



Genetic analyses of the major and minor locus groups of bacterial wilt resistance in tobacco using a diallel cross design

Y.L. Qian^{1*}, J. Chen^{2*}, J.J. Dong³, Z.C. Wu⁴, Y.H. Liu³, B.Y. Xue³, F.W. Shao³ and X.Y. Sun¹

¹Tobacco Research Institute, Anhui Academy of Agricultural Science, Hefei, China

²Institute of Agricultural Economy and Information, Anhui Academy of Agricultural Science, Hefei, China

³Anhui Provincial Corporation of China National Tobacco Corporation, Hefei, China

⁴Institute of Crop Science, Chinese Academy of Agricultural Sciences, Beijing, China

*These authors contributed equally to this study.

Corresponding author: X.Y. Sun

E-mail: sxyxscn@yahoo.com

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ABSTRACT. Tobacco germplasm samples with various levels of resistance to bacterial wilt were selected to construct F_1 combinations of parental inbred lines and orthogonal diallel crosses using samples collected in 2009 (15 germplasms), 2010 (15 germplasms), and 2011 (16 germplasms). A total of $1/2P(P + 1)$ experimental materials were used for analysis. Based on the analyses of major and minor locus groups, genetic effects on the incidence rate and index of bacterial wilt in tobacco were investigated on the 15th and 25th day during the early stage. Significant effects were observed in major locus groups, but not in minor locus groups. Specifically, adjacent major locus groups ($J_1 = 13,056$ and $J_1 = 13,055$; $J_1 = 14,080$ and $J_1 = 14,079$) were detected in both the first and second analyses with considerable effects. Based on the additive effects of minor locus groups on the rate and index of bacterial wilt, the effects on the incidence rates of

Yunyan 85, DB101, and RG11 as well as the effects on the disease index of the latter two germplasms reached the maximum. This was consistent with the disease resistance indicators of these tobacco varieties in the field (corresponding broad heritability >20%). Genetic homozygous dominant loci (+ +) increased the rate of bacterial wilt (susceptible), whereas homozygous recessive loci (- -) reduced the index of bacterial wilt (resistant) with considerable additive effects and low dominant effects, suggesting that the inheritance of the bacterial wilt rate and index in tobacco mainly relies on additive inheritance.

Key words: Tobacco bacterial wilt; Major and minor locus groups; Genetic analysis; Bacterial wilt resistance in tobacco