Chapter-5

BEHAVIOUR GENERICS

A survey of literature reveals the fact that individual differences in behavior are somehow related to genetic differences among individuals. Behavioral traits are known to respond to both natural and sexual selection and can be heritable too. The heritability estimates for behaviors are broadly comparable to other kinds of morphological traits (Meffert et.al 2002; Stirling et.al. 2002), and they also show adaptive, heritable geographic variation. The study of heritability of behavioral traits in animal (including human) behavior is known as **behavior genetics**. The field has formed from an overlap of genetics, ethology and psychology.

In recent years increasing evidence that behavior can be studied from a phylogenetic perspective (Brooks and McLenan, 1991) and an appreciation of behavior's role in evolutionary processes such as speciation and reproductive isolation (Boughman 2002) have all contributed to interest in bridging the gap between genetics and behavior and stimulated the development of the field of behavior genetics. The study of the relations between heredity and behavior is of fundamental importance, not only for understanding behavior itself, but also for a more complete understanding of biology.

The fact that behavior indeed has a genetic basis is brought home by the following observations:

- Behaviors are species specific
- Behaviors often breed true
- Behaviors change in response to alteration in DNA (i.e. genes)
- Behavior shows phyletic relationships
- In humans, some behaviors run in families.

Although genes may play a role in many behaviors, they never determine them. There are no genes that directly code for a behavior - genes only code for proteins. The gene-derived proteins direct the formation of neural circuits in the brain, and it is these circuits that serve as the true foundations of behavior. The external environment also exerts a strong influence on how all genes are expressed in behavior via a development of nervous and hormonal mechanisms.

Approaches to the Study of Behavior Genetics

- **Classical (or Mendelian) genetics:** It examines the distribution of hereditary characteristics of behaviors from one generation to the next. With selective breeding, the presence/absence of specific behaviors can be tracked through the outcomes of sexual reproduction.
- **Quantitative genetics :** It explores the inheritance of traits that are often subject to significant environmental influences and usually involve a great number of underlying genes. Quantitative approaches are essential to studying the degree to which relatedness among individuals is matched by resemblances in behavioral characteristics.
- **Population Genetics :** It concerns itself with mechanisms that change the relative occurrence of genes within a population. It examines how gene frequencies change or become stabilized within populations through behavioral forces such as sexual selection, mating systems, dominance, or territoriality.
- **Developmental Genetics :** Developmental genetics explores how genetics interfaces with ontogenetic processes in behavior. Genetics plays an integral role in the control of cell growth and differentiation, formation of tissues, organs and hormone systems, as well as in the emergence and critical timing of learning opportunities, cognitive abilities, and emotional systems.

Basic queries : Any enquiry into the study of behavioral genetics revolves around the following questions

- Is the behavioral trait genetic?
- If so, what is the nature of the genetic influence (in other words, is it inherited in a Mendelian pattern or is it something more complex)?
- Where in the genome are the genes located?
- What proteins (gene products) do the genes encode?
- How does each gene product function?

Techniques and Strategies of Behavioral Genetics

Observation vs. Experimentation **:** There have been two main approaches to behavior-

genetic analysis: the experimental approach and the observational approach. Human studies in behavioral genetics rely primarily on observational data over which we have no experimental control. It is not possible or ethical to manipulate experimentally who marries whom. Animal studies on the other hand provide an important alternative for studying certain kinds of behavior because the researcher can set up carefully selected patterns of mating under tightly controlled environmental conditions. The investigator who employs laboratory studies has some degree of control over the subjects being studied. This allows that investigator and others to replicate the work. Both the approaches are complimentary to each other and a synthesis of both approaches has become one of the goals of behavior-genetic analysis.

Human Studies

Two different methods are employed in behavioral genetic analysis in human beings. They include

- *Methods based on the principles of genetic epidemiology*: In genetic epidemiology (the study of the clustering of specific traits in families and populations), the goal is to provide designs that permit quantification of genetic and environmental effects.
- *Methods that employ the technology of molecular genetics*: In molecular genetics, the goals are to establish the biochemical basis of genetic effects.

