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ABSTRACTS

Behavior Genetics Association Abstracts

Laura A. Baker.[1] Differential Experience Within Twin Pairs: Another Reconsideration of the Equal-Environments Assumption?[2] In an effort to identify and measure sources of within-family environmental variation important to personality characteristics, 143 monozygotic (MZ) and 65 dizygotic (DZ) adult twins (mean age, 35.2 years) reported retrospectively on within-pair differences in their experiences while growing up. This was the first study of twins to employ the Sibling Inventory of Differential Experience (SIDE; Daniels and Plomin, *Dev. Psychol.* 747–760, 1985), which was developed specifically for studying the within-family environment. The instrument yielded 11 subscales for each individual, reflecting his/her perceptions of the direction and amount of differences between self and cotwin in three areas of "experience": parental treatment, peer-group characteristics, and interactions with each other. Regarding the absolute amount of perceived difference, the twins were generally in moderate agreement with each other on the 11 subscales, regardless of zygosity (median intraclass twin correlation = 0.40 for both MZ and DZ pairs). However, MZ twin pairs reported significantly fewer average differences in their early experiences ($P < 0.05$) than same-sex DZ pairs on every scale, suggesting that genetic influences in the SIDE scales may be more important than previously concluded from the sibling/adoption design. Moreover, to the extent that the SIDE does measure the "environment," this result calls into question the assumption of comparable environmental similarity for both twin types used when estimating heritability from twin designs. On the other hand, the perceived amount of differential experience in these twins bore little or no relationship to actual differences in personality variables, including extraversion, neuroticism, psychoticism, and gender identification, thereby lessening the concern about violation of the critical "equal-environments" assumption in twin studies of personality.

C. S. Bergeman.[3] Genotype–Environment Interaction in Extraversion and Neuroticism: Identical Twins Reared Apart.[4] The primary focus of this study is to identify specific genotype–environment (GE) interactions as they contribute to individual differences in temperament in later life. The best available test of a GE interaction in human analysis is provided by identical twins separated early in life and reared apart. A sample of 99 pairs of identical twins reared apart has been identified in the Swedish Twin Registry, as part of the Swedish Adoption/Twin Study of Aging (SATSA). This analysis explored GE interactions using a

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[4] Supported by NIA Grant AG-04563. SATSA is an ongoing study conducted at the Department of Environmental Hygiene of the Karolinska Institute in Stockholm, Sweden, in collaboration with the Institute for the Study of Human Development at The Pennsylvania State University. Coinvestigators in this study are G. E. McClearn, Lars T. Friberg, John R. Nesselroade, Nancy Pedersen, and Robert Plomin.

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short form of the Eysenck Personality Inventory (EPI) to measure Extraversion and Neuroticism and the Moos' Family Environment Scale (FES) and socioeconomic status (SES) as measures of the rearing environment. Hierarchical multiple regression was used to detect interactions between the temperament and the environmental variables, after the "main effects" of genotype (as estimated from the cotwin's score) and environment were removed. Analyses provided evidence for 6 significant GE interactions (of 24 interactions examined), with the GE interactions between the Extraversion variable and the control-related dimensions of the FES suggesting that environment may have a greater impact on individuals with a genotype to score low on the Extraversion measure.

R. G. Burright, George Schreer, Sharon Doring, and P. J. Donovick.[5] Watching One Paw Clap: Behavioral Laterality in Male and Female Binghamton HET Mice. R. L. Collins selected lines of mice for degree of paw preference; relations among pawedness, gender, structural brain asymmetry, and other behavioral characteristics of these lines have been reported (cf. Lipp, Collins, and Nauta, *Brain Res.* 310:393–396, 1984; Ward, Giguere, and St-Yves, *Behav. Genet.* 16:575–584, 1986). Using Collins' phenotypic test, we obtained paw use to obtain food in Binghamton heterogeneous (HET) mice of both sexes; we then recorded the direction of turning either during the righting reflex or when escaping from a water maze. Adult HET mice (34 males, 32 females) were tested at least once in the Collins' food-retrieval task under modified 24-h (male) or 48-h (female) deprivation schedules. About 65% of the mice showed relatively high degrees of paw preference, but more females than males met the criterion for strong laterality. After reaching for maple-flavored Maypo, high-lateralized mice tended to eat directly from their paws, but less lateralized animals often scratched at the food tube with both paws and then ate the oats from the floor of the test chamber. After return to ad lib. feeding, all mice were given either five righting-reflex trials or five free-choice trials to escape from a trident-shaped water (19°C) maze. Strongly lateralized males tended to turn more consistently in the direction of their paw preference than either the less lateralized "brothers" or the females. Findings are discussed in the context of general issues regarding behavioral laterality, cerebral asymmetry, and gene–environment coaction.

Ch. Capron[6] and M. Duyme.[6] Crossfostering and IQ: Preliminary Results.[7] The adoption method provides a means of dissociating genetic and prenatal factors from postnatal environmental factors. The study presented here used a crossfostering design. Differences in postnatal environments are expressed in terms of socioeconomic categories on the INSEE scale (a French 86-point scale). Four groups were composed: (1) children from lower socioeconomic categories adopted by high-SES parents, (2) children born to low-SES parents adopted by low-SES parents, (3) children born to high-SES parents adopted by low-SES parents, and (4) children born to high-SES parents adopted by high-SES parents.

Results show that Group 1 children have higher IQ scores (14 points higher on the WISC-R) than children in Group 2 but lower scores (14 points) than children in Group 4. Data for Group 3 are currently being analyzed. Preliminary findings for this group suggest that performance in Group 3 is notably higher than in Group 2. These findings do not point toward an interaction effect between the SES of the biological parents and the SES of the foster parents as regards IQ scores (full scale).

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Gregory Carey.[8] Is Extraversion a Unitary Trait?[9] Twin similarity on higher-order personality traits such as extraversion and neuroticism has been extensively reported. However, broad temperament dimensions are composed of a number of lower-order traits, and multivariate studies of the lower-order traits that comprise extraversion and neuroticism are infrequent. Here, analyses are reported for four extraversion subtraits as measured by items from the California Psychological Inventory (CPI) on the National Merit twin sample. The four subtraits are (1) attraction to social events, (2) inhibition in talking to strangers, (3) dislike of public speaking, and (4) leadership. These traits were defined by a content analysis of CPI items originally in the extraversion dimension reported by Loehlin (*Behav. Genet.* 12:417–428, 1982) and verified by principal-component analysis. The results suggest that single genotypic and single environmental factors are not sufficient to account for the covariance among the subtraits.

M. Carlier,[10] P. L. Roubertoux,[10] M. L. Kottler,[11] and H. Degrelle.[11] The Y Chromosome and Aggression in Mice.[12] Results reported by several authors indicate that the Y chromosome may be correlated to differences in attack behavior between certain inbred strains of mice. In a dyadic encounter with an A/J standard opponent, NZB attack this opponent more frequently than CBA/H in the same situation. The reciprocal F_1's differ. Two experiments were conducted to test for a Y-chromosome effect. (1) Reciprocal F_1 males were backcrossed to each parental strain H and N. (2) Two consomic strains were developed: N-YH (7 generations of backcrosses), with N autosomes and H Y chromosome; and H-YN (11 generations of backcrosses), with H autosomes and N Y chromosome. Results show that the presence of the N-Y chromosome is related to an increase in the number of attacks only for subjects bearing between 25 and 50% N autosomes. Plasma testosterone concentration was assayed for subjects from the two parental strains H and N and from the two consomic strains. Males bearing N autosomes have a higher testosterone concentration but the Y chromosome (H vs. N) is not related to between testosterone concentration and number of attacks is positive and significant.

Crista M. Carmichael,[13] D. T. Lykken,[13,14] and A. Tellegen.[13] Social Attitudes and the Trait of Traditionalism in Twins Reared Together and Twins Reared Apart. Data gathered from participants in the Minnesota Twin Registry and the Minnesota Study of Twins Reared Apart are analyzed to assess the relative contributions of genetic and environmental influences to social attitudes and to the personality trait of traditionalism. Twins in both samples were administered an attitudes and opinions questionnaire and the Minnesota Personality Questionnaire (A. Tellegen, *Brief Manual for the Differential Personality Questionnaire*, (1978/1982), as part of a comprehensive personality assessment. Attitude and personality data were collected by mail for Minnesota Twin Registry participants and early participants in the Minnesota Study of Twins Reared Apart. Later reared apart twins completed both questionnaires as they were incorporated into the standard personality assessment procedure.

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The reared-apart sample consists of 49 MZA and 23 DZA twin pairs and 2 sets of MZA triplets. The reared-together sample consists of 484 MZT and 335 DZT twin pairs. Genetic and environmental contributions for each of the 14 attitude items and the Traditionalism scale are estimated using a biometrical model-fitting procedure. Results from the present study are compared with those of previous twin studies of attitudes (N. G. Martin, L. J. Eaves, A. C. Heath, R. Jardine, L. M. Feingold, and H. J. Eysenck, *Proc. Natl. Acad. Sci. USA* 83:4364–4368, 1986).

C. Cohen-Salmon,[15] L. Lhotellier,[15] and J. L. Mogenet.[16] Maternal Effects in Senescent Mice: Preliminary Results.[17] Two groups of female mice, mature (aged 400 days) and senescent (aged 750 days), were reared in nine groups. Three parental strains (DBA/2J, C57BL/6J and BALB/cJ) and their six reciprocal F_1 were used. Neurosensorial functioning, bottle licking, rhythms of activity, exploration, short- and long-term memory, perseveration, and weight were investigated. The preliminary results indicate an unusual number of maternal effects at 400 and at 750 days. An analysis of weight at 400 and 750 days, including, moreover, groups of young mice (60 days), shows an amplification of maternal effect with age. This result may imply that age could amplify or reveal certain effects of the early maternal environment.

Hilary Coon[18] and Gregory Carey.[18] Twins and Musical Ability: An Analysis of If–Then Relationships.[19] Analyses of musical ability data from the Loehlin and Nichols National Merit Scholarship study are presented. Musical ability is indexed by three measures: interest in music, performance, and receiving honors in music. These variables pose a challenge for behavior genetic analysis since they do not conform to the assumptions of traditional linear models. For example, the association between performance and receiving honors forms an "if–then" relationship; one cannot obtain honors without performance. Several methods were employed to deal with these relationships, and the following conclusions appeared regardless of the method used. First, twin correlations were always high, ranging from 0.49 to 0.94 in MZ twins and 0.45 to 0.80 in DZ twins. Second, although there was evidence for heritable variation, the effects of common environment were almost always larger than the effects of heredity. Third, marital assortment was not of sufficient magnitude to account for these common environment effects. This preliminary analysis suggests that in the young adults in this sample, musical ability is influenced more by shared family environment than by shared genes.

