

Inheritance of Operant Learning Performance in Mice *)

by

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Die Vererbung der Fähigkeit von operanten Lernen bei Mäusen

Synopsis: To assess the inheritance of differences of operant learning ability in two inbred mouse strains (CBA = "bad learners" versus 102 = "good learners"), groups of ten male or of ten female subjects of altogether 12 generations were tested simultaneously in individual standardized lever boxes. The animals were required to press the lever for food reward in an automated nocturnal 15-hour contingency subdivided into alternating 30 minutes ON-phases and 60 minutes OFF-phases. An additional food pellet was presented at the start of each ON-phase. Data on the number of lever presses, rewards and errors from both sexes of the two strains, their F_1 and F_2 hybrids, and respective backcross generations were obtained in eight consecutive test sessions. These results and their ratio (Z-values) demonstrated a striking pattern resemblance of performance levels in the parental generations of CBA- and 102-strains as well as in the subsequent generations. Hence, it is concluded that long-term operant performance studies yield reliable data for a quantitative approach in behavioral genetics.

Since a linear model ($Y = a + bX$) seemed to fit best the experimental results, the intercept (a) and the slope (b) of the performance curves in all 12 generations groups were determined for both sexes. The slope (b) of the learning curve revealed a rather good measure for the operant learning performance and therefore was analysed in more detail for both learners and nonlearners. A unidirectional additive-dominance model with no non-allelic interactions was found to describe best the inheritance of b. Heritabilities varying between 0.0118 and 0.76 favour the view that operant learning belongs to the characters with a medium to relatively high reproductive fitness. With respect to the inheritance of operant learning performance, the two parental strains under investigation differed by only independently segregating genetic unit. The genotypic variance amounted to 60 and the environmental variance to 40 % of the phenotypic variance.

1. Introduction:

There are few experimental results concerning the inheritance of learning ability and learning performance in mammals (FESTING 1973a, b, LASSALLE et al. 1979, SCHRODER & SUND 1984). As to our knowledge, nothing has been done hitherto with respect to the genetic analysis of operant behavior performance in vertebrates. This paper describes an attempt to analyse the genetic basis of operant learning in both sexes of the laboratory mouse (*Mus musculus domesticus*).

2. Material and Methods:

2.1. Animals:

To ascertain the feasibility of an analysis of the genetic basis of operant learning, after a pilot study with six Neuherberg mouse strains (C57BL/6J/Han, BALB/c, C3H/Hc, 102, CBA, NMRI), two inbred mouse strains

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(102 –formerly 101–, and CBA) were selected for the hybridization experiments. With the exception of the NMRI albino strain, all others were inbred and propagated exclusively by brother x sister mating since more than 50 generations. Although some of the six strains exhibited larger differences in operant learning behavior than did 102 and CBA, these two strains were chosen because they did not segregate into different color phenotypes in subsequent F_2 and backcross generations. The mice were bred and kept as specific pathogen free mouse strains as described previously (SCHRÖDER 1977). At weaning (21 - 28 days old) the mice were separated by sex and housed in groups, five or fewer per standard Macrolon cage (25 x 20 x 14 cm³). Water and Altromin^(R) food pellets were available *ad libitum*.

2.2. Apparatus:

To assess the learning ability in operant learning tests, isolated test mice were required to press a lever in a Skinner box for food reward. A nocturnal test session lasted 15 hours (16:00 - 07:00) with alternating 30 min of light and 90 min of dark phases. Only in light phases, a bar press was rewarded by a food pellet, while lever actions in the dark phases remained unrewarded. The mice had unlimited access to tap water. Each test cage was equipped with individual custom-built electronic circuitry which controlled the test program and the record of data automatically. Accordingly, interactions between experimenter and subjects could be minimized during the test sessions. Ten mice could be tested simultaneously (fig. 1). Thus, 10 males and 10 females were tested for each of the 12 different generations (cf. table 1). A total of 240 mice within 3 years were analysed in this study as described elsewhere in more detail (BORNHAUSEN et al. 1980).

Table 1: Percent genomic composition of the 12 different generations with respect to the parental (maternal, mat., and paternal, pat.) genetic material.

Generation Origin		Genome (%)	
		102	CBA
P ₁	102 inbred strain	100 (50 pat + 50 mat); Y	0
P ₂	CBA inbred strain	0	100 (50 pat + 50 mat); Y
F ₁	(102 ♂ x CBA ♀) – F ₁	50 pat; Y	50 mat
F ₁ *	(CBA ♂ x 102 ♀) – F ₁	50 mat	50 pat; Y
F ₂	(102 ♂ x CBA ♀) – F ₂	50 pat; Y	50 mat
F ₂ *	(CBA ♂ x 102 ♀) – F ₂	50 mat	50 pat; Y
B ₁	(102 ♂ x CBA ♀) – F ₁ ♂ x 102 ♀	75 (50 mat + 25 pat); Y	25 mat
B ₁ *	(CBA ♂ x 102 ♀) – F ₁ * ♂ x 102 ♀	75 mat	25 pat; Y
B ₂	(102 ♂ x CBA ♀) – F ₁ ♀ x 102 ♂	75 pat; Y	25 mat
B ₃	(102 ♂ x CBA ♀) – F ₁ ♂ x CBA ♀	25 pat; Y	75 mat
B ₃ *	(CBA ♂ x 102 ♀) – F ₁ * ♂ x CBA ♀	25 mat	75 (50 mat + 25 pat); Y
B ₄	(102 ♂ x CBA ♀) – F ₁ ♀ x CBA ♂	25 pat	75 (50 pat + 25 mat); Y

2.3. Data analysis:

The total number of bar presses in light (rewarded) and dark (unrewarded) phases were compared to each other using the approximation of the binomial distribution by the normal distribution with $P = 0.25$ and $Q = 0.75$. According to a formula given by SACHS (1973), viz. $\hat{z} = (x - nP) / (\sqrt{nPQ})$, where x = the number of rewarded bar presses and n = the sum of the number of rewarded bar presses + that of unrewarded bar presses, a mouse was designate a learner when the number of rewarded bar presses significantly exceeded that of the unrewarded ones, i.e. $\hat{z} \geq 1.65$. Accordingly, all mice were distinguished into learners ($\hat{z} \geq 1.65$) and nonlearners ($\hat{z} < 1.65$).

