Study on Reaction of Sunflower Lines and Hybrids to 

Macrophomina phaseolina (Tassi) Goed. causal Agent of Charcoalrot Disease

Mahtab Rafiei, Alireza Dalili Siavash Rayatpanah, Abasali Andarkhor and Masoud Soltani Najaf Abadi

Abstract: Charcoal rot is one of the most important diseases of sunflower in the world. The disease is threat for the sunflower crops in north of Iran. Different methods were applied for the disease management. The use of resistant cultivars is considered as one of the most important methods. In this study ten sunflower genotypes obtained from the seed and plant improvement institute of Iran, were evaluated to Macrophomina phaseolina. In this experiment response of the genotypes was investigated against to charcoal rot in vitro and farm condition. In vitro study showed that genotype RF81-74*AF80-460/2/1 with 39.89 and genotype RF81-137/1*AF81-228 with 50.67 had lowest and highest disease index. In the farm condition genotypes RF81-74*AF80-460/2/1, RF81-1/2*AF81-112, RF81-1/2*AF80-452/2/2, RF81-106/1*AF80-448/1/2, HYSUN33 and AZARGOL showed significantly low incidence of Macrophomina phaseolina (0.33%) followed by genotype RF81-65*AF80-429/2/3 (13.67%). The results demonstrated different response of sunflower genotypes to Macrophomina phaseolina.

Key words: Macrophomina phaseolina - Sunflower - Disease index - Incidence - in vitro

INTRODUCTION

Sunflower (Helianthus annuus L.) is an oilseed species characterized with high production, wide range of growing season, growth in different soil condition, growth in low humidity condition and its content of high quality oil [1].

Macrophomina phaseolina is the most important pathogens on sunflower and more than 500 plant species. [2]. The charcoal rot is serious for the sunflower crop throughout the world. The diseases can decrease 12% in yield from 12 million hectares of the world [3, 4].

The pathogen causes root or stem rot and sometimes caused early death of maturing plants [5]. The fungus is seed and soil borne pathogen [6, 7]. The disease develops under warm and dry weather condition [8].

Different researcher studied sunflower genotypes to M. phaseolina. Gul et al. [9] investigated some sunflower genotypes to M. phaseolina in green house and farm condition. The results indicate reaction of genotypes was different to the agent. Resistant of four sunflower hybrids were evaluated to M. phaseolina and the reaction was different to the agent [10].

Asad et al. [11] investigated response 10 sunflower genotypes to M. phaseolina. The results showed that genotypes 953-102 and IMP1141 were moderately resistant to the fungus. Kumar et al. [12] inoculated some sunflower hybrids by M. phaseolina. The reaction of LDMRSH-3 and HS-1 genotypes was susceptible to charcoal rot disease. Dalili et al. [13] evaluated some sunflower genotypes to M. phaseolina. The reaction of genotypes was very different to the agent of disease.

The pathogen was reported on different crops from Iran [14-17]. The charcoal root rot of sunflower is threat for the sunflower crop in north provinces of Iran. Development of resistant varieties is one of the most important methods for the management of the disease. The present study was carried out with the objective of sunflower genotypes screening against charcoal rot.
MATERIAL AND METHODS

Sampling and Fungal Isolation: Eighteen Samples were collected from the infected stems and roots of soybean (Glycine max L.), sesame (Sesamum indicum L.) and sunflower (Helianthus annuus L.) plants from Mazandaran Province in northern Iran, during 2011-2012 (Table 1). The infected tissues were sterilized in 0.8% sodium hypochlorite for 1 min and small pieces were excised and placed on potato dextrose agar (PDA). The plates were incubated at 28±2°C in the darkness for four days. Purification was developed by single microesclerotium on PDA at 28±2°C [18]. The isolates used in the investigation are present in Table 1.

