TOWARDS IDENTIFICATION OF SSR MARKERS LINKED TO TSWV RESISTANCE IN PEANUT (*Arachis hypogaea* L.)

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Introduction

Spotted wilt caused by tomato spotted wilt virus (TSWV) is one of the major diseases affecting peanut (*Arachis hypogaea* L.) production in the Southeastern USA (Fig. 1). Occurrence, severity, and symptoms of spotted wilt disease are highly variable from season to season making it difficult to efficiently evaluate breeding populations for resistant line selection. Molecular markers linked to spotted wilt resistance could overcome this problem and allow selection of resistant lines regardless of seasonal conditions and periods.

Objectives

The objective of this study is to identify simple sequence repeat (SSR) markers linked to TSWV resistance in peanut through

1) evaluating the TSWV reaction of the F_2 and $F_{2:3}$ populations;
2) screening polymorphic SSR markers between the two parental lines of the F_2 population,
3) mapping the TSWV resistance loci using SSR genotyping of the F_2 population.

Fig. 1 Plant stunting is a typical symptom of spotted wilt.

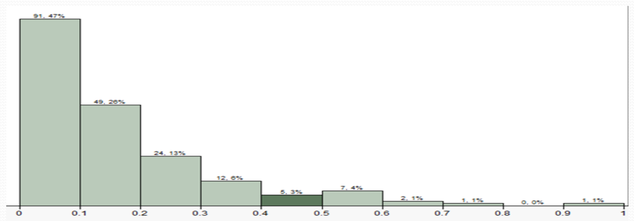

Fig.2 ELISA results distribution of the F2 population

Materials and methods

- A total of 199 F_2 progeny derived from the cross between Florida-EP^{TM}'113', a TSWV resistant variety and Georgia Valencia, a highly susceptible cultivar were evaluated by ELISA (enzyme-linked immunosorbent assay) for the presence of TSWV.
- The $F_{2:3}$ population were further phenotyped using a visual 1 to 10 scaling method on both canopy and seed coat and ELISA Immunostrip.
- For genotyping, a total of 2116 SSR markers with high polymorphic information content or mapped on peanut linkage groups were screened against the two parental lines of the F_2 segregating population.
- Map construction: The polymorphic SSR markers will be used to genotype the F2 mapping population to map the spotted wilt resistance gene loci.

Results

- The ELISA and Immunostrip results confirmed that most of the symptomatic plants were infected by TSWV with some exceptions, which didn't display visual symptoms but exhibited positive ELISA reactions.
- The phenotype distributions in both F2 population ELISA results and $F_{2:3}$ population visual scoring method results show the reasonable segregation based on TSWV resistance investigation (Fig. 2).
- Totally, 294 polymorphic SSR markers were found and will be used to map the TSWV resistance conferred by Florida-EP^{TM}'113' and to identify the flanking markers linked to spotted wilt resistance (Table 1, Fig 3).

Table. 1 The summary table of total 2116 SSR markers been screened. It shows the amplifiable and polymorphic information by each linkage group

Linkage group	Total SSRs screened	amplifiable SSRs	polymorphic SSRs	Amplifiable ratio	polymorphic ratio
A01	110	98	19	0.89	0.17
A02	75	66	14	0.88	0.19
A03	128	120	23	0.94	0.18
A04	99	87	7	0.88	0.07
A05	89	81	9	0.91	0.10
A06	98	92	14	0.94	0.14
A07	62	54	15	0.87	0.24
A08	99	90	3	0.91	0.03
A09	86	78	19	0.91	0.22
A10	82	76	6	0.93	0.07
B01	87	78	18	0.90	0.21
B02	71	63	19	0.89	0.27
B03	94	88	8	0.94	0.09
B04	95	88	7	0.93	0.07
B05	75	71	8	0.95	0.11
B06	82	78	10	0.95	0.12
B07	77	69	12	0.90	0.16
B08	82	75	6	0.91	0.07
B09	74	65	15	0.88	0.20
B10	70	68	11	0.97	0.16
No AABB genome information SSRs	19	15	1	0.79	0.05
No linkage group information SSRs	362	307	50	0.85	0.14
Total	2116	1907	294	0.90	0.14

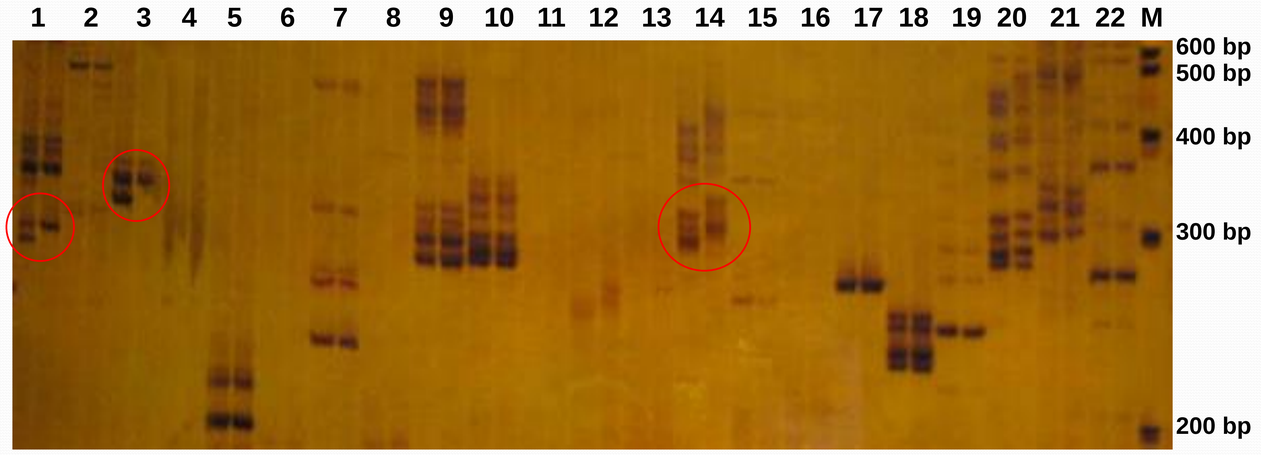

Fig. 3 The SSR markers shown on polyacrylamide gel electrophoresis (PAGE) between two different parental lines. Lane 1~22 represent different SSR markers and the red circles indicate the polymorphic markers.

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