T(IIR;VIR)R2459

Translocation that fuses two chromosomes end-to-end. II is attached at its right tip to the right end of VI. The II centromere is inactive. II markers pi (23%), arg-5 (18%), ure-1 (19%), fl (10%), trp-3 (2%), rip-1 (0%) linked to breakpoint and to VI markers (trp-2, 6% to 11%; ylo-1, 14%). Wild morphology. Homozygous-fertile. T × N ascospores 75% black; unordered asci 33% 8:0, 44% 6:2, 20% 4:4, 1% 2:6, 2% 0:8 (Black : White ascospores, 113 asci). 2:1 allele ratio for II and VI aberration-linked markers is produced by nondisjunction to form unstable disomics which can break down only in such a way as to be scored as T. Progeny are in a ratio of 1 normal chromosome sequence: 2 translocation sequence. Barren progeny (putative stable duplications) are infrequent (1 to 2%). Cytologically, many bridges and fragments are seen following anaphase I. The fragments are asymmetrical. Pachytene analysis shows two chromosomes joined at their tips. Origin: Present in rol-2; inl A strain FGSC 1350. Linkages shown by Perkins and Björkman, subsequent analysis by Barry.