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A FUNCTIONAL GENOMIC APPROACH TO ANALYZE HERBIVORY RELATED TRANSCRIPTS IN TEA

ABSTRACT

Tea Mosquito Bug (*Helopeltis theivora* Waterhouse) is one of the most dreaded tea pests of NE India causing a loss of 15-20 lakh kgs of made tea per year. Plant resistance to insect is most often a quantitatively inherited trait. Molecular marker technology is one such approach to dissect quantitative traits into discrete genetic loci allowing the effects of individual loci to be studied. Suppression Subtractive Hybridisation (SSH) is another powerful technique in functional genomics that can be used to develop tools to discriminate between insect resistant and susceptible varieties. In the present study SSH libraries were constructed for *Helopeltis* resistance in tea showed abundance of transcripts viz. those encoding insect resistant proteins, hsp's, chaperones and a myriad of other stress responsive genes known to play important role in insect resistance mechanism in other plants. Moreover, SSR markers derived from stress associated ESTs were evaluated in a segregating population showing variable resistance to *Helopeltis* infestation. This approach would facilitate new methods of marker assisted selection (MAS) to efficiently breed superior *Helopeltis* resistant varieties.

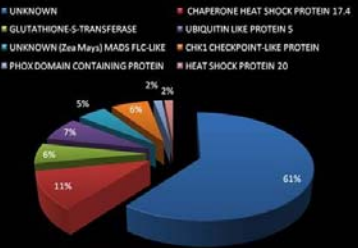
CANDIDATE GENE APPROACH

SUSCEPTIBLE VARIETY (DRIVER) TV1 **RESISTANT VARIETY (TESTER) 19/22/4**

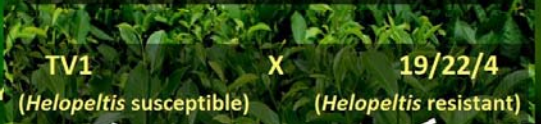


IDENTIFICATION OF CANDIDATE GENES RELATED TO THE TRAIT

Helopeltis responsive genes

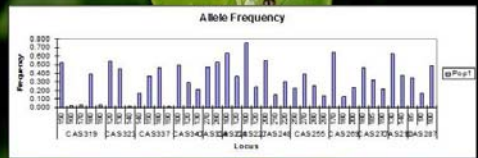
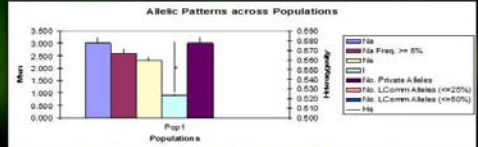
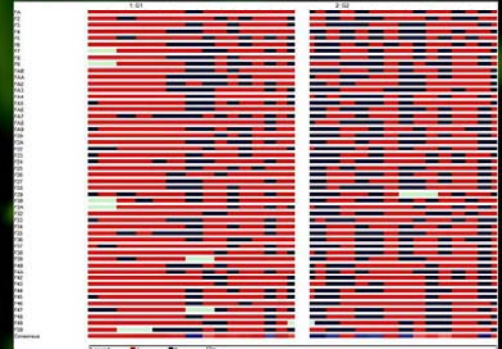


MOLECULAR MARKER APPROACH



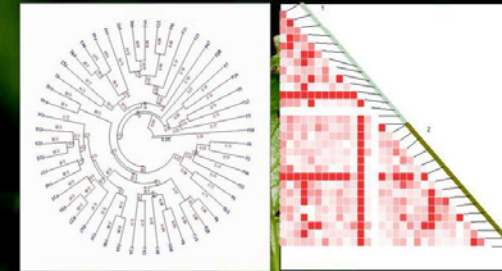
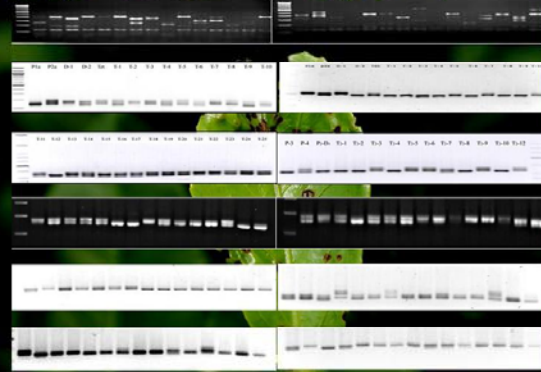
MAPPING POPULATION OF 90 PLANTS

