## GENETIC AND PHYSICAL MAPPING OF ROOT-KNOT NEMATODE RESISTANCE ON CHROMOSOME 11 OF ACALA NEMX COTTON Philip A. Roberts Congli Wang Dept. Of Nematology University Of California Riverside, CA Mauricio Ulloa USDA-ARS, WICS Shafter, CA

## Abstract

Root-knot nematode (RKN) Meloidogvne incognita resistance in Gossypium hirsutum 'Acala NemX' cotton is conferred by the recessive gene rkn1 (locus  $Mi_{2h}$ -C11) on chromosome 11. The concentration of RKN, reniform nematode and other disease resistance factors on chromosome 11 indicates that much can be gained by molecular genetic and physical mapping analysis of this genomic region. We have conducted gene action analysis by inheritance and quantitative trait loci mapping of the RKN resistance in Acala NemX. We also conducted analysis of the resistance in Acala NemX in conjunction with RKN resistance in other Upland, Pima, and diploid cotton germplasm sources. Comparison focused on resistance segregation and expression in resistant x resistant and resistant x susceptible crosses, and on DNA sequence information of the various alleles of markers linked to RKN resistance and markers framing the chromosome 11 resistance region. The comparative studies have revealed probable ancestral origin and introgression pathways of RKN resistance into the Acala NemX background, which occurred by artificial (man-made) introgression. Various crosses with RKN resistance sources indicated that allelic interaction, epistasis, and heterosis operate in the expression of resistance depending on resistance source and genetic background. In addition, annotated complete sequence of G. hirsutum 'Acala Maxxa' BAC clones anchored to chromosome 11 according to mapped BAC-end sequence derived markers (MUSB) is being used to derive additional markers for screening an Acala NemX source ('N901') BAC library, in efforts to develop a physical framework of the resistance region. Our ultimate objective is to accelerate the incorporation of RKN resistance in commercial cultivars by increasing knowledge about the inheritance and genome organization of the resistance, and developing markers for marker assisted selection for RKN resistance.