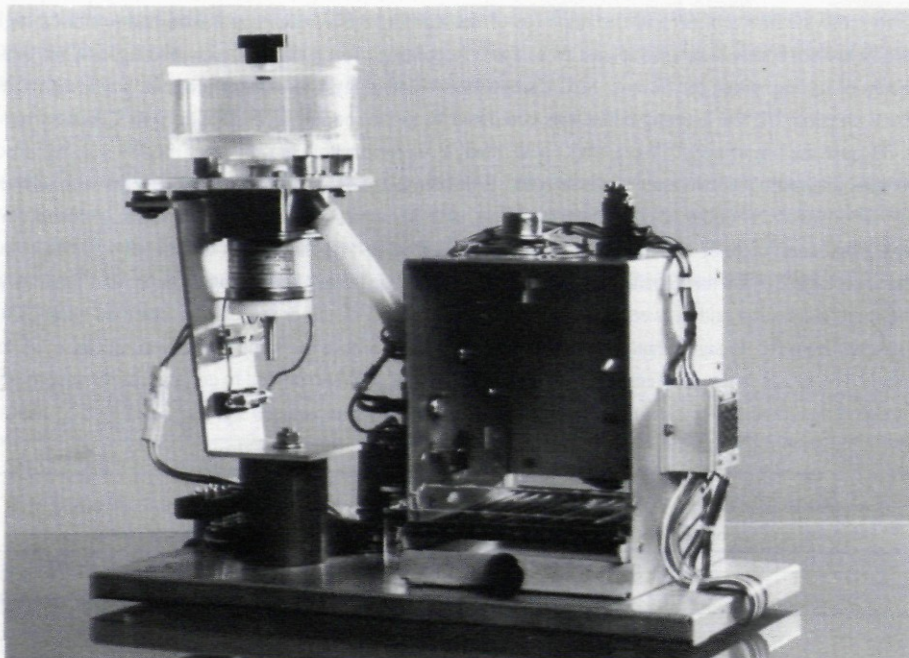


Fig. 1a: Skinner-box as used for the present experiments.



Fig. 1b: A set of ten Skinner-boxes as used for the simultaneous record of operant learning performance.

To score the intercept (a) and the slope (b) of the learning curve, each test mouse had to run through 8 successive test sessions which were at least 24 hs apart. Accordingly, each animal under investigation had to pass 120 hours of testing within the Skinner box. Using a regression analysis computer program provided by STATGRAPHICS, version 2.1, the learning curve was computed from the individual \bar{z} -values of the 8 successive sessions. Because the linear model ($Y = a + bX$) best fitted the experimental data, all other models (e.g. reciprocal, exponential and multiplicative ones) were rejected. From the individual parameters (a and b) of each of the 10 mice of either sex in any of the 12 different generations, arithmetic mean (\bar{x}), standard error (SE), standard deviation (SD), and coefficient of variation ($CV = SD/\bar{x}$) were calculated by the help of a respective STATGRAPHICS program (cf. table 2). The mean parameters were compared to each other both between males and females within the same generation and between the 12 different generations of either sex using a standard t-test (SACHS 1973). Apart from P_2 , no significant sex differences were found within the same generation. Because of this, the weighed means of males and females of the same generation could be pooled to compare them with those of other generations (table 2b - table 4). Altogether 256 double (dual) comparisons were adjusted by the means of multiple comparisons (Bonferroni-Holm procedure; HOLM 1979).

Table 2a: Arithmetic mean (\bar{x}), standard error (SE), standard deviation (SD), and percent coefficient of variation (CV) of the parameter b of the linear model ($Y = a + bX$) for males and females of the 12 different generations.

Generation	σ^2				σ^2			
	\bar{x}	SE	SD	CV (%)	\bar{x}	SE	SD	CV (%)
P_1	1.50	0.29	0.92	61.33	1.02	0.28	0.88	86.27
P_2	1.20	0.27	0.87	22.50	0.65	0.15	0.49	0.75
F_1	0.92	0.39	1.24	134.78	0.95	0.32	0.97	102.11
F_1^*	0.84	0.30	0.96	114.29	0.67	0.29	0.92	137.31
F_2	1.61	0.15	0.48	29.91	1.60	0.27	0.85	53.13
F_2^*	2.17	0.13	0.42	19.35	1.47	0.49	1.56	106.12
B_1	1.54	0.26	0.77	50.00	1.01	0.21	0.64	63.37
B_1^*	0.92	0.32	1.00	108.70	1.24	0.22	0.71	57.26
B_2	0.81	0.34	1.09	134.57	2.09	0.28	0.80	38.28
B_3	1.43	0.39	1.16	81.12	0.43	0.13	0.41	95.35
B_3^*	1.66	0.52	1.64	98.80	1.05	0.18	0.58	55.24
B_4	1.19	0.27	0.86	72.27	1.72	0.18	0.55	31.98

Table 2b: Variances of b.