J. S. de Belle,[20] A. J. Hilliker,[21] and M. B. Sokolowski.[20] Genetic Localization of the Rover Sitter Larval Foraging Polymorphism in *Drosophila melanogaster*.[22] The heredity of rover/

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sitter, a naturally occurring larval foraging polymorphism in *Drosophila melanogaster* was analyzed using 16 reciprocal crosses. Results indicated that rover/sitter differences are autosomally based and fit a single-gene model of inheritance, with rover completely dominant to sitter (de Belle and Sokolowski, *Heredity*, 59:73–83 1987). Rover/sitter differences are attributable to the second pair of chromosomes in both laboratory (Sokolowski, *Behav. Genet.* 10:291–302, 1980), and naturally derived (Bauer and Sokolowski, *Can. J. Genet. Cytol.* 27:334–340, 1985) strains. Recently the trait has been further localized to the left arm of chromosome 2 (*2L*) by generating rover and sitter compound autosome strains. In the present study we identify the rover/sitter genetic locus. This was accomplished by the irradiating a rover strain and performing two behavioral screens for sitters over several generations. In 11 lines isogenous for chromosome 2, lethality corresponds with transformation of the behavioral phenotype to sitter. One year later five lethal lines still maintain "extreme" sitter phenotypes. Three of these five lines fail to complement. These results suggest that we have identified the genetic locus responsible for differences in the rover/sitter foraging polymorphism. Recombinant mapping of the lethals using dominant second-chromosome markers (*Sp, Bl, and* L^2) has localized rover/sitter to the left of *Sp* on the distal end of chromosome 2*L*. We call this gene *for* (foraging).

Christopher M. de Fiebre[23] and A. C. Collins.[23] Enhancement of Desensitization to Nicotine-Induced Seizures via Nicotine/Ethanol Copretreatment in LS and SS Mice.[24] Nicotine and ethanol are often used simultaneously. In an attempt to ascertain whether common genes influence response to both of these drugs, we have examined the nicotine response and the nicotinic receptors of LS and SS mice. Previously, we have reported that the LS is the more nicotine sensitive of the two lines as measured by a battery of tests, including sensitivity to nicotine-induced seizures (C. M. de Fiebre, L. J. Medhurst, L. L. Miner, and A. C. Collins, *Soc. Neurosci. Abstr.* 12:919, 1986). Studies with inbred mice have indicated that nicotine-induced seizure sensitivity is positively correlated with levels of hippocampal α-bungarotoxin (BTX) binding (L. L. Miner, M. J. Marks, and A. C. Collins, *J. Pharmacol. Exp. Ther.* 239:853–860, 1986). Unlike inbred mice, the more seizure susceptible LS mice do not have greater hippocampal BTX binding than SS mice. Last year we reported that nicotine pretreatment caused a decrease in the nicotine-induced seizure sensitivity of these selected lines (C. M. de Fiebre and A. C. Collins, *Behav. Genet.* 16:615, 1986). Such a decrease in sensitivity, a behavioral desensitization, could be due to desensitization of nicotinic receptors. Here we report that simultaneous pretreatment with nicotine and ethanol enhances the desensitization produced by nicotine alone. This is consistent with findings in *Torpedo* that alcohols stabilize nicotinic receptors in a desensitized state (A. P. Young and D. S. Sigman, *Mol. Pharmacol.* 20:498–510, 1981).

Lisabeth Fisher DiLalla[25] and Irving I. Gottesman.[25] Forecasting Delinquency and Criminality: Resurrection of the Hathaway–Monachesi Data Set. Characteristics were identified which were particular to delinquents who continued on as criminals as adults ("continuous antisocials") and which differentiated them from those delinquents who ceased such activity after adolescence ("garden variety") and from those adults who were criminal but were not delinquent as adolescents ("late bloomers"). Fifteen thousand three hundred ninth graders were originally assessed via the MMPI, teacher ratings, and school records (S. R. Hathaway and E. D. Monachesi, *Analyzing and Predicting Juvenile Delinquency with the MMPI*, University of Minnesota Press, Minneapolis, 1953). Family data on criminality and drinking behavior were examined for a subset of 75 boys with more than one delinquency offense and 75 controls with no delinquency offenses. The best-fitting path model showed a signif-

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icant path from father's criminality (0.33) and drinking (0.32) to subject's delinquency and from mother's criminality (0.36) to subject's adult criminality. The low base rate of criminality for women suggests that women who are criminal have more predisposing factors. Given that delinquency is a "stage" common to adolescence, only those delinquents with a genetic predisposition toward antisocial behavior may continue as criminal adults.

L. J. Eaves[26] and N. G. Martin.[27] Religion and Education as Cultural Mediators of Values: An Empirical Test.[28] Conflicting models for the role of biological and cultural inheritance in the transmission of social attitudes are reexamined in a large twin study of educational attainment, social attitudes, religious affiliation, and church attendance. We show that previous claims that family resemblance in social attitudes is entirely cultural are unjustified. However, we cannot substantiate the conflicting claim that it is purely genetic. A large part of the variance ascribed to the genetic consequences of assortative mating in a previous study is shown to be due to the similarity between twins in their religious beliefs and practices. Since these variables are shown to be almost entirely cultural, we have no reason to doubt that cultural inheritance plays at least as great a role as biological inheritance in the creation of family resemblance in attitudes.

Frank R. George,[29] L. J. Porrino,[29] and S. R. Goldberg.[29] Differences in Locomotor Activation and Lethality in Response to Acute Administration of Cocaine Across Several Rat Genotypes. The pharmacology of cocaine has been widely studied, but little is known about the contribution of genotype in determining response to this drug. The present study was conducted to establish a data base of cocaine-related behavior and to use genetic correlations in examining the biological substrates which mediate responses to cocaine. The following rat stocks were used: NBR/NIH, ACI/HSD, F344/CR1BR, LEW/CR1BR, and S-D/CR1BR. Severalfold differences in the *efficacy* of cocaine in producing locomotor stimulation were found, with NBR rats displaying the greatest maximum response and F344 rats showing the least locomotor response. Large *potency* differences were also found, with NBR rats being the most sensitive, while rats from the LEW and F344 strains were the least sensitive. Large differences in lethality response to cocaine were also seen; 50% of NBR rats tested at 40 mg/kg and 100% of NBR rats tested at 60 mg/kg died shortly after injection, while no LEW or S-D rats died even at 60 mg/kg. These data should aid researchers interested in exploring the mechanisms of behavioral and physiological responses to cocaine.

David M. Gilliam[30] and E. P. Riley.[30] Differential Effects of Prenatal Alcohol Exposure in Long-Sleep and Short-Sleep Mice: Offspring Mortality and Maze Performance.[31] Long-Sleep (LS) and Short-Sleep (SS) mice provide a tool to investigate how genetic differences in alcohol sensitivity influence susceptibility to prenatal alcohol effects. Pregnant LS and SS mice were intubated on days 7 through 18 of pregnancy (PD 7 to 18) at 1200 and 1800 h with either 4.5 g/kg ethanol (E) or an isocaloric amount of sucrose (S). An untreated control (C) group was maintained for each line. Maternal weight gain from PD 7 to PD 18 was similar

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across groups ($\bar{X}$= 62%). The number of live offspring was greater for LS than SS dams ($\bar{X}$'s = 8.6 and 7.4, respectively) but was unaffected by prenatal history. Birth weights were lower for E than S pups ($\bar{X}$'s = 1.17 and 1.31 g, respectively) and lower for S than C pups ($\bar{X}$ = 1.35 g). At 20 days of age, offspring mortality was greatest for LS E pups (59%) compared to all other groups (≤17%). At 22 days of age, offspring were trained to remain on a submerged platform. On 2 subsequent days, animals were tested in a spatial water maze. During training LS E offspring required more trials to remain on the platform compared to all other groups. During maze learning, latencies decreased within each test session. Average latency across days for LS E offspring was longer than for controls, while average latency did not differ among SS groups. These results suggest genetic differences in alcohol sensitivity influence offspring mortality and maze performance following prenatal alcohol exposure.

Sheila B. Gilligan[32] and C. Robert Cloninger.[33] Phenotypic Variation in Measures of Harm Avoidance, Novelty Seeking, and Reward Dependence.[34] Cloninger (*Psychiat. Dev.* 3:167–226, 1986) has postulated three independently determined dimensions of personality, each associated with a specific monoamine neuromodulator influencing stimulus–response patterns. Harm avoidance (HA), modulated by serotonin, involves intense response to aversive stimuli and passive avoidance of punishment/nonreward. Novelty seeking (NS), influenced by dopamine, relates to exploratory activity and a positive response to novel stimuli. Reward dependence (RD), associated with norepinephrine activity, leads to resistance to extinction of behaviors that relieve punishment or are rewarded. Phenotypic variation of HA, NS, and RD was evaluated in 503 pedigrees, ascertained through alcoholic, sociopathic, and control subjects. Multiple regression of psychometric test scores for a separate, student population gave predictors, accounting for 70, 56, and 26% of the variance of HA, NS, and RD, respectively. In the pedigrees, HA, NS, and RD were uncorrelated (r_{HA-NS} = 0.09, r_{HA-RD} = 0.00, r_{NS-RD} = 0.00). Means for HA and RD in females (6.45, 0.14) were higher than those in males (4.65, −0.07), whereas NS was greater in males (9.18 vs. 8.58). Correlations in first-degree relatives varied for like-sex vs. unlike-sex pairs; no significant mate correlations were found. Measures of HA, NS, and RD were good predictors of heterogeneous forms of alcoholism in families of male alcoholics. Loss of control over drinking was associated with ↑HA, ↓NS, ↑RD, while ↓HA, ↑NS, ↓RD described the inability to abstain from ethanol; moreover, similar personality patterns were found in relatives, regardless of sex.

Benson E. Ginsburg[35] and Bonnie Frank Carter.[36] The Seville Statement on Violence: An International and Interdisciplinary Response to the Question of Biological Determinism.[37] The Seville Statement addresses the question of whether we are a genetically violent species. In our view, "violence" must be differentiated from "aggression," and biogenetic sources

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of variation from psychogenetic sources. Laboratory selection for increased aggression has been effective in many species, demonstrating that genetic variation exists for such behavior and that most social species have been selected to be only moderately agonistic. Moreover, different genotypes react differently to similar environmental conditions. Family, twin, and adoption studies implicate genetic factors in instances of self-directed aggression. Low CSF levels of serotonin and dopamine metabolites and high response levels of cortisol to dexamethasone suppression are associated with some types of suicidal and homicidal behaviors. Biology predisposes species and individuals to variability and sets limits to their potential to interact with psychosocial factors. The Seville Statement attempts to summarize and disseminate the most accurate biological information which provides a basis for optimism about the future of humankind.

