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1229/30/31
2013

I. Abstract

Project Title: GENETIC MARKERS TO ENHANCE BREEDING OF PEANUT FOR DISEASE RESISTANCES

Project Investigator: Peggy Ozias-Akins, University of Georgia, Tifton Campus

Summary:

Control of pests and diseases in peanut requires considerable economic input for chemicals and application costs. Genetic resistance reduces or in some cases eliminates the need for certain chemical control. Mapping the genes that confer pest and disease resistance allows the identification of linked molecular markers that can be subsequently used for marker-assisted selection (MAS). In an effort to improve late leaf spot (LLS) resistance in peanut, we have evaluated a segregating population from the cross Florida-07 (susceptible) x SPT-06-06 (resistant) in the field for three years, and have observed wide segregation for LLS resistance. Molecular markers associated with this resistance have been identified. Development of additional molecular markers to identify those that are more tightly linked to resistance is almost complete and genotyping with these additional markers should yield dozens that potentially can be used for MAS.

II. Main Body of Report

Project Title: GENETIC MARKERS TO ENHANCE BREEDING OF PEANUT FOR DISEASE RESISTANCES

Project Investigators: Peggy Ozias-Akins, University of Georgia, Tifton Campus

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Objectives:

1) Phenotype segregating population Florida-07 x SPT-06-06 for late leaf spot (LLS) resistance in a replicated trial to collect a second year of data.
2) Construct a framework simple sequence repeat (SSR) map for all lines of this population and explore the utility of single nucleotide polymorphism (SNP) markers.
3) Translate genetic markers for leaf spot resistance into assays that can be used to enhance peanut breeding efforts in an efficient and cost-effective manner.

Procedures:

Phenotyping of this segregating population for late leaf spot resistance was conducted in replicated trials in 2012, 2013, and 2014. Ratings for late leaf spot were made at three time points during the season and followed the Florida 1-10 scale.

The population was screened with molecular markers polymorphic between the parents and a genetic map was produced using standard statistical methods. In order to increase map density, a highly reliable computational method to identify single nucleotide polymorphisms (SNPs) was developed and validated by sequencing a small set of SNPs.

Results and Discussion:

Significant variation for late leaf spot resistance was identified in the population Florida-07 x SPT -06-06, which consists of 192 recombinant inbred lines (RILs). Lines with high levels of resistance in both 2012 and 2013 were selected for increase and analysis of agronomic traits. The tails of resistant and susceptible lines are shown in the Table. These lines will be used for additional molecular study.

RIL	Average RANK	st dev	2012	2013	2014
Resistant					
1028	4.67	3.51	5	8	1
952	7.00	9.54	18	1	2
1036	9.00	1.73	8	11	8
980	10.00	7.00	15	2	13
954	10.67	9.07	21	4	7
1040	16.33	15.95	3	34	12
1043	18.00	10.44	30	13	11
1062	19.33	6.43	12	22	24
953	20.33	17.90	10	41	10

999	20.67	16.01	37	5	20
Susceptible					
940	172.33	13.32	157	179	181
1056	173.33	23.67	146	187	187
1066	175.33	5.86	182	173	171
1038	176.00	17.78	190	182	156
971	177.00	20.07	186	154	191
1012	177.00	5.29	171	181	179
1042	177.00	3.61	180	178	173
924	178.33	2.08	179	180	176
1075	181.00	5.20	184	175	184
917	186.67	4.04	189	189	182

A framework simple sequence repeat (SSR) map for all 192 lines of this population was constructed with 79 marker loci. Quantitative trait loci (QTL) mapping identified 2 QTL that were significantly associated with late leaf spot resistance, one from the resistant and one from the susceptible parent. A denser map that will enable better definition of LLS QTL will require SNP markers; however, true SNPs in peanut have been difficult to identify because of its polyploid nature and similarity between the two sub-genomes. Therefore, we have invested a considerable amount of time in developing a computational method to call SNPs with high confidence. SNPs from the respective parents have been included for development of an Affymetrix SNP array with 60,000 features. The population segregating for LLS resistance will be genotyped with this array in order to identify SNPs that are closely segregating with LLS resistance and those will be transitioned to an alternative marker platform for marker-assisted selection. We have determined that KASP assays (a type of SNP assay) are economically feasible for breeding programs.