The Development of Behavior 2

- Heritability
- Single-gene effects on development
- Evolution and behavioral development
Basic Concepts of Heritability

- **Genotype** is the suite of genes possessed by an individual, whereas **phenotype** is a trait that an individual exhibits because of gene-environment interactions.

- **Coefficient of relatedness** ($r$): represents the average % of genes that two individuals will share based upon their relationship. A parent will contribute half of its **alleles** (forms of each gene) to an offspring ($r=0.5$). The coefficient is 0.5 for full siblings etc.
Assessing Heritability: Human Twin Studies

- Monozygotic (MZ) twins are derived from the same egg and sperm \( (r = 1.0) \) (“identical twins”)
- Dizygotic (DZ) twins are from different gametes and share half of their alleles \( (r = 0.5) \) (“fraternal twins”)
- MZ twins raised apart offer insight into genetic influences, as they share all of their genes – what about shared environment?

Oskar Stohr was raised Catholic in Nazi Germany; Jack Yufe as Jewish in the Caribbean. They both like sweet liqueurs, store rubber bands on their wrists, etc
Assessing Heritability

- A study of MZ and DZ twins raised apart demonstrates the influence of genes on personality, temperament, social attitudes.

- The amount of the phenotypic variability between individuals that can be accounted for by genes is called the heritability for that phenotype, which ranges from 0 to 1.

- Heritability is ~0.5 for personality scores and ~0.7 for IQ (averages from multiple studies).
Heritability & Human Behavior

• We can also look at unrelated individuals that are reared together from a very early age.
• On IQ tests, the concordance rate for these individuals was only 0.26 (0.45 for full sibs reared together).

### TABLE 1 Familial correlations for IQ scores: Predicted values based on the genetic differences hypothesis and the actual correlations

<table>
<thead>
<tr>
<th>Category</th>
<th>Predicted correlation</th>
<th>Actual median correlation</th>
<th>Number of studies</th>
</tr>
</thead>
<tbody>
<tr>
<td>Identical (MZ) twins reared together</td>
<td>1.0</td>
<td>0.85</td>
<td>34</td>
</tr>
<tr>
<td>Identical (MZ) twins reared apart</td>
<td>1.0</td>
<td>0.75</td>
<td>5</td>
</tr>
<tr>
<td>Fraternal (DZ) twins reared together</td>
<td>0.5</td>
<td>0.58</td>
<td>41</td>
</tr>
<tr>
<td>Siblings reared together</td>
<td>0.5</td>
<td>0.45</td>
<td>69</td>
</tr>
<tr>
<td>Parent-genetic offspring</td>
<td>0.5</td>
<td>0.39</td>
<td>32</td>
</tr>
<tr>
<td>Parent-adoptive offspring</td>
<td>0.0</td>
<td>0.18</td>
<td>6</td>
</tr>
</tbody>
</table>

*Sources: Bouchard and McGue [137]; Bouchard [134]*
Outline

- Heritability
- Single-gene effects on development
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How many genes are required to see a difference in phenotype?

- Often many. But sometimes only one!

- If one parent has two dominant alleles (homozygous AA) and one has two recessive alleles (homozygous aa), all of the offspring will have one dominant and one recessive allele (Aa), and thus they are heterozygous for the trait and will have the dominant phenotype.

- If both parents are heterozygous (Aa), 3/4 of the offspring will express the dominant phenotype (one AA, two Aa); 1/4 will be of the recessive phenotype (aa).
Natural variation in larval foraging behavior

- Drosophila melanogaster
- Fruit fly larvae of the “sitter” strain move very little on a petri dish with food in it, whereas “rovers” move a lot.
Foraging behavior inherited as a single gene trait

Parents

rover x sitter

F1

100% rovers

F1 x F1

rover x rover

F2

rover rover rover sitter
foraging (for)

- *for* gene encodes a PKG
- this enzyme is expressed in olfactory system
- rovers have high PKG activity
Foraging behavior inherited as a single gene trait

Parents: \( \text{for}^R/\text{for}^R \times \text{for}^s/\text{for}^s \)

F1: \( \text{for}^R/\text{for}^s \)

F1 x F1: \( \text{for}^R/\text{for}^s \times \text{for}^R/\text{for}^s \)

F2: \( \text{for}^R/\text{for}^R, \text{for}^R/\text{for}^s, \text{for}^R/\text{for}^s, \text{for}^s/\text{for}^s \)
Based on previous studies on fruit fly larvae you know that the \( for^R \) allele is dominant to the \( for^s \) allele and that the \( for^R \) allele is responsible for the “rover” phenotype. You have identified a larva that exhibits the “rover” phenotype. What is the genotype of this individual?