V_P	=	phenotypic variance		
V_G	=	genotypic variance		
V_E	=	environmental variance		
V_P	=	$V_G + V_E$		
V_E	=	$V_{P_1} + V_{P_2} + V_{F_1} + V_{F_1}^*$ (only environmental variance possible)		
V_P	=	$V_{F_2} + V_{F_2}^* + V_{B_1} + V_{B_2} + V_{B_3} + V_{B_4} + V_{B_1}^* + V_{B_3}^* + V_E$		
V_P	=	37.37 (Learners + Nonlearners)		
V_P	=	8.83 (Learners)		
V_G	=	22.45 (Learners + Nonlearners)		
V_G	=	5.32 (Learners)		
V_E in % of V_P :	39.93 (Learners + Nonlearners)		39.75 (Learners)	
V_G in % of V_P :	60.07 (Learners + Nonlearners)		60.25 (Learners)	

To determine whether or not an additive-dominance model fits the results to be presented, the scaling test as proposed by MATHER (1949) and MATHER & JINKS (1970, pp. 71 - 73) was applied. The number of independently segregating units was estimated according to the formula

$$n = \sqrt{1/2 (P_1 - P_2) / 1/2 (P_1 - P_2) - e}$$

in which \bar{P}_1 and \bar{P}_2 are the arithmetic means of the parental generations and e is the mean standard error of the non-segregating generations P_1 , P_2 , and F_1 (cf. table 3). Estimates of the additive, dominance, and interaction parameters (cf. table 4) were carried out according to the formalism given by JINKS & JONES (1958) and MATHER & JINKS (1970, p. 70). The heritability of b (cf. table 5) was estimated using the formulae provided by McCLEARN & DEFRIES (1973) and WHITNEY et al. (1970).

Table 3: The scaling test according to MATHER (1949) and MATHER & JINKS (1970) and the number of independently segregating units.

Parameter *) \pm Standard deviation	Nonlearners + learners	Learners ²
A	-0.13 ± 3.14	0.08 ± 1.78
B	0.42 ± 2.95	-0.08 ± 1.64
C	3.03 ± 5.76	1.19 ± 2.93

* Formulas were used as follows:

$$A = 2 \overline{BC_1} - \bar{P}_1 - \bar{F}_1;$$

$$V_A = 4 \overline{V_{B_1}} + \overline{V_{P_1}} + \overline{V_{F_1}};$$

$$B = 2 \overline{BC_2} - \bar{P}_2 - \bar{F}_1;$$

$$V_B = 4 \overline{V_{BC_2}} + \overline{V_{P_2}} + \overline{V_{F_1}};$$

$$C = 4 \bar{F}_2 - 2 \bar{F}_1 - \bar{P}_1 - \bar{P}_2;$$

$$V_C = 16 \overline{V_{F_2}} + 4 \overline{V_{F_1}} + \overline{V_{P_1}} + \overline{V_{P_2}};$$

in which

\bar{P}_1 , \bar{P}_2 , \bar{F}_1 , \bar{F}_2 , $\overline{BC_1}$ and $\overline{BC_2}$ are the arithmetic means of P_1 , P_2 , F_1 , F_2 , BC_1 and BC_2 , while $\overline{V_{P_1}}$, $\overline{V_{P_2}}$, $\overline{V_{F_1}}$, $\overline{V_{F_2}}$, $\overline{V_{BC_1}}$ and $\overline{V_{BC_2}}$ are the respective variances.

F_1 and F_2 values are the weighed means of $\sigma^+ + \sigma^-$ of $F_1 + F_1^*$ and of $F_2 + F_2^*$ respectively.

Number (n) of independently segregating units.

$$n = \sqrt{\frac{1/2 (\bar{P}_1 - \bar{P}_2)}{1/2 (\bar{P}_1 - \bar{P}_2) + e}} \quad \text{where } e = \text{mean standard error of the non-segregating generations } (P_1, P_2, F_1)$$

$$n = 0.97 \text{ (Nonlearners + Learners)}$$

$$n = 0.84 \text{ (Learners)}$$

3. Results:

3.1. Genomic composition of the 12 different generations:

Table 1 concerns the percent genomic composition of the 12 different generations with respect to the paternal (pat) and maternal (mat) genetic material of the original parental strains 102 and CBA including the origin of the Y-chromosome. Summing up the different backcross generations B_1 , B_1^* , B_2 , B_3 , B_3^* and B_4 , we have to distinguish between two different types: Backcrosses with an average of 75 % 102 + 25 % CBA genomic material (BC_1) and those with 25 % 102 + 75 % CBA (BC_2). The pooled data of males and females of BC_1 contain the weighed means of B_1 , B_1^* and B_2 , while those of BC_2 comprise the weighed means of B_3 , B_3^* , and B_4 (figs. 1 and 2).

Table 4: Estimates of the additive, dominance, and interaction parameters according to JINKS & JONES (1958) and MATHER & JINKS (1970).

Parameter ± Standard deviation	Nonlearners + learners	Learners
m	4.73 ± 7.14	3.92 ± 3.84
[d]	0.39 ± 0.88	0.30 ± 0.54
[h]	- 5.54 ± 13.58	- 2.35 ± 7.17
[i]	- 2.74 ± 5.54	- 1.18 ± 2.81
[j]	- 0.55 ± 3.69	0.16 ± 2.11
[l]	2.45 ± 8.67	1.18 ± 4.66

The magnitude of effects of nonallelic interactions on the means can be estimated by the parameters m, [d], [h], [i], [j] and [l]. Because these estimates of the interaction parameters are within the order of magnitude of their standard deviations, there is no evidence of nonallelic interactions for slope.

