RESPONSE OF Solanum lycopersicum L. (Tomato) TO Tuta absoluta AND Glomus clarum USING SIMPLE SEQUENCE REPEAT (SSR) MARKER Olawuyi, O.J. and Nsi, I.M.

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Introduction

Tomato (*Solanum lycopersicum* L.) is a self-pollinated annual crop which belongs to the family Solanaceae and the order Solanales (Singh *et al.*, 2016). It is a tropical crop used for numerous purposes viz: juice, tomato paste, ketchup, a variety of sauces etc. it is a cheap source of many essential nutrients such as lycopene, carotene, flavonoids, vitamin C and a host of other vitamins (Kimura and Sinha, 2008). Just like other crops, it is sensitive to a number of diseases and attacked by pests of which *Tuta absoluta* is one of them.

Tuta absoluta is one of the most devastating pests of tomato as it feeds on leaves, burrows stems, attacks flowers and bores both unripe and ripe fruits leading to the production of unhealthy fruits and results in losses leading to a downturn in the global tomato market (Chhetri, 2018). Over the years, heavy reliance on chemical pesticides of which incidences of misuse, doubling of required doses, and wrong application all aimed at protecting crops from further attack had been reported (Zekeya *et al.*, 2017). These pesticides are environmental hazard which pose health risks to consumers as they get stored up at different stages of the food chain hence, the need to adopt an effective and more environmentally friendly approach of using beneficial microorganisms such as the use of Arbuscular Mycorrhizal Fungus (*Glomus clarum*) (Olowe *et al.*, 2018). SSR markers have been used in marker assisted breeding due to their high reproducibility, co-dominance, specificity and wide genome coverage (Olawuyi and Onuoha, 2017).

Aim of the Study

This study aimed at investigating the response of tomato to *Tuta absoluta* and *Glomus clarum* using morphological and molecular techniques

Materials and Methods

A total of eight tomato varieties were collected from TechnoServe Nigeria Limited, Katsina State, National Centre for Genetic Resources and Biotechnology, Ibadan and Ojoo market, Ibadan in Nigeria and evaluated using Complete Randomized Design with three replicates and three treatments which comprised of *Glomus clarum* + *Tuta absoluta*, *Tuta absoluta* alone and Control (uninoculated). Seedlings were raised for 4 weeks in nursery before transplanted into poly pots containing 8kg sterilized sandy-loam soil and transferred to the screen house in the Department of Botany, University of Ibadan. Five (5) grams of *G. clarum* was inoculated to the varieties according to the procedure described by Olawuyi *et al.* (2014) and *Tuta absoluta* was infested on the plants 1 week after. Growth, agronomic, and yield characters were evaluated, percentage incidence was calculated according to the method described by Rasheed *et al.* (2018) and severity of infestation was assessed using the visual rating scale described by Anjorin *et al.* (2013). Amplification of DNA and detection of polymorphisms from young apical leaves were carried out using SSR primers; LEGA003, LECA001, LEAAT005 and LETAA001in accordance with the procedure described by Lorenz (2012).

Morphological data was analyzed using SAS 9.1 statistical software and means were separated using Duncan Multiple Range Test at P 0.05 while binary data generated for molecular data was analyzed for genetic diversity parameters using Power Marker software V 2.5.

Results and Discussion

There was significant difference between *Glomus clarum* and *Tuta absoluta* treated plants across growth, agronomic and yield characters. The tomato varieties had varied influence on growth, agronomic and yield characters in accordance with the results obtained by Biswas *et al.* (2015) who reported significant varietal effect on growth characters of tomato. This could be due to the fact that these characters are controlled and expressed by certain genes which are particular to each variety. Also, plants with *G. clarum* showed reduced percentage incidence (13%) and severity of infestation (27%) when compared to *T. absoluta* alone (19% and 40%) and control (23% and 35%). This could have been due to *G. clarum* which induced activation of tomato defense mechanism, optimum nutrient uptake and damage compensation which was also reported by Olawuyi *et al.* (2013), Olawuyi *et al.* (2014) and Olowe *et al.* (2018). Primer LEAAT005 had the highest allele number (4), gene diversity (0.73), and polymorphic information content (0.67) while the highest major allele frequency of 0.67 was observed in LEGA003.

