Behavior of New Entries and Developed Tomato Hybrids Carrying *Ty-2* Gene

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ABSTRACT

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Tomato yellow leaf curl disease (TYLCD) is a serious problem hampering tomato production worldwide. In the Mediterranean Basin, disease incidence and severity are higher in the dry season increasing whitefly (*Bemisia tabaci*) populations. Effectiveness of resistance to *Tomato yellow leaf curl virus* (TYLCV) depends on both tomato host resistance and TYLCV complex species. So far, six different *Ty* tomato resistance genes have been identified. Two main TYLCV complex species, *Tomato yellow leaf curl virus-Israel* (TYLCV-Is) and *Tomato yellow leaf curl Sardinia virus* (TYLCSV), have been identified in Tunisia. The present work aimed to evaluate entries heterozygous for *Ty-2* gene to help predict hybrid performance. Two tomato entries homozygous for the *Ty-2* TYLCV resistance gene, one tomato hybrid homozygous for *Ty-2* and two heterozygous hybrids were included, besides two susceptible tomato entries. Resistance response to TYLCD was recorded based on disease incidence and severity levels. Data analysis was performed according to presence/absence of *Ty-2* gene and taking into account homozygosity and heterozygosity of *Ty-2*. Generalized linear model analysis was applied to check significance of individual factors' effects (*i.e.* effect of tomato entries or tomato groups of entries based on presence or absence of homozygous/heterozygous *Ty-2* gene, block unit within the field trial and the year of the trial) on the dependent variables (disease incidence and severity). Further multi-comparison tests gave evidence on significant effect of *Ty-2* homozygous gene tomato entries on TYLCD incidence and severity levels. The results were discussed with special focus on the relevance use of heterozygous hybrid tomato varieties.

Keywords: Heterozygous, resistance genes, tomato, *Tomato yellow leaf curl virus* (TYLCV), Tunisia

Tomato yellow leaf curl disease (TYLCD) is caused by a complex of monopartite and bipartite begomoviruses belonging to the family Geminiviridae and vectored by the adult sweet potato whitefly (*Bemisia tabaci*). Begomoviruses infect a wide range of botanical families, including Solanaceae (tomato, tobacco, pepper, petunia), Cucurbitaceae (melon, watermelon, squash, gourd), Fabaceae (common bean, soybean, lima bean, mung bean, cowpea), Euphorbiaceae (cassava) and Malvaceae (cotton, okra) (Seal et al. 2006). Begomoviruses cause serious

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tomato (*Solanum lycopersicum*) yield losses particularly in tropical and subtropical regions (Cohen and Lapidot 2007; Ji et al. 2007b; Moriones & Navas-Castillo 2000; Varma et al. 2003; Rybicki 2015).