Charles R. Goodlett,[38] D. M. Gilliam,[39] and J. R. West.[38] Differential Susceptibility of Long-Sleep (LS) and Short-Sleep (SS) Mice to Brain Weight Reduction Following Prenatal Alcohol Exposure.[40] The LS and SS lines of mice, selectively bred for differences in ethanol-induced hypnosis, were compared for differences in susceptibility to neuromorphological effects following prenatal alcohol exposure. Breeding pairs were obtained from the University of Colorado, and the matings, experimental treatments, and maintenance of offspring until adulthood were performed at SUNY—Albany. Dams from the two lines were intubated from gestational day 7 to day 18 either with two daily doses of 4.5 g/kg of alcohol (separated by 6 h each day) or with an isocaloric amount of sucrose. Other dams served as nonintubated controls. Separate groups of dams showed that there were no significant line differences across days in blood alcohol concentrations, and the average BAC was 345 mg/dl. The adult offspring were weighed, then perfused with sodium sulfide followed by 1% paraformaldehyde/1.25% glutaraldehyde for later evaluations of hippocampal morphology. Brains were carefully extracted and weights were obtained. In the LS line, prenatal alcohol treatment significantly reduced both the brain weight and the body weight relative to the two control groups. However, the brain weight of the SS line was unaffected by the alcohol treatment relative to the untreated control group, even though body weights were reduced. Interestingly, the SS group given sucrose had the lowest average brain weight obtained. Thus, genetic differences in alcohol sensitivity influence the susceptibility to prenatal alcohol effects.

Susanne A. Graf[41] and Marla B. Sokolowski.[41] The Rover/Sitter *Drosophila* Foraging Polymorphism as a Function of Larval Development and Food Patch Quality.[42] This study is the first in a series addressing the effects of larval development and food availability on the maintenance of the rover/sitter foraging polymorphism. Prior to this study larval foraging behavior had been characterized only in third-instar larvae on a highly concentrated homogeneous food source. Under these conditions rovers had significantly longer foraging trails than sitters. We tested foraging behavior on each of 4 days during the larval period (age), and in patches of different food quality (substrate), to determine if these factors influence the expression of the behavior. We found that (1) rovers consistently travel farther than sitters regardless of age or substrate quality, (2) the rover/sitter phenotype begins to express itself early in larval development, (3) the development of locomotor behavior within each morph shows a significant increase occurring in sitters from 72 to 96 h posthatch and in rovers from 48 to 72 h as well as from 72 to 96 h posthatch, and (4) larvae of the two morphs do not differ in developmental time or growth rate. We conclude that rover/sitter differences are expressed in environments of different food quality and throughout most of

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larval development. These results indicate that potential for uncovering selection pressures at different points in the life history that may act differentially on the two morphs in natural populations.

Jean-Marie Guastavino,[43] Glyn Goodall,[43] and Albert Ly.[43] Can Behavioral Strategies Depend upon a Single Mutant Gene in Mice? Most mice mutations are detected on the basis of anatomical or gross behavioral abnormalities. It seems reasonable to suppose that such mutations may also affect less visible aspects of behaviors as in *Drosophila* mutants. A large number of behaviors have already been investigated in staggerer mutant mice, and here we address two new issues concerning this mutant's behavioral strategies. When placed in a low temperature, young staggerers lose body temperature faster than controls. The difference is less obvious for adults. Behavioral measures reveal that the equivalent survival is obtained through the use of different strategies. Normals seem primarily to depend upon thermogenesis by activity, whereas staggerers rely on huddling in a confined location. These strategies, while both effective, are based on opposing mechanisms. The second illustration involves learning to swim to an invisible submerged platform. In this learning task both groups are capable of improving their performance but do so again using two different strategies. The normals reduce the distance they swim, implying that they learn the location of the platform. Inversely, the staggerers do not reduce the distance they swim, but because they swim progressively faster, they attain the platform as quickly as normals. These results incite us to analyze the behavior of mutant mice in greater detail, as done for *Drosophila*, in order to uncover the complex effects of single genes.

Ruth Guttman[44] and Benson E. Ginsburg.[45] The Pharmacogenetics of Agonistic Behavior in Male Mice.[46] *d*-Amphetamine has been shown to have profound behavioral effects that vary with the genotype. In the present study, the effects of *dl*-amphetamine on the agonistic behaviors of male BALB and C57BL/6 mice and their reciprocal F_1 progeny were assessed. Differences between the strains were dose dependent. BALB's amassed higher aggression scores at 5.0 mg/kg i.p. than at 2.5 mg, where C57's peaked, while the F_1 hybrids showed identical responses at both doses, resembling the BALB's at the lower dose and exhibiting intermediacy at the higher dose. "Chase" and "wrestle" were identical to the C57's in control F_1's, whereas "attack" and "tail rattle" showed intermediacy. These data are consistent with known differences in dopaminergic innervations in these strains, and the effects of amphetamine considered as a dopamine agonist fit the neurochemical and behavioral data.

Andrew C. Heath.[47] Marital Concordance for Alcohol Consumption: Contributions of Spousal Selection and Marital Interaction.[48] Estimates of the marital correlation for drinking habits in the U.S. population are substantial, ranging from 0.5 to 0.7 (e.g., D. Cahalan, I. H. Cisin, and H. M. Crossley, *American Drinking Practices*, Rutgers Center of Alcohol Studies, New

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Brunswick, N.J., 1969). We cannot infer from such marital correlations whether spousal resemblance results from assortative mating or from social interaction between spouses. In the Virginia Twin Register Alcohol Survey (VATRAS), we are obtaining self-report and rating data on alcohol use by adult twin pairs and their spouses. Different mechanisms of assortative mating and spousal interaction lead to distinctive patterns of correlations between twin pairs and their spouses (A. C. Heath and L. J. Eaves, *Behav. Genet.* 15:15–30, 1984; A. C. Heath, *Acta Genet. Med. Gemellol.*, in press, 1987). Under spousal interaction, for example, marital correlations will be much higher, relative to correlations between twin and cotwin's spouse and between the spouses of twin pairs, than would be predicted under most models of mate selection. Analyses, combining rating and self-rating data, suggest that spousal interaction is a relatively minor determinant of marital resemblance for drinking habits. For other variables, notably political affiliation, marital interaction has more marked effects.

Martha M. Hotz[49] and Fred W. Turek.[49] Inbred Strain Analysis of Circadian Rhythms in the Golden Hamster. One of the species most studied for both the formal properties and the physiology of circadian (i.e., about 24-h) rhythms in mammals is the golden hamster (*Mesocricetus auratus*). The rhythm of wheel-running activity has often been used in this species, as it is very precise and easily monitored. Although a certain degree of individual variability has been noted, very little is presently known about the genetic basis (if any) of these differences. To address this question, a number of rhythm parameters were compared in five different inbred strains (MHA, PD4, LHC, CB, and LSH) and a common outbred stock [LAK:LVG(SYR)] under various lighting conditions. Significant strain differences were found in the time of activity onset relative to the light–dark cycle (the primary time cue) under both long (14 h light/day) and short (6 h light/day) days. A strong genetic correlation was found in onset times in long and short days, with MHA, LHC, and PD4 representing "early" and LSH and CB representing "late" strains. Significant strain differences were also found in the free-running (i.e., without time cues) period of the activity rhythm both in a constant light environment and when animals were blind. Strain differences were also observed in constant light in the incidence of "splitting" of the activity rhythm into two separate bouts. Early strains tended to have shorter free-running periods and show less splitting than late strains. These results suggest that further investigation of these strains may prove useful in determining physiological correlates underlying their circadian differences.

Nina J. Jackson,[50] G. A. Harshfield,[50] Q. Chong-Guang,[50] J. P. Henry,[50] T. J. Opgenorth,[50] and C. E. Grim.[50] The Effects of Psychosocial Stress on Birth Outcome. The effects of psychosocial stress on birth outcome were observed in CBA/USC, a behaviorally active yet not agonistic strain of mice. Two levels of stress were induced by two different psychosocial environments. The Henry–Stephens model induces a high level of stress by preventing the establishment of a dominance hierarchy. The open-field model induces an intermediate level of stress but does allow for the establishment of social order. The control group consisted of 10 sets of breeding pairs (one male and two females). In the Henry–Stephens environment, 10 males and 10 females were observed for 7 weeks. All of the females in the Henry–Stephens model became pregnant but showed no signs of the pregnancies reaching full gestation. In the open-field model, eight females and four males were observed, of which all females became pregnant. Forty-six pups were born; 36 survived 24 h, 10 of which survived 48 h, with only 1 surviving beyond 72 h. The control mice yielded 120 pups, with one one death.

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These data indicate that birth outcome is differentially affected by differing levels of psychosocial stress. In our current project the males are removed following female impregnation to determine if females are able to carry the pregnancies to full term and rear the pups without disturbance.

Ronald C. Johnson,[51] Anwar R. Abdel-Rahim,[52] and Craig T. Nagoshi.[53] Egyptian Spouse Resemblances in Measures of Cognition and Personality: Comparisons with Korean and American Data. Fifty-seven, Egyptian families were tested on measures of cognition and of personality. Spouse, parent–child, and sibling correlations were very high, as compared with Hawaii and Colorado data but were about the same magnitude as family correlations obtained in an earlier study conducted in Korea. Various explanations for the differences in the United States vs. Egypt and Korea were considered. It seems probable that the differences result from differing degrees of spouse resemblance in arranged vs. love marriages.

B. C. Jones,[54] J. Reyes,[55] R. Vega,[56] E. Reyes,[57] and J. M. Masserano.[58] Differential Effect of Infantile Handling on Tyrosine Hydroxylase in Three Inbred Murine Strains. Previous work has shown the effects of handling mice in infancy to differ in two strains, C57B1/10J and BALB/cJ. Adult behaviors which evince this strain-handling interaction include avoidance (B. C. Jones, L. E. Kauffman, M. A. Langston, and E. Reyes, *Behav. Genet.* 13:539, 1983) and alcohol selection (B. C. Jones, R. N. Goldstine, M. Kegel, M. Gurley, and E. Reyes, *Alcohol* 2:327, 1985). In the present study, 60 female mice from three strains, C57B1/10J, BALB/cJ, and DBA/2J, were assigned to handling for the first 20 days of life or control conditions. At 60–80 days of age, they were sacrificed, and their brains removed and dissected into frontal cortex, corpus striatum, and hypothalamus. Total tyrosine hydroxylase (TH) was determined by the coupled decarboxylase method (J. C. Waymire, R. Bjur, and N. Weiner, *Anal. Biochem.* 43:588, 1971). The results revealed strain-related differences ($P < 0.001$) among means in hypothalamic TH, with BALB > C57 > DBA. The strain × handling interaction approached significance ($P = 0.07$). In BALB's, compared to controls, handling produced a 17% increase in hypothalamic TH. In C57's and DBA's, handling reduced TH by 17 and 11%, respectively. These preliminary results present neurochemical evidence for genetically based differential sensitivity to early environments.

