CHAPTER 2

Study of pattern of inheritance of selected courtship traits of

*Drosophila melanogaster*
2.1 Introduction

*Drosophila melanogaster* has a well-characterized sequential pattern of male courtship behavior with the orientation followed by wing extension, wing vibration ("singing"), licking of genitalia, and attempt to court/copulate (Bastock and Manning, 1955; Bastock, 1967; Speith and Ringo, 1983; Hall, 1994a; Greenspan, 1995, 1997; Yamamoto *et al*., 1997; Greenspan and Ferveur, 2000). With mutational analysis, many genes which are responsible for specific male courtship behavior have been identified (Hall *et al*., 1982; Hall, 1994a; Greenspan, 1997; Yamamoto *et al*., 1997, 1998; Goodwin, 1999; Yamamoto and Nakano, 1998, 1999; Greenspan and Ferveur, 2000; Mackay, 2001; Sokolowski, 2001). Although, the basic courtship pattern and mating has been studied in *Drosophila melanogaster* and a few other species, the genetics of sexual behavior is poorly understood. Because of the complexity of these traits both in inheritance and in action, and lack of appropriate techniques for the genetic analysis of these complex traits, little is known about their inheritance. However, such knowledge on the genetic structure and the pattern of inheritance is necessary to understand the role of these genes in the development of the complex behavioral phenotype. Now a few modern molecular markers such as Restriction Fragment Length Polymorphs (RFLP) and Rapid Amplified DNA polymorphism (RAPD) are available to analyze such complex polygenic traits. Application of these techniques for understanding the genetic structure of such complex traits requires a preliminary knowledge on the distribution pattern of genes on the karyotype. Although complete genetic map along with the sequence is available for *Drosophila* the genetic architecture and the nature of genetic control of behavioral traits has not yet been studied. Therefore, the present study has been made to locate the sexual behavioral traits viz., orientation, tapping, wing vibration and copulation duration on
the chromosomes of *D. melanogaster* and to know their pattern of inheritance. The genetic crosses of Mendelian inheritance and linkage studies were made in the present study using the courtship variants selected (vide Chapter 1).

### 2.2 Materials and methods

**Fly stocks used:** The high and low lines of courtship traits selected from the Oregon K (*org k*) strain of *Drosophila melanogaster* were used for the present study. The courtship traits studied were orientation (fast orientation [*for*] and slow orientation [*sor*]), tapping (maximum tapping [*mxtp*] and minimum tapping [*mntp*]), wing vibration (maximum wing vibration [*mxwv*] and minimum wing vibration [*mnwv*]) and copulation duration (long copulation duration [*lcd*] and short copulation duration [*scd*]). Yellow body (*y*), brown eye (*bw*) and ebony body (*e*) mutants were used as I, II and III chromosome markers respectively. These stocks were reared on wheat cream agar medium seeded with yeast and maintained at 20±2°C.

**Crossing experiment:** To study the pattern of inheritance, three sets of experiments were conducted. 1. First it was assumed that the variants of a given courtship trait (eg maximum tapping and minimum tapping, [*mxtp*] and [*mntp*]) are monogenic and are alleles of the same locus; 2. Second it was assumed that the variants of the courtship traits are digenic, controlled by two alleles. 3. If any one of the above assumptions is true, the genes should have been located on any one of the four chromosomes. To verify these assumptions linkage experiments were conducted using appropriate markers. The possible combinations of crosses made are represented in Figs. 5 to Figs. 11.
Parents: 

\[ \text{for} \quad \text{for} \quad \text{sor} \quad \text{sor} \]

Genotype:

\[ \begin{array}{c}
\text{for} \\
\hline \\
\text{sor} \\
\text{sor}
\end{array} \]

Gametes:

\[ \begin{array}{c}
\text{for} \\
\text{sor}
\end{array} \times \begin{array}{c}
\text{for} \\
\text{sor}
\end{array} \]

F1 progeny:

\[ \begin{array}{c}
\text{for} \\
\text{sor}
\end{array} \]

If for is dominant, phenotype of F1 male is slow orienting.
If for is not dominant, phenotype of F1 male is slow orienting.

\[ \text{self crossed} \]

Gametes:

\[ \begin{array}{c}
\text{for} \\
\text{sor} \\
\text{sor}
\end{array} \times \begin{array}{c}
\text{for} \\
\text{sor} \\
\text{sor}
\end{array} \]

F2 progeny:

\[ \begin{array}{c}
\text{for} \\
\text{sor} \\
\text{sor} \\
\text{sor}
\end{array} \]

If for is dominant, phenotype of F2 male is fast and slow orienting in the ratio of 1:1.
If for is not dominant, phenotype of F2 male is normal and slow orienting in the ratio of 1:1.