Heterosis will occur only when [h] is negative and greater than [d].

[h] is not greater than [d] in the present study.

The parameters of the six calculated experimental generations P_1 , P_2 , F_1 , F_2 , BC_1 and BC_2 are the formulas given by JINKS and JONES (1958) and JINKS (1970).

$$m = 1/2 \bar{P}_1 + 1/2 \bar{P}_2 + 4 \bar{F}_2 - 2 \bar{BC}_1 - 2 \bar{BC}_2 \quad \text{with} \quad V_m = 1/4 V_{P_1} + 1/4 V_{P_2} + 16 V_{F_2} + 4 V_{BC_1} + 4 V_{BC_2}$$

$$[d] = 1/2 \bar{P}_1 - 1/2 \bar{P}_2 \quad \text{with} \quad V_{[d]} = 1/4 V_{P_1} + 1/4 V_{P_2}$$

$$[h] = 6 \bar{BC}_1 + 6 \bar{BC}_2 - 8 \bar{F}_2 - \bar{F}_1 - 1/2 \bar{P}_1 - 1/2 \bar{P}_2 \quad \text{with} \quad V_{[h]} = 36 V_{BC_1} + 36 V_{BC_2} + 64 V_{F_2} + V_{F_1} + 2.25 V_{P_1} + 2.25 V_{P_2}$$

$$[i] = 2 \bar{BC}_1 + 2 \bar{BC}_2 - 4 \bar{F}_2 \quad \text{with} \quad V_{[i]} = 4 V_{BC_1} + 4 V_{BC_2} + 16 V_{F_2}$$

$$[j] = 2 \bar{BC}_1 - \bar{P}_1 - 2 \bar{BC}_2 + \bar{P}_2 \quad \text{with} \quad V_{[j]} = 4 V_{BC_1} + V_{P_1} + 4 V_{BC_2} + V_{P_2}$$

$$[l] = \bar{P}_1 + \bar{P}_2 + 2 \bar{F}_1 + 4 \bar{F}_2 - 4 \bar{BC}_1 - 4 \bar{BC}_2 \quad \text{with} \quad V_{[l]} = V_{P_1} + V_{P_2} + 4 V_{F_1} + 16 V_{F_2} + 16 V_{BC_1} + 16 V_{BC_2}$$

Table 5: Estimates of heritability of b:

$$\text{heritability } (h^2) = \frac{V_G}{V_P} = \frac{V_G}{V_G + V_E}$$

$$h^2 = \frac{1/8 (\bar{P}_1 - \bar{P}_2)^2}{1/8 (\bar{P}_1 - \bar{P}_2)^2 + V_E} \quad \text{where } \bar{P}_1 \text{ and } \bar{P}_2 \text{ are the phenotypic means of the parental generations, } (\sigma^2 + \varrho^2) \text{ and } V_E \text{ is estimated from the variance within the isogenic generations } (P_1, P_2, F_1, F_2^*).$$

$$h^2 = 0.0049 \text{ (Learners + Nonlearners)}$$

$$h^2 = 0.0118 \text{ (Learners)}$$

Characters with low heritabilities are related to those most closely connected with reproductive fitness (FALCONER 1960).

$$h^2 = \frac{[\bar{B}_1 - \bar{B}_2]}{[\bar{B}_1 - \bar{B}_2] + e} \quad \text{where } \bar{B}_1 \text{ and } \bar{B}_2 \text{ are the phenotypic means of } \sigma^2 + \varrho^2 \text{ of the backcross generations } BC_1 \text{ (75 \% } 102 + 25 \% \text{ CBA) and } BC_2 \text{ (25 \% } 102 + 75 \% \text{ CBA), and } e \text{ is the mean standard error of the non-segregating generations.}$$

$$h^2 = 0.41 \text{ (Learners + Nonlearners)}$$

$$h^2 = 0.76 \text{ (Learners)}$$

According to the second formula the operant learning performance seems to be a quantitative character of medium fitness.

3.2. Significant differences of the slope (b):

The mean values of the parameter b for the linear model ($Y = a + bX$) as calculated from the individual \bar{z} -values of every 10 males and 10 females, respectively, are given in fig. 2. Although the b's between males and females often differed significantly, higher values for males within the same generation were found only in P_2