A. Methods using principles of genetic epidemiology: These include the following approaches

a. *Family studies*: An obvious place to look for genetic effects is within families. Family studies are useful because families are easy to find, and most family studies can provide information about

- genetic influences on a trait,
- mode of inheritance (for single-gene traits), and sometimes
- number of genes involved (for polygenic, or multiple-gene, traits).

The obvious problem with relying on resemblance among family members is that while we can conclude from family resemblance that there may be genetic influences on a trait, but we need more specialized approaches to separate genetic influences from shared environmental influences.

b. *Twin studies* : Twin studies are extremely important in studying human subjects, because humans cannot be bred for certain traits and are hard to manipulate in an experimental fashion. *Monozygotic twins*, commonly known as *identical twins*, are genetically identical. *Dizygotic twins*, or *fraternal twins*, are no more genetically similar than non-twin siblings are.

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- Therefore, if monozygotic twins share a behavioral trait significantly more frequently than dizygotic twins do, it can be assumed that behavior has a genetic component.
- If identical and fraternal twins are similar for a particular trait, this is evidence for a shared environmental contribution to the trait.

The ability to separate genetic and shared environmental influences using twins is a powerful advantage of using twins (Fig 11). A further advantage is that both members of a twin pair are the same age. Since many behaviors are affected by age or developmental stage, this is an important advantage over family studies, where age can differ by an entire generation. A disadvantage of relying on twins is that they are more difficult to find than families. A critical implicit assumption is that identical twins and fraternal twins share environments to the same extent, which may be an overly simplistic assumption.

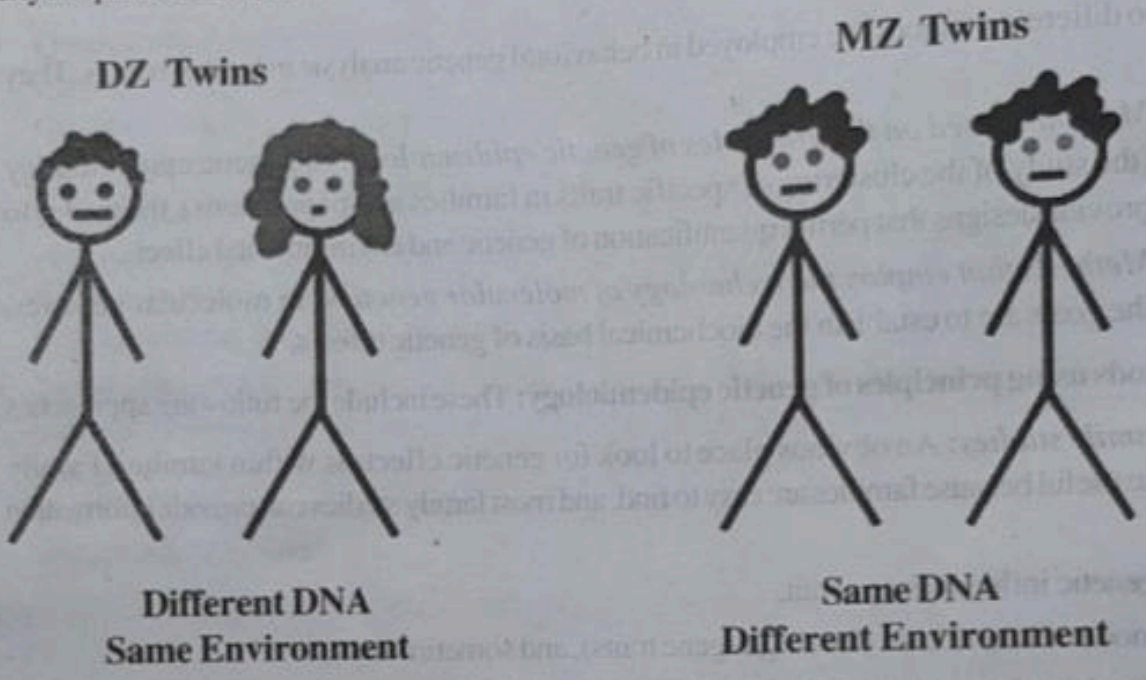

Fig 11. ***Showing the comparison of monozygotic (MZ) and dizygotic (DZ) twins***

