

Table 1: Demographics of mice tested.

Genotype	Sex	Mean age (days)	Minimum age (days)	Maximum age (days)	N
3xTg-AD	Female	296.27	154	558	11
3xTg-AD	Male	366.00	366	366	1
B6129	Female	403.00	172	756	13
B6129	Male	373.00	298	574	4

Subjects

Due to the small number of male mice, only females are included in this analysis. There are 24 female mice included in this study. There was no significant difference in age between the 3xTg-AD and B6129 mice ($t_{20} = -1.5, p = 0.149$; Table 1).

Discrimination

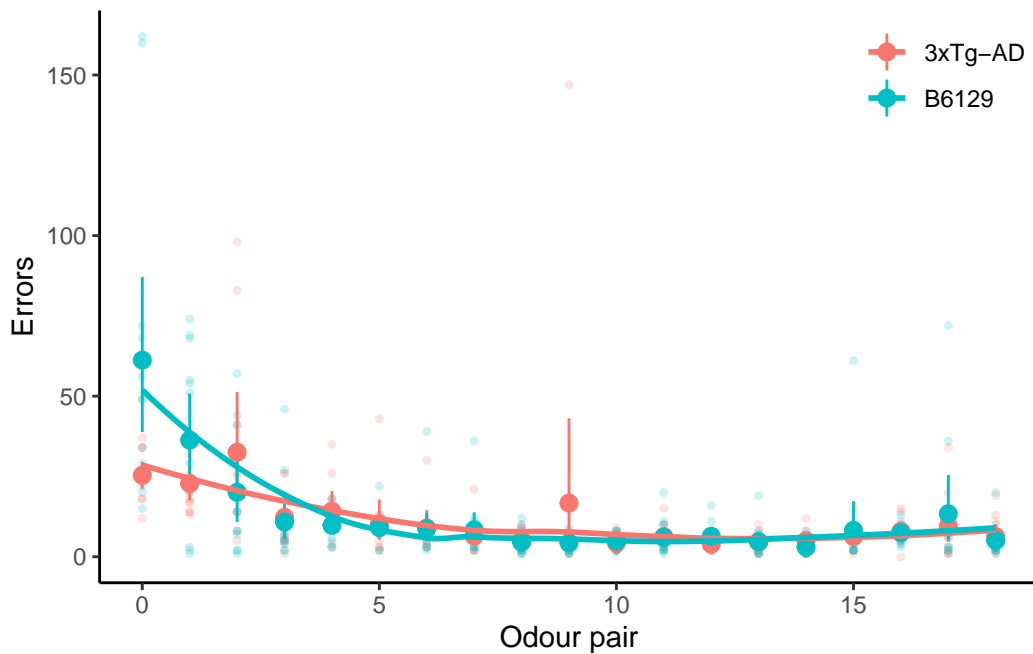


Figure 1: Errors ($\pm 95\%$ CI) made by the mice at on each odour pair during the discrimination stages.

The discrimination trials were assessed with linear mixed effects models on the number of errors made on each odour pair. The errors made decreased as the mice advanced through the odour pairs (Figure 1).

Table 2: AICc model table for discrimination.

geno	op	geno:op	df	logLik	AICc	delta	weight
	-1.28		4	-1922.91	3853.92	0.00	0.46
+	-1.01	+	6	-1921.19	3854.57	0.65	0.33
+	-1.28		5	-1922.69	3855.52	1.60	0.21
			3	-1959.86	3925.78	71.86	0.00
+			4	-1959.62	3927.33	73.41	0.00

The model with just an effect of odour pair best explained the data (Table 2), this model differed from the null model ($\chi^2_1 = 74, p < 0.0001$).

