

Information on chromosome rearrangements

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Information on chromosome rearrangements

Abstract

Chromosome rearrangements

T(IV;V)AR11r

The VR break point is between al-3 and cot-2.

T(V-IV)AR33

Cytological observations indicate a break point near the tip of chromosome 2S (linkage group VL), translocating the nucleolus organizer to the tip of another chromosome. Duplications should thus contain two organizers.

T(I;VI)T51M158, T(I;VI)T51M166

Fewer than 50% of ascospores are black in the intercross, indicating that the two are structurally different although they arose in the same experiment.

Tr(IR-IR)T54M94

ad-9 is not covered in duplications.

T(V;VI)T54M117 un

Reciprocal translocation. VR (linked al-3) interchanged with VI (near yla-1). Slow growing, variable heat-sensitive, often not progressing beyond the germ tube after ascospore germination. T x N ascospores 50% black; unordered asci 22% 8:0, 2% 6:2, 53% 4:4, 6% 2:6, 16% 0:8 (Black:White ascospores, 141 asci). Origin: 74A, UV. Aberration detected and analyzed by Perkins.

T(II;III)T54M140b

The II break is probably between bal and arg-5, based on coverage of bal but not arg-5 in presumed disomics.

T(II-VII)P73B159 wc

Duplication-generating translocation. Involves II (near arg-5) and VII (probably at wc). Phenotype wc. T x T slightly fertile. T x N ascospores 50% black; unordered asci 34% 8:0, 11% 6:2, 18% 4:4, 5% 2:6, 32% 0:8 (Black:White ascospores, 199 asci). Origin: sn cr; al-3 inl, EMS. Detected and analyzed by Perkins. Duplications are slow growing, barren in crosses by non-duplication. FGSC 3039, 3040.

T(I;V)ALS111

The VR break point is between or near pab-2 and pyr-6.

T(I-III)Y112M4i ad-3B

cys-13 is not covered in duplications.

T(IV;VII)ALS122

Reciprocal translocation, IV (near pdx) interchanged with VII (near wc). Wild phenotype. Homozygous-fertile. T x N ascospores 50% black; unordered asci 34% 8:0, 7% 6:2, 11% 4:4, 8% 2:6, 40% 0:8 (Black:White ascospores, 153 asci). Origin: rg cr a UV. Detected and analyzed by Perkins. Original strain probably contained a dominant meiotic mutant (D.A. Smith unpublished), from which the translocation has been separated. FGSC 2986, 2987.

T(II;III)ALS132

Reciprocal translocation. II (linked arg-5) interchanged with III (linked acr-2). Wild phenotype. Homozygous fertile. T x N ascospores 50% black; unordered asci 30% 8:0, 5% 6:2, 27% 4:4, 6% 2:6, 32% 0:8 (Black:White ascospores, 328 asci). Origin: rg cr a UV. Detected and analyzed by Perkins.

T(IV-1)NM152

pho-3 is covered in duplications (Nelson et al. 1976 *Genetics* 84, p. 187). arg-2 is not covered.

T(I;II;III)Y155M64 ad-3A

Complex rearrangement. Involves IR (at ad-3a), IIR (near fl) and III (linked acr-2). ad-3A phenotype. T x N ascospores 10 to 20% black; unordered asci 0% 8:0, 2% 6:2, 17% 4:4, 33% 2:6, 48% 0:8 (Black:White ascospores, 64 asci). Origin: 74A, X-rays. Called A9 by de Serres. Chromosome rearrangement inferred from anomalous crossing over in IR (de Serres 1971 *Genetics* 68:384). Break points identified and further analysis by Perkins. Barren duplications of two types are produced in crosses by Normal. FGSC 3037, 3038.

T(IV-VI)ALS159

pho-3 is covered in duplications (Nelson et al. 1976 *Genetics* 84, p. 187). mtr is covered. psi is not

T(I;II)ALS172

Reciprocal translocation. IR (near un-18) translocated to IIL (left of ro-3). Wild phenotype. Homozygous-fertile. T x N ascospores 50% black; unordered asci 20% 8:0, 0% 6:2, 63% 4:4, 5% 2:6, 13% 0:8 (Black:White ascospores, 158 asci). Origin: rg or a UV. Detected and analyzed by Perkins. FGSC 3035, 3036.