Jaakko Kaprio,[59] Markku Koskenvuo,[59] Kauko Heikkila,[59] H. Langinvanio,[59] Seppo Sarna,[50] and Richard J. Rose.[60] Maximum-Likelihood Estimation of Genetic and Environmental Parameters in Behavioral Data from a Finnish Twin-Family Cohort.[61] Extraversion and neu-

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[61] Research with the Finnish Twin Cohort has been supported by the Council for Tobacco Research, USA-Inc. R.J.R. was supported by a Senior Research Fellowship (TW 01019) from the John E. Fogarty International Center and by NIAAA Grant AA-06232.

roticism scores and self-report data on frequency, quantity, and density of social drinking were obtained from adult offspring of MZ and DZ twin parents and age-matched MZ and DZ twin pairs during questionnaire surveys of the population-based Finnish twin cohort. The data set includes some 2800 adults related to one another as full or half-siblings, first cousins, or MZ or DZ cotwins. Rat data were age banded separately by sex and z score transformed. Maximum-likelihood estimates of the genetic, environmental, and maternal sources of variance were made from the mean squares obtained from nested ANOVAs of these age/sex-standardized data using the Minuit optimization routines.

Kenneth S. Kendler.[62] The Sporadic vs. Familial Classification Given Etiologic Heterogeneity. Environmental factors are etiologically important in many non-Mendelian familial disorders in man. Because such disorders often occur as "sporadic" cases (i.e., an individual with no affected relatives), it is tempting to assume that such cases represent an "environmental" form of the disorder. This paper presents a thorough evaluation of the sensitivity, specificity, and positive and negative predictive power (PPV and NPV) of this "sporadic vs. familial classification." The model assumes etiologic heterogeneity, with a subpopulation of cases due to a "major" environmental event acting independent of genotype and the remaining cases resulting from a generalized SML. Sibship size is modeled by a truncated negative binomial distribution. Schizophrenia and major depression are used as examples. For rare disorders such as schizophrenia this classification has a high sensitivity and NPV but a low specificity and PPV. As the disorder becomes more common, as with major depression, sensitivity and NPV fall while specificity and PPV rise. The power of the method increases substantially with increasing sibship size up to four or five, but further increases in power are minimal. MZ twins add considerable power to the method. In contrast, aunts and uncles add little, if anything. Both a correlational (phi) and an agreement-based (kappa) statistic indicate that, in most realistic circumstances, the relationship between etiology and family history is modest.

Sjeng Kerbusch,[63] Toon Vendrik,[63] and Jo Vossen.[63] Attention in Appetitively Motivated Discrimination Learning in Rats: Preliminary Results. A Skinner-box version of the original Krechevski hypothesis box was developed in which a rat started discrete trials by pressing a bar opposite to the intelligence panel. The rat had to choose between two (other) levers in order to receive food reward. Spatial stimuli, lights, and sounds served as cues. The order of lights and sounds in each set of four consecutive trials made it possible to determine to which stimulus aspect animals reacted. For each set of five trials win/stay–lose/shift strategies could be detected. After pretraining animals of four inbred strains (WAG/Rij, A*C/Kun, BN/Rij, and G/CPB) and six F_1-hybrid genotypes were tested in a solvable discrimination task with light as the discriminatory stimulus. Number of trials needed to meet a strong criterion (14 consecutive choices correct, or 17 of 18, 20 of 22, or 22 of 25 trials), number of trials spent on each of 10 different response strategies, and mean and variability of time spent on each response strategy were analyzed. Eighty-three to 95% of the rats' choices could be assigned to a systematic response strategy; genotypical differences were found, hybrids not deviating from midparental values. No interstrain variation was found for percentages of trials the rat followed irrelevant strategies such as tone, place alternation, and perseveration; no systematic variation was found in the length of trial blocks in which rats would stick to the same strategy. Strains did differ with respect to the number of trials to meet criterion, the slowest strain needing 350 trials, and the fastest 40 trials. No directional dominance for fast learning was found, as hybrids did not deviate from midparental values.

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Genotypical variation existed for the number of trials as well as the number of blocks rats employed the correct strategy. Strains learning within fewer trials needed fewer opportunities to learn in terms of times as well as number of trials they responded to the right rule. Again, no hybrid vigor was found. The hypothesis is put forward that appetitively motivated learning shows a genetic architecture different from that of aversively motivated learning. In learning to avoid noxious stimuli, hybrid superiority is found for all aspects of learning. In appetitive learning no directional dominance is found and intermediate inheritance seems to be the rule.

K. A. Kerns,[64] A. D. Fernando,[64] M. Rosenblatt,[64] and S. A. Berenbaum.[64] Sex Differences in Spatial Ability in Children.[65] There is considerable evidence that sex differences in spatial ability exist in adults, with males outperforming females at every age after puberty. It is difficult, however, to find sex differences in children younger than 13. This is due, in part, to the lack of adequate measures of spatial ability for use with children. We report the use of spatial tests for children that are similar to those that have been used with adults and may be measuring ability comparable to adult spatial ability. Five tests of mental rotation, spatial visualization, and left–right orientation were given to 123 children between 9 and 13 years of age. The first sample included 39 males and 42 females (mean age, 10.6 years), and the second sample, 21 males and 21 females (mean age, 11.7 years). Significant sex differences were found on three tests on both samples, with the magnitude of the difference ranging from 0.4 to 1.0 standard deviation. These data indicate that sex differences in spatial ability can be found if appropriate tests are used. We are now examining (a) the relationship between these spatial tests and early childhood activities and (b) the similarity between children's performance on these tests and the spatial ability of their parents.

Jean Michel Lassalle,[66] Barbara Bulman-Fleming,[67] and Douglas Wahlsten.[67] Variation of Spatial Knowledge in *Mus musculus:* Maternal and Genetic Effects.[68] Mice from two inbred strains, BALB/c j wah and C57BL/6 j wah, and the two reciprocal F_1's were assessed for sensitivity to familiar-objects rearrangement in the open field. Ovarian grafting and cross-fostering methods were used to study the effects of both pre- and postnatal maternal factors. All the animals were from grafted ovaries and had been fostered to a normal female at birth. The experiment was designed so that each genotype experienced the four combinations between the inbred and the hybrid pre- andpostnatal maternal environment. Stepwise correlation analysis indicated that variables such as litter size at birth, group size between weaning and experiments, and body weight at the age of the measure did not influence the performance. Results were analyzed using unbalanced hierarchical ANOVA designs. They show a significant genotype effect attributable mainly to BALB/c mice, which are less active, are more neophobic, and habituate more slowly to the objects. Spatial rearrangement of the objects in the experimental group results in a significant increase in exploratory activity when compared to the control group, indicating spatial memory. When applied at the genotypic level, the hierarchical ANOVA shows that all genotypes but BALB/c learn and memorize the spatial arrangement of the objects in the open field. There is also a significant

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postnatal maternal effect, inducing both better habituation and greater renewal of exploration.

R. J. Marley,[69] R. K. Freund,[69] and J. M. Wehner.[69] Anesthetic, Hypothermic, and Anticonvulsant Responses to Flurazepam in LS and SS Mice.[70] LS and SS mice, in addition to differing in ethanol sensitivity, also differ in response to agents acting on the GABAergic system. To characterize further differences between these two lines in response to GABAergic agents, we have conducted a series of experiments to measure the sensitivity of LS and SS mice to the anesthetic, hypothermic, and anticonvulsant effects of the benzodiazepine, flurazepam (FLU). The anesthetic potency was measured as the duration of the loss of righting response following the administration of FLU. FLU (75–300 mg/kg) induced a dose-dependent loss of righting response in both lines. The LS line displayed a twofold greater sensitivity to the anesthetic effects of FLU than did the SS line. A dose-dependent decrease in body temperature was also observed following the administration of FLU (25–150 mg/kg), but the two lines did not differ on this measure. When we measured the anticonvulsant effects of FLU (1–6 mg/kg) against seizures induced by 3-mercaptopropionic acid, an inhibitor of GABA synthesis, the SS mice displayed a threefold greater sensitivity to the anticonvulsant effects of FLU. We have also observed similar responses with the benzodiazepine, diazepam. These studies demonstrate that LS and SS mice differ in response to benzodiazepines, but the nature of these differences is dependent on the type of response measured and/or the dose of drug. The lack of a consistent pattern of differences implies that the observed differences in benzodiazepine sensitivity are not due to pharmacokinetic differences. Additionally, the mechanisms underlying the various responses to benzodiazepines seem to be mediated by different genetic factors.

Barbara J. Martin[71] and R. K. Freund.[71] The Effect of Genotype on Nicotine-Induced Increases in Plasma Corticosterone.[72] The administration of nicotine to rodents induces dose-related increases in levels of plasma corticosterone (CCS). In the absence of pharmacological intervention, an increase in glucocorticoid synthesis is generally observed as a homeostatic response to stress. Despite the prediction that nicotine use would aggravate the stress response, many smokers report a "calming effect" of nicotine. To understand the mechanisms explaining this paradox we investigated the effects of genotype and desensitization on plasma CCS. Initially, time courses were established for levels of CCS in C3H, C57/BL, DBA, and A/J inbred strains after a 2 mg/kg i.p. injection of nicotine. For all populations tested, nicotine-induced CCS levels were significantly elevated as compared to saline controls. Peak CCS levels (measured at 25–30 min) increased across nicotine doses of 0.5–2.0 mg/kg with the following rank order: A > C57 = DBA > C3H. To test the hypothesis that tolerance to the effects of nicotine could result in an attenuated stress response, acute desensitization studies were conducted using C57/BL, C3H, and DBA inbreds. There appears to be a strain-selective effect of nicotine or saline preinjection on the nicotine challenge-induced release of CCS. This suggests that genotype mediates the sensitization response and may explain the existence of "relaxation" and "stress" smokers.

N. G. Martin.[73] Evolutionary Inferences from Twin Studies. The mere demonstration of genetic variation tells us nothing about the evolutionary processes shaping a trait. However,

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Mather's concept of "genetic architecture" provides a heuristic for making inferences about selection. In particular, evidence of dominant or epistatic variance and its direction may hint at the selection history. The twin design is a poor one for detecting genetical nonadditivity, but with the very large numbers now available from some registries, certain inferences are possible. On the other hand, twins are an ideal way to detect certain types of genotype × environment interaction. If scales of measurement can be trusted, one can infer which genotypes are more sensitive to the environment and which less so. The genetic architecture of such environmental sensitivity *per se* may indicate whether there has been selection to buffer the genotype against environmental insults or, conversely, to allow the individual to exploit favorable environmental circumstances when they are present. Eaves has suggested that traits exhibiting genotype–environment covariation may have been subject to kin selection. Twins in conjunction with singletons are ideally suited to detecting sibling effects of competition and cooperation and several examples are now available. In conjunction with spouse data twins allow the detection of assortative mating and exploration of the effects of such mating on linkage disequilibrium, and hence covariation, between fitness traits.