Table 1: Growth, agronomi	ic and yield characters	of Tomato as affected by	Glomus clarum and	Tuta absoluta
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Treatments	Plant height (cm)	Leaf length (cm)	Number of leaves	Stem girth (cm)	Leaf width (cm)	Presence of flowers	Number of flowers	Number of dead flowers	Presence of fruits	Number of fruits	Fruit fresh weight (g)
Glomus clarum + Tuta absoluta	95.07ª	5.55ª	11.97ª	0.58ª	2.59 ^a	3.64ª	3.78ª	1.31ª	1.56 ^{ab}	0.18 ^b	0.75ª
Tuta absoluta alone	85.68 ^c	5.06 ^c	11.60 ^a	0.53°	2.46 ^b	2.97 ^b	3.27 ^b	1.27 ^a	1.26 ^b	0.45 ^a	1.13 ^a
Control	89.25 ^b	5.23 ^b	11.64 ^a	0.56 ^b	2.44 ^b	3.46 ^a	3.25 ^b	1.13 ^a	1.76 ^a	0.28 ^b	0.97 ^a

Means with different letters in the same column are significantly different at P < 0.05 according to Duncan Multiple Range Test (DMRT).

Table 2: Genotypic effect on growth, agronomic and yield characters of Tomato

Tomato varieties	Plant height (cm)	Leaf length (cm)	Number of leaves	Stem girth (cm)	Leaf width (cm)	Presence of flowers	Number of flowers	Number of dead flowers	Presence of Fruit	Number of fruits	Fruit fresh weight (g)
Dan Eka Jibia	80.16 ^d	5.25 ^c	10.16 ^{de}	0.58 ^a	2.35°	3.76 ^a	3.66 ^c	1.39 ^c	1.35 ^{bc}	0.24 ^c	0.99 ^{abc}
Rukuta Mani	78.76 ^{de}	5.52 ^{ab}	11.29 ^c	0.58 ^a	2.64 ^a	3.62 ^a	1.34 ^e	0.23 ^e	0.53 ^{de}	0.26 ^c	0.15 ^c
Dan Eka Mani	74.88 ^{ef}	5.26 ^c	9.60 ^e	0.53 ^b	2.66 ^a	3.50 ^a	2.49 ^d	0.61 ^d	0.97 ^{cd}	0.09 ^c	0.71 ^{bc}
Rukuta Jibia	71.09^{f}	4.97 ^d	10.39 ^{de}	0.56 ^a	2.37°	2.48 ^b	1.21 ^e	0.32 ^{de}	0.53 ^{de}	0.03 ^c	0.31 ^c
Ojoo market	60.38 ^g	4.84 ^d	10.75 ^{cd}	0.47 ^c	2.07 ^d	2.19 ^b	0.69 ^e	0.34 ^{de}	0.00 ^e	0.00°	0.00°
NGB00717	105.44 ^c	5.44^{abc}	13.40 ^b	0.57 ^a	2.49 ^b	3.72 ^a	5.18 ^b	2.03 ^b	3.61 ^a	0.53 ^b	0.99 ^{abc}
NGB00725	128.87 ^a	5.67 ^a	14.78 ^a	0.57 ^a	2.70 ^a	3.78 ^a	6.35 ^a	2.49 ^a	3.44 ^a	0.91 ^a	2.48 ^a
NGB00710	120.42 ^b	5.31 ^{bc}	13.52 ^b	0.56 ^a	2.69a	3.81 ^a	6.59ª	2.48 ^a	1.79 ^b	0.58 ^b	1.97 ^{ab}

Means with different letters in the same column are significantly different at P < 0.05 according to Duncan Multiple Range Test (DMRT)

Table 3: Gene diversity, Allele number, and Polymorphic information content of SSR primers

Molecular Markers	Major Allele Frequency	Sample Size	Allele No.	Gene Diversity	Polymorphic Information Content
LEGA003	0.67	24	3	0.50	0.44
LECAA001	0.46	24	3	0.64	0.57
LEAAT005	0.33	24	4	0.73	0.67
LETAA001	0.63	24	3	0.50	0.41
Mean	0.52	24	3.25	0.59	0.52



Key: AMF: Glomus clarum, Pest: Tuta absoluta





Week 4 Week 5 Week 6 Week 7 Week 8 Week 9Week 1 Week 1 Wee

Key: AMF: Glomus clarum, Pest: Tuta absoluta



Conclusion and Recommendation

Plants treated with *Glomus clarum* reduced the infestation of *Tuta absoluta*. Primers LEAAT005 and LECAA001 detected the highest genetic polymorphism and could be used in marker assisted breeding of other *Solanum spp*. The tomato varieties; NGB00717 (NACGRAB), NGB00725 (NACGRAB) and Dan Eka Jibia (Technoserve), Dan Eka Mani (Technoserve) were highly tolerant to *Tuta absoluta* and could be recommended for breeding of tomato against *Tuta absoluta*.

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