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Upland Cotton (Gossypium hirsutum L.) x Hawaiian Cotton (G. tomentosum Nutt. Ex. Seem.) F₁ Hybrid Hypoaneuploid Chromosome Substitution Series

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Interspecific germplasm introgression enables unique opportunities for genetic analysis and improvement of domesticated plants, but is commonly impeded by barriers to transmission and recombination, insufficient genetic resolution, and the difficulty of deriving economically suitable products. Such impediments are mitigated to varying extents by the breeding of chromosome substitution lines; however, the difficulty of developing such lines varies widely among crop species and chromosomes. In this manuscript, the development of 45 interspecific F₁ monosomic (2n=51) and monotelodisomic (2n=52) substitution hybrids of G. hirsutum L. inbred TM-1 (2n=52, [AD]₁ genome) with G. tomentosum Nutt. ex Seem., a wild cotton (2n=52, [AD]₃ genome) species endemic to dry and rocky coastal areas of the Hawaiian Islands, is reported. Hypoaneuploid plants that lack specific chromosomes or chromosome arms were identified based on phenotypic syndromes, and conventional meiotic metaphase I configuration analysis of acetocarmine-stained microsporocytes ("pollen mother cells"). Characteristics of the hybrids were largely intermediate compared with those of the parental species, including hairy silvery-green to gray-green palmately veined leaves, a muted but distinctly sulfur-yellow corolla and yellow pollen, no central petal spot, a strongly exerted stigma, the absence of nectaries, and short brown seed fiber. Each hypoaneuploid F1 interspecific hybrid in the series is heterozygous for all parental nuclear polymorphisms except where G. tomentosum loci are rendered hemizygous because of the absence of a specific G. hirsutum arm segment or chromosome. These hypoaneuploid chromosome substitution stocks are an additional resource for localization of genomic markers and for development of backcross substitution lines; therefore, these stocks provide a stepping stone toward high-resolution chromosome-specific genetic dissection of complex traits, germplasm introgression, and cotton improvement.

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