S. C. Maxson.[74] The Evolution of the Mammalian Y Chromosome.[75] It has been proposed that the mammalian X and Y chromosomes originated from a common ancestor. Meiotic pairing of the X and Y chromosomes has been taken as evidence of this chromosomal homology and has been considered as consistent with DNA sequence homology. Homologies have been found for DNA sequences of the X and Y chromosomes in mice (Nallaseth and Dewey, *Nucleic Acid Res.* 14:5295–5307, 1986) and in humans (Bishop *et al.*, *J. Mol. Biol.* 178:403–417, 1984). Some, but not all, of these DNA homologies are in the meiotic pairing region of the human and X and Y chromosomes (Simmler *et al.*, *Nature* 317:692–697, 1985). These DNA homologies in the short arms of the human X and Y chromosomes may be conserved sequences. Other homologies are found between the DNA sequences on the short or long arms of the Y chromosome and the long arm of the X chromosome. At least three of these are the result of X–Y transpositions in primate evolution (Goodfellow *et al.*, *J. Med Gent.* 22:329–344, 1985). Similar chromosomal transfers have occurred in rodent evolution. A retroviral sequences appeared on the Y chromosome of aboriginal and commensal mice about 1 to 3 million years ago (Phillips *et al.*, *Nature* 297:241–243, 1982). This may have been an autosomal or X chromosomal to Y chromosomal transposition. Also, about 4 to 8 million years ago three families of repeat sequences appeared on the Y chromosome of species of the subgenus *Mus*. At least one of these may be an X–Y transposition. Taken together these findings suggest that although some of the DNA sequences and genes of the mammalian Y chromosome may be highly conserved, most of the the DNA sequences of the Y chromosome in each mammalian lineage have a relatively recent origin. This conclusion has implications for the findings of developmental and behavioral effects of the mouse Y chromosome.

Joanne M. Meyer.[76] Actul Versus Perceived Weight: Bias Effects in the Reports of Twins and their Parents.[77] Questionnaire responses regarding body weight and perceived body size (indicated by nine silhouettes) were obtained from twins (377 MZ and 821 DZ pairs, ages 20 to 56) and their parents (813 mothers and 554 fathers). In addition, the twins reported

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the body sizes of their cotwins, parents, spouses, and cotwins' spouses, while the parents reported the size of their spouses and twin offspring. From this, we considered (1) the reliability of body silhouettes as weight indices, (2) the magnitude of biases in the perception of family members, (3) the genetic basis of these biases, and (4) the effect of bias on the detection of family similarities. Significant differences over age (twins > parents) and sex (females > males) were found for the reliability of silhouette indices. Generational effects were also apparent in the perception of relatives' body sizes—twins were the best raters of their cotwins, and wives were the best raters of their husbands. A genetic basis for bias was seen in the perception of mothers by male twins: the correlation between MZ males was 0.86, and that between DZ males, 0.67. Finally, biases in twins' reports of relatives resulted in the detection of greater maternal and assortative mating effects than were found from self-ratings and actual weight data. Heritability estimates from self-ratings were significantly lower than those derived from cotwin ratings and weight data. We emphasize the limitation of interpretations based on family ratings and suggest path analytic methods to model biases.

Daniel P. Moloney[78] and Thomas J. Bouchard, Jr.[78] Do Individual and Familial Background Characteristics Explain Variance in IQ, Well-Being, and Job Satisfaction? An Adoption Study of Twins Reared Apart. An attempt to account for the variance of several outcome life measures of mental health (e.g., well-being, job satisfaction, and a full-scale score on the General Behavior Inventory), as well as IQ, was conducted via regression for a sample of 49 reared-apart MZ twin pairs, 2 reared-apart MZ triplet sets, and 23 reared-apart DZ twin pairs. The study of individuals reared by genetically unrelated parents allows the estimate of environmental influences unconfounded by hereditary influences. Predictor variables were grouped into two blocks. The first group contained background characteristics of the adoptive family home environment similar to "family background" (S. Scarr and R. Weinberg, *Am. Sociol. Rev.* 43:674–692, 1978) and was based upon a life-history interview and selected items from the Minnesota Briggs Life History Form. The second group contained life-history characteristics of the individual and was derived from both life-stress and life-history interviews (e.g., number of marriages, occupational level, etc.). A parallel analysis included spouses of reared-apart twins, raised by their own biological families.

Mary R. Moster,[79] P. W. Fox,[79] and R. Little.[79] Genetic Contributions to Perceptual Motor Performance. This study investigates the contribution of genetic factors to individual differences in a perceptual motor skill. Prior studies in this area (Q. McNemar, *J. Genet. Psychol.* 42:70–97, 1933; D. Q. Marisi, *Acta Genet. Med. Gemellol.* 26:197–204, 1977) have used MZ and DZ twin pairs who shared a common rearing environment. The present study, in contrast, is part of a comprehensive assessment of MZ and DZ twins and triplets reared apart from birth. Fifty MZA twin pairs and 22 DZA twin pairs practiced a pursuit rotor task for 50 trials under a 20 s/10 s work–rest schedule, over two practice sessions. Time-on-target measures from successive trials were blocked in groups of five to obtain reliable measures of performance at various stages of practice. A preliminary analysis of 53 pairs, using the first five and last five trials, showed intraclass correlations of 0.56 and 0.68 for MZA twin pairs and −0.01 and 0.61 for DZA twin pairs. Intraclass correlations for all 50 trials were 0.71 for MZA twin pairs and 0.25 for DZA twin pairs. The data suggest decreasing genetic influence with practice on the pursuit rotor task.

Craig T. Nagoshi[80] and R. C. Johnson.[81] Between- vs. Within-Family Factor Analyses of Cognitive Abilities.[82] Confirmatory LISREL factor analyses of the 15 cognitive abilities tests

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from the Hawaii Family Study of Cognition were conducted on between-pair (BP) means and within-pair (WP) differences for 370 AEA (Americans of European ancestry) and 116 AJA (Americans of Japanese ancestry) sibling pairs. Although difference chi-square significance tests indicated that the between-pair factor structures were significantly different from the within-pair structures for both AEA and AJA siblings, congruence coefficients for the estimated loadings on the four specific cognitive abilities factors and on the second-order general intelligence factor indicated that the BP and WP structures were very similar for the two groups. The similarity of the BP and WP structures suggests that the genetic and environmental influences underlying cognitive abilities are "intrinsic" in nature, i.e., not just due to between-family differences in culture, status, values, and fortuitous cross-assortative mating.

Donald J. Nash[83] and Robert S. Ackley.[84] Effects of the Microphthalmic White Gene on Audiogenic Seizure Susceptibility in Mice. Audiogenic seizure susceptibility in mice has provided a useful model for the study of human epilepsies. The microphthalmic white gene (Mi^{wh}) in mice produces a number of abnormalities including severe inner-ear defects and extreme eye anomalies including microphthalmia and cataracts. This study examined effects of the gene on audiogenic seizure susceptibility. A congenic inbred strain provided mice which were identical in genetic background except for single-gene substitutions at the microphthalmic locus. The three genotypes tested were $Mi^{wh}/Mi^{wh}/Mi^{wh}+$, and $+/+$. Mice were exposed to the sound stimulus once for a 1-min period at ages ranging from preweaning stages to early adulthood. All three genotypes demonstrated age-related changes in seizure susceptibility. In addition, striking differences were noted in the frequencies of seizures among the three genotypes. In general, the heterozygotes were more susceptible than the homozygous Mi^{wh}/Mi^{wh}. Preliminary studies involving measurements of auditory evoked potentials indicate that mice bearing either one or two mutant genes are severely hearing impaired.

M. C. Neale.[85] Evidence for Cultural Transmission and Assortative Mating for a Measure of Conservatism in a Sample of Twins and Their Parents.[86] An adaptation of a conservatism scale was completed by a sample of twins and their parents on the population-based Virginia Twin Register. Unweighted least-squares factor analysis revealed a high degree of factor structure between the twin and the parent of twin subgroups. The first factor loads largely on items concerning conservative or liberal issues and accounts for approximately 41% of the variance. Age-corrected variance–covariance matrices were calculated for three types of pedigree: twins with both parents ($N = 385$), twins with their mother ($N = 257$), and twins without parent data ($N = 1161$). Each pedigree type was divided into five groups according to the sex and zygosity of the twins. We discriminate between scalar sex differences in the strength of the effect of genetic or environmental factors and nonscalar differences in which different factors are operating in the two sexes. A model of sex-limited genetic and cultural transmission in the presence of assortative mating was developed and fitted to the data. Results indicate that variation in conservatism in the sample is associated with common and specific environmental factors, with no evidence of additive gene action in either sex. The marital correlation is high (0.49) and there is evidence for both scalar and nonscalar sex limitation for nonparental common environmental variation, but no differences in cultural transmission are associated with sex of parent or child. The absence of genetic

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variation differs from the results of other studies using similar scales, so differences in sampling procedures are considered.

M. Nosten.[87]The Cytoplasm and Uterine Environment (Either Alone or in Interaction with the Genotype) Affect the Rate of Preweaning Development in Mice.[88] The joint use of ovarian transplantation *in situ* and adoption methods provides a means of testing for genotype and maternal effects (uterine, cytoplasmic, and postnatal), which can be additive and/or interactive with each other. Techniques and controls, as used in our laboratory, have been described previously (Nosten and Roubertoux, *Physiol. Behav.* in press, 1987). Preweaning sensory–motor and weight development of two inbred strains of mice, NZB and CBA/H, were measured using the Fox battery, as adapted in our laboratory (Carlier, Roubertoux, and Cohen-Salmon, *Physiol. Behav.* 30:837–844, 1983). Such effects were tested during adulthood in both exploratory (open-field) and passive (shuttle-box) avoidance. A cytoplasmic effect on age at eyelid opening (AEO) was obtained in 1985 and was replicated in 1986. Comparisons between backcrosses (HN/H and NH/H) lead us to believe that this cytoplasmic effect is related to environment rather than to inheritance (Nosten and Roubertoux, *Physiol. Behav.* in press, 1987). Uterine effects are shown; some, such as on weight or AEO, interact with the genotype. The first results, for tests in adulthood, suggest that, for variables such as ambulation (squares number), maternal environment has no effect but genotype is significant.