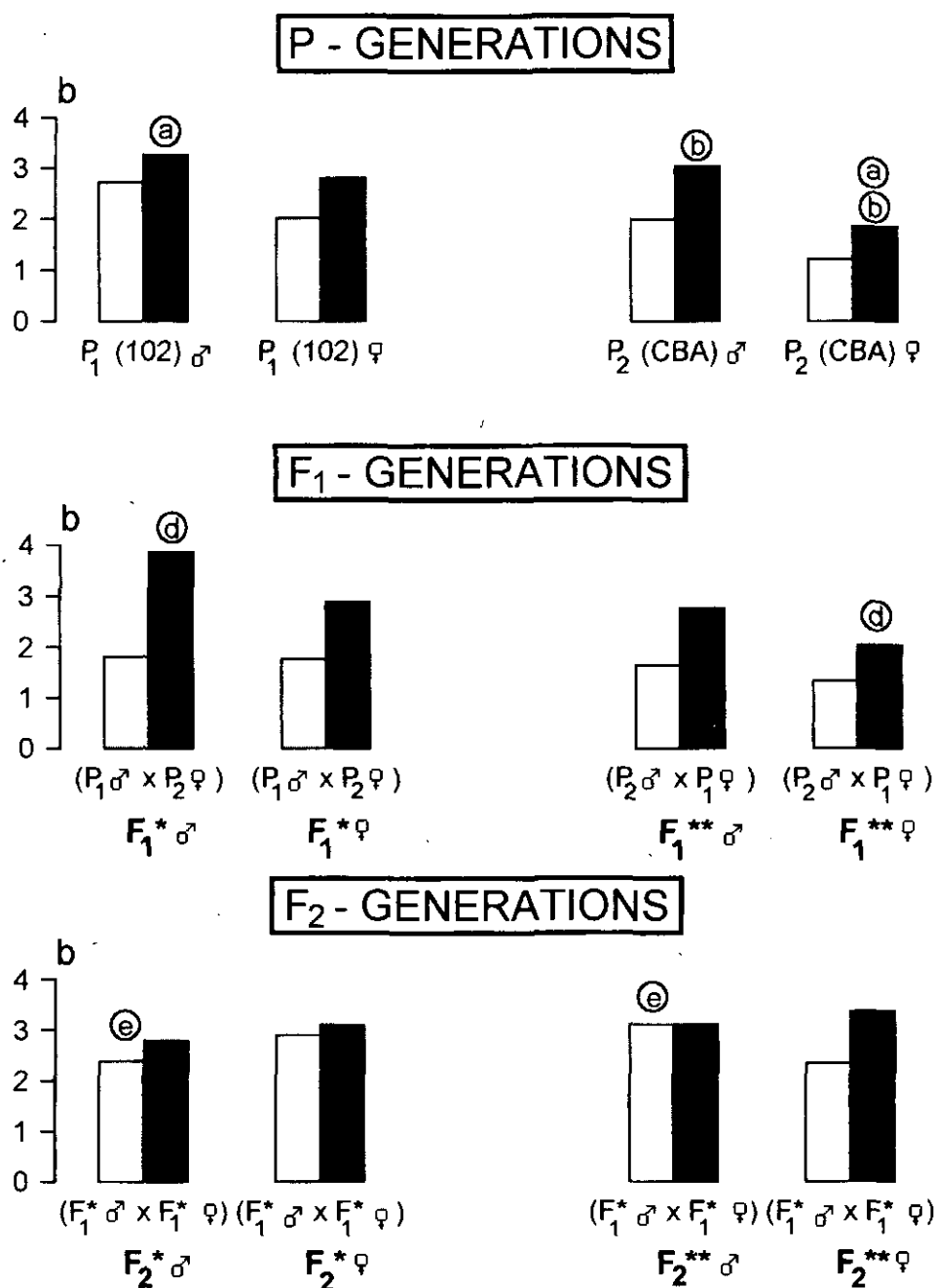


Fig. 2a: Histograms of the slope (b) from the learning curve ($Y = a + bX$) of males and females of the different 12 generations distinguished into all individuals (learners + nonlearners) and learners only. a) - t): significant differences ($p \leq 0.05$).
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BACKCROSS GENERATIONS

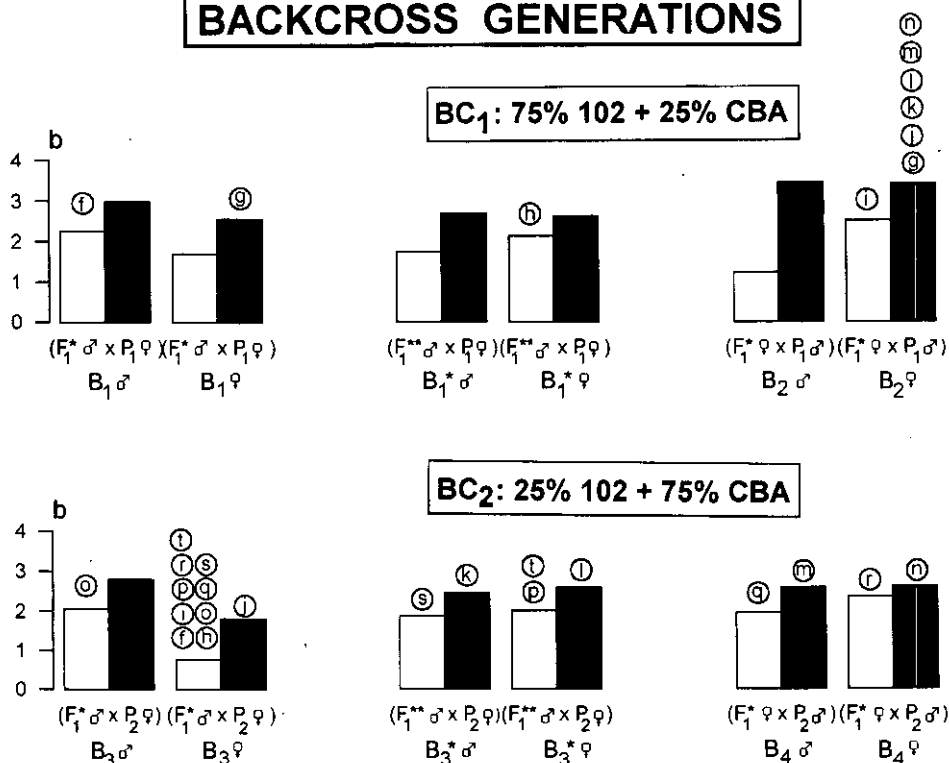
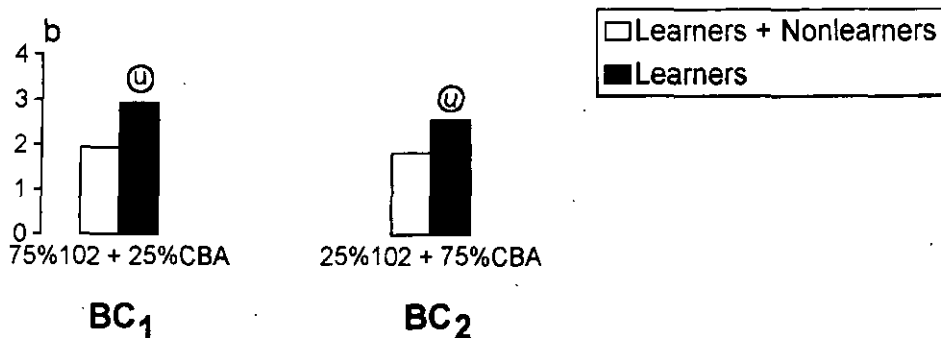


