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EVALUATING THE USE OF COTTON CHROMOSOME SUBSTITUTION LINES WITH A NEWLY DEVELOPED MODEL

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When using chromosome substitution (CS) lines in cotton breeding program it is important to separate the effects of a target chromosome from the remaining chromosomes. However, the genetic effects due to all target chromosomes cannot be separated with the traditional additive-dominance (AD) model. In this presentation, we will demonstrate the use of a newly developed chromosome model (an extended AD model) and its software. With this new chromosome model, the following analyses are provided: (a) detect the genetic effects due to specific substituted chromosomes or chromosome arms and (b) detect the genetic effects due to specific chromosomes or chromosome arms in the lines crossed with these CS lines. Data from several CS lines and TM-1 crossed with five commercial cultivars grown in two environments will be used to illustrate the use of this new chromosome model. Thus, the new model will not only be useful to determine effects of the chromosomes of interest in various cotton lines, but also be able to unify both genetic and breeding studies. Furthermore, this new model can be also used to detect single marker associated effects when marker data for parents used for crossing are available. The computer program can be obtained through email request at jjenkins@ars.usda.gov.