Reversal

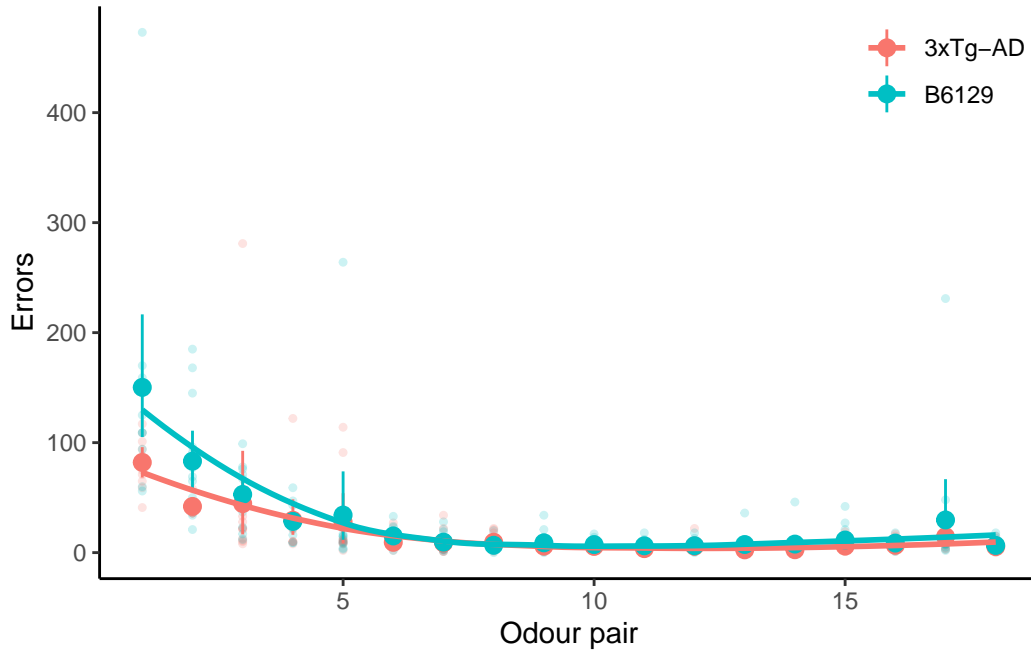


Figure 2: Errors ($\pm 95\%$ CI) made by the mice at on each odour pair during the reversal stages.

The reversal trials were assessed with linear mixed effects models on the number of errors made on each odour pair. The errors made decreased as the mice advanced through the odour pairs (Figure 2). The model with effects of genotype, odour pair, and the genotype by odour pair interaction best explained the data (Table 3), this model differed significantly from the null model of just an effect of odour pair ($\chi^2_3 = 104, p < 0.0001$).

Table 3: AICc model table for reversal.

geno	op	geno:op	df	logLik	AICc	delta	weight
+	-2.83	+	6	-2121.78	4255.77	0.00	0.76
+	-3.67		5	-2124.06	4258.27	2.51	0.22
	-3.67		4	-2127.30	4262.69	6.93	0.02
+			4	-2171.37	4350.84	95.07	0.00
			3	-2173.80	4353.66	97.90	0.00

Table 4: AICc model table for total errors.

geno	df	logLik	AICc	delta	weight
+	3	-159.28	325.76	0.00	0.83
	2	-162.15	328.87	3.11	0.17

Total errors

The total errors made were assessed with linear models. The model with an effect of genotype best explained the data (Table 4), this model differed significantly from the null model ($F_1 = 5.9, p = 0.0233$; (Figure 3)).

Retest

The number of errors made during the retest was assessed with linear models. The null model best explained the data for the number of errors made during the retest (Table 5), indicating no significant effects of genotype nor sex (Figure 4).

Table 5: AICc model table for retest errors.

geno	df	logLik	AICc	delta	weight
	2	-77.88	160.55	0.0	0.79
+	3	-77.77	163.26	2.7	0.21

