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Abstract A total of 206 mapped SSR markers distributed on the 26 linkage groups of the most recent Gossypium hirsutum genetic maps were used to monitor the introgression of diploid species chromosome fragments in the framework of three different breeding programmes involving the G. hirsutum x G. raimondii x G. sturtianum (HRS), G. hirsutum x G. longicalyx (HL) and G. hirsutum x G. australe (HA) interspecific hybrids. In these three hybrids, the rate of reduction of the diploid parent specific SSR numbers were respectively 31 % for G. longicalyx, 38 % for G. sturtianum, 46 % for G. raimondii and 42 % for G. australe while the number of specific G. hirsutum SSRs remained almost unchanged. An important part of this variability in the amplification of the diploid species specific SSR alleles in the interspecific hybrids can be explained by the high level of heterozygosity observed in the different parent species which was respectively 94.4 % for G. longicalyx, 62.1 % for G. sturtianum, 65.5 % for G. raimondii but only 12 % for G. australe . The possible influence of other factors mentioned in the literature to explain this phenomenon is discussed.