Development of New Interspecific Monosomic F_1 Substitution Stocks for Investigations in Cotton Genome

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As it is known a complete coverage of cotton (*Gossypium hirsutum* L.) genome with hypoaneuploids is not still realized. Therefore the detection of new types of aneuploids especially in different cytogenetic collections is very useful. In Uzbekistan, long-term investigations towards development of cytogenetic stocks that use different types of irradiation as a source of aberrations are carried out. As a result, many translocation lines and primary monosomics in cotton *G. hirsutum* were isolated. Parts of them are characterized by phenotypic differences that indirectly suggest the possibility of detection of some new interchanges and chromosome deficiencies. At present the possibilities for unifying identification are limited. We have already begun to use interspecific monosomic F_1 hybrids from the crosses of the monosomic lines from our collection and *G. barbadense* L. as a donor parent for chromosome assignment of chromosome-specific SSR markers. As a lot of SSRs have already been assigned to the chromosomes in cotton, *G. hirsutum*, the investigations for their chromosome associations will preliminarily be allowed to identify monosomes from our collection. We crossed 36 monosomic lines and a *G. barbadense* doubled haploid line known as 3-79 (USA), and 5904-I variety (Uzbekistan), *G. barbadense*. As a result, hybrid seeds were obtained for 47 combinations, 36 involved 3-79 and 11 involved 5904-I. At present, F_1 hybrid monosomics were isolated in 15 hybrid populations. In 3 hybrid families, 3 hybrid chromosome deficient plants were detected in each F_1 monosomic progeny, in 5 families 2 monosomics were isolated, and in remaining 7 families, 1 monosomic per progeny was identified. These results pointed out both the ability of monosomic detection in various hybrid backgrounds and differences in monosome transmission rates. In addition, the presence of additional univalents was observed in two hybrid monosomic progenies with a frequency of 1.22 ± 0.15 (hybrid monosomic Mo11×3-79) to 1.45 ± 0.15 (Mo17×3-79) average per cell. Similar desynaptis effects were present in the parental and daughter monosomics in selfed Mo11 and Mo17 progenies. It suggested that gene (s) weakening chromosome pairing were present. These F_1 hybrid monosomics also differed in their morphology within the same hybrid family that pointed out the possibility of univalent shifts due to irregular chromosome disjunction in meiosis. All other F_1 hybrid monosomics were characterized with usual chromosome pairing that will allow them to be used for chromosome assignment of SSR markers.