Strategies to control the disease focus on reducing sources of inoculum, controlling *B. tabaci* population, use of physical (*e.g.* whitefly-proof screens, UV-absorbing plastic sheets, and reflective plastic mulches), chemical (insecticide applications) or cultural (virus-free seeds, virus-free transplants, crop-free periods, rouging symptomatic plants and weed management) methods (Riley and Srinivasan 2019). Besides, another alternative control method using salycilic acid as a resistance-inducing factor was shown to effectively enhance TYLCD tomato resistance in both resistant and susceptible tomato cultivars (Li et al. 2019). However, in general TYLCD control is not possible after infection because of very low efficient spray level of *B. tabaci* and whitefly resistance to some commonly used pesticides (Antignus et al. 2001; Horowitz et al. 2007). Thus, the use of resistant varieties combined with other strategies of control can contribute to significantly reduce the incidence of the disease. So far, six TYLCD resistance *Ty* genes have been identified (Dhaliwal et al. 2020) and their chromosomal locations mapped, *i.e.*, *Ty-1* (Zamir et al.1994) and its allele *Ty-3* on chromosome 6 (Ji et al. 2007a; Verlaan et al. 2013), *Ty-2* on chromosome 11 (Kalloo & Banerjee 1990; Hanson et al. 2000; Yang et al. 2014), *Ty-4* on chromosome 3 (Ji et al. 2009), recessive *ty-5* on chromosome 4 (Anbinder et al. 2009; Hutton et al. 2012; Wang et al. 2018), and *Ty-6* on chromosome 10 (Hutton and Scott 2014; Gill et al. 2019). These resistance genes were originally discovered and introgressed from several tomato wild species including *S. peruvianum* (*ty-5*), *S. chilense* (*Ty-1* and *Ty-3*, *Ty-4* and *Ty-6*), and *S. habrochaites* (*Ty-2*) (Kasrawi et al. 1988; Pico et al. 1996. Hanson et al. 2000; Hanson et al. 2006; Ji et al. 2007a, c). Gene function studies were conducted for *Ty-1/Ty-3*, *ty-5* and *Ty-2*. *Ty-3* encoding for a DFDGD-class RNA-dependent RNA polymerase which function is still unclear (Verlaan et al. 2013). Lapidot et al. (2015) discovered that *ty-5* gene is a loss-of-function mutant allele of the Pelota gene due to a T-to-G transversion in the coding region in cultivated tomato. *Ty-2* was found to be synonymous with *TYNBS1*, a functional resistance gene which is an *NB-LRR* (nucleotide-binding domain and leucine-rich repeat-containing) gene (Yamaguchi et al. 2018). In general, TYLCD resistance is positively correlates with lower levels of virus accumulation: *i.e.* the virus level was found to be 10% lower in tomato lines carrying *Ty-1/Ty-3* compared to virus level in susceptible tomato cultivars (Verlaan et al. 2013). Similar results were reported with *Ty-2* (Barbieri et al. 2010).

The present work aimed to evaluate heterozygous entries for one *Ty* gene intending to help predict hybrid performance. The impact of *Ty-2* gene at heterozygous status has not been tested in tomato yet. Hence, two tomato entries homozygous for the *Ty-2* TYLCV resistance gene, one tomato hybrid homozygous for this gene and two heterozygous hybrids were involved in this work. Additionally, two susceptible tomato entries, with no *Ty* gene, were added as susceptible controls. Resistance response to TYLCD was recorded based on incidence and severity levels of the disease. Data analysis was performed according to presence/absence of *Ty-2* resistance gene only. Results were discussed with special attention to relevance of heterozygous hybrid tomato varieties utilization.

MATERIALS AND METHODS

Experimental site.

Field trials were conducted in the Marj Ellil - Route Regueb in Kairouan in central region of Tunisia, during two consecutive seasons in 2015 and 2016 from February to August. Kairouan is under a Mediterranean climate.

Plant material and experimental design.

Seven tomato entries (E1 to E7) were included in the study (Table 1): two tomato lines and one hybrid homozygous for *Ty-2* and two hybrids heterozygous for *Ty-2*. Additionally, two susceptible tomato entries, lacking Ty genes, were added as susceptible controls. Resistance response to TYLCD was recorded based on incidence and severity levels of the disease. Tomato hybrids E3, E4 and E5 were obtained from crosses using either tomato accessions, obtained from The World Vegetable Center gene bank in Taiwan (WorldVeg), or with the inbred line variety Rio Grande (Table 1). The cross schemes are written as female parent crossed with the male parent so in all crosses resistant parents were used as the pollen donor. Tomato entries were categorized into 3 groups (Grp1 to Grp3) based on presence/absence of the homozygous/heterozygous *Ty-2* gene (Table 1). The experimental design was a Randomized Blocks Design (RBD), with an arrangement of grouping the heterogeneous units into homogenous blocks, using 3 blocks and 16-20 plants per plot. All entries were represented in each block. Plant spacing was 40 cm within- and 100 cm between- rows. In addition, in order to ensure homogeneous infection of the experimental site by *B. tabaci*, tomato Rio Grande variety, known as a susceptible genotype to TYLCD, was planted in the border of the entire field trial.