C. Adoption studies : Both twins and other family members share environmental influences to some extent. The study of children who have been adopted at an early age provides a unique opportunity to separate genetic effects cleanly from shared environmental effects.

- Any systematically observed similarity for a given trait between biological parents and adopted-away children must reflect genetic, rather than environmental, effects.
- In contrast, any systematically observed similarity between adoptive parents and children they have adopted must reflect shared environmental effects.

The clean distinction between shared effects that are genetic in origin and shared effects that are environmental in origin makes the adoption study design appealing and powerful. On the other hand, adoption studies are extremely difficult to conduct because there are very few children who are adopted in contemporary society, and there are serious issues of confidentiality that make it difficult to link adopted children to their biological parents.

B. Methods using molecular genetic technology :

The methods described above cannot be used to actually locate genes. Molecular genetic technology describes a set of methods involving the direct study of DNA. These methods include

a. ***Linkage analysis*** : Linkage analysis is used to "map" (or locate) genes by studying their transmission in families with respect to other genes (or genetic markers) of known location.

- If trait and marker are transmitted together within families or shared by siblings, the gene is inferred to be close to the marker. The gene and the marker are then said to be linked.
- If there is no relationship between relatives sharing a marker allele and relatives sharing a trait, it is assumed that there is no gene for the trait in the vicinity of the marker.

Linkage analysis has been used classically for Mendelian traits. For complex traits, types of linkage analyses known collectively as non parametric methods (in that basic genetic parameters, such as mode of transmission, do not have to be specified for the analysis to be valid) are used. The basic principle is the same: if relatives — commonly, sibling pairs — share both trait and marker alleles, the gene must be close to the marker location. When this method is applied to traits that vary continuously, such as a presence or absence of a disease, it is known as quantitative trait locus (QTL) mapping. If a gene that affects such a trait is identified, then it is known as a QTL for that trait. For quantitative traits, it is frequently expected that multiple QTLs will have an influence.

b. ***The candidate gene approach*** : In many cases, scientists can formulate a reasonable hypothesis about whether known genes might influence a behavioral trait. If a known gene is thought to influence a trait, it is referred to as a candidate gene. Researchers then can test the hypothesis that the gene affects the trait by conducting an association study. In an association

study, a comparison is made between observations of particular alleles of the candidate gene in populations of individuals with or without the trait. If a particular allele is observed more often in the group with the trait than in the group without the trait, one possible explanation is that the allele plays a role in influencing the trait. Often, there are, however, alternative explanations for genetic associations that have nothing to do with the gene influencing the trait. For example, the candidate gene may simply be linked to another gene that actually is responsible for influencing the trait. It is the responsibility of scientists conducting studies of this sort to consider carefully all possible alternative explanations, and only when alternatives are eliminated to make a claim that a gene and a trait are associated.

c. *Large scale approaches* : Unfortunately, a candidate-gene-by-candidate-gene approach is often inefficient. Thus, investigators are increasingly turning to the enormous amount of data available through the genome sequencing of many organisms. Use of this information allows researchers to adopt a more unbiased approach, simultaneously examining up to thousands of genes at once. Genomic tools also allow scientists to associate genetic variants, including single nucleotide polymorphisms (SNPs), with specific behaviors or even with different gene expression patterns using microarray comparisons. Often, the genes identified through these large-scale genomic approaches are designated as candidate genes, and the effects of these candidates are then verified through more traditional approaches wherein individual genes and their functions are examined.

