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GENETICS OF BLACK SHANK RESISTANCE IN TOBACCO

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ABSTRACT

The inheritance of resistance in four cultivars of tobacco to black-shank showed that resistance was dominant over susceptability in F1 and a ratio of nine resistance to seven susceptibe plants was obtained in F2, suggesting that resistance was controlled by two dominant complementary genes. F2 results were confirmend through back cross studies.

INTRODUCTION

Black-shank caused by phytophthora parasitica var. nicotianae is one of the serious and destructive disease of flue-cured tobacco in Pakistan especially in N.W.F.P. The wide spready occurrence, epidemic nature and general severity of the disease has stopped cultivation of tobacco as a commercial crop in certain areas of N.W.F.P. The disease has become epidemic where monoculture is practised, on soil rich in organic matter and where warm humid weather prevails. The inheritance of host plant resistance to black-shank had been investigated by many workers. Apple [8] studied nicotiana tabacum X N.plumbaginifolia F_2 families for resistance to race 0 and 1, found, that this character is controlled by a single dominant gene. Goin and Apple [12] also observed that black shank resistance is controlled by a high dominant gene. In another experiment of back cross of 402 X 8 N. plumbaginaflia, Apple [7] found that a single dominant gene is responsible for its inheritance. Oka [6] reported that black resistance selected from two back crosses of bright yellow with (N. tabaccum XN.tungifora)