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Annual Report & Summary

**Project (00098511) Report**

**Genetic mapping the gene loci underlying spotted wilt resistance in peanut**

In this project, we proposed to 1) develop and identify the polymorphic SSR markers between the selected resistant and susceptible parents, and 2) genotype and phenotype the F2 segregating populations to genetically map the TSWV resistance gene loci to develop the resistance linked markers. This is a multiple year project as described in the full proposal. For year 2012 with fund of $26,000, we proposed to complete the first objective: develop and identify the polymorphic SSR markers between the selected resistant and susceptible parents. Meanwhile, with the available funding, beside the proposed activities in the proposal, we did phenotypic evaluation of the TSWV segregating population. The main progresses are summarized as below.

To develop and identify the polymorphic SSR markers between the selected resistant and susceptible parents, we have selected and ordered a total of 2116 SSR markers, which have high polymorphic information content (PIC) or mapped on peanut linkage groups based on the recently publications. These 2116 markers have been screened against the two parental lines of the $F_2$ segregating population: UF113, which is TSWV resistant, and Georgia Valencia, which is TSWV susceptible using polyacrylamide gel electrophoresis system with silver staining (Fig. 1). In total, 294 polymorphic SSR markers were screened (Table 1). The average amplifiable rate is about 90% and polymorphic rate is about 14%. Linage group B02 has the highest marker polymorphic rate of 27% and linkage group A03 has the lowest polymorphic rate 3%. The number of SSR primers being screened on linkage group A03 is the most (128) and resulted in 23 polymorphic markers on linkage group A03, which has the highest number of polymorphic marker in the whole linkage groups. Linkage group A08 has the least number of polymorphic markers (3). These 294 polymorphic markers will be used to map the TSWV resistance and to identify the flanking markers linked to spotted wilt resistance.

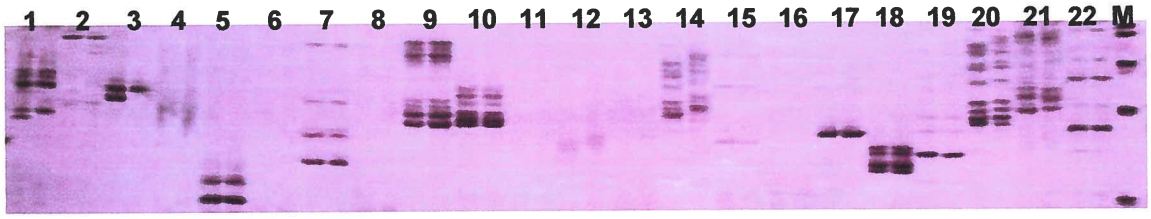


Fig 1. The SSR markers shown on polyacrylamide gel electrophoresis (PAGE) between two different parental lines. Lane pair 1-22 represent different SSR markers and lane pair 1,3 and 14 show the polymorphism.

Table 1. The summary list of the 2116 SSR markers been screened. It shows the amplified 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 |

In addition, we did phenotypic evaluation of the $F_2$ segregating population with 199 individuals using both enzyme-linked immunosorbent assay (ELISA) method and a 1 to 10 visual scoring method in the field. The ELISA was used to evaluate the relatively TSWV amount in $F_2$ progeny. It shows a reasonable segregation and verified this $F_2$ population can be used to map the TSWV resistance (Fig. 2). The 1 to 10 visual scoring was conducted in $F_{2:3}$ population to observe the occurrence and severity of spotted wilt. In both location, Marianna (Fig.3) and Citra (Fig.4), the distributions display the segregation based on TSWV resistance investigation.