ANIMAL STUDIES

Historically many studies in behavioral genetics have been conducted using nonhuman species. Behaviorists have used the fruit fly *Drosophila* extensively to study the genetics of simple behaviors, such as geotaxis (attraction to gravity) and phototaxis (attraction to light). Hundreds of mutations that affect behavior have been identified in the fruit fly. A closer biological relative to humans is the mouse, which is a mammal. The mouse and human genomes have been shown to overlap substantially, with many DNA segments containing genes in the same order in the two species (synteny) and with very similar DNA sequence and identical function (homology). The methods in behavior genetic analysis of animals include

a. *Selection studies* : This approach provides a powerful tool for detecting genetic influences on behavior. In selection studies, quantitative traits are measured in animals of mixed genetic background, which leads to a continuous distribution of phenotypes. Those animals that exhibit high and low extremes of the trait are selected as parents for the next generation. This process is repeated over a number of generations. If the trait is genetic, there will be divergence over time in the value of the trait in the offspring of parents selected for high and low values.

b. *Inbreeding* : In order to differentiate the genetic and environmental factors contributing to a behavior, it is useful to be able to hold one factor constant. Inbreeding provides a second strong approach for detecting genetic variation in quantitative traits. Inbred animals are strains in which siblings have been mated over many generations, resulting in strains in which all animals are virtually genetically identical and all genes are homozygous. Differences between strains are attributed to genetic influences, whereas variability within strains is attributed to environmental influence. A great deal of information about genetic and environmental influence is also obtained from derived generations such as the F1, which is the cross between two inbred strains resulting in offspring all of which are heterozygous at all genes, with one allele from one parental strain and the other allele from the second parental strain. All individuals in the F1 generation are genetically identical heterozygote types that are used to infer the presence of genetic influences.

c. *Knockout studies* : An important technique in molecular analyses of behavioral genetics is the knockout study. Transgenic and knockout mice result from new technologies that permit an investigator to insert a foreign gene or delete a specifically targeted gene, respectively. Mice are literally designed to express or fail to express certain traits by inserting or subtracting genes from embryonic cells and then reinserting them into a female to gestate. In most knockout studies, a mechanism is designed so that researchers can turn on and off the gene, usually by treatment with an antibiotic. This is accomplished by combining the inserted or deleted gene with another gene susceptible to antibiotics. The production of mice with specific deletion of targeted genes (knockouts) has provided a useful tool in understanding the mechanisms underlying behavior. For example, by knocking out the gene that codes for a nerve-cell receptor for the neurotransmitter serotonin, scientists increased the aggressiveness of male mice. Similar studies are allowing profound increases in the ability to understand the activity of specific genes.

EXAMPLES OF GENETIC CONTROL OF BEHAVIOR :

Examples demonstrating genetic control of various aspects of behavior are outlined as follows

EXAMPLES IN ANIMALS

1. Learning : One of the best-known experiments in the behavioral science literature is the Tryon bidirectional selective breeding study of maze- learning in rats, begun in 1925 and continued until 1940.

- Tryon started with a heterogeneous foundation population. After the population had been tested in a multiple T-maze, rats were bred selectively on the basis of their scores (errors and time). This was the beginning of the Tryon 'bright' and 'dull' strains, maintained ever since in reproductive isolation.

- In succeeding generations, brights were mated with brights, and dulls with dulls. The performance of the two strains gradually diverged and by the eighth generation there was little overlap between them.

Many aspects of Tryon's elegant experiment have been replicated for the same and different behavior patterns in the same and different species. Later, it was also demonstrated that the brights were not superior to the dulls in all other learning tasks. In fact, sometimes the converse was true. However, brights were superior when the new test resembled the original test. These results suggest two things.

- First, there is no single 'super-gene' for learning in the rat.
- Secondly, this innate ability of the brights tends to be relatively task specific.

