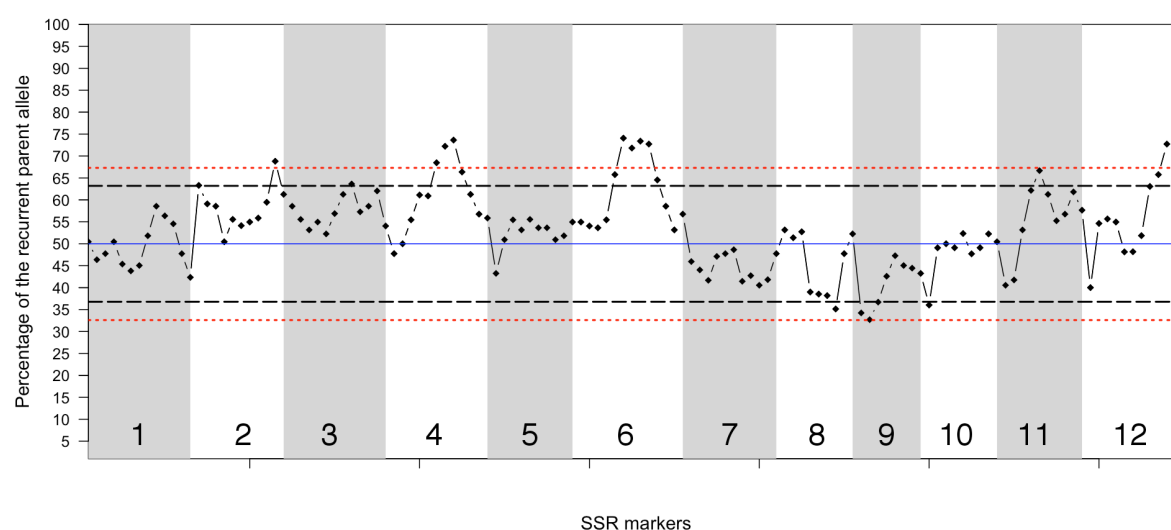


Development and GBS-genotyping of Introgression Lines (ILs) using two wild species of rice, *O. meridionalis* and *O. rufipogon*, in a common recurrent parent, *O. sativa* cv. Curinga. *Molecular Breeding*. Arbelaez J. D., Moreno L. T., Singh N., Tung C.-W., Maron L. G., Ospina Y., Martinez C. P., Grenier C., Lorieux M., McCouch S. Department of Plant Breeding and Genetics, Cornell University, emails: srm4@cornell.edu

Online Resource 5. (a) Segregation distortion analysis of SSR markers mapped in the BC₁F₁ from *CUR/MER*. Each point represents the percentage deviation with respect of the recurrent genotypic class expected (50 %, solid blue line). The dash black line and the dotted red line represent the critical values for a probability value of 0.5 and 0.01 respectively. (b) Markers with strong segregations distortion in the *CUR/MER* BC₁F₁ linkage analysis. The genotypic classes are defined as homozygous *CUR* class (hmz. *CUR*) and heterozygous class (heterozygote). A significance threshold level of 0.01 was set to identify markers with strong deviation from a chi-square test.

a)

CUR/MER segregation distortion



b)

Marker	Chr	Chi-square	p-value	Genotypic hmz. class	Genotypic htz. class	Skewed genotypic class	% hmz.	Associated sterility gene
RM425	2	15.42	0.000086	75	34	hmz. <i>CUR</i>	68.81	-
RM6314	4	15.14	0.000100	76	34	hmz. <i>CUR</i>	68.47	<i>s-e-2, ga-6, ga-10*</i>
RM142	4	21.33	0.000004	78	30	hmz. <i>CUR</i>	72.22	<i>s-e-2, ga-6, ga-10*</i>
RM3839	4	24.58	0.000001	81	29	hmz. <i>CUR</i>	73.64	<i>s-e-2, ga-6, ga-10*</i>
RM1018	4	11.78	0.000598	73	37	hmz. <i>CUR</i>	66.36	<i>s-e-2, ga-6, ga-10*</i>
RM136	6	11.04	0.000894	73	37	hmz. <i>CUR</i>	65.77	<i>Su-Cif***</i>
RM3183	6	25.04	0.000001	80	28	hmz. <i>CUR</i>	74.07	<i>Su-Cif***</i>
RM19983	6	20.95	0.000005	79	31	hmz. <i>CUR</i>	71.82	<i>Su-Cif***</i>
RM20086	6	23.86	0.000001	80	29	hmz. <i>CUR</i>	73.39	<i>Su-Cif***</i>
RM20208	6	22.73	0.000002	80	30	hmz. <i>CUR</i>	72.73	<i>Su-Cif***</i>
RM23662	9	11.04	0.000894	38	72	heterozygote	34.23	-
RM5799	9	12.46	0.000416	34	70	heterozygote	32.69	-
RM5526	9	7.72	0.005475	40	69	heterozygote	36.70	-
RM7120	11	12.00	0.000532	72	36	hmz. <i>CUR</i>	66.67	<i>S-3</i>
RM463	12	11.04	0.000894	72	38	hmz. <i>CUR</i>	65.77	<i>ga-13**</i>
RM28607	12	22.73	0.000002	80	30	hmz. <i>CUR</i>	72.73	<i>ga-13**</i>
RM6396	12	21.63	0.000003	80	30	hmz. <i>CUR</i>	72.07	<i>ga-13**</i>
RM1227	12	18.24	0.000019	78	32	hmz. <i>CUR</i>	70.27	<i>ga-13**</i>

* *ga-6, ga-10, s-e-2* and *S-3* genes were listed by Kinoshita (1991, 1993)

** *ga-13* was listed by Rha et al. (1995)

*** The dominant suppressor *Su-Cif* was listed by Matsubara et al. (2003).