Table 1. Tomato entries (E) and corresponding groups (Grp) representing different combinations of *Ty* resistance genes screened for TYLCD resistance in Tunisia

Current code	Original code/Name	Status of *Ty-2* gene	Group Nb.	Source
E1	CLN2498E	*Ty* 2 Hm	Grp1	WorldVeg
E2	CLN2498D	*Ty* 2 Hm	Grp1	WorldVeg
E3	E2* E1	*Ty* 2 Hm	Grp1	This work
E4	E6*E1	*Ty* 2 Ht	Grp2	This work
E5	Rio Grande*E1	*Ty* 2 Ht	Grp2	This work
E6	CLN1466P	None	Grp3	WorldVeg
E7	CLN2026D	None	Grp3	WorldVeg

E2*E1, E6*E1 and Rio Grande*E1 represent the crosses' codes for hybrid production; Hm and Ht refer to homozygous and heterozygous, respectively.

Disease incidence and severity scoring.

TYLCD incidence and severity were recorded weekly for two months, starting the fifth week after planting when TYLCD symptoms occurred first. Symptom severity assessment was performed based on a scoring scale from 1 to 5 adapted from Lapidot et al. (2006) and Lapidot et al. (1997) where:

1: no symptoms.
2: slight leaf curl.
3: substantial curl with or without lightyellowing.
4: substantial curl with substantial yellowing.
5: substantial curl + yellowing + stunting or death of the plant.

A single score was assigned to each tomato plant according to detectable symptoms.

Incidence and severity scores (I% and S%, respectively) were calculated for each plot using the following formula:

$$I\,(\%) = \frac{PA \times 100}{PT}$$

where I: disease incidence; PA: number of symptomatic plants as soon as a visible symptom was observed; PT: total number of plants in the plot.

$$S(\%) = \sum_{i=1}^{5} \frac{iYi \times 100}{5N}$$

where S: disease severity; i: class; Yi: number of plants in class i; N: total number of plants.

Data analysis.

Only data from the last evaluation were subjected to statistical analysis to detect possible effect of tomato entries on the disease incidence and severity levels. Similarly, based on the presence or absence of homozygous/heterozygous *Ty-2* gene, effect of tomato entries group (Grp) on the disease incidence and severity was investigated.

Then, two generalized linear models (GLM) were written as:

$$Y_{ijk} = \mu + E_i + B_j + Yr_k + e_{ijk}$$

where μ: mean; E_i: tomato entry i effect (from 1 to 7); B_j: block j effect (from 1 to 3); Yr_k: year k effect (1 or 2, respectively for year 2015 and 2016); e_{ijk}: residual for E_i at B_j and Yr_k; Y_{ijk}: severity or incidence of E_i at B_j and Yr_k, and

$$Y_{ijk} = \mu + Grp_i + B_j + Yr_k + e_{ijk}$$

where μ: mean; Grp_i: group of tomato entries i effect (from 1 to 3); B_j: block j effect (from 1 to 3); Yr_k: year k effect (1 or 2, respectively for year 2015 and 2016); e_{ijk}: residual for Grp_i at B_j and Yr_k; Y_{ijk}: severity or incidence of Grp_i at B_j and Yr_k.

Data analyses were applied using Generalized Linear Model (GLM) to check significance of the effects of individual factors on the dependent variables (*i.e.* incidence and severity rates).

Following GLM analyses, data distribution was tested for normality using the Shapiro-Wilk test and Q-Q plot of residuals. ANOVA (analysis of variance) was applied followed by an adequate post hoc test for mean comparison if data were normally distributed. The Tukey Kramer multi-comparison test was used if results of the Levene's test showed equal variances, whereas Dunnett's test was applied in the case of heterogeneous variances. The Kruskal Wallis test, a non-parametric test, was applied when normality was rejected. If a significant effect was shown using Kruskal Wallis test, a post hoc test, Bonferroni multi-comparison test was used. The 95% confidence level was applied with all the tests. All of the statistical analyses were carried out using the SPSS 25 program (IBM 2017).

RESULTS

Experimental field infestation.

High levels of both incidence and severity scores were recorded from the Rio Grande plots (Table 2). The field trial was obviously highly infected by *B. tabaci* during the experimental trials over the two trial periods year 1 and year 2 (2015 and 2016, respectively). Consequently, homogeneous infection over the trial plots was observed.