M. Nosten,[89] M. H. Francois,[89] and P. L. Roubertoux.[89] Effect of the Strain of the Opponent on Attacking Behavior in NZB.[90] The effect of the strain of the opponent on attacking behavior in males, tested in dyadic encounters, has already been described. In a preliminary experiment, it was shown that, for NZB males aged 65 ± 4 days, tested in a dyadic encounter in the presence of C57BL/6 (B6) or BALB/C (C) males, the latency of the first attack is shorter and the number of attacks higher with a C opponent (François, unpublished data, 1986). This result has been duplicated with the same strains and endocrine and genetic correlates have been investigated. These studies have shown the following. (1) The amount of marking secretions, supposed to serve as a basis for olfactive discrimination of the opponents, is found to be greater for C than for B6. (2) The concentration of plasma testosterone, as measured by the Abraham method, is higher in C. (3) Sensitivity to testosterone, investigated by the injection of testosterone propionate in B6 and C castrated males, has shown that, for target organs such as submandibular glands and seminal vesicules, C is more sensitive. Genetic correlates and hypotheses concerning the major histocompatibility system (H2) are currently being tested by the recombinant inbred method.

Sonoko Ogawa[91] and Stephen C. Maxson.[91] A Study of the Role of Progesterone in Aggressive Behavior in Virgin and Pregnant Mice from Three Inbred Strains. The physiological mechanism of female aggressive behavior, which appears associated with the changes in repro-

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ductive states, remains unknown. Although it has been assumed that gonadal steroids might induce aggressive behavior, the findings as to the kind of steroid(s) and the direction of their effects are controversial. A series of experiments was conducted to test the hypothesis that progesterone might have facilitatory effects on aggressive behavior in virgin and pregnant mice. Females from three different inbred strains (AKR/J, BALB/cN, and DBA/2J) were used. These strains are variable in the levels of aggressive behavior (measured with eight behavioral acts) in both a repeated-tests study (Ogawa and Makino, *Behav. Neur. Biol.* 40:195–204, 1984) and a single-test study (Ogawa and Maxson, *Behav. Genet.* 16:630–631, 1986.) During pregnancy, AKR is extremely aggressive, DBA is moderately aggressive, and BALB is absolutely nonagressive. In addition, virgin AKR females are exceptionally aggressive and show fluctuating levels of aggression over the estrous cycle. The present study examined (i) whether these behavioral variations among strains and reproductive states could be correlated with the variations in the plasma levels of progesterone, (ii) the effects of exogenous progesterone administered in a very early stage of gestation on the onset of aggression in a nonaggressive strain and the levels of aggression in aggressive strains, and (iii) the effects of ovariectomy and replacement with progesterone or progesterone plus estradiol on the levels of aggression.

Kay Phillips,[92] Robert Plomin,[93] David W. Fulker,[92] and J. C. DeFries.[92] General Cognitive Ability of 7-Year-Old Children in the Colorado Adoption Project (CAP): Path Analysis of Genetic and Environmental Transmission.[94] WISC-R scores of 127 adopted and 87 nonadopted 7-year-old children were compared to first principal-components scores of their biological, adoptive, and nonadoptive parents, who had been administered a battery of specific cognitive abilities tests over 6 years earlier. A reparameterization of the the CAP path model (D. W. Fulker and J. C. DeFries, *Br. J. Math. Stat. Psychol.* 36:175–188, 1983) was fitted to observed covariances among family members to yield maximum-likelihood estimates of heritability, cultural transmission, genotype–environment (G–E) correlation, assortative mating, and selective placement. A significant heritability estimate of 0.35 was obtained, which compares favorably with estimates of 0.08 and 0.15 at ages 1 and 2 (Bayley) and 0.12 and 0.22 at ages 3 and 4 (Stanford–Binet) obtained from a somewhat larger proportion of the entire sample using the same estimation procedure. Estimates of cultural transmission at ages 1 through 4 and 7 were 0.03, 0.05, 0.11, 0.09, and 0.02, respectively. In general, no G–E correlation or selective placement effects were evident. Estimates of phenotypic assortment range from 0.22 to 0.27 for wed and unwed couples.

Timothy H. K. Platt.[95] Molecular Genetic Analysis of Sex Determination in Mice: A Model System for the Molecular Genetic Analysis of a Behavioral Phenotype.[96] In mammals, the Y chromosome mediates both gonadogenesis and spermatogenesis. It is also known to influence such traits as histocompatibility, sperm-head morphology, pubertal but not adult testosterone level, and the traits of male sexual behavior and tendency toward aggressive behavior. An immediate goal in my laboratory is the isolation and characterization of the Y chromosomal gene responsible for initiating differentiation of the primitive bipotental gonads to become testes: the Y chromosomal gonadogenesis gene. Function of this gene initiates a cascade of events involving large numbers of other genes scattered throughout the genome, but it is not responsible for initiating development of all of the male phenotype:

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XX^{Sxr} karyotype males, bearing the *Sxr* region of the Y chromosome which includes this gene, are sterile. It is not known if this gene influences those behaviors known to be influenced by the Y chromosome. If animals with an XX karyotype, transgenic for specific Y chromosomal genes could be produced, questions such as this could be answered. I discuss the developmental biology of the testis, the molecular genetics of the *Sxr* region of the Y chromosome, and isolation of the testis determination gene from DNA of XX^{Sxr} males. I also discuss the production of transgenic mice and the prospects for using such animals as coisogenic strains, differing by precisely known DNA sequences, in behavior genetic analysis. Such animals could be used both to test for behavioral phenotype and to dissect out biochemical and neurological mechanisms precisely responsible for the behavior in exact detail.

Susan M. Resnick,[97] R. Arlen Price,[97] Edward M. Moss,[97] John T. Walkup[98] Raquel E. Gur,[97] Ruben C. Gur,[97] and James F. Leckman.[98] Regional Brain Structure and Function in Twins with Tourette Syndrome.[99] Few studies have focused on brain structure and function in Tourette syndrome (TS). None have utilized new neuroimaging techniques in twins with TS. We have applied these methods to four pairs of MZ twins with varying severities of TS and one set of triplets (affected MZ twins and an unaffected DZ cotriplet). Magnetic resonance imaging (MRI) provided a measure of brain anatomy. Regional brain function was assessed behaviorally by a standard neuropsychological battery and physiologically (in subjects over age 18) by the ^{133}Xe inhalation method of regional cerebral blood flow (rCBF). Measurement of rCBF was obtained during three conditions: resting baseline, verbal analogy task, and spatial line orientation task. Examination of MRI scans yielded no consistent anatomic abnormalities. In contrast, within-pair differences on neuropsychological tasks suggested an association between severity of TS and right hemispheric dysfunction, localized to more posterior regions.

Treva Rice[100] and J. C. DeFries.[100] Multivariate Path Analysis of Parent–Offspring Resemblance and Measures of the Home Environment in the Colorado Adoption Project.[101] A multivariate path model of parent–offspring resemblance and a measured index of the home environment were fitted to data from the Colorado Adoption Project to assess the extent to which the behavior–index relationships are genetically and environmentally mediated. In addition to the direct effect of the home environment on children's behavior, three types of indirect influences are possible: a "pure" environmental effect, a pure genetic effect, and a combined environmental–genetic effect. The model was fitted to two parental and offspring behavioral measures (verbal and spatial abilities) and to four "environmental" indices (paternal education and occupation and two factors based on Caldwell and Bradley's Home Observation for Measurement of the Environment; HOME). The offspring behavioral measures and the HOME were assessed when the children were 4 years of age. In general, the results suggest that the influences of parental occupation and education on offspring's behavior are genetically mediated. In addition, the home environment has both direct environmental and indirect genetic effects on childhood abilities.

John Ringo[102] and Harold Dowse.[102] Phenocopies of *Period* Mutants Produced by Light Deprivation of Wild-Type *Drosophila*. The *period* (*per*) gene of *Drosophila melanogaster* affects

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the period of circadian activity rhythms. Normally reared wild-type individuals in free run have periods of about 24 h and lack ultradian (very short period) rhythms, in contrast to individuals homozygous for any of the three classes of mutant *per* alleles: *short* (*s*), exhibiting shortened circadian periods; *long* (*L*), exhibiting lengthened circadian periods as well as ultradian rhythms; and *null* (*O*), lacking normal circadian rhythms but exhibiting ultradian rhythms similar to those of per^L. However, completely light-deprived wild-type individuals usually exhibit characteristics of per^O or per^L: ultradian rhythms and either no circadian rhythms or circadian rhythms with lengthened periods. Among chronically light-deprived wild-type individuals, we observed 55% with per^O behavior, 29% with per^L behavior, and 16% with wild-type behavior. We hypothesize that the wild-type *per* gene and exposure to light are both necessary to couple ultradian oscillators to produce a circadian oscillator.

Lucy Rodriguez[103] and Marla B. Sokolowski.[103] The Effect of Soil Moisture and Temperature on *Drosophila* Pupation Behaviors.[104] Strains of *D. melanogaster* were established by collecting flies emerging from pupae in two distinct pupal microhabitats, on fruit and off fruit, from a pear orchard in Southern Ontario. These strains, called Ml and M4, respectively, were used to study several pupation behaviors known to be inherited polygenically. A strong positive correlation was found when larval pupation behavior was measured in (1) vials, (2) a field assay consisting of fruit on soil and, (3) a soil moisture selection apparatus. M1 larvae pupated low in vials, on fruit in the field assay, and in the highest soil moisture. M4 larvae pupated higher in vials, more off fruit in the field assay, and in dryer soils than M1. The pupation behavior of M1 was more affected by extreme temperatures than that of M4. There was also a significant effect of soil moisture and temperature on the tendency to remain on the food source for larvae of both strains. The differential sensitivity of these strains to soil moisture and temperature helps to explain their different pupal microhabitats in nature. These results also show the importance of gene × environment interactions in habitat selection.

Richard J. Rose[105] and Jaakko Kaprio.[106] Shared Experience and the Similarity of Adult Personality: New Evidence for Effects of E_2.[107] That siblings' shared experience makes no contribution to their behavioral similarities is an increasingly accepted, albeit implausable, notion. We challenge it with evidence from Finnish and Indiana twin studies. The Indiana data employed nine factors identified in the first item factor analysis of normal adult MMPI responses. Data from 410 twin pairs, ages 14–34, yield evidence of significant effects from shared experience for four of nine factors: MZ/DZ correlations for the extraversion scale, 0.60 and 0.42, suggest that one-fourth of its variance arises from experiences shared by siblings matched on age and gender. The Finnish data reveal shared environmental influences for 2320 pairs of adult MZ twins categorized by their social interaction patterns. MZ cotwins in more frequent interactions with each other were more alike. The effect of social contact on cotwein resemblance is large and linear and is no artifact of age: in stepwise multiple regressions of double-entry matrices of the MZ data, it retained significance when tested after effects of age and gender were first removed.

