Dissection of Genetic Overlaps between Brown Spot and Black Shank Disease Resistances in Tobacco (*Nicotiana tabacum* L.) Line Beinhart-1000

Cai-hong JIANG, Yuan-ying WANG, Min REN, Xing-wei ZHANG, Aiguo YANG, Lirui CHENG, Quanfu FENG, Cheng-gang LUO

(Tobacco Research Institute of Chinese Academy of Agricultural Sciences; Qingdao, 266101, China)

Abstract

To investigate the genetic basis of resistances to brown spot and black shank diseases in tobacco (*Nicotiana tabacum* L.), two F_2 populations (including 115 and 220 individuals, respectively) were developed from the crosses between the common resistance line Beinhart-1000 and two susceptible cultivars G140 and XHJ, respectively. A total of 7 QTL affecting on resistances to fungal disease were identified on chromosomes 2, 3, 6, 8 and 12, respectively. As for brown spot disease, the two QTL were mapped on chromosomes 3 and 8, which explained 10.7% of the total phenotypic variance. As for black shank disease, a total of 5 QTL were mapped on chromosomes 2, 3, 6 and 12, which explained 29.6% of the total phenotypic variance. Upon comparison of QTL identified for brown spot and black shank disease resistances, we found one QTL shared the same genome region with similar gene actions, clearly suggesting that genetic overlap existed between the two major kinds of fungal disease resistances. Therefore, it is possible to breed a new cultivar with resistance to both brown spot and black shank diseases using Beinhart-1000 as a resistant source though maker assisted selection (MAS).

Introduction

Brown spot and black shank diseases are considered as the two of the major fungal diseases affecting tobacco (*Nicotiana tabacum* L.) production and quality in the world. The most effective approach to control the two kinds of diseases is growing resistant tobacco cultivars. For this purpose, it is necessary to study the genetic basis of brown spot and black disease resistance. The cigar tobacco line, Beinhart-1000, is not only considered as a good resistance source to blank shank disease, but also to brown spot disease. A number of classical genetics studies have indicated that brown spot resistance and black shank resistance from the resource were genetically complex quantitative traits. This makes the breeding of resistant tobacco cultivars difficult.

In recent years, molecular marker technology have facilitated our understanding of genetic basis of complex quantitative traits. As for brown spot disease, three QTL were mapped by 196 SSR markers based on a cross between susceptible Chinese cultivar Changbohuang and resistant Chinese cultivar Jingyehuang. As for black shank disease, two major QTL were located on chromosomes 4 and 8. The resistant alleles for the two major QTL come from resistant line Beinhart-1000. In addition, a total of 11 QTL affecting resistance to black shank disease were detected using a recombination inbred lines (RIL) derived from a cross between Florida301 and a susceptible cultivar Hicks. Among of them, one QTL with the largest effects was also found to have the largest effect on resistance in a Beinhart-1000 × Hicks doubled haploid (DH) population.

Although several QTL for resistances to brown spot disease and black shank disease have been reported, our understanding of genetic the genetic relationship between brown spot disease resistance and black shank disease resistance is also unknown. Therefore, the objective of present study were to identify QTL affecting the two kinds of fungal diseases and analyzed the genetic relationships between the two resistance, provide some useful information for tobacco breeding of biotic stress by MAS.

Materials

Parents: Beinhart-1000, G140 and XHJ;

A total of 110 F_2 individuals for resistance to brown spot disease (Beinhart-1000 × G140);

A total of 220 F_2 individuals for resistance to black shank disease (Beinhart-1000 × XHJ).