Table 2. Disease severity and incidence rates of susceptible Rio Grande variety around the experimentation plot

Plot	Year	N	Severity (%)			Incidence (%)		
			Mean ± SE	Min (%)	Max (%)	Mean ± SE	Min (%)	Max (%)
1	**1**	**3**	65.1±1.9	62.3	67.0	96.7±2.4	93.0	100
1	**2**	**3**	63.2±2.0	60.2	65.3	96.3±2.7	92.3	100
2	**1**	**3**	66.6±1.8	65.3	69.3	97.8±3.0	93.3	100
2	**2**	**3**	68.9±1.6	66.7	71.3	97.8±1.5	95.7	100
3	**1**	**3**	69.9±1.0	68.3	71.3	98.3±1.1	97.0	100
3	**2**	**3**	68.2±2.7	64.3	72.3	98.3±1.6	96.0	100
4	**1**	**3**	68.9±2.3	66.3	72.3	99.0±1.3	97.0	100
4	**2**	**3**	64.4±1.6	62.7	66.7	97.5±1.8	94.7	100

Generalized linear model analysis.

GLM analysis was applied to quantify the degree of association between three independent variables (E/Grp, B and Yr) to a dependent variable, TYLCD incidence or severity. Significant results of composite tests were found with both incidence and severity, either in the case of models including E or Grp. Models of incidence based on E, B and Yr independent variables or Grp, B and Yr independent variables came out with p = 0.036 and 0.021, respectively. The p values were lower than 0.001 in both GLMs with severity as the dependent variable (severity by E, B and Yr and severity by Grp, B and Yr). Accordingly, significant global effect of all tested models is concluded.

Furthermore, effects of each GLM were tested using Wald χ^2 test. Independent variable Yr showed no significant effect with all GLMs, whereas independent variable B had a significant effect on severity only when associated to E and Yr (p = 0.041). The independent variable E had a significant effect on both dependent variables, incidence and severity, with a p = 0.008 and $p < 0.001$, respectively. Similarly, independent variable Grp was significantly associated with incidence and severity with a p = 0.004 and $p < 0.001$, respectively.

TYLCD resistance response based on incidence.

Incidence data set and corresponding residuals were not normally distributed either if incidence is expressed by E or by Grp. Kruskal Wallis test, a non-parametric test, was conducted to examine differences on TYLCD incidence according to E and Grp factors. Significant differences were found for E (χ^2 = 13.183,

$p = 0.040$ and df = 6) and Grp ($\chi^2 = 10.162$, $p = 0.006$ and df = 2). A pairwise comparison test showed no significant differences of the effect of E on TYLCD incidence based on adjusted significance using the Bonferroni correction ($p = 0.05$) (Figure 1), while the same comparison test showed significant differences between Grp on TYLCD incidence. Indeed, Grp1 (entries homozygous for *Ty-2*) was significantly different from Grp2 (heterozygous for *Ty-2*) ($p = 0.017$) and Grp3 (homozygous for susceptible allele) ($p = 0.031$) (Figure 2). Grp2 and Grp3 were not significantly different. TYLCD incidences of Grp1, Grp2 and Grp3 were 96.72%, 99.54% and 99.07%, respectively. *Ty-2* gene seems to have no effect on TYLCD incidence when heterozygous.

Tomato entries heterozygous for *Ty-2* behaved similarly as susceptible tomato entries lacking *Ty-2*.