Other studies concerned with learning in rodents have involved such measures as: shock avoidance, water escape, preference for or aversion to auditory stimuli, discrimination, and several types of maze-learning.

2. Foraging : Animal species vary greatly in the behaviors they use to obtain food; however, the genes that contribute to these actions have been highly conserved.

In the fruit fly *Drosophila melanogaster*, foraging behavior is influenced by the activity of a certain enzyme called cGMP-dependant protein kinase (PKG).

- Fly larvae with high PKG levels typically have long food-finding paths outside of their food patch, and they are therefore called "rovers." The opposite is true of so-called "sitter" larvae, which have low PKG levels (Osborne *et al.*, 1997).
- The rover and sitter traits are inherited as a single major gene called *for*, with a different allelic variant for each trait (for^R and for^S, respectively) that has multiple phenotypic effects and is influenced by minor genes (de Belle & Sokolowski, 1987).
- However, both the genetic and phenotypic expression of *for* can be influenced by the environment. Specifically, for^R is more common in larvae from crowded environments, whereas for^S is predominant in larvae from sparsely populated surroundings (Sokolowski *et al.*, 1997).
- Moreover, when food is scarce, even for a brief period, rover flies with the for^R allele can act like sitters (Sokolowski, 2001). Thus, both internal and external factors can influence foraging behavior in *Drosophila*.

Once the *for* gene was associated with foraging behavior in fruit flies, it was used as a candidate gene to study similar behaviors in other species.

- For example, the fruit fly *for* gene shows high sequence homology to the *Amfor* gene in honeybees. Changing *Amfor* expression can alter the foraging behavior of a honeybee,

thereby transforming the bee from a "nurse" (a bee that cares for the young) to a "forager" (a bee that leaves the hive to find pollen and nectar). Like the rover fruit fly, the forager honeybee has higher levels of the PKG enzyme than do nurse bees (Ben-Shahar *et al.*, 2002).

- Researchers have also noted that an orthologue of *for*, called *egl-4*, is associated with food-related behavior in the roundworm *C. elegans* (Fujiwara *et al.*, 2002).

Taken together, these findings suggest that *for* could be used as a candidate gene for behaviors concerning food acquisition in other species.

3. Sexual behavior : Male courtship in the fruit fly *Drosophila melanogaster* was one of the first behaviors for which researchers found strong evidence for specification by a gene, namely, the so-called "fruitless" gene (abbreviated *fru*). In male fruit flies, courtship is a complex, ritualistic behavior that involves many visual, olfactory, gustatory, tactile, and acoustic cues, as well as intricate motor output directed toward attracting a suitable mate (i.e., a female that has not recently mated). During courtship, the male fruit fly orients to the female, taps her with his forelegs, sings a courtship-specific song by vibrating one wing, probes the female's genitalia, and then curves his abdomen to mate.

- The fruitless gene first emerged as a candidate gene for sexual behavior when it was discovered that male flies with *fru* mutations were sterile due to defective performance of courtship and copulation (Gill, 1963).
- Years later, the mutated gene present in these flies was cloned, and the protein that it encodes was identified as a transcription factor (Ito *et al.*, 1996; Ryner *et al.*, 1996).
- Researchers also determined that the *fru* gene is spliced differentially in males and females and that this gene generates various sex-specific messenger RNAs (Demir & Dickson, 2005; Kyriacou, 2005).
- Interestingly, not only does the male pattern of splicing elicit male courtship behavior, but it also influences sexual orientation, as evidenced by the finding that male splicing in otherwise normal females generated male behavior (e.g., singing) that was directed toward other females (Figure 2; Demir & Dickson, 2005).

Functional conservation of the *fru* gene has only been shown in one other species, the malaria mosquito *Anopheles gambiae* (Gailey *et al.*, 2006), and a mammalian homologue for *fru* does not exist. Even so, *fru* is a good example of how genes can specify aspects of a complex inborn behavior.

