RESPONSE OF Solanum lycopersicum L. (Tomato) TO Tuta absoluta AND Glomerus clarum USING SIMPLE SEQUENCE REPEAT (SSR) MARKER

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INTRODUCTION

Tomato (Solanum lycopersicum L.) belongs to the family Solanaceae and the order Solanales (Czihak et al., 2010). It is sensitive to a number of diseases and affected by devastating pests of which Tuta absoluta is one of them (Chettri et al., 2010).

Several approaches have been employed in the management of Tuta absoluta but none of these are effective in the management of the virus (Olaleye et al., 2016). Several attempts have been made in the management of Tuta absoluta but none of these are effective in the management of the virus. The use of SSR (Simple Sequence Repeat) marker and its derivatives are useful tools for identification and characterization of nematode species (Olaleye et al., 2016).

This study aimed to investigate the response of tomato to Tuta absoluta and Glomerus clarum using morphological and molecular techniques.

MATERIALS AND METHODS

Eight tomato varieties were collected from Yewa, Ile-Ife, and Osun States, Nigeria. Complete Randomized Design was used with three replicates and 3 treatments (Glomerus clarum, Tuta absoluta, and Control) for each variety. A screen house experiment was conducted in a 9 x 12 pots where the seedlings of G. clarum was inoculated to the varieties and the T. absoluta was infected in the plants week before flowering.

Growth, yield, and yield characters were determined while percentage inoculation was calculated according to the method described by Ramírez et al. (2010) and severity of infestation was measured using the visual rating scale described by Mazzola et al. (2013).

Amplification of RNA from insects and detection of polymorphisms from young adult leaves were carried out using SSR primers: LEGAC, LECAM, LECAD, LWSAD, and LETA401.

RESULTS AND DISCUSSION

There was no significant difference between Glomerus clarum and Tuta absoluta treated plants across the growth, yield, and yield characters.

Plants treated with G. clarum showed reduced percentage inoculation (14%) and severity of infestation (22%) compared to T. absoluta (20% and 46%) and control (23% and 25%) as seen in Table 1 and 2 respectively. This could be due to G. clarum which induced activation of tomato defense mechanisms, optimum nutrient uptake and damage compensations in response to the attacks of the pests (Olaleye et al., 2016) and Olawuyi et al. (2018).

Amplification of RNA from insects and detection of polymorphisms from young adult leaves were carried out using SSR primers: LEGAC, LECAM, LECAD, LWSAD, and LETA401 (Table 2).

RESULTS CONT’D

Table 2: Gene diversity, Allele number, and Polymorphic information content of SSR primers

<table>
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<tr>
<th>Molecular Markers</th>
<th>Major Allele Frequency</th>
<th>Allele No.</th>
<th>Gene Diversity</th>
<th>Polymorphic Information Content</th>
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</thead>
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<tr>
<td>LEGAC03</td>
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<td>3</td>
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<td>24</td>
<td>3</td>
<td>0.50</td>
</tr>
</tbody>
</table>

RESULTS CONT’D

Figure 1: Effect of treatments on percentage incidence of Tuta absoluta at different growth stages

REFERENCES


Chettri, B.L. 2010. Tomato leafminer (Tuta absoluta) an emerging agricultural pest: control and management strategies: a review. World Scientific News 11:30-43


