

Table 3 Genetic parameter estimates for the simple (additive-dominant) and complete (additive-dominant-epistatic) models and Relative contribution of parameters (“m”, “a”, “d”, “aa”, “ad” and “dd”) for the simple and complete models, adjusted based on the mean of evaluated characters, in six generations (P1, P2, F1, F2, RC1F1 and RC2F2) obtained from five oat crosses (CR).

Parameters ⁽¹⁾	Grain yield per plant (GY P ⁻¹)				
	CR1 ⁽⁶⁾	CR2 ⁽⁶⁾	CR3 ⁽⁶⁾	CR4 ⁽⁶⁾	CR5 ⁽⁶⁾
m	4.34 ^{ns}	-12.60**	1.98 ^{ns}	7.08**	22.96**
a	2.50**	1.25*	1.94**	-1.21**	-0.30 ^{ns}
d	36.56**	83.42**	39.22**	14.25*	-32.34**
aa	9.58**	27.54**	12.63**	5.26*	-11.73**
ad	-2.30 ^{ns}	-2.13 ^{ns}	8.90*	-2.63 ^{ns}	-6.46*
dd	-10.12 ^{ns}	-48.56**	-24.28**	-7.78 ^{ns}	22.59**
m/a. d. aa. ad. dd	3.14	6.37	0.45	26.57	50.51
a/m. d. aa. ad. dd	47.79	4.21	29.92	31.21	0.73
d/m. a. aa. ad. dd	27.65	32.66	21.65	13.97	13.73
aa/m. a. d. ad. dd	15.65	30.88	18.46	15.04	13.36
ad/m. a. d. aa. dd	1.02	0.2	10.51	4.55	5.79
dd/m. a. d. aa. ad	4.72	25.65	18.99	8.63	15.86
Parameters	Number of panicles per plant (NP P ⁻¹)				
	CR1 ⁽⁶⁾	CR2 ⁽⁶⁾	CR3 ⁽³⁾	CR4 ⁽⁶⁾	CR5 ⁽³⁾
m	-0.33 ^{ns}	-2.01 ^{ns}	8.60**	3.77*	5.37**
a	2.42**	0.02 ^{ns}	1.77**	-2.15**	-0.66**
d	22.77**	27.91**	-2.78*	3.93 ^{ns}	-0.43 ^{ns}
aa	8.69**	12.91**	-	4.27*	-
ad	-0.28 ^{ns}	-4.15 ^{ns}	-	1.33 ^{ns}	-
dd	-13.67*	-17.47**	-	-1.60 ^{ns}	-
m/a. d. aa. ad. dd	0.02	1.19	93.87	5.82	98.41
a/m. d. aa. ad. dd	64.07	0.01	3.68	84.89	1.4
d/m. a. aa. ad. dd	11.85	25.31	2.43	0.82	0.18
aa/m. a. d. ad. dd	14.31	45.87	-	7.61	-
ad/m. a. d. aa. dd	0.01	5.16	-	0.93	-
dd/m. a. d. aa. ad	9.71	22.54	-	0.31	-
Parameters	Panicle weight per plant (PP)				
	CR1 ⁽⁶⁾	CR2 ⁽³⁾	CR3 ⁽³⁾	CR4 ⁽³⁾	CR5 ⁽³⁾
m	6.33**	3.26**	3.53**	4.26**	3.91**
a	-0.56**	0.13 ^{ns}	-0.29 ^{ns}	1.19**	0.61*
d	-3.88 ^{ns}	2.05**	1.51*	1.62**	1.82**
aa	-2.46*	-	-	-	-
ad	1.06 ^{ns}	-	-	-	-
dd	4.61*	-	-	-	-
m/a. d. aa. ad. dd	47.12	90.06	94.97	90.17	91.63
a/m. d. aa. ad. dd	34.99	0.14	0.61	6.72	2.12
d/m. a. aa. ad. dd	2.2	9.79	4.41	3.1	6.23
aa/m. a. d. ad. dd	7.19	-	-	-	-
ad/m. a. d. aa. dd	1.61	-	-	-	-
dd/m. a. d. aa. ad	6.88	-	-	-	-

Note: ⁽¹⁾ m: means of homzygous lines derived from F₂; a: additive gene effect; d: mean of deviations due to dominance; aa: additive x additive interactions; ad: additive x dominant interactions; dd: dominant x dominant interactions; ^{ns}Non-significant; * and ** Significant at (p<0,05) and (p<0,01) probability, respectively; ⁽³⁾Additive-dominant model; ⁽⁶⁾Additive-dominant complete model; CR1 (UPF 16/UPF 18); CR2 (UPF 16/UFRGS 7); CR3 (UPF 16/URPEL 15); CR4 (UPF 18/UFRGS 7) and CR5 (UPF 18/UFRGS 17)