4. Taxes : Genetic analyses have been made on the taxes of *Drosophila*.

- In one investigation starting with unselected *(free-mating)* wild-type fruit flies, the response to gravity was measured by the number of turns toward or away from the pull of gravity in a vertical T-maze.

- A distribution of scores was obtained, some flies making more positive (or negative) responses than others.
- From the free-mating foundation population, a positive line was started by mating together flies making the most positive responses (approaching the pull of gravity), and a negative line by mating those making the most negative responses.
- Henceforth, in each generation, though both lines contained individuals with positive and negative scores, mating were made in the positive line between only the most positively scoring individuals, and in the negative line between only the most negatively scoring individuals.
- In a few generations the mean scores diverged markedly. But they remain separated only while selection pressure is continued.

The changes in the distributions of scores resulting from control of the mating system (the response to selection) indicate the presence of genetic correlates for the trait being studied.

5. Nest-cleaning in bees : One of the problems facing the honey-bee is the American foul brood disease (a bacterial infection) which kills its larvae and pupae. If the dead are not removed, the infection will spread.

- One investigator worked with two strains of bees. One was resistant to American foul brood disease, and the other was susceptible to it. It was noted that the resistant strain would remove infected larvae while the susceptible strain left most of the infected individuals in the nest.
- This hygienic behavior is composed of two steps: uncapping the cell, and removing the infected larva or pupa from the cell. (For simplicity one can call the resistant strain hygienic and the susceptible strain non-hygienic.)
- When the investigator crossed the hygienic strain with the non-hygienic strain, the F1 from this cross resembled the non-hygienic strain. This indicated that the gene or genes for hygienic behavior were recessive.

This is an example of a behavior that has been analyzed into two components, and for each of which a gene correlate has been found. Rothenbuhler (1964) suggested that these two traits were controlled in a simple Mendelian manner by two recessive loci. More recent molecular evidence from quantitative trait loci (QTL) linkage mapping has identified multiple specific stretches of DNA with genes that underlie variation in this trait. This work suggests that the genetic basis of hygienic behavior is considerably more complex, and that seven QTLs are associated with hygienic behavior, each controlling only 9-15% of the observed phenotypic variance.

6. Social behavior in rodents : The effect of individual genes on affiliative behavior has been studied in two species of voles. The prairie vole Microtus ochrogaster is monogamous,

biparental, and highly social. By contrast, the montane vole Microtus montanus is promiscuous, maternal, and minimally social.

- The hormones oxytocin and vasopressin exert complementary effects on these behaviors in the prairie vole, as they appear to do in rats and mice. Moreover, the anatomical distribution of oxytocin and vasopressin receptors in the brain differs markedly between the two vole species.
- Vasopressin administration stimulates affiliative behavior in prairie voles but neither in montane voles nor in mice.
- When a prairie vole vasopressin receptor gene (V_{1a}) was transferred into mice, thereby creating an anatomical distribution similar to that of the prairie vole, the mice began to exhibit affiliative behavior in response to vasopressin.

These results argue that changing the pattern of V_{1a} distribution is sufficient to alter this social behavior. This interpretation is further supported by the fact that the V_{1a} receptor genes are virtually identical between the two vole species that differ in affiliative behavior, except for the presence in prairie voles of a small segment in the region of the gene that is likely to regulate its expression. Thus, it appears that subtle changes in the expression pattern of the vasopressin receptor V_{1a} may account for these substantial differences in social behavior in these rodent species.

7. Migration paths of European Warblers : For several decades studies conducted on the European Sylvia warblers (Garden warblers -*Sylvia borin* and Blackcaps-*Sylvia atricapailla* particularly) have shed light on the various aspects of migration such as the underlying mechanisms. These birds have proved to be excellent models for studying migration as they contain migrant populations that fly to different regions as well as non-migrant populations that remain sedentary.

- The Blackcaps breed throughout Europe, parts of western Asia and North Africa; those populations from Central and North Europe migrate to Southern Europe and parts of North Africa.
- Similarly, the Garden warblers migrate from Europe to Northern Africa.