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David C. Rowe,[108] J. L. Rodgers,[108] and C. St. John.[109] Connections Between Delinquency and Sexual Maturation in Adolescence: A Sibling Analysis.[110] In both the popular imagination and behavioral research, precocious sexual maturation and delinquency are related behaviors. This paper reports on sibling analyses of this relationship in two data sets. The first consists of the retrospective reports of college students and their siblings; the second, concurrent reports of young adolescents and their siblings from the ADSEX project on adolescent sexual development. Preliminary analyses of the college data set have confirmed the relationship between sexual maturation and delinquency. For example, early intercourse (<18 years) correlates with delinquency 0.41 and 0.31 for males and females, respectively. Family background effects proved important in both sexes, but the results were stronger and more consistent in males. Lack of relationships in opposite-sex pairs suggest different shared family environmental or genetic determination in the two sexes. Other analyses place upper bounds on genetic and shared family environmental covariance. The analyses of the ADSEX data on 334 sibling pairs are just beginning. The rapid social and biological changes in adolescence make this an ideal period for intensive behavioral genetic research.

Ellen J. Rubin,[111] T. J. Bouchard,[111] and N. L. Segal.[111] Self-Reported Family Background Characteristics of a Reared-Apart Twin Sample. An environmental questionnaire (Block Environmental Questionnaire) created by adding 9 items to an original 92-item Q-sort (Block, 1971) was administered to a sample of reared-apart twins. The Q-sort format was changed to a 9-point Likert scale in which each statement received a rating ranging from "very untrue" to "very true." The 101-item questionnaire consists of items selected to permit a comprehensive description of an individual's upbringing. A sample statement is, "My home was a warm and affectionate place." The questionnaire was completed by 128 subjects, consisting of 44 pairs of reared-apart twins (25 MZA pairs and 19 DZA pairs), 1 set of reared-apart triplets (MZA), and 23 spouses of twins reared apart. Data were also available for 1 member from each of 14 reared-apart twin pairs (11 MZA and 3 DZA). These data were factor analyzed, using the principal-axis method with Varimax rotation. Six factors were interpretable. On the basis of inspection of factor loadings, the factors were called Positive Maternal Care, Negative Paternal Care, Parental Competence and Culture, Authoritarian Family Values, Stable Family Environment, and Father Extraversion. Intraclass correlations on factor scores are presented for MZA and DZA twins, and these are compared with comparable intraclass correlations for Rearing Family SES, Rearing Family Educational Level, and personality. Rearing Family SES was coded using the Duncan SEI system, outlined by Mueller and Parcell (1981). Rearing Family Education level was assessed as years of schooling completed. Personality measures were taken from the Multidimensional Personality Questionnaire.

J. Philippe Rushton.[112] How Generalizable Are Within-Group Heritabilities to Between-Group Differences? Group differences (age, sex, socioeconomic, race) have been observed on important traits of social behavior shown to be about 50% heritable within populations and related to evolutionarily based reproductive strategies (J. P. Rushton, *Person. Indiv. Diff.* 6:441–452, 1985). It is difficult, however, to demonstrate the heritability of the group differences. It is often stated that heritabilities calculated on one population cannot be gen-

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eralized to another. Support for this position comes from the finding that, with the removal of environmental impediments, there are intergenerational increases in the heritability of educational attainment and health. On the other hand, the evidence also shows that heritabilities are sometimes remarkably robust across samples. For example, in tests of genetic similarity theory (J. P. Rushton, R. J. H. Russell, and P. A. Wells, *Behav. Genet.* 14:179–193, 1984) in which assortment is predicted to be higher on the more genetically influenced of traits, we find that heritabilities calculated in the Hawaii Family Study for one population (e.g., Japanese-Americans in Hawaii) predict assortative mating coefficients in other populations (e.g., European-Americans living in Colorado). Another study found that item heritabilities based on Australian twins predicted friendships among Canadians and item heritabilities in Britain. Models for generalizing differential heritability estimates and for establishing the genetic basis of group differences are called for.

Andrew Smolen,[113] T. N. Smolen,[113] and J. L. van de Kamp.[113] Genetic and Neurochemical Studies of Seizure Susceptibility of Mice During Pregnancy.[114] During pregnancy mice are more susceptible to flurothyl-induced seizures than are nonpregnant controls. A number of inbred strains and selected lines of mice were screened for this trait, and we identified two inbred strains, A/Ibg and BALB/cByJ, which were resistant to the pregnancy-associated increase in seizure susceptibility. These two strains, along with C57BL/6Ibg and DBA/2Ibg, which both have an increased susceptibility to seizures during pregnancy, are being used to investigate potential neurochemical alterations in pregnant mice which may influence this behavior. In studies with HS mice the role of brain catecholamines in mediating the increase in pregnancy-associated seizures was examined. Concentrations and turnover of norepinephrine (NE) and dopamine (DA) in control, pregnant (days 17–18), and delivery-day mice were measured in hippocampus, striatum, midbrain, and cortex of individual animals using an HPLC-EC method. There were no significant changes in DA levels or turnover during pregnancy and parturition, except for a small increase in turnover rate in the hippocampus of pregnant animals. The concentration of hippocampal NE decreased during pregnancy and rose at parturition. The turnover of NE was depressed in all four regions during pregnancy, and it remained depressed in hippocampus and striatum at parturition. Hippocampal NE turnover was most affected, dropping from 101 to 19 and 25 ng NE/g tissue/h for control, pregnant, and delivery-day mice, respectively. These data imply a role for NE, but not DA, in the mediation of increased seizure susceptibility during pregnancy.

Toni N. Smolen,[115] A. Smolen,[115] E. I. Han,[115] and J. L. van de Kamp.[115] Genotype- and Age-Dependent Responses to Ethanol in Young Long-Sleep (LS) and Short-Sleep (SS) Mice.[116] We have investigated both genotype- and age-dependent responses to EtOH in young (20–35 days) and adult (55–90 days) LS and SS mice bred for differences in duration of EtOH sleep time or loss of the righting response (LRR) following EtOH. EtOH response was measured with a battery of physiological and behavioral tests, including respiration rate, heart rate, body temperature, Y-maze activity, and rotarod performance. Also, LRR, waking blood (WBE) and brain (WBrE) EtOH levels, and blood EtOH elimination rate (BEER) were assessed at six ages and three doses of EtOH. Blood and brain EtOH levels were compared in separate groups of mice at LRR and upon awakening in order to test for the development of acute tolerance. EtOH levels were measured using an enzymatic assay. Although genotype played an important role in EtOH response, there was little effect of age on most of the measures taken. LS mice were, in general, more sensitive to EtOH than

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SS at all ages tested. LRR, WBE, WBrE, and BEER were stable in both LS and SS after 20 days of age. LS mice eliminated EtOH at a slightly lower rate than SS mice. There was no evidence for acute tolerance in either line or at any age tested. These results suggest that young mice do not differ substantially from adults in their response to EtOH.

Steven R. Sundby[117,118] and S. Scott Panter.[117,118] Genetic Differences in Susceptibility to Iron- or Hemoglobin-Dependent Tissue Damage.[119] The phenotypic expression of different neurological disorders following head trauma depends upon both genetic and environmental elements. To explore genetic factors that might contribute to a predisposition to trauma-related brain damage, we studied the outcome of iron- or hemoglobin-dependent processes in brain homogenates of six inbred strains and one outbred line of mice. Our standard assay measured thiobarbituric acid-reactive substances (TBARS), which are considered to be an index of oxidative tissue damage. Two interesting trends were noted. First, TBARS generated by 0.5 μM ferrous sulfate or 150 μM hemoglobin added to brain homogenates from C57B1 animals (/6J and /10J) were consistently below the mean of all strains and lines. When brain homogenates from albino animals (Balb/cBJ and A/J inbreds and SW outbreds) were examined, the generation of TBARS was consistently elevated. We conclude that one genetic factor predisposing an individual to brain damage following head trauma might be the susceptibility of the brain itself to iron- or hemoglobin-mediated damage. We conclude that the susceptibility of the brain itself to iron- or hemoglobin-mediated tissue damage may contribute to a genetic predisposition to an untoward outcome following head trauma.

Marla B. Sokolowski.[120] *Drosophila* Larval Behaviors.[121] We use *Drosophila* larval behaviors as a model system to understand the importance of behavior genetics in microevolutionary processes. During development, changes occur in (1) larval behavioral phenotypes, (2) genetic contributions to differences in these phenotypes, and (3) selection pressures which act on them. Prior to pupation, larval locomotory behavior changes from foraging, where differences are controlled by a single second chromosome-based gene, to wandering, controlled by second- and third-chromosome polygenes. The rover/sitter polymorphism comprises a naturally occurring suite of correlated behavior patterns. Rovers have long foraging trails and pupate high in vials and on fruit, whereas sitters have short foraging trails and pupate low in vials and close to or on fruit in the laboratory and the field. Selection pressures differentially affect rovers and sitters as follows. (1) Larval parasitoids of *Drosophila* differentially parasitize rovers and sitters; field evidence shows a relationship among the species of parasitoid, its searching behavior, and the larval morph it most frequently parasitizes. (2) Roving and sitting may influence food acquisition when patch size and interpatch distance vary. (3) Larvae that pupate on the fruit (sitters) have greater adult emergence in dry environments than those that pupate off the fruit (rovers). The opposite is true in wet environments. Our understanding of evolutionary responses to natural selection is heightened now that we have identified major genes which effect quantitative behavioral traits as well as suites of genetically correlated traits.

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Dace S. Svikis,[122] R. Pickens,[122] D. Lykken,[123] L. Heston,[123] and P. J. Clayton.[123] Familial Influences in Twin Concordance for Alcoholism.[124] The present report is based on preliminary analysis of questionnaire data from 132 same-sex twin pairs, where at least one member of each pair met DSM-III criteria for alcohol abuse/dependence. There was no significant difference in the mean age and sex ratio for the 59 MZ and 73 DZ pairs. MZ and DZ probands reported a similar number of pathological use symptoms (mean, 7.6 and 7.5, respectively). MZ twins showed higher concordance rates than DZ twins for DSM-III diagnoses of alcohol abuse/dependence. Concordance rates were 52.5 for MZ twins and 38.4 for DZ twins. Concordance for alcohol abuse/dependence was related to the drinking pattern of the biological parents. When neither parent was a "heavy" drinker ($N = 22$), concordance rates for alcohol abuse/dependence were 54.4 for MZ and 29.3 for DZ twins. When one parent was a heavy drinker ($N = 23$), concordance rates were 43.5 for MZ and 55.6 for DZ twins. When both parents were heavy drinkers ($N = 6$), concordance rates were 100.0 for MZ and 44.4 for DZ twins. For both MZ and DZ twins, heavy-drinking mothers tended to marry heavy-drinking fathers, while light/moderate-drinking fathers tended to marry light/moderate-drinking mother ($P < 0.005$).

