Inheritance studies on *Fusarium* wilt resistance in long duration pigeon pea (*Cajanus cajan* (L.) Millsp.)

Anil Kumar Singh¹, Dhirendra Kumar Singh, Rajeev Kumar, Mahendra Narain Singh, and Ved Prakash Rai²*

Department of Genetics and Plant Breeding, Institute of Agricultural Sciences, Banaras Hindu University, Varanasi-221 005, India.

Received: 29-11-2016 Accepted: 10-07-2017 DOI: 10.18805/LR-3805

ABSTRACT

*Fusarium* wilt (FW) is a major fungal disease of pigeon pea causing huge economic losses annually and breeding of FW resistant cultivars is essential as other control measures such as fungicides are expensive and harmful to environment. To understand the inheritance of FW resistance, nine populations each of F₁, F₂ and BCSF, (F₁ × susceptible parent) derived from crossing between three adopted but susceptible long duration pigeonpea cultivars (MA-6, MAL-13 and MAL-18) with three FW resistant lines (BSMR-846, BWR-23 and BDN-2029). All F₁ plants were resistant to FW indicating the dominance of resistance. The χ² test for goodness-of-fit showed F₂ segregation ratio of 13:3 (one dominant and one recessive), 15:1 (two dominant genes) and 3:1 (one dominant gene) in BSMR-846, BWR-23 and BDN-2029, respectively. The information generated on the genetics of FW resistance will be helpful in development of high yielding and stable wilt resistant, long duration pigeonpea varieties.

Key words: Dominance, *Fusarium* wilt resistance, Genetics, Long duration, Recessive

INTRODUCTION

*Fusarium* wilt (FW) caused by *Fusarium udum* Butler is an important fungal disease prevalent in all pigeonpea growing areas worldwide, being more severe in Indian subcontinent (Jain and Reddy, 1995; Gwata et al., 2006). Yield losses of wilt susceptible crops ranged from 16 to 47% (Prasad et al., 2003) or even 100% (Reddy et al., 1990) causing losses up to 71 million US $ annually in India alone (Reddy et al., 1993). Wilt symptoms usually appear during flowering and pod stage of the crop. In addition, the symptoms may also appear in early growth stages. Though, FW can be managed through adoption of certain agronomic practices such as crop rotation, field sanitation, seed and soil treatment and mixed cropping with sorghum (Jain and Reddy, 1995), the cultivation of FW resistant varieties appears to be the best option for stabilizing the pigeonpea production. Therefore, enhancement of resistance to FW in pigeonpea is a major challenge, which needs to be addressed on priority basis. Although, *F. udum* was identified in India by Butler in 1908, only a limited number of resistant sources have been identified so far (Nene et al., 1989; Khare et al., 1994). Currently, none of the long duration pigeonpea variety in India is resistant to FW (Singh et al., 2011).

A thorough understanding of the inheritance of FW resistance in pigeon pea will be useful in initiating an effective breeding programme (Kamboj et al., 1990; Zhang et al., 2007). Several studies have been conducted in this direction and number of genes have been identified which confer FW resistance in different pigeon pea genotypes. This include two complementary genes with recessive and dominant expression (Shaw, 1936), duplicate genes (Joshi, 1957), a single dominant gene (Saxena and Sharma, 1990), two independent dominant genes (Singh et al., 1998), a major dominance gene with minor poly genes (Sharma, 1986), two complementary genes (Okiror, 2002), single or two independent/complementary dominant genes (Changaya et al., 2012; Singh et al., 2016), one dominant and one recessive gene (Saxena et al., 2012).

At present information about physiological races and genetic diversity of the FW pathogen in pigeon pea is also limited and inconclusive (Tiwari and Dhar, 2011). The presence of pathogenic variability may also influence the results of genetic studies and breeding efforts hence specific information on the presence of different variants and their relative virulence is essential to employ appropriate breeding strategies for enhancement of FW resistance (Patil et al., 2013). The present investigation is an attempt to understand the genetics of resistance to FW involving diverse susceptible/ resistant genotypes of mostly long duration pigeon pea. The breeding materials generated from this study will be useful for mapping of FW resistance and in conventional breeding programmes.

*Corresponding author’s e-mail: vprai.genetics@gmail.com*

¹College of Agriculture and Research Station, Indira Gandhi Krishi Vishwavidyalaya, Korea- 497 335, Chhattisgarh (India)

²Agricultural Research Station, Navsari Agricultural University, Tanchha, Bharuch - 392025, Gujarat (India)
MATERIALS AND METHODS

Three long duration FW susceptible pigeon pea genotypes viz., MA-6, MAL-13 and MAL-18 (developed at Banaras Hindu University, Varanasi, India) and three FW resistant donors viz., BSMR-846, BWR-23 and BDN-2029 (FW resistant pigeon pea genotypes obtained from Agricultural Research Station, Badnapur, Maharastra, India) were selected for the present study (Table 1). The crosses were made in all possible combinations (excluding reciprocals) to obtain nine F1 hybrids. The nine F1 along with parents were grown in crossing blocks during rainy season 2010-2011 and each F1 plant was backcrossed to susceptible parent to generate (BCSF1) plants. The F1 plants were also selfed to procure the nine respective F2 generations.