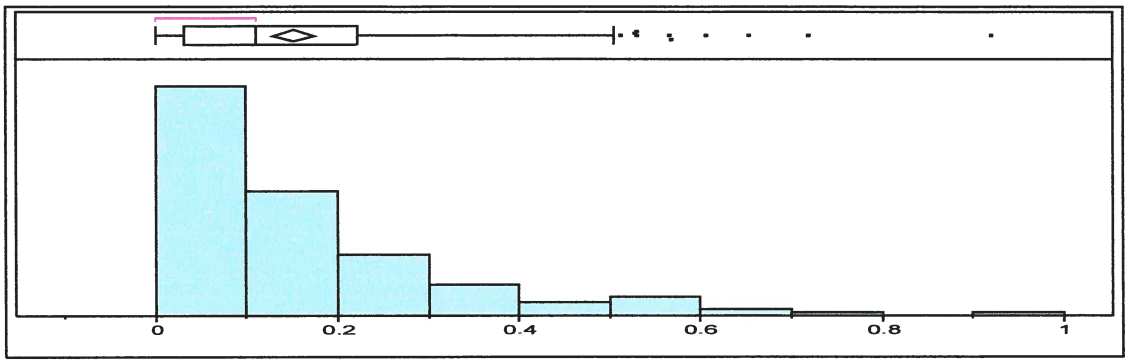


Fig 2. Frequency distribution of enzyme-linked immunosorbent assay (ELISA) method results in $F_2$ population with 199 individuals.

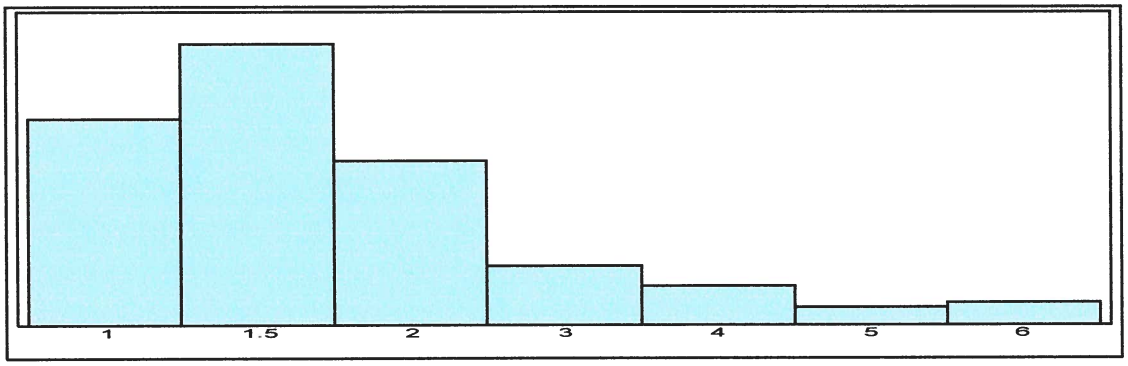


Fig 3. The frequency distribution of 1 to 10 visual scoring method in $F_{2:3}$ population in Marianna.

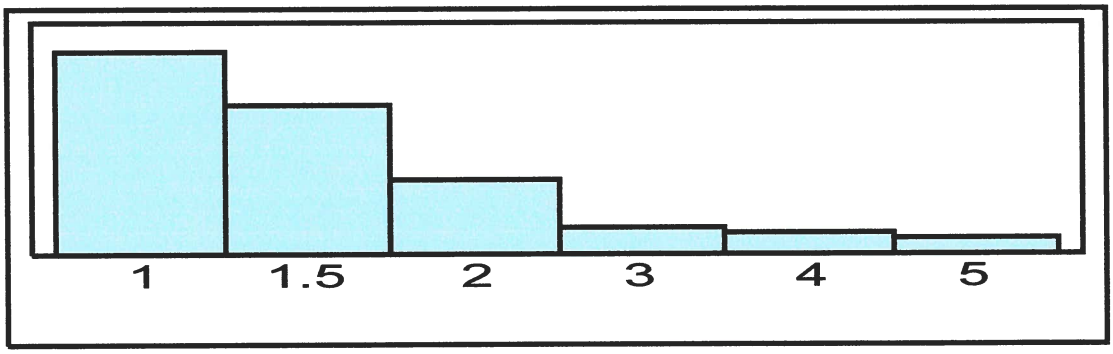


Fig 4. The frequency distribution of 1 to 10 visual scoring method in $F_{2:3}$ population in Citra.

In summary, the nearly 300 polymorphic SSR markers located on all over the peanut linkage groups coupled with the field and lab phenotypic data we have collected on the segregating population provided us the strong basis for mapping the TSWV resistance gene loci. With further funding, we should be able to have the whole project accomplishment successfully by identifying the flanking markers linked to the TSWV resistance gene loci.