L. A. Thompson,[125] Kay Phillips,[125] David W. Fulker,[125] and Robert Plomin.[126] Infant Predictors of Adult IQ: Preliminary Results from the Colorado Infant Twin Project.[127] The predictive validity of measures of infant intelligence is assessed using a midparent/midtwin design in a sample of 83 families participating in the Colorado Infant Twin Project. Infant twins are tested at 67, 73, and 79 weeks of gestational age on a battery of tests that yield 31 scores. Parents are administered the WAIS and a battery of specific cognitive abilities tests from the Hawaii Family Study of Cognition (HFSC). Regression of midtwin on midparent results in 13 (of 62) significant regressions ranging in size from 0.16 to 0.42. Heritability estimates calculated using a maximum-likelihood approach show some evidence of heritable variation for 19 of the 31 measures, with an average heritability of 0.21. Multiple regression analyses indicated that 13 of the measures might form a highly predictive composite score. These measures were z scored and summed to form a single score. Estimates of heritability and common environmental variance for this single composite score are 0.30 and 0.24, respectively, and regressions of midtwin on midparent are 0.56 ± 0.12 ($P < 0.001$) and 0.52 ± 0.14 ($P < 0.001$) for WAIS IQ and the first unrotated principal component of the HFSC battery. These preliminary results strongly suggest that valid measures of infant intelligence can be found, that there is continuity in mental development, and that this continuity is at least in part genetically mediated.

M. Upchurch[128] and J. M. Wehner.[128] A Mechanistic and Genetic Analysis of Spatial Learning in Mice.[129] The Morris water task is a test of spatial learning in which a rodent is trained to find a submerged platform in a pool containing opaque water. Spatial ability is tested by removing the platform from the pool and obtaining a difference score between the number of times the animal crosses the platform's former location and the mean number of times it crosses other possible platform locations to which it has not been trained. C57BL/6Ibg

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(C) mice show a preference for crossing the trained platform site, with a mean difference score of 1.99 ± 0.377, while DBA/2Ibg (D) mice show no search preference and have a difference score of 0 ± 0.516. The cholinergic system has been implicated in the regulation of spatial learning. C57 mice were treated with the cholinergic agonist oxotremorine (OXO) by chronic infusion for 5 days at 0.5 mg/kg/h so that they showed a 20–30% loss of muscarinic receptors in cortex and hippocampus. OXO-treated mice had a reduced spatial learning ability (difference score, −0.13 ± 0.686; 4.04 ± 1.309 for saline-treated controls). The similarity between OXO-treated C57 mice and untreated DBA mice suggested that DBA mice may lack normal cholinergic function. A classical Mendelian cross suggested a relatively simple genetic contribution to spatial learning, with evidence of heterosis. Difference scores were 7.43 ± 1.123 for C × D F_1 hybrids, 4.23 ± 0.537 for D × C F_1 hybrids, 3.90 ± 2.318 for CD × D backcrosses, 4.90 ± 2.138 for CD × C backcrosses, and 4.00 ± 1.466 for F_2 hybrids. Additional backcrosses and F_2 hybrids are being tested.

Steven G. Vandenberg.[130] A Status Report on the Fragile X Syndrome.[131] A great deal of research has been reported in the last few years on the fragile X syndrome of mental retardation. As a consequence, several questions have been answered—such as the incidence, symptomatology, and sex distribution. On the other hand, a number of other questions have been raised—such as the precise mode of inheritance, the expression of the disorder in females, and the transmission of the disorder by apparently normal males. These topics are reviewed briefly.

Philip A. Vernon.[132] The Heritability of Measures of Speed of Information Processing.[133] One hundred pairs of adult twins (48 MZ pairs and 52 DZ pairs) and 25 pairs of nontwin siblings have been administered a standardized intelligence test (the Multidimensional Aptitude Battery) and eight reaction-time tests measuring the speed with which they can process different kinds of information in short- and in long-term memory. More twins and siblings are currently being tested. Preliminary analyses indicate a substantial heritability for intelligence and for several of the speed of information-processing measures. For the latter, heritabilities range from 0.318 to 0.914 (M = 0.594), and in general, the more complex reaction-time tests and/or those involving long-term memory had higher heritabilities than did the less complex and/or those involving short-term memory. In addition, the higher the heritability of a reaction-time test, the higher was its loading on the general speed factor extracted from these tests' intercorrelations and the more highly it was correlated with intelligence.

Douglas Wahlsten.[134] Insensitivity of Analysis of Variance to Heredity–Environment Interaction.[135] Linear models aimed at partitioning variance among genetic and environmental components generally assume the separate and additive effects of the components on the phenotype in question. Sensitivity of analysis of variance to interaction and nonlinear effects was tested with several realistic models of heredity–environment relationships. Expected

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results were derived for a simple experiment involving five inbred strains reared in five different environments, and these results were then subjected to the usual analysis of variance. Under conditions commonly employed in behavior genetics research, the analysis failed to detect significant interaction effects for most reasonable models, or it suggested that interaction was negligible compared to main effects. A modification of the usual procedure to test interaction is proposed, whereby the profile of simple main effects of heredity at the different levels of environment is routinely inspected. Visible departures of this profile from a horizontal line should alert us to the presence of interaction and prevent wrongful acceptance of a hypothesis of additivity. The power of a test of alternative linear and nonlinear models, even relatively complex ones, can be assessed using the bootstrap sampling procedure. Applications of this approach are discussed.

Ronald M. Weigel[136] and John C. Crabbe.[137] Statistical Issues in the Use of Difference Scores Versus Regression Residuals in Selection Experiments.[138] Behavior geneticists are often interested in selecting for breeding on the basis of changes in a variable between an initial and a final measurement. Unreliability of these variables results in regression to the mean, providing a biased estimate of true change, with the greatest bias associated with extreme scores. Since directional selection is for extreme scores, these biases are exacerbated in selection experiments. Statisticians recommend using regression residuals derived from the regression of final on initial scores as estimates of true change controlling for regression to the mean. However, this method cannot be used readily in selection experiments, because reliable estimates of heritability cannot be obtained. We present data from a study of selection for hypothermic response to an acute dose of ethanol in mice, comparing the use of regression residuals versus difference scores as a basis for selection. Correlations between change and residual scores were high (mean = 0.80). Almost 75% of the mice chosen for breeding using change scores would also have been chosen using the residual method. Generalizability of the results is discussed. Additional methods for decreasing bias in the estimate of change in selection experiments are presented.

Kimerly J. Wilcox,[139,140] Ilo E. Leppik,[140] S. Scott Panter,[139,140] and V. Elving Anderson.[139,140] Reading Epilepsy in Identical Twins.[141] Two pairs of identical female twins with primary reading epilepsy have been identified from the records of the Minnesota Twin registry (courtesy of Dr. David Lykken). Primary reading epilepsy is a rare disorder manifested during reading by jerking sensations of the mouth, jaw, tongue, or throat, followed by a transient loss of consciousness and/or a generalized seizure. Several studies have suggested a genetic component (cf. R. F. Daly and F. M. Forster, *Neurology* 25:1051–1054, 1975). Pair 1 is 31 years old; Twin B began having seizures at the age of 18 and has had a total of six or seven generalized tonic–clonic (GTC) seizures. Twin A had one GTC seizure at age 19. Both have continued to experience jaw jerking when reading. Their oldest brother has been treated for a seizure disorder. Pair 2 is now 43 years old. Both twins first experienced absence-type seizures, preceded by jaw jerking, at age 15. Both also have seizures evoked by writing and reading musical scores. There is no family history of seizures. Pair 2 was extensively studied by Daly and Forster in 1972. We are extending this research to identify biochemical markers

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of genetic risk for seizures and to explore possible physiologic mechanisms. Previous research has suggested that some seizure patients have altered levels of certain amino acids or the plasma protein haptoglobin. In Pair 2, however, no abnormal patterns of plasma proteins are detected by two-dimensional gel electrophoresis. Plasma amino acid levels are within normal limits, although several are at the low end of the range.

Kunio Yamazaki,[142] G. K. Beauchamp,[142] O. Matsuzaki,[142] J. Bard,[143] L. Thomas,[143] and E. A. Boyse.[143] Participation of the X and Y Chromosomes in the Individual Chemosensory Identity of Mice According to Genotype.[144] The major histocompatibility complex (MHC) of the mouse imparts to each mouse an odor that reflects its genetic constitution at this region of chromosome 17 (K. Yamazaki, E. A. Boyse, V. Mike, H. T. Thaler, B. J. Mathieson, J. Abbott, J. Boyse, Z. A. Zayas, and L. Thomas, *J. Exp. Med.* 144:1324–1335, 1976). Sensory recognition of these differential odors influences reproductive behavior and evokes neuroendocrine responses critical to the maintenance of pregnancy (K. Yamazaki, G. K. Beauchamp, C. J. Wysocki, J. Bard, L. Thomas, and E. A. Boyse, *Science* 221:186–188, 1983). To determine whether other parts of the mouse genome contribute to individual scent marking, and so may similarly exert a selective force on loci other than the MHC, mice differing genetically only in their X and/or Y chromosomes were tested for individuality of scent in the Y-maze system previously employed to investigate MHC-related scent distinctions. It was found that the X and Y chromosomes each confer individuality of scent related to genotype. However, the MHC appears to be most salient since the order of odor intensity, judged by comparative ease of Y-maze training, was the MHC (most intense), the X chromosome, and the Y chromosome (least intense).

Rowe A. Young.[145] Genetic Variations in Motor and Cognitive Patterns Associated with Reading Disabilities—Diagnosis and Remediation.[146] Previous work in the Behavioral Genetics Laboratory at the University of Connecticut has demonstrated that variations in laterality patterns based on visual processing of linguistic and nonlinguistic symbols and auditory processing of phonemes that were maladaptive in some dyslexia-affected families were not necessarily maladaptive in others and that the effectiveness of coping strategies depended on matching these to the underlying aberrations. The present work reports a paper-and-pencil test that is proving to be a highly effective diagnostic instrument applicable to a broad range of ages and practical to administer in a group setting. Two highly maladaptive patterns based on the new instrument are reported, and a technique that is providing the remediation from one of these is discussed and evaluated from both an empirical and a theoretical point of view, with implications for application to other maladaptive patterns.

Michele Zimowski[147] and R. Darrell Bock.[147] Spatial Ability and Fluent Expression: Are They Reciprocally Related? Tests of spatial visualizing ability (mental rotations) and those of fluent expression (word fluency, coding speed) show pronounced sex differences in many populations. On average, males excel in spatial ability, and females excel in fluent expression.

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Moreover, the partial correlation of measures of these abilities, partialing out general verbal ability, has been found to be negative in several studies. In factor analytic studies, however, spatial ability, fluent expression, and verbal ability typically load on different factors. This paradox is investigated in light of studies in the literature and new data. A theory of the determinants of these abilities is advanced.