Fig. 2a: Continued.

(CBA) for learners (standard t test; $P < 0.05$; fig. 2a). Because no correlation between the parental origin of sex chromosomes (table 1) and the success in operant learning could be found, sex differences are apparently not attributable to the influences of sex chromosomes but rather to the percent composition of the parental genomes, 102 and CBA, respectively. The pooled data with a higher percentage of 102 ("good learner") genomic material (BC₁) revealed a significantly higher numeric value of b for learners than that with a higher percentage of CBA ("bad learner") genomic proportion (fig. 2b). The learning curves ($Y = a + bX$) of the parental and backcross generations (fig. 3) as calculated from \bar{z} of the pooled b values of males and females reflect the same situation as described by the histograms of b (fig. 2) and revealed significant differences for learners + non-learners between P_1 (102) and P_2 (CBA) as well as for learners between BC₁ and BC₂.

3.3. Variances of b :

Apart from the inbred generations and their F_1 hybrids, the measured variance corresponds to the phenotypic variance (V_P) which consists of the genotypic (V_G) and the environmental (V_E) variances. Only environmental variances occurred in P_1 , P_2 , F_1 , and F_1^* generations (table 2). Although both the phenotypic and genotypic variance of learners amounted to about one fourth of those of all individuals, there was no significant differences between all individuals (learners + nonlearners; 39.93 %) and learners (39.75 %) with respect to the environmental variance expressed in percent of the phenotypic variance (table 2b).



@ - u; significant differences between different crosses of the same generation (t-test; $p < 0.05$)

Fig. 2b: The pooled data of the slope (b) from the learning curve of males and females of the backcross generations BC₁ (75 % 102 + 25 % CBA) and BC₂ (25 % 102 + 75 % CBA) as calculated from the weighed means of B₁; B₁*, B₂, (BC₁) and those of B₃, B₃*, B₄ (BC₂) distinguished into all individuals (learners + nonlearners) and learners only. u) significant difference ($p \leq 0.05$).

3.4. Estimation of the additive, dominance, and interactions parameters:

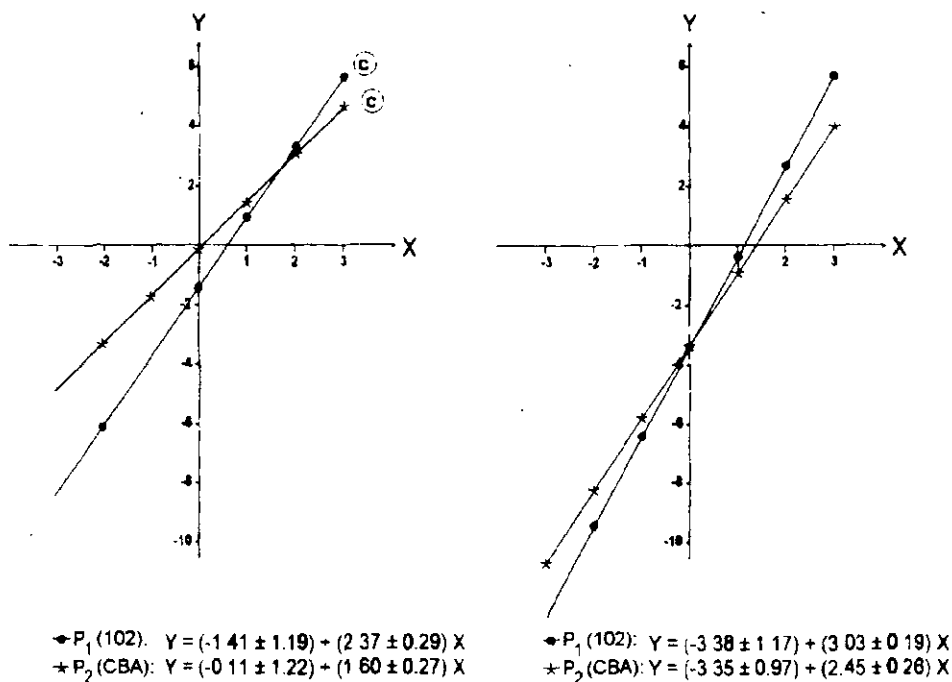
The expectations for the scaling test (table 3; MATHER 1949, MATHER & JINKS 1970) all reduce to zero when no interaction is present, but each type of test depends on characteristic combinations of interactions for its departure from zero. Since the means of the parameters A, B, and C are all within the order of magnitude of their standard deviations, they do not deviate from zero, which means that no non-allelic interactions occur.