Cross breeding studies on these species revealed the following

- In studies on Blackcaps from southern Germany, researchers were able to show that hybrids of migratory and non-migratory populations developed migratory activity; the degree of activity was found to be intermediate to that of the parents.
- Using a series of cross breeding experiments it was determined that the direction of orientation was also under genetic control as the offspring of migratory and non-migratory species showed directional preferences that matched those of the migratory parents.
- Cross breeding experiments between Austrian Blackcaps (which fly in a southeasterly

direction) and German Blackcaps (which fly southwesterly) determinec that the offspring flew in an intermediary direction.

- Additional cross breeding experiments between German Blackcaps and Blackcaps from the Canaries showed that the pattern of activity was found to be intermediate to that of the parents.

Thus through several studies on European warblers, it was shown that the ability to migrate is hereditary as well as the direction in which the birds migrate. The degree of activity (intense migration versus sedentariness) was also inherited.

7. Cricket song : Whereas Drosophila males tap females to make sure they are the right species, the cricket female (Gryllidae) listens for the appropriate song to find the right male. The male cricket's song is species specific, and a number of experiments have shown that the female can correctly identify the song of her male conspecific. When two species of crickets were crossed, it was found that the F1 hybrid sang a song that was intermediate between those of both species. And even more surprisingly, the female hybrid is attracted more to her hybrid brother than to either parental strain.

EXAMPLES IN HUMANS

1. Schizophrenia : Schizophrenia is a chronic and disabling mental illness involving onset in early adulthood; deterioration in level of function; and psychotic symptoms (inability to distinguish between one's thoughts and reality), such as auditory and visual hallucinations and paranoia. Until the 1960s, many psychiatrists accepted the idea that schizophrenia was caused principally by family environmental factors, for example, the interaction between the pre schizophrenic child and his or her mother. A series of landmark adoption studies carried out in the 1960s demonstrated that the risk for schizophrenia of adopted-away offspring of schizophrenic parents was higher than the risk to adopted-away offspring of non schizophrenic parents. Those results were confirmed by subsequent studies. In addition, twin studies consistently have shown increased concordance (sharing of diagnosis) for identical compared to fraternal twins. Family studies also have shown increased rates of schizophrenia in siblings, parents, and children of schizophrenics. Recent linkage studies have provided fairly consistent evidence that a gene predisposing to schizophrenia resides on chromosome 6 and less consistent but still reasonably good evidence for genes in other chromosomal locations.

2. Dyslexia : Genes have been mapped for specific reading disability (dyslexia) in humans. Reading disability has been shown to run in families, where siblings and parents of reading-disabled children perform worse on reading tests than siblings and parents of children who are not reading disabled. Twin studies have shown higher concordance rates in identical twins compared to fraternal twins, which suggests that reading disability is moderately genetic in origin. Recent

research has provided evidence that there is a gene involved in reading disability on chromosome 6 and another on chromosome 15. Although only the approximate locations of the genes have been identified, and not the genes themselves or the mechanism through which they influence reading disability, it is interesting that the two genes appear to influence different component processes of reading skill. Phonological awareness is related to a region on chromosome 6 and single-word decoding is related to a region on chromosome 15.

3. Bipolar affective disorder : Bipolar affective disorder, also known as manic-depressive illness, is characterized by both episodes of depression (sad mood, alterations in sleep and appetite, feelings of hopelessness and worthlessness) and mania (euphoric or irritable mood, increased activity, racing thoughts, and decreased sleep). Bipolar affective disorder is different from major depression, which has a slow onset but generally lasts for months and is more common than bipolar disorders. Bipolar disorder involves rapid mood swings, and the manic periods can be as short as days or as long as months. Family and twin studies have consistently indicated a strong genetic component. Recent linkage studies have identified at least two potential locations for genes that increase susceptibility for bipolar affective disorder, but at present no specific genes have been identified.