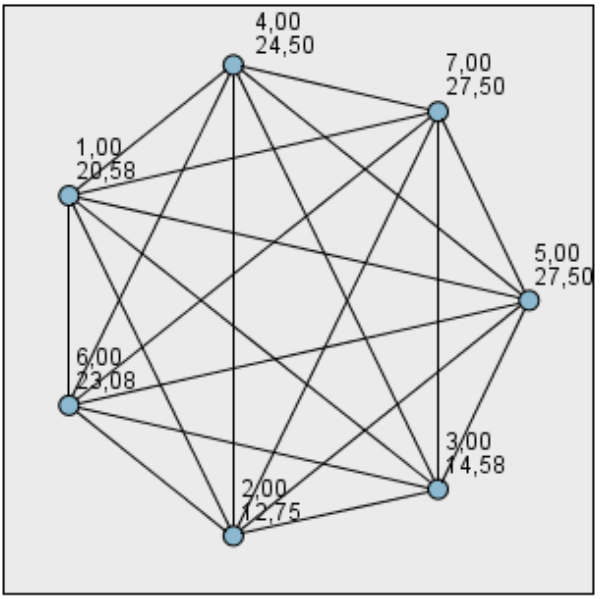

Fig. 1. Pairwise comparisons of E mean effect on TYLCD incidence by Bonferroni test using Bonferroni significance correction. Each node shows the sample average rank of E.

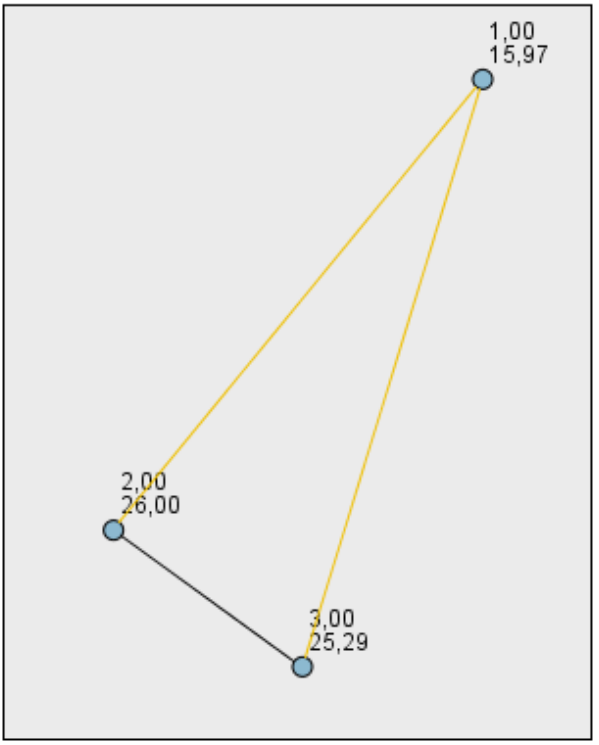

Fig. 2. Pairwise comparisons of Grp mean effect on TYLCD incidence by Bonferroni test using Bonferroni significance correction. Each node shows the sample average rank of Grp.

TYLCD resistance response based on severity.

GLM analysis showed that both E and B independent variables were significantly associated to TYLCD severity. Considering variable B, severity data were normally distributed, and heterogeneous variance was shown based on Levene's test. Subsequently, a post hoc multi-comparison test was required. Data analysis using Dunnett's test showed no significant differences between B1, B2 and B3 (blocks 1, 2, 3, respectively). Hence, no significant effect of individual levels of B on severity was found.

Severity data set and corresponding residuals were shown to be normally distributed either when severity was expressed by E or by Grp. Variance homogeneity was proven using Levene's test within severity by Grp data (p = 0.070), so multi-comparison was carried out using Tukey Kramer's test, whereas heterogeneous variance was shown within severity by E data (p = 0.211). Then, multi-comparison Dunnett's test was performed.

Mean's multi-comparison tests showed significant differences between E and Grp on severity levels (Table 3). In fact, TYLCD severity levels of *Ty-2* homozygous lines E1, E2 and E3 with severity rate of 50.88%, 52.49 % and 50.76 %, respectively, were significantly different from TYLCD severity levels of susceptible tomato lines (E6 and E7), with severity rate of 73.89% (E6) and 68.64%

(E7). On the other hand, heterozygous tomato hybrid E5 behaved similarly as a susceptible line based on TYLCD severity. Indeed, E5 was significantly different from homozygous tomato lines with higher TYLCD severity level. In addition, it showed no significant differences compared to susceptible tomato lines (Table 3). However, heterozygous *Ty-2* tomato line E4 showed no significant difference of TYLCD severity compared to all other tomato entries: E4 seemed to have an intermediate behavior, since it showed a severity level that was not significantly different neither from homozygous *Ty-2* entries nor from susceptible tomato controls.