There is still another procedure to estimate the magnitude of the effects of non-allelic interactions on the means (MATHER & JINKS 1970, p. 90). For this purpose, a minimum of six family means are required for the estimation of the six parameters, m, [d], [h], [i], [j], and [l] (table 4). The six families can be provided by the parents, F₁, F₂, and first backcross generations of a cross between the two true breeding (inbred) lines. In the present case, two calculations were performed in which the six families were either P₁, P₂, F₁, F₂, B₁, B₃, or P₁, P₂, F₁*, F₂*, B₁*, B₃*, respectively. The perfect fit solution is then given by the formulae of JINKS & JONES (1958). Because the estimates both for nonlearners + learners and learners alone of the interaction parameters are all within the order of magnitude of their standard deviations, there is no evidence of non-allelic interactions for the inheritance of the slope of both sexes which confirms the results of table 3. This also holds true for the calculations of the intercept (a) which are not specified in this paper.

Consequently, the inheritance of a and b can be explained by an additive-dominance model in which no non-allelic interactions occur.

3.5. Estimation of the number of independently segregating units:

The number of independently segregating genetic units can be estimated by the formula of table 3. Because the values for both all individuals (nonlearners + learners) and learners approaches unit, we may conclude that both inbred lines (102 and CBA) distinguish from each other by only one independently segregating genetic element. This necessarily must not mean a single gene locus should be responsible for the difference



Learners + Nonlearners

Learners

Fig. 3a

Fig. 3a + b: The learning curves ($Y = a + bX$) as calculated from \bar{z} of the pooled data parameters (a and b) of males and females distinguished into all individuals (learners + nonlearners) and learners only. Only the parental generations P_1 (102) and P_2 (CBA) (fig. 3a) and the pooled backcross generations BC_1 and BC_2 (fig. 3b) are presented. c) and u): significant difference ($p \leq 0.05$).

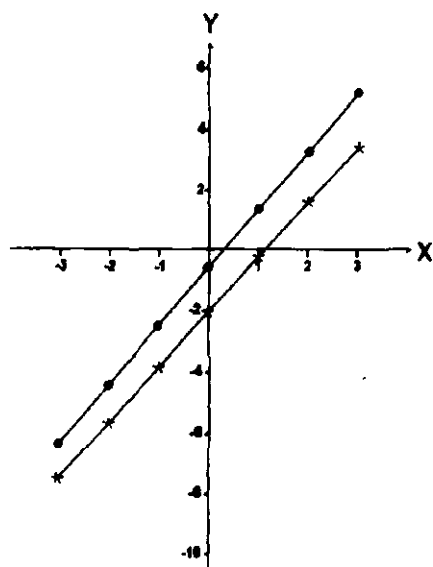
between the two lines but rather could stand for polygenes sharing one linkage group.

3.6. Estimation of heterosis:

Heterosis will occur only when $[h]$ is negative and greater than $[d]$. In addition, heterosis is more likely to occur if the signs of all $[h]$'s are the same, that is, dominance is unidirectional (table 4). Because the signs of all $[h]$'s are negative while those of $[d]$ are positive, $[h]$ is not greater than $[d]$. Thus, table 4 represents the pooled data of males and females. In details not explained here, b of females might be due to over- (or super-) dominance at some or all loci responsible for the inheritance of b .

3.7. Estimates of heritability of b :

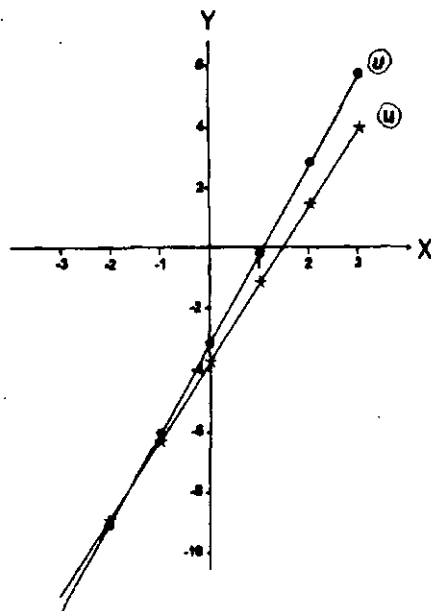
The heritability (h^2) is defined as the ratio of additive genetic variance to phenotypic variance (FALCONER 1960). Two estimates of heritability (h^2) for the slope (b) in the linear model (table 5) were performed accord-



$$\bullet BC_1 Y = (-0.56 \pm 0.72) + (1.94 \pm 0.16) X$$

$$+ BC_2 Y = (-2.03 \pm 0.52) + (1.83 \pm 0.14) X$$

Learners + Nonlearners



$$\bullet BC_1 Y = (-3.13 \pm 0.77) + (2.93 \pm 0.12) X$$

$$+ BC_2 Y = (-3.72 \pm 0.59) + (2.56 \pm 0.10) X$$

Learners

Fig. 3b.

ing to two formulae given by McCLEARN & DEFRIES (1973) and WHITNEY et al. (1970). According to the first formula using the means of the parental strains, the calculations of heritability resulted in numeric values of 0.0049 for all individuals and 0.0118 for learners, while the use of the second formula with the means of backcross generations resulted in heritabilities of 0.41 for all individuals and 0.76 for learners. Since the characters with lowest heritabilities are those most closely connected with reproductive fitness while the characters with the highest heritabilities are those that might be judged on biological grounds to be the least important as determinants of natural fitness (FALCONER 1960, pp. 167 - 168), operant learning as described by the linear model seem to be a quantitative character varying between very high and medium fitness.