A. \( for^R/for^R \)

B. \( for^R/for^s \)

C. \( for^s/for^s \)

D. A or B

E. B or C
Single gene mutations

• Single gene mutations in fruit flies can affect daily rhythms, courtship behavior, learning

• Do these experiments tell us that single genes code for a specific behavior?

• Genes code for proteins, not behaviors!
Single Gene Mutations in Mice

• If a male mouse is introduced to a female, he investigates her a lot at the first meeting and progressively less thereafter (familiarity with her odor)

• **Oxytocin** (like vasopressin) is a neuropeptide that is found in numerous brain regions that regulate social behavior

• What happens with male mice missing the gene for oxytocin (**oxytocin “knockout mice”**) (Oxt⁻⁻) compared to “wild-type” mice (Oxt⁺⁺)?
Oxytocin knockout mice

(A) Picture of two mice

(B) Graph showing inspection duration (seconds) vs. trial.
- Purple line: $Oxt^{-/-}$
- Green line: $Oxt^{+/+}$

Y-axis: Inspection duration (seconds)
X-axis: Trial

New female
Oxytocin receptor (OXTR) polymorphisms and attachment in human infants

37+ SNP’s for OXTR gene on chromosome 3

Frances S. Chen¹*, Maria E. Barth², Stephen L. Johnson³, Ian H. Gotlib⁴ and Susan C. Johnson⁵*

Showing raw data for SNP rs2254298, which is on chromosome 3.

Jump to a gene: [Go] a SNP: rs2254298 [Go]

or a chromosome: [1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 X Y MT]

« Return to your whole genome.

<table>
<thead>
<tr>
<th>Gene</th>
<th>Position</th>
<th>SNP</th>
<th>Versions</th>
<th>Kiran Soma’s Genotype</th>
</tr>
</thead>
<tbody>
<tr>
<td>OXTR</td>
<td>8802228</td>
<td>rs2254298</td>
<td>A or G</td>
<td>GG</td>
</tr>
</tbody>
</table>

FIGURE 1 | Percentage of infants classified as secure as a function of rs2254298 genotype and ethnicity. Group A includes infants with the AA or AG genotype. Group G includes infants with the GG genotype. The effect of genotype on attachment security was significant in the non-Caucasian group (p < 0.005).
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Phenotypic Variation in Garter Snakes

- Selection can operate differently in separate populations of the same species, producing phenotypic variation.

- *T. elegans* is found in both wet coastal areas of California and drier inland areas of North America.

- **Observation:** Coastal snakes prey extensively on banana slugs; inland snakes eat fish and frogs by ponds

Studies by Stevan Arnold
Distribution of Thamnophis elegans in California

- **T. e. elegans**
- **T. e. terrestris**
- **T. e. vagrans**
- **Intergrades**

**SWALLOWING FISH**

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Question: Why do the diets of these two populations of the same species differ?

Hypothesis: The differences in diet exhibited by the snakes are due, at least in part, to hereditary food preferences (due to a genetic difference between the two populations).

Predictions: The slug preference of coastal snakes and the slug aversion of inland snakes should still be present if the snakes are separated from their mothers and siblings after birth and raised in the same environment.
Uniform environment experiments: animals from both populations were raised in the same environment.
Responses of newborn, naive garter snakes to slug cubes

- Isolated newborn snakes offered freshly thawed slug cubes.
- In addition, young snakes from both populations were interested in frog smells on cotton swabs, but only coastal snakes liked the slug smells on cotton swabs.
Why are there different selection pressures on the two populations?

- Using abundant slugs for food probably allowed the snakes to move into coastal areas (even a 1% benefit to reproduction could produce the current pattern of dietary preferences in only 10,000 years!).

- The data also suggest that the slug preference is being selected against in the inland population. It is not clear why.