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TABLE 2

Sperm genotypes and descriptive parameters for progeny of crosses to normal females

Male[a]	N[b]	X2	Y2	XY2	02	ND[c]	D[d]	R_X[d]	R_Y[d]
$+/cry^+Y$	160	13326	11471	1	3	0.025	1.00 (1.00–1.00)	0.62 (0.14–1.0)	0.54 (0.12–0.88)
Xh^-/cry^+Y	165	1318	436	76	3115	19.3	0.61 (0.58–0.64)	0.27 (0.24–0.31)	0.09 (0.08–0.10)
$+/cry^-Y^e$	121	9843	6600	40	254	2.4	0.99 (0.99–0.99)	0.49 (0.41–0.57)	0.33 (0.27–0.38)
Xh^-/cry^-Y	164	1022	221	29	2845	17.5	0.62 (0.58–0.67)	0.22 (0.18–0.26)	0.05 (0.04–0.06)

[a] +, Ste^{W12}; Xh^-, $Df(1)X1$, Ste^{W12} Bx; cry^+Y, B^SY y^+; cry^-Y, B^Scry^1Y y^+.

[b] Number of males crossed. Matings were performed with one male and three females.

[c] (Exceptional progeny)/male.

[d] X–Y disjunction and chromosome-specific sperm recoveries (see text): $D = 1/(1+\sqrt{XY \cdot 0/X \cdot Y})$, $R_x = \sqrt{X \cdot XY/Y \cdot 0}$, and $R_y = \sqrt{Y \cdot XY/X \cdot 0}$. Support intervals found using the method of maximum likelihood are shown in parentheses.

[e] Results from BELLONI et al. (2000).

Footnotes indicated by letters