One row plot of each of the parents and F1s, two rows of BCSF1 and eight rows of each F2s were grown in compact family block design in wilt sick plot at Agricultural Research Farm, Institute of Agricultural Sciences, Banaras Hindu University, Varanasi, India during rainy season 2011-2012. As per availability of the seeds, the plot size of few segregating population (F2 and BCSF2) of respective crosses was reduced. Each plot consisted of one row of 3 meter length with spacing of 75 × 25 cm between and within rows, respectively. Recommended agronomic practices were followed to raise a good crop. Chopped wilted pigeon pea plant stems (5-8 cm long) were uniformly buried into the soil across the field every year to artificially enhance and maintain the F. udum inoculum load (5 × 106 spores per ml-1).

To access the uniformity of disease incidence, one infector row of susceptible check ‘Bahar’ was planted after every 10 rows of test entries. The scoring of the susceptible (completely or partially wilted) and resistant (wilt free) plants of each population of each crosses was done as per the standard method (Nene and Kannaiyan, 1982). Chi-square (χ2) test was applied to assess the goodness of fit to appropriate genetic ratio for the estimation of number of gene(s) governing FW resistance.

RESULTS AND DISCUSSION

The parents, F1, F2 and BCSF1 of each of the nine crosses were screened for wilt incidence in wilt sick plots. All F1 exhibited resistant reaction to FW, indicating the dominance of resistance over susceptibility (Table 2). Dominant control of FW resistance was also reported by a number of scientists (Shaw, 1936; Joshi, 1957; Changaya et al., 2012; Saxena et al., 2012). F1 plants of three populations, MA-6 × BSRM-846, MAL-13 × BSMR-846 and MAL-18 × BSMR-846 segregated in the ratio of 13R:3S, indicating digenic inheritance with one dominant and one recessive gene for FW resistance in the resistant parent BSMR 846 (Table 1). The BCSF1 plants segregated in the expected ratio of 1R:1S (Table 3). The results substantiated that the resistant parent, BSMR-846, possessed one dominant and one recessive gene for resistance. Saxena et al. (2012) analysed four F1 pigeon pea populations derived from cross between a susceptible male sterile line (ICPA 2051) and four FW resistant restorer lines (ICPL 20106, ICPL 20116, ICPL 20136 and ICPL 87119) and found a genetic ratio of 13R:3S. They suggested that one dominant (Wr/Wr1) and one recessive (wr2wr2) gene conferred resistance to FW disease in these pigeon pea lines. The involvement of single dominant gene for FW resistance in pigeon pea is also reported by (Pastor-Corrales et al., 1994; Okioro, 2002; Changaya et al., 2012). Involvement of one or more recessive genes for control of FW resistance has also been reported by some researchers (Jain and Reddy, 1995; Kumar et al., 2009).

In F2 populations of three other crosses involving the resistant parent BWR-23, namely, MA-6 × BWR-23, MAL-13 × BWR-23 and MAL-18 × BWR-23 segregated with a good fit to 15R:1S (Table 2) indicating the involvement of two independent dominant genes governing resistance to FW. Further, the BCSF2 population of these crosses exhibited 3R:1S segregation ratio (Table 3). From these results, it was quite obvious that the resistant parent, BWR-23 possessed two independent dominant genes for FW resistance. The F2 populations of three crosses viz., MA-6 × BDN-2029, MAL-13 × BDN-2029 and MAL-18 × BDN-2029, involving BDN-2029 as the resistant parent, segregated into 3R:1S exhibited monogenic dominant control of resistance. The ratios in BCSF2 (1R:1S) further confirmed the significance of a single dominant gene for controlling FW resistance in crosses derived using BDN-2029 as resistant parent (Table 3).

Table 1: Details of the pigeon pea genotypes used in the present study.

<table>
<thead>
<tr>
<th>Genotype</th>
<th>Full name</th>
<th>FW reaction</th>
<th>Phenotypic characteristics</th>
</tr>
</thead>
<tbody>
<tr>
<td>MA-6</td>
<td>Malviya Arhar-6</td>
<td>S’</td>
<td>Semi-spreading, yellow flower, purple pod, highly resistant</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>to Sterility Mosaic Virus</td>
</tr>
<tr>
<td>MAL-13</td>
<td>Malviya Arhar Long-13</td>
<td>S</td>
<td>Spreading, light yellow flower, long green pods with</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>constricted locules having purplish black streaks and resistant</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>to Sterility Mosaic Virus</td>
</tr>
<tr>
<td>MAL-18</td>
<td>Malviya Arhar Long-18</td>
<td>S</td>
<td>Spreading, yellow flower, purple pod, highly resistant to</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>Sterility Mosaic Virus</td>
</tr>
<tr>
<td>BSMR-846</td>
<td>Badnapur Sterility Mosaic</td>
<td>R</td>
<td>Semi compact, yellow flower with red streaks, pod green with</td>
</tr>
<tr>
<td></td>
<td>Resistant-846</td>
<td></td>
<td>streaks</td>
</tr>
<tr>
<td>BWR-23</td>
<td>Badnapur Wilt Resistant-23</td>
<td>R</td>
<td>Flower red, pod green with streaks</td>
</tr>
<tr>
<td>BDN-2029</td>
<td>Badnapur-2029</td>
<td>R</td>
<td>Semi compact, dark red flower, pod green with purplish streaks</td>
</tr>
</tbody>
</table>

'S = susceptible; R = resistant.