4. Discussion:

Previous investigations concerned the inheritance of an orientation task in mice testing the learning ability to escape a water-bath in five successive trials (LASSALLE et al. 1979; SCHRODER & SUND 1984). Remarkable similarities were found between this task and the results of the present study: 1. An additive-dominance model with no non-allelic interactions was found to describe both the inheritance of the water-escape performance and of operant conditioning in the Skinner-box. Unidirectional dominance occurred in both cases. 2. Low heritabi-

lities which are related to those characters closely connected to reproductive fitness (FALCONER 1960) were found in both experimental sets. However, also medium heritabilities occurred in operant learning. 3. Heterotic effects were likely in the inheritance of water-escape learning ability and operant learning with the difference that heterotic effects occurred persistently in the escape-learning experiments for all aspects under investigation, while heterosis could be guaranteed in operant learning only for the inheritance of the slope (b) in females. Sex differences appeared in both studies but at a lesser degree in operant learning. Despite these differences between escape learning and food reinforced lever presses, it is of considerable interest that both kinds of learning performance seem to be inherited in a similar manner, viz. by an additive-dominant polygenic system with no non-allelic interactions of the genes in question. That heterotic effects do not occur in the same way in both kinds of inheritance may be attributed to the non-adjusted hormonal state of the test mice which seems important for the motivation to seek food. Because of these similarities, a common genetic basis for both operant and escape learning seems to exist. That only one independently segregating unit was found for the difference of operant learning in both parental strains may be an indication for the inheritance by linkage groups which contain different gene loci. These loci might be closely linked to each other thus forming a "supergene" (DARLINGTON & MATHER 1949) complex (hitchhiking gene group) and thus not subjected to and therefore also protected from genetic exchange processes. This often occurred during evolution to stabilize groups of genes coacting in the realization of characters with both a high functional correlation and reproductive fitness (e.g. courtship strategies and intermale aggressiveness in the guppy; FARR 1983). Although genotypic variance shares in 60 % of the total phenotypic variance, the remaining 40 % for the environmental variance indicates the high adaptive capacity of operant learning.

A lot of previous behavior-genetic studies confirm the present findings: Positive additive-genetic and dominance correlations between two mouse phenotypes were also found for locomotory and rearing activity (CRUSIO 1993). A genetic architecture of ambidirectional dominance and additive genetic variation apparently has been established for all exploratory behaviors of the mouse (CRUSIO 1984, CRUSIO et al. 1984, CRUSIO & VAN ABELEN 1986). Furthermore, the quantitative-genetic analysis of isolation-induced aggression in mice revealed that the interstrain differences were correlated with more than one single locus (SCHICKNICK et al. 1993). As far as investigated hitherto, additive genetic variation was present for all phenotypes of hippocampal variation in the mouse (CRUSIO et al. 1986). Generally, additive genetic effects and/or ambidirectional dominance were found to be characteristic of most species-specific behavior elements, suggesting an evolutionary history of stabilizing selection (GERLAI et al. 1990).

5. Zusammenfassung:

Um die Vererbung der Unterschiede in der Fähigkeit zum operanten Lernen (Konditionierung) bei zwei Mäuse-Inzuchtstämmen (CBA = "Schlechte Lerner" im Vergleich zu 102 = "gute Lerner") zu analysieren, wurden jeweils zehn männliche oder weibliche Mäuse von insgesamt 12 unterschiedlichen Generationen in einzelnen, mit Hebeln standardisiert ausgestatteten Skinner-Boxen gleichzeitig getestet. Die Tiere mussten in einer automatischen nächtlichen 15-Stunden-Sitzung jeweils einen Hebel drücken, um ein Futter-Pellet als Belohnung zu erhalten. Die 15 Stunden waren in 30-Minuten-Phasen mit Licht und Futterbelohnung ("ON") und 60-Minuten-Dunkelphasen ohne Belohnung ("OFF") unterteilt, die einander abwechselten. Bei Beginn einer "ON"-Phase wurde jeweils ein zusätzliches Futter-Pellet gereicht. Daten über die Zahl der Hebeldrücke, Belohnungen und Fehler wurden von beiden Geschlechtern der beiden Stämme, ihrer F₁- und F₂-Hybriden sowie der entsprechenden Rückkreuzungsgenerationen in acht aufeinanderfolgenden Test-Sitzungen erhalten. Diese Ergebnisse und ihre Relativwerte (\bar{z}) zeigten ein auffallend ähnliches Muster der Leistungsniveaus sowohl in den Elterngenerationen der CBA- und 102-Stämme als auch in den nachfolgenden Generationen. Langzeitunter-

suchungen der operanten Lernleistung können deshalb zuverlässige Daten für die quantitative Verhaltensgenetik liefern.

Da ein lineares Modell ($Y = a + bX$) am besten die experimentellen Ergebnisse beschrieb, wurden Intercept (a) und Anstieg (b) der Lernkurven für alle 12 Generationen bei beiden Geschlechtern bestimmt. Als Maß für die Lernleistung wurde der Anstieg der Lernkurve (b) näher analysiert, und zwar getrennt für Lerner und Nichtlerner. Ein Modell der in eine Richtung weisenden additiv-dominanten Genwirkung ohne Wechselwirkung nicht-allelischer Gene erwies sich zur Beschreibung der Vererbung von b als geeignet. Heritabilitätswerte zwischen 0.0118 und 0.76 für Lerner rechtfertigen die Annahme, dass das operante Lernen zu den Eigenschaften mit einer mittleren bis relativ hohen reproduktiven Fitness gehört. Die beiden untersuchten parental Ausgangsstämme unterschieden sich hinsichtlich der Vererbung ihrer operanten Lernfähigkeit durch nur eine unabhängig aufspaltende genetische Einheit. Die genotypische Varianz betrug 60 und die Umwelt-Varianz 40 % der phänotypischen Varianz.

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