TYLCD severity data analyses based on Grp of tomato lines showed significant differences of Grp1 to Grp2 and Grp3 (Table 3). Grp1 included tomato lines homozygous for *Ty-2* resistance gene, whereas Grp2 comprised tomato lines heterozygous for *Ty-2* resistance gene, and Grp3 had no resistance gene. Definitely, effectiveness of *Ty-2*, as a resistance gene to TYLCD, was only demonstrated with tomato lines harboring homozygous *Ty-2* gene.

Table 3. TYLCD severity as expressed among tomato entries (E1-E7) and *Ty-2* gene groups (Grp1-Grp3)

Entry/Group of Entries	N	Mean ± Std Error	Minimum (%)	Maximum (%)
Severity by entry (Dunnett's test)				
E1	6	50.88 ± 1.91a	44	55
E2	6	52.49 ± 2.56a	43	60
E3	6	50.76 ± 1.69a	48	59
E4	6	66.01 ± 3.27ab	56	79
E5	6	71.13 ± 1.68b	66	76
E6	6	73.89 ± 3.83b	60	84
E7	6	68.64 ± 2.76b	60	77
Severity by Group of entries (Tukey Kramer's test)				
Grp1	18	51.38 ± 1.15a	43	60
Grp2	12	68.57 ± 1.91b	56	79
Grp3	12	71.27 ± 2.39b	60	84

In summary, tomato entries homozygous for *Ty-2* (Grp1) were significantly different from susceptible tomato entries (Grp3) for TYLCD severity. The group of heterozygous tomato (Grp2) behaved similarly as the group of susceptible tomato entries (Grp3). These results suggest that *Ty-2* should be homozygous to achieve better TYLCD resistance, especially under high whitefly and inoculum pressure.

DISCUSSION

In Tunisia, TYLCD is one of the major threats particularly occurring during dry season in open field tomato growing areas due to high whitefly population density. Both TYLCV-Is and TYLCSV do exist in Tunisia all over tomato production areas. Mnari-Hattab et al. (2014) reported the occurrence of both TYLCV species. Many TYLCD resistant tomato hybrid varieties have been developed harboring

one or more *Ty* resistance genes. In Tunisia, all commercial tomato varieties, even those commonly known as highly tolerant to TYLCV (*e.g.* Saada, Savera, Tisey, Berna and Kismat varieties), still show TYLCD symptoms under high inoculum pressure and/or early infection.

In a previous work, we carried out a tomato field trial aiming to screen TYLCD resistance resources (Elbaz et al. 2016). The screening was applied to a set of tomato entries homozygous for one or several *Ty* genes, including*Ty-1/Ty-3*, *Ty-2* and *ty-5*. The work demonstrated that tomato lines with *Ty-1*/*Ty-3* and *Ty-2* genes offered the highest levels of resistance to begomoviruses, whereas a line homozygous for *Ty-2* alone displayed relatively low levels of TYLCD resistance. Similarly, the combination of *Ty-2* and *ty-5* in homozygous condition showed better resistance than *ty-5* alone. In similar work performed in Oman, Al-Shihi et al. (2018) found that tomato lines homozygous for *ty-5* performed the best, possibly due to the presence of a different begomovirus species than those occurring in Tunisia.

Ty-2 resistance gene was shown to have an additive effect of tomato resistance against begomoviruses in Tunisia (Elbaz et al. 2016). This additive effect of *Ty-2* gene was confirmed by Tabein et al.(2017), when pyramiding *Ty-1*/*Ty-3* and *Ty-2* in tomato hybrids. Accordingly, the *Ty-2* gene, a dominant resistance gene, was shown to act with a minor additive effect against this disease. Moreover, the impact of *Ty-2* gene at heterozygous status has not been tested in tomato yet.

As a case study, the present work aimed to evaluate TYLCD resistance of tomato entries heterozygous for *Ty-2* gene compared to tomato entries homozygous for *Ty-2*. The study also included susceptible tomato entries lacking *Ty* genes.