T(IV-VII)ALS175

Involves VIIIR (near arg-10) and IVR (near pan-1). This duplication-producing rearrangement is not a simple insertional, and may involve another chromosome.

T(II-V)ALS176

un-5 and het-d are covered in duplications. The simple duplications cover all known IIR markers. In addition, IIL markers are sometimes found to be heterozygous, supposedly in disomics from 3:1 segregations. These occur with frequencies of several percent. If het-c in IIL is heterozygous, a class of brown-flat inhibited duplications is seen, which are distinguishable from het-D / het-d duplications (in IIR) by their coarser morphology and surface growth, with browning trunk hyphae on a GCP agar surface. In contrast, D/d duplications have finer subsurface hyphae. Translocation stocks FGSC 2414, 3014 are het-D; FGSC 3013, 2415 are het-d. (All four are het-C and can readily be used to test the het-d constitution of normal laboratory strains, which are mostly het-C.)

T(II -> [IV;V])AR179

Cytologically, one break point is observed to be in chromosome 2S (linkage group VL) proximal to the nucleolus organizer. AR179 should then be a good genetic marker for VL.

T(I -> V)ALS182

Quasiterminal translocation. A IR segment involving met-6 and IR markers distal to it is translocated to the VL tip (satellite). Cytologically, the translocated segment of I is seen abutting the nucleolus at pachynema. met-6 is covered in Dp(IR -> VL)ALS182 duplications from the cross x Normal. Viable duplications are also produced by intercrosses of ALS182 with T(IR -> VL)AR190, which shares the same break point at the VL tip; these intercross duplications include his-2 through thi-1 but do not include un-2 proximally or met-6 distally. FGSC 2973, 2974.

T(I -> V)AR190

Generates viable duplications from intercrosses with T(I -> V)ALS182, including the loci his-2 through thi-1, but not un-2 or met-6.

T(I -> ;II;VII)AR217

FGSC 3033, 3034.

T(III -> ;III;V)D305

ro-2 is not covered in duplications.

T(IV -> I)B362i

Fertility is reduced in I x I crosses. FGSC 2935, 2988. met-1 (in IVR) is covered in duplications. Markers shown not covered: cut, psi, pyr-1, pdx, pt, col-4, cot-1.

T(III;VI)B362r

FGSC 3011, 3012.

T(II -> IV)R2394

A IIL segment near pyr-4 is translocated to IV. Markers shown not covered in duplications: pi, het-6, pyr-4, ro-3, het-c, thr-2, bal, fl.

T(I;II)EB2501

Reciprocal translocation. I (near mt) interchanged with II (near bal). Wild phenotype. Homozygous fertile. T x N ascospores more than 50% black; unordered asci 43% 8:0, 14% 6:2, 30% 4:4, 3% 2:6, 11% 0:8 (Black:White ascospores, 101 asci). Excess black spores and 6:2 asci are unexplained. (Germination of black spores has been close to 100% in some crosses, so inclusion of inviable duplication-deficiency products in a pigmented spore does not occur.) Cytology: Chromosome I is aberrant; the second aberrant chromosome was not identified. Origin: Separated from a stock of met-1 (38706). Detected and analyzed by Barry.

T(II;VI)P3340

Reciprocal translocation. II (linked arg-5) interchanged with VI (linked yla-1). Wild phenotype. T x N ascospores 50% black; unordered asci 26% 8:0, 2% 6:2, 47% 4:4, 1% 2:6, 24% 0:8 (Black:White ascospores, 300 asci). Origin: Found in an exceptional perithecium that shot 50% white ascospores, in an otherwise normal cross of Adiopodoume A (FGSC 430) x fl⁺ a. Detected and analyzed by Perkins.

In(IL -> IR)H4250

The following Inversion stocks contain the tol suppressor of A/a vegetative incompatibility: FGSC 1947, 3032.

T(I -> III)4540 nic-2

rg is not covered in duplications.

T(I;V)P5166

The VR break point is near pyr-6.

T(VI -> [I;III])Y16329

un-4 is covered in duplications.

T(I -> II)39311

csp is covered in duplications. The following translocation stocks contain the tol suppressor of A/a vegetative incompatibility: FGSC 2985, 2976.