MORPHOLOGICAL CHARACTERIZATION

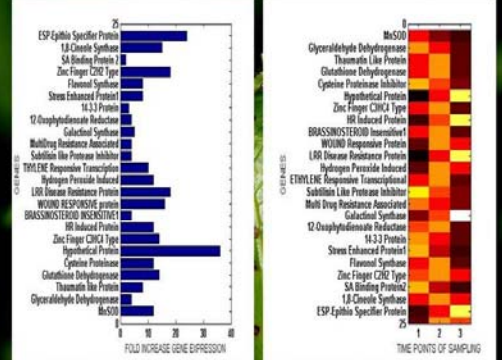


ESTs RELATED TO Helopeltis (PEST) INCIDENCE/RESISTANCE

ACB9790.1	namo-like protein [Camellia sinensis]	66-38
CAQ0009.1	papain-like cysteine protease [Hordaea vulg...	36-36
EEF4007.1	acyl-CoA thioesterase, putative [Ricinus commun...	48-39
BAE5544.1	mitogen-activated protein kinase kinase [Nico...	86-43
NP_067998.1	SRP5 (STRESS INDUCED PROTEIN 5)	10-30
ACM7866.1	protease inhibitor/seed storage/lipid transfer	66-19
NP_003302683.1	cytochrome oxidase [Populus trichocarpa]	28-39
AAR3440.1	glyoxalase 3-phosphate dehydrogenase	48-19
NP_197907.1	ubiquinol cytochrome C reductase complex	48-11
CAQ0009.1	papain-like cysteine protease [Hordaea vulg...	36-36
NP_101432.1	ATMBFB/MBFB (multi-protein bridging factor	48-33
AAK8293.1	salicylic acid-binding protein 2 [Nicotiana ta...	28-14
ARA1438.1	glyoxal oxidase [Vitis pseudoreticulata] csmh	66-08
ACF0619.1	ethylene-responsive transcriptional coactivator	38-33
NP_003308810.1	sterol 14-alpha demethylase [Populus trichoc...	38-23
NP_062896.1	LUG (LEUNIG) [Arabidopsis thaliana] sap1Qa	48-56
ARR4418.1	meroidiol/lincolol synthase 2 [Antirrhinum majus]	48-31
NP_101684.2	AP2s (acclimation of photosynthesis to enviro	10-49
NP_100966.1	protease inhibitor/seed storage/lipid transf	78-10
NP_066907.1	phosphatidic acid phosphatase-related / P-APs	38-54
EEF43970.1	1,8-cineole synthase, chloroplast precursor	78-50
ARR3466.1	LRK-like disease resistance protein [Brassica	38-08
AAK84874.1	subtilisin-like protease [Gossypium somaliense]	10-21
NP_07881.1	ATMFRP1 (Arabidopsis thaliana multidrug resi	66-26
ARR0000.1	lipoxigenase 2 [Acciostia deltoidea]	38-23
NP_00119356.1	SPAL1 (SPIRAL-1 LIKE) [Arabidopsis]	78-12
CAK06433.1	casein-like 3 [Pinus abies]	98-110
ACF0860.1	PAE [Litchi chinensis]	10-34
ACK07266.1	cysteine protease-like protein [Arachis hypogaea]	10-40
102D1A	Chase A, Crystal structure of Kinasin-Like Calmodu	28-17
ACG33961.1	calreticulin-3 precursor [Zea mays]	10-34
ACD3497.1	12-oxophenylacetate reductase 2 [Zea mays]	98-94
NP_074376.1	reticulon family protein [Arabidopsis thalia	10-42
102D1A	Chase A, Crystal structure of Kinasin-Like Calmodu	28-17



PHYLOGENY ANALYSIS AND LINKAGE DISEQUILIBRIUM



SCORING / ANALYSIS WITH VARIOUS SOFTWARES (TASSEL, NTSYS, GenAlex)

