improving the resistance of conventional varieties, the parents of hybrid rice, and the cultivar new resistant parents of hybrid rice.

xa5, a recessive gene, expressed at the whole period. Zhongzu14, a late Indica variety and Xieyou zhong 1, a hybrid combination of Zhongzu 14 and CMS Xieqingzao A, which got through Zhejiang Province authorized committee of crop variety, were the successfully examples of pyramiding xa5 and minor genes together through MAS and anther culture (Wang et al., 2004; Ma et al., 2010).

Xa7 together with xa5 is from DV85 and mediates resistance to bacterial blight at adult-period. Kang18, Kang2 1 and Kang25 gaining from the progenies of the cross of Minghui63 and TD lines, which are the derive lines of Xa7, are severe resistant to bacterial blight (Zhou et al., 1993). Subsequently, Kanghui63, Kanghui98 and D205, which both confer resistance to bacterial blight, were also the restorers, and the new hybrids combinations: Kangyou63, Kangyou98 and fengyou205 were cultivared and registered in Anhui, Yunnan and Jiangsu (Ding et al., 2005. Kangyou 98 were also validated in Anhui, Henan and Hunan and renamed as Ilyou98 (Xu et al., 2006).

Xa21, a broad spectrum gene which stems from Oryza rufipogon with its resistance enhanced gradually from seedling stage to adult-plant stage, are wide applied to improve the parents of hybrid rice resistance to bacterial blight. The restorers, 9311, 6078, Zberapa820, Zhonghui218, R8006, R1176, Kang4183, and the male sterile, 3178S were improved or cultivated using MAS and the registered cultivars (province level and national grade) had Ilyou8820, Xieyou218, Zhongyou218, Zhongyou6 (ZhangYou6 and Guodao1), Zhongyou1176, Guodao3, Shuangyou4183 (Chen et al., 2000; Tong et al., 2003; Pei et al., 2004; Cao et al., 2005; Cao et al., 2006; Luo et al., 2005).

The transgenic restorers and male sterile lines with Xa21 had Minghui63, Yanhui559, SWR20, C418, T461 and Wan21A, Peiai64S. Kangyou87, the hybrid combination of Wan21A and R18, passed the late japonica rice regional test in Anhui province (Zhou et al., 2002; Peng et al., 2001; Li et al., 2001; Ma et al., 2000; Ni et al., 2001; Rao et al., 2003; Zhao et al., 2000).

Xa23, a broad spectrum gene found from Oryza longistaminata by Zhang Qi, could rapidly become a major source resistance to bacterial blight in improving the resistance of hybrid rice since the varieties with Xa21 have been infected by some new races. Due to the short-time application, the most materials improved and cultivated by Xa23 are lines. The modified restorers and male sterile lines with Xa23 using MAS had C6201, C6271, C6351, Minghui 86, C418, HB1471, HB1473, K10, H705, H706, ZR21-sk1, Jin23 A and Zhongjia A, the combination of K10 and Funong S along with ZR21-sk1 and II-32A displayed outstanding. Moreover, the preliminary results were achieved on transgenic
technology (Li et al., 2006; Xia et al., 2010; Chen et al., 2009; Zheng et al., 2009; Fan et al., 2011; Chen et al., 2009; Liu et al., 2011; Huang et al., 2009; Ji et al., 2007; Zhang et al., 2008).

3.2 Polygenic polymerization

In recent years, the varieties with genes of broad spectrum have been largely planted in various regions resulting in accelerated mutation of Xoo races. For instance, the China Xoo race VIII, infected the cultivars with Xa21. In order to strengthen resistance, broaden spectrum and prolong the resistance of varieties, pyramiding several genes into one cultivar seems to be necessary.

The genes polymerized together commonly containing 2 to 4, both the dominant genes and the recessive genes, which should broaden the spectrum and enhance the resistance of varieties to Xoo.

At present, the familiar gene polymerization combinations have Xa4/Xa21, Xa21/Xa23, Xa7/Xa21, Xa4/Xa21/Xa23, Xa4/xa5/xa13/Xa21. Shuhui207 and Kanghui527 with Xa4/Xa21 were bred (Deng et al., 2006; Huang et al., 2003; Wang et al., 2006), the hybrid rice combination Dyou17, deriving from the cross of D35A/Kanghui 527, were through variety identification in Sichuan province. The new line R106 with Xa21/Xa23, the improved-Hua 201S lines, YR7016 and YR7023 with Xa4/Xa21 were also obtained (Luo et al., 2005; Lan et al., 2011). The lines harboring different combinations of two, three and four genes were gained and displayed highly resistance and broad spectrum (Deng et al., 2005; Yi et al., 2006; Zhou et al., 2008; Basharat et al., 2006). The author analyzed the lesion length of the new hybrid combinations reacting to Xoo participated in south regional test from 2007 to 2011, the result shows that 86.5% of combinations are susceptible, 36.4% of which are susceptible, 42% of which are moderate susceptible, the others are moderate resistant or resistant, only Bo II you 829 t and Chun you xiang ning jing 2 tested in South China photosensitive late indica group in 2009 and the middle and lower reaches of Yangtze river for late japonica group in 2011 respectively achieved resistance level (Figure 2).

Figure 2 The new hybrid crosses participating in the south regional test reacting to bacterial blight from 2007 to 2011

4 Summary and prospect

The relationship between host and pathogenic bacteria is a process of mutual evolution. The resistant varieties released may result in changement of group members of pathogenic bacteria, either the compatible races become dominant or the present incompatible races vary.

Xa4 used in Indica rice in early stage and Xa21 largely applied in hybrid rice can be invaded successively. So it is possible that bacterial blight breaks out again under the hybrid rice widespread planted. Now the advices proposed how to alleviate the damage caused by bacterial blight are as follow:

(1) Exploring new resistant sources. Exploring the new resistant sources controlling the new infected races is the effective method since the natural law is that the new resistant sources conferring resistance to the new incompatible races must exist.

(2) Distributing the resistant cultivars reasonably. The group structure of pathogenic bacteria differs in different areas which plant cultivars with diverse background. It is pivotal to clear the genetic background of the varieties, the genetic structure of bacteria population and the dynamics of races so that the efficient resistant cultivars can be released and the new effective cultivars can be replaced in time before the loss of resistance of the former since the adaptability of bacteria is produced to the local
varieties in long-term evolution.

(3) Utilizing polygenic polymerization. Bacterial blight is the typical disease fitting gene-for-gene hypothesis, the products encoded by the resistant gene in host can interact with the proteins expressed by the avr gene in incompatible races. The mutation rate occurring at several avr genes at the same time is severe low, moreover, the interaction between the resistant genes can strengthen resistance level and broaden spectrum.

(4) The research on function of Xa27 shows that the expression of Xa27 is indispensable to prevent the infection of bacteria. The plants with Xa27 of its promoter replaced can resist the compatible races, which means the scientists could create the new resistant sources using genetic engineering technology in the future.

The wide spread of hybrid rice provides the condition for rapid reproduction of Xao. The breeding for disease resistance should be considered together with the high yield and quality to achieve the object of high yield, high efficiency, high quality, ecological and safe.

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