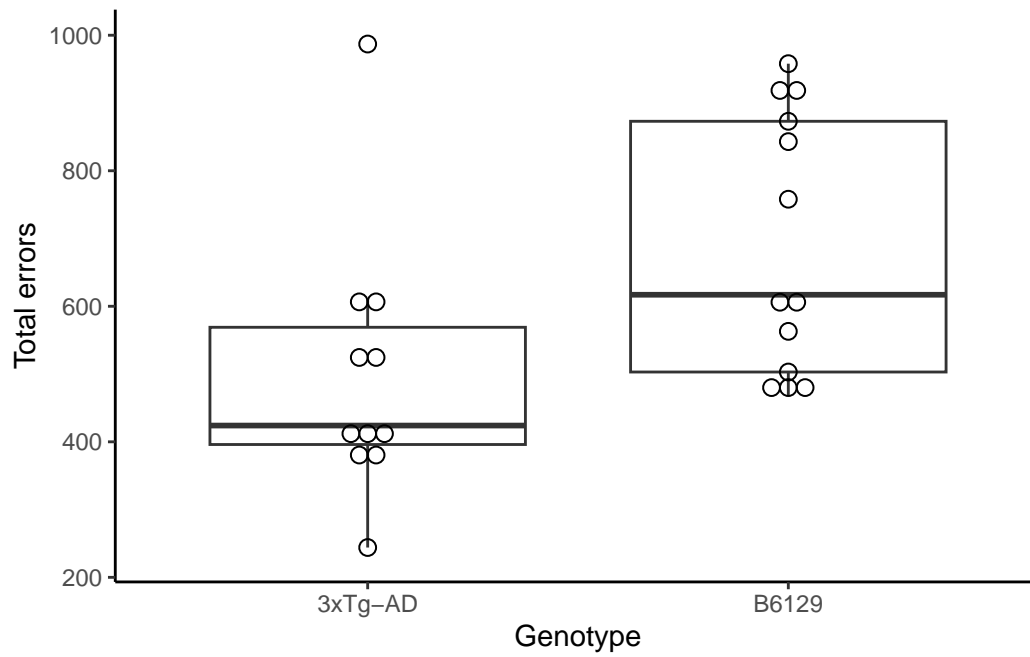


Figure 3: Total errors made, excluding retest.

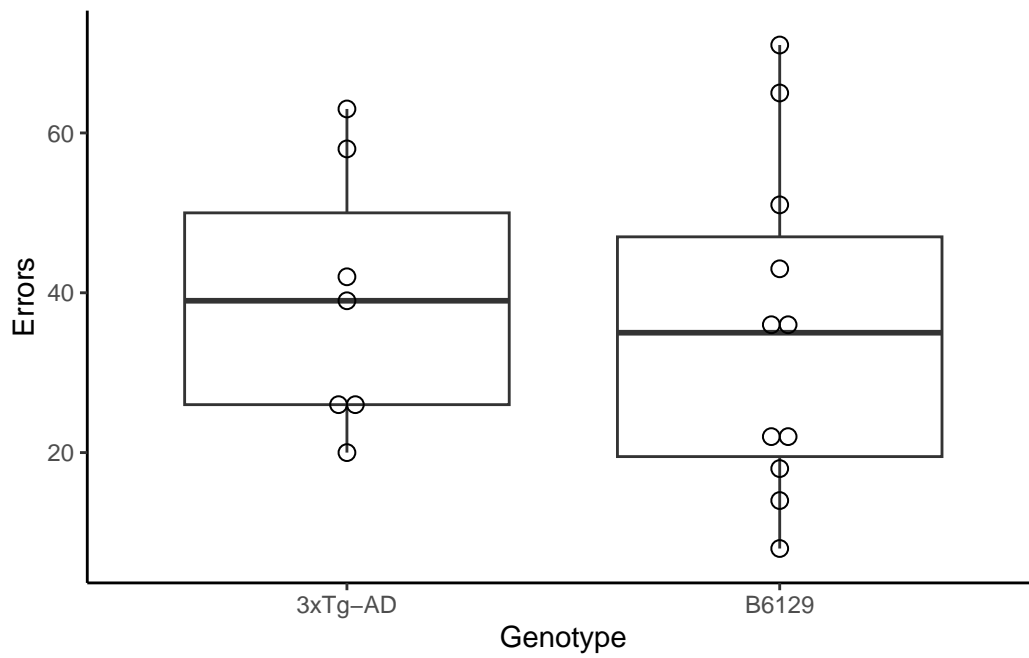


Figure 4: Total errors made during retest.