Supplementary Information

The role of Drosophila mismatch repair in suppressing recombination between diverged sequences

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Supplementary Table S1– Total Flies Scored for Each DSB Repair Phenotype

Genotype	DSB repair assay	Experiment number	No. Progeny (No. of individual germlines)	Total number of each phenotype (% of total)		
				y+ w– NHEJ, intersister HR, no DSB	y+ w+ intra-chromosomal HR	y–w– SSA
msh6$^{-/+}$	DR-*white*	1	284 (11)	184 (64.8)	94 (33.1)	6 (2.11)
		2	282 (13)	168 (59.6)	106 (37.6)	8 (2.84)
		3	73 (3)	41 (56.2)	32 (43.8)	0 (0.00)
		4	127 (8)	69 (54.3)	57 (44.9)	1 (0.787)
		5	1157 (13)	729 (63.0)	414 (35.8)	14 (1.21)
		Total	**1923 (48)**	**1191 (61.9)**	**703 (36.6)**	**29 (1.51)**
		Mean % (±S.E.M.)		**59.6 (±1.98)**	**39.0 (±2.29)**	**1.43 (±0.496)**
	DR-*white.mu*	1	268 (12)	206 (76.9)	58 (21.6)	4 (1.49)
		2	153 (10)	112 (73.2)	38 (24.8)	3 (1.96)
		3	106 (4)	77 (72.6)	28 (26.4)	1 (0.943)
		4	117 (7)	84 (71.8)	33 (28.2)	0 (0.00)
		5	1092 (13)	813 (74.5)	271 (24.8)	8 (0.733)
		Total	**1736 (46)**	**1292 (74.4)**	**428 (24.7)**	**16 (0.922)**
		Mean % (±S.E.M.)		**73.8 (±0.892)**	**25.2 (±1.09)**	**1.03 (±0.334)**
msh6$^{-/-}$	DR-*white*	1	113 (4)	68 (60.2)	44 (38.9)	1 (0.885)
		2	275 (7)	137 (49.8)	136 (49.5)	2 (0.727)
		3	48 (3)	35 (72.9)	12 (25.0)	1 (2.08)
		4	93 (8)	66 (71.0)	27 (29.0)	0 (0.00)
		5	116 (5)	69 (61.1)	42 (37.2)	5 (1.77)
		Total	**645 (27)**	**375 (58.4)**	**261 (40.7)**	**9 (1.40)**
		Mean % (±S.E.M.)		**63.0 (±4.17)**	**27.6 (±2.62)**	**1.23 (±0.353)**
	DR-*white.mu*	1	361 (16)	254 (70.4)	101 (28.0)	6 (1.66)
		2	273 (9)	145 (53.1)	123 (45.1)	5 (1.83)
		3	11 (2)	11 (100)	0 (0.00	0 (0.00)
		4	63 (6)	42 (66.7)	21 (33.3)	0 (0.00)
		5	113 (5)	74 (65.5)	37 (32.7)	2 (1.77)
		Total	**821 (38)**	**526 (63.8)**	**282 (34.3)**	**13 (1.55)**
		Mean % (±S.E.M.)		**71.1 (±7.78)**	**27.8 (±7.50)**	**1.05 (±0.430)**

Supplementary Table S2 – Frequency of Nonhomologous End-Joining Events

DSB repair assay	Genotype	Experiment number	No. y+w– isolates analyzed	No. NHEJ with processing (%)
DR-*white*	*msh6*$^{-/+}$	1	3	0 (0)
		2	13	1 (7.69)
		3	11	0 (0)
		4	9	0 (0)
		5	25	2 (8.00)
		Total	**61**	3 (4.92)
	msh6$^{-/-}$	1	0	0 (0)
		2	7	0 (0)
		3	6	2 (33.3)
		4	12	1 (8.33)
		5	10	0 (0)
		Total	**35**	3 (8.57)
DR-*white.mu*	*msh6*$^{-/+}$	1	2	1 (50)
		2	11	0 (0)
		3	5	0 (0)
		4	11	0 (0)
		5	26	2 (7.69)
		Total	**55**	3 (5.45)
	msh6$^{-/-}$	1	14	1 (7.14)
		2	10	1 (10)
		3	1	0 (0)
		4	7	0 (0)
		5	10	0 (0)
		Total	**42**	2 (4.76)