Experimental method

The two F_2 populations were evaluated for field resistance by artificial inoculation and genotyped with 83 and 70 polymorphic SSR markers. The position of the detected QTL were determined by composite interval mapping (CIM) using the software Cartographer 2.5. A logarithm of odds

Results and analysis

Significant differences of resistance to two kinds of diseases were observed between Beinhart-1000 and susceptible parents, indicating that Beinhart-1000 was not only a good resistant resource for improvement of brown spot resistance, but also for blank shank resistance. The F_2 population for brown spot expressed transgressive segregation and continuous variations, indicating the polygenic characteristics of the brown spot disease resistances. Reversely, score of disease severity for black shank was not fitted to a normal distribution and no F_2 individuals exhibited higher resistance to blank shank disease than parent Beinhart-1000, indicating that all resistant alleles existed in the parent Beinhart-1000, whereas all susceptible alleles existed in the susceptible parent (Fig. 1).

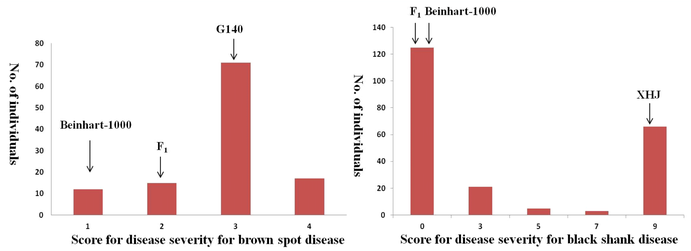

Fig 1. Frequency distribution of score for disease severity in the two F_2 populations

A total of 2 QTL affecting on resistance to brown spot disease were identified. They distributed on chromosomes 3 and 8 and explained 14.4 and 15.9% of the phenotypic variance, respectively (Table 1). The Beinhart-1000 alleles of the locus on chromosome 8 increased resistance while the Beinhart-1000 alleles of the other locus decreased resistance, indicating that some favorable alleles for resistance derived from low value parent. As for resistance to blank shank disease, a total of 5 QTL were mapped on chromosomes 2, 3, 6 and 12, which explained 2.9 to 4.1% of the phenotypic variance. For all these QTL, the resistant alleles were from parent Beinhart-1000.

Upon comparison of QTL identified for brown spot and black shank disease resistances, we found that two QTL for brown spot and black shank located in the neighboring region with same flanking marker M653 (Fig. 2). The Beinhart-1000 alleles at the two QTL were in same directions. The results clearly suggested that genetic overlap existed between the two kinds of fungal disease resistances.

Table 1 QTL affecting resistances to brown spot and black shank diseases

Trait	Genetic map	Interval region	LOD	Additive effect	R^2
Resistance to brown spot	3	M653-M524	3.1	-0.130	14.4
	8	M122-M935	3.4	0.057	15.9
Resistance to black shank	2	M252-PT61322	3.6	-0.254	6.2
	3	M653-M161	3.2	-1.239	6.0
	3	M790-M378	4.1	-0.184	6.7
	6	M355-M415	2.9	-0.240	5.6
	12	M745-M706	3.4	-1.289	5.1

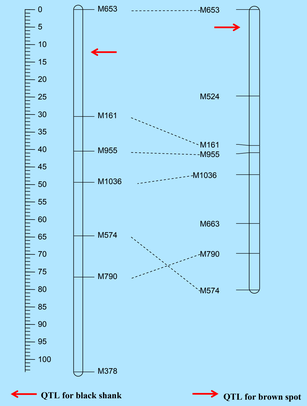

Fig.2 QTL flanking with marker M653 for resistances to two kinds of diseases

Conclusions

1. **The cigar tobacco line, Beinhart-1000, exhibiting highly resistances to both brown spot disease and black shank disease, is a good resource for improvement of brown spot and black shank resistances.**
2. **Based on molecular marker technology, a total of 7 QTL in this study were identified on chromosomes 2, 3, 6, 8 and 12, respectively. As for brown spot disease, the two QTL were mapped on chromosomes 3 and 8, which explained 10.7% of the total phenotypic variance. As for black shank disease, a total of 5 QTL were mapped on chromosomes 2, 3, 6 and 12, which explained 29.6% of the total phenotypic variance.**
3. **Genetic overlaps between brown spot and black shank resistances were detected in this study.**
4. **It is possible to breed a new cultivar with brown spot and black shank resistances by pyramiding the favorable alleles by MAS.**

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