All tomato entries showed symptoms caused by TYLCV infection. TYLCD incidence of tomato entries in this study varied from 95.95% to 100%. These tomato entries showed severity levels higher than 68% over the two year trials. These registered rates of TYLCD incidence and severity indicated high begomovirus pressure. Moreover, tomato entries homozygous for *Ty-2* gene (E1, E2 and E3) were significantly different from all other entries except E4 tomato line. E4, heterozygous for *Ty-2*, had an intermediate behavior between resistant (E1, E2 and E3) and susceptible (E6 and E7) entries. The occurrence of the intermediate genotype such as E4 line indicated that resistance level response might be explained not only based on genetic effect but also by other factors like plant vigor (Kasrawi et al. 1988), weather conditions and whiteflies abundance (Moriones and Navas-Castillo 2000). In addition, the mean of tomato entries of Grp1 with homozygous *Ty-2* gene, either line entries or hybrid entry, showed the lowest levels of TYLCD severity compared to Grp2 (hybrids heterozygous for *Ty-2* gene) and Grp3 (susceptible lines with no *Ty* gene).

Our work showed that *Ty-2* was more efficient when homozygous. Consequently, resistance levels of tomato hybrids heterozygous for *Ty-2* are questionable especially in case of severe epidemic. To address this issue, we suggest that TYLCD resistant tomato varieties should be homozygous for *Ty-2*. This implies that the two parental lines involved in a genetic cross aiming to produce a tomato TYLCD resistant F_1 hybrid, are both homozygous for *Ty-2*. Similar results were reported by Vijeth et al. (2018). They showed that when challenged to a high disease pressure by using controlled inoculation by whiteflies, all tomato TYLCD resistant lines crossed with a susceptible tomato parent produced

susceptible hybrids except for two crosses (among a total of seven hybrids) where the hybrids were classified as tolerant. On the other hand, most crosses involving two resistant lines produced resistant hybrids. Nevertheless, conclusion from the present work needs to be further verified with other *Ty* genes since this study involved only *Ty-2*. In particular, *Ty-1/Ty-3* gene needs to be considered during future investigation in the context of Tunisian epidemiological TYLCD. Based on our results and those of Vijeth et al. (2018), we expect that the highest resistance against TYLCD in Tunisia would be obtained from tomato hybrids homozygous for *Ty1*/*Ty-3* and *Ty-*

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RESUME

Elbaz M., Timoumi M. et Hanson P. 2022. Comportement de nouvelles entrées et hybrides de tomate développés portant le gène *Ty-2*. Tunisian Journal of Plant Protection 17 (1): 1-14.

La maladie de la feuille jaune en cuillère de la tomate (Tomato yellow leaf curl disease, TYLCD) est une menace sérieuse pour la production de tomate dans le monde entier. Dans le bassin méditerranéen, l'incidence et la sévérité de la maladie sont plus élevées pendant la saison sèche qui favorise les populations élevées de la mouche blanche (*Bemisia tabaci*). L'efficacité de la résistance au virus de la maladie de la feuille jaune en cuillère de la tomate (*Tomato yellow leaf curl virus*, TYLCV) dépend à la fois de la résistance de la plante hôte, ici la tomate, et des espèces présentes du complexe TYLCV. Jusqu'à présent, six gènes différents Ty de résistance chez la tomate ont été identifiés. En Tunisie, deux principales espèces du complexe TYLCV, *Tomato yellow leaf curl virus-Israel* (TYLCV-Is) et *Tomato yellow leaf curl Sardinia virus* (TYLCSV), ont été identifiées. Le présent travail vise à évaluer les entrées de tomate hétérozygotes pour le gène *Ty-2* afin d'aider à prédire les performances des hybrides. Deux entrées de tomates homozygotes pour le gène de résistance *Ty-2* au TYLCD, un hybride de tomate homozygote pour *Ty-2* et deux hybrides hétérozygotes ont été inclus, en plus de deux entrées de tomates sensibles. La réponse de résistance au TYLCD a été enregistrée en fonction de l'incidence et des niveaux de sévérité de la maladie. L'analyse des données a été réalisée selon la présence/absence du gène *Ty-2* et en tenant compte de l'homozygotie et de l'hétérozygotie de *Ty-2*. L'analyse en modèle linéaire généralisé a été appliquée pour vérifier la signification des effets des facteurs individuels (c'est-à-dire l'effet des entrées de tomate ou des groupes d'entrées de tomate en fonction de la présence ou de l'absence du gène *Ty-2* homozygote/hétérozygote, de l'unité expérimentale dans l'essai sur le terrain et de l'année de l'essai) sur les variables dépendantes (incidence et sévérité de la maladie). D'autres tests de comparaisons multiples ont révélé un effet significatif des génotypes de tomate ayant le *Ty-2* à l'état homozygote sur l'incidence et les niveaux de sévérité de la maladie TYLCD. Les résultats ont été discutés avec une attention particulière à la pertinence des variétés de tomates hybrides hétérozygotes.