4. Alcohol and drug dependence : Both alcohol and drug abuse have distinct and overlapping genetic predisposing factors. This is not surprising given that most drugs of addiction and alcohol act on the same reward pathway in the brain, the nucleus acumbens and ventral tegmentum. There is suggestive evidence for the genetic association of several specific genes and alcohol dependence. There is some evidence that the genetic factors leading to alcohol dependence differ between men and women.

5. General cognitive ability (intelligence) : Intelligence, the general capacity to learn and solve problems, has been shown in numerous studies to be heritable, genetic factors. The observation that there is a significant genetic contribution to intelligence is not seriously disputed because of the amount of work done in this area, an enormous body which has been subject to extremely careful scrutiny. No specific genes contributing to normal variation have been indisputably identified, but many genes contributing to very low intelligence (such as mental retardation) are known.

Conclusion

Genetic factors, once thought to be straightforward and fixed, are mind-numbingly complex and responsive to outside stimuli, and they are only one of many elements that affect behavior. Behavior genetics conceives of behavior as an essentially biological phenomenon, in fact, as a most essential mechanism of species adaptation and survival. Every aspect of behavior that is studied is intimately involved in the ability of organisms to adapt to their environment. Through behavior genetics, animal behavior is linked with the fundamental biological phenomena of

reproduction and evolution. Significantly parallels can be drawn between such genes-and-behavior systems in animals and those in humans, with hope for potential future treatment of abnormal behaviors such as schizophrenia and autism.

PRACTICE QUESTIONS :

- ***Multiple choices***

1. Changes in gene frequencies is the subject matter of
   a. Classical genetics
   b. Quantitative genetics
   c. Population genetics
   d. Developmental genetics
2. Observation approach to the study of population genetics is used for
   a. Human beings
   b. animals
   c. Both a and b
   d. Neither a nor b
3. Which of the following twins are genetically identical?
   a. Monozygotic
   b. Dizygotic
   c. Fraternal
   d. None of the above
4. Which chromosome in human beings contains the gene for single word decoding?
   a. 6
   b. 8
   c. 15
   d. 12
5. Sexual behavior in *Drosophila* is controlled by the gene named
   a. *fru*
   b *for*
   c. *Amfor*
   d. V_{1a}
6. A gene known to influence a particular trait is called
   a. QTL
   b. SNP
   c. Candidate gene
   d. Knockout gene
7. Foraging behavior in *Drosophila* is controlled by the gene named
   a. *fru*
   b *for*
   c. *Amfor*
   d. V_{1a}
8. Family studies in humans provide information on
   a. Genetic influences on a trait
   b. Mode of inheritance of traits
   c. Number of genes involved in multiple traits
   d. All of the above

9. Tryon studied rats to decipher the effect of genes on

a. Foraging
b. Sexual behavior
c. Learning
d. Locomotion

10. Drosophila larvae having long food finding paths are called

a. Foragers
b. Sitters
c. Rovers
d. Nurses

- ***Very short answer type***

1. What does genetic epidemiology deal with?
2. Name the approaches to the study of genetic epidemiology in humans.
3. What is a candidate gene?
4. What is QTL mapping?
5. How are transgenic mice designed?
6. What is the name given to reading disability in humans?
7. What is schizophrenia?
8. Name an innate behavior controlled by genes in animals.
9. What component of behavior is under the control of *for*^{s} gene in Drosophila?
10. Give one characteristic feature of inbred animals.

- ***Short answer type***

1. Give five arguments in favor of genetic basis of behavior.
2. What are the basic queries in any study of behavior genetics?
3. Explain the genetic basis of social behavior of rodents.

- ***Write short notes on***

1. Knockout mice
2. Candidate gene approach
3. Twin studies
4. Genetic basis of dyslexia

- ***Long answer type***

1. What is behavior genetics? Enumerate the techniques of behavior genetics in animals and cite three examples of genetical control of behavior.