Evaluation of M. phaseolina isolates Pathogenicity and Sunflower Genotypes Resistance in vitro: In this experiment 3 isolates were selected from soybean, sunflower and sesame. Resistant was evaluated at the seedling stage on 10 sunflower genotypes in a completely randomized design. Each treatment was replicated three times and included two plates with six seeds per plate. Seeds of the different genotypes were sterilized with 2% sodium hypochlorite for 4 min and rinsed twice in sterile water. Seeds were placed on 6-day-old colonies of the M. phaseolina isolate (on PDA plates) and incubated at 28°C ± 2 in the dark condition.

Evaluation was done after six days, using the following severity assessment key:

0 = healthy seed, 1 = discoloration of a portion of the seedling in contact with the mycelium, 2 = seed teguments invaded by mycelium and sclerotia but healthy seedling, 3 = seed teguments free from the fungus but seedling infected, 4= seed tegument and seedling infected, 5= seed infected and not germinated.

The disease index was calculated by multiplying the number of seeds by the degree of disease severity [19]. Analysis of variance (ANOVA) of the data was performed with the MSTAT-C program.

RESULTS AND DISCUSSION

Evaluation of M. phaseolina isolates Pathogenicity and Sunflower Genotypes Resistance in Farm Condition: Ten sunflower genotypes were sown in Dashtenaz research station, Agricultural and natural research center of Mazandaran, in field with 20 microsclerotia per gram of soil (20). Each plot consisted of four rows of 5 m length spaced 70 cm apart. The plant to plant spacing was maintained at 25 cm. Crop management factors such as land preparation, crop rotation, fertilizer and weed control were followed as recommended for local area. The experiment was conducted based on Completely Randomized Design with three replications. Disease incidence was calculated by dividing the number of infected plants with total number of plants multiplying it with100 [21]. All the analyses were performed using the MSTAT-C program.

Table 1: Macrophomina phaseolina isolates from Mazandaran Province in north of Iran: locality, host plants

<table>
<thead>
<tr>
<th>Isolate No.</th>
<th>Host</th>
<th>Locality</th>
</tr>
</thead>
<tbody>
<tr>
<td>Se1</td>
<td>Sesame</td>
<td>Behshar</td>
</tr>
<tr>
<td>Se2</td>
<td>Sesame</td>
<td>Behshar</td>
</tr>
<tr>
<td>Se3</td>
<td>Sesame</td>
<td>Amir Abad</td>
</tr>
<tr>
<td>Se4</td>
<td>Sesame</td>
<td>Hossein Abad</td>
</tr>
<tr>
<td>Se5</td>
<td>Sesame</td>
<td>Jouibar</td>
</tr>
<tr>
<td>Se6</td>
<td>Sesame</td>
<td>Tous Kola</td>
</tr>
<tr>
<td>Se7</td>
<td>Sesame</td>
<td>PanbehCholeh</td>
</tr>
<tr>
<td>Se8</td>
<td>Sesame</td>
<td>Hamid Abad</td>
</tr>
<tr>
<td>Su1</td>
<td>Sunflower</td>
<td>Behshar</td>
</tr>
<tr>
<td>Su2</td>
<td>Sunflower</td>
<td>Amir Abad</td>
</tr>
<tr>
<td>Su3</td>
<td>Sunflower</td>
<td>Hossein Abad</td>
</tr>
<tr>
<td>Su4</td>
<td>Sunflower</td>
<td>Rostam Kola</td>
</tr>
<tr>
<td>Su5</td>
<td>Sunflower</td>
<td>DashteNaz</td>
</tr>
<tr>
<td>So1</td>
<td>Soybean</td>
<td>Behshar</td>
</tr>
<tr>
<td>So2</td>
<td>Soybean</td>
<td>Amir Abad</td>
</tr>
<tr>
<td>So3</td>
<td>Soybean</td>
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<tr>
<td>So5</td>
<td>Soybean</td>
<td>DashteNaz</td>
</tr>
</tbody>
</table>

Table 2: Analysis of variance pathogenicity of M. phaseolina on sunflower genotypes in vitro