Mots clés: Hétérozygote, gènes de résistance, tomate, *Tomato yellow leaf curl virus* (TYLCV), Tunisie

الملخص

الباز، منيرة ومنعم تيمومي وبيتر هانسون. 2022. سلوك إدخالات جديدة وهائجن من الطماطم مطوَّرة حاملة للجين 2-yT.
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يعد مرض تجعد أوراق الطماطم الصفراء (TYLCD) تهديدا خطيرا لإنتاج الطماطم في جميع أنحاء العالم. في حوض البحر الأبيض المتوسط تكون معدلات الإصابة بالأمراض وشدتها أعلى في موسم الجفاف الذي يسمح بوجود أعداد كبيرة من الذبابة البيضاء (*Bemisia tabaci*). تعتمد فعالية مقاومة فيروس تجعد أوراق الطماطم الصفراء (TYLCV) على كل من المقاومة الجينية لصنف الطماطم وأنواع الفيروس الموجودة. حتى الآن تم تحديد ستة جينات Ty مختلفة لمقاومة هذا المرض. في تونس تم التعرف على نوعيْن رئيسييْن من نوع هذا الفيروس وهما فيروس تجعد الأوراق الصفراء للطماطم-إسرائيل (TYLCV-Is) وفيروس سردينيا لتجعد أوراق الطماطم الصفراء (VSTYLC). يهدف هذا العمل إلى تقييم إدخالات مختلفة من الطماطم حاملة للجين في صيغته المتماثلة أو الهجينة غير المتماثلة للجين للمساعدة على التنبأ بالأداء الجيني في مقاومة المرض. تم تضمين اثنين من إدخالات الطماطم ذات الصيغة الجينية المتماثلة للجين Ty-2 مع هجين طماطم واحد متماثل الصيغة للجين Ty-2 وهجينيْن اثنين غير متماثلي الصيغة الجينية لجين المقاومة Ty-2، بالإضافة إلى صنفيْن من الطماطم الخالية من أي مقاومة للمرض. تم تسجيل مدى مقاومة المرض بناء على نسبة حدوث المرض ومدى شدته. وقد تم إجراء تحليل البيانات باعتبار تواجد أو عدم تواجد الجين Ty-2 مع مراعاة صيغة التماثل من عدمها التي يتواجد عليها هذا جين. التحليل الإحصائي للمعطيات مكن من التحقق من مدى أهمية تأثيرات العوامل الفردية (أي تأثير إدخالات الطماطم أو مجموعات إدخالات الطماطم المكونة بناء على وجود أو عدم وجود الجين Ty-2 باعتبار صيغة التماثل الموجود عليها هذا الجين، ووحدة التجربة الميدانية وسنة التجربة) على المتغيرات صلب الدراسة (نسبة المرض وشدته). أعطت اختبارات المقارنة المتعددة دليلا على التأثير المعنوي لجين المقاومة المتماثل yT-2 على مستوى نسبة مرض TYLCD وشدته صلب مختلف إدخالات الطماطم. تمت مناقشة النتائج مع إيلاء اهتمام خاص لأهمية أصناف الطماطم الهجينة غير المتماثلة.

كلمات مفتاحية: اللاتماثل الجيني، تونس، جينات المقاومة، طماطم، فيروس تجعد أوراق الطماطم الصفراء (TYLCV)

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