<table>
<thead>
<tr>
<th>K Value</th>
<th>Source</th>
<th>Degrees of Freedom</th>
<th>Sum of Squares</th>
<th>Mean Squares</th>
<th>F Value</th>
</tr>
</thead>
<tbody>
<tr>
<td>2</td>
<td>Isolate</td>
<td>2</td>
<td>66.067</td>
<td>33.033</td>
<td>5.48**</td>
</tr>
<tr>
<td>4</td>
<td>Genotype</td>
<td>9</td>
<td>926.000</td>
<td>102.889</td>
<td>17.08**</td>
</tr>
<tr>
<td>6</td>
<td>Isolate * Genotype</td>
<td>18</td>
<td>142.600</td>
<td>7.922</td>
<td>1.3155**</td>
</tr>
<tr>
<td>7</td>
<td>Error</td>
<td>60</td>
<td>361.333</td>
<td>6.022</td>
<td></td>
</tr>
</tbody>
</table>

Coefficient of Variation: 5.71%
** significant at level 1%
ns = not significant
Eighty four isolates of *M. phaseolina* from different geographical regions of Mexico were studied and the isolates were grouped in 43 distinct pathotypes [22]. Study on pathogenicity of *M. phaseolina* indicated high levels of variation in pathogenicity of the fungus [23].

Investigation of *M. phaseolina* isolates showed great variability in pathogenicity among isolates from different host species [24]. Pathogenicity of some isolates of *M. phaseolina* that belong to different country was investigated. The results showed the pathogenicity of isolates was different and the most aggressive isolates were from Mexico, Brazil and Colombia [25].

Means comparison of different plants species reaction showed that there was significant difference (P<0.01) on the rate of disease index, hence, the sunflower genotypes were placed in different groups (Table 4). The results showed that genotype RF81-74*AF80-460/2/1 with 39.89 and genotype RF81-1371*AF81-228 with 50.67 had lowest and highest disease index.

**Evaluation of Sunflower Genotypes Resistance to *M. phaseolina* in Farm Condition:** Evaluation of sunflower genotypes resistance in farm condition demonstrated that sunflower cultivars and hybrids showed different response to *M. phaseolina*. Analysis of variance showed that the sunflower genotypes were significantly different (P< 0.01) on the reaction to *M. phaseolina* (Table 5).

Mean comparison of different plants species reaction showed that significant difference (P<0.01) on the rate of disease index, hence, the sunflower genotypes were placed in different groups (Table 6). The results indicated that genotypes RF81-74*AF80-460/2/1, RF81-1/2*AF81-112, RF81-1/2*AF80-452/2/2, RF81-1061*AF80-448/1/2, RF81-65*AF80-429/2/3, RF81-1371*AF81-228, HYSUN33, AZARGOL with 24.42, 24.42 and 22.20 % and genotype Allstar 65% had lowest and highest disease incidence.

There are different studies about reaction of sunflower to *M. phaseolina*. Some sunflower varieties or lines were studied in field condition to *M. phaseolina*. Disease incidence was estimated at flowering stage. Eight sunflower lines were resistant against charcoal rot. Three sunflower varieties or lines were moderately susceptible and lines viz. G-32 and G-66 were indicated highly resistant to charcoal rot [26].

The reaction of 20 genotype of sunflower was investigated to charcoal rot under farm and green house condition. The results of green house demonstrated genotypes CMS19 × R43, Bline 1052/1 and CMS 350.1 ×R43 with 24.42, 24.42 and 22.20 % and genotype Allstar...
with 51/06% had lowest and highest disease incidence. Also the farm study showed that genotypes CMS 19× R43, Bline 1052/1 and CMS 350/1 × R43 with 25.49, 26.39 and 33.40 % have the lowest disease incidence and were more tolerance to charcoal rot

Five sunflower genotypes (SC-83, SC-92, SF-177 and HO-1) were investigated. The genotypes showed that different reaction to M. phaseolina. HO-1, SC-92 and SC-83 sunflower varieties indicated susceptible response to M. phaseolina (27).

REFERENCES