Test cross

\[ \text{for} \quad \text{for} \quad \text{sor} \quad \text{sor} \]

Gametes:

\[ \begin{array}{c}
\text{for} \\
\text{sor} \\
\text{sor}
\end{array} \times \begin{array}{c}
\text{for} \\
\text{sor} \\
\text{sor}
\end{array} \]

Test cross progeny:

\[ \begin{array}{c}
\text{for} \\
\text{sor} \\
\text{sor} \\
\text{sor}
\end{array} \]

If for is dominant, phenotype of test cross male progeny is fast and slow orienting in the ratio of 1:1.
If for is not dominant, phenotype of test cross male progeny is normal and slow orienting in the ratio of 1:1.

Fig 5 - If the trait is monogenic and X-linked
Parents: ![Diagram](image.png)

Genotype: 
- `for` ![Diagram](image.png)
- `sor` ![Diagram](image.png)

Gametes: 
- `for` ![Diagram](image.png)
- `sor` ![Diagram](image.png)

F1 progeny: 
- `for` ![Diagram](image.png)
- `sor` ![Diagram](image.png)

If `for` is dominant, phenotype of F1 male is fast orienting.
If `sor` is dominant, phenotype of F1 male is slow orienting.
If both are not dominant, phenotype of F1 male is normal.

self crossed

Gametes: 
- `for` ![Diagram](image.png)
- `sor` ![Diagram](image.png)
- `for` ![Diagram](image.png)
- `sor` ![Diagram](image.png)

F2 progeny: 
- `for` ![Diagram](image.png)
- `sor` ![Diagram](image.png)
- `for` ![Diagram](image.png)
- `sor` ![Diagram](image.png)

If `for` is dominant, phenotype of F2 male is fast and slow orienting in the ratio of 3:1.
If `sor` is dominant, phenotype of F2 male is fast and slow orienting in the ratio of 1:3.
If both are not dominant, phenotype of F2 male is fast orienting, normal and slow orienting in the ratio of 1:2:1.

Test cross 

Gametes: 
- `for` ![Diagram](image.png)
- `sor` ![Diagram](image.png)
- `sor` ![Diagram](image.png)

Test cross progeny: 
- `for` ![Diagram](image.png)
- `sor` ![Diagram](image.png)
- `sor` ![Diagram](image.png)

If `for` is dominant, phenotype of test cross male progeny is fast and slow orienting in the ratio of 1:1.
If `sor` is dominant, phenotype of test cross male progeny is slow orienting.
If both are not dominant, phenotype of test cross male progeny is normal and slow orienting in the ratio of 1:1.

Fig 6 - If the trait is monogenic and autosomal
Parents:  
\[ \text{for} X + \text{for} \]

Genotype:  
\[ + + \]

Gametes:  
\[ + \text{for} \]

F1 progeny:  
\[ + + \]

If \textit{for} is dominant, phenotype of F1 male is normal.
If \textit{for} is not dominant, phenotype of F1 male is normal.

self crossed

Gametes:  
\[ + + \]

F2 progeny:  
\[ + + + + \]

If \textit{for} is dominant, phenotype of F2 male is fast orienting and normal in the ratio of 1:1.
If \textit{for} is not dominant, phenotype of F2 male is normal.

Test cross  
\[ F1 \text{ for} X \text{ for} \]

Gametes:  
\[ + + \]

Test cross progeny:  
\[ + + + + \]

If \textit{for} is dominant, phenotype of test cross male progeny is fast orienting and normal in the ratio of 1:1.
If \textit{for} is not dominant, phenotype of test cross male progeny is normal.

Fig 7 - If the trait is digenic and X-linked (direct cross)
Parents:  
\[ 
\begin{array}{c}
\text{for} \\
+ \\
\end{array}
\begin{array}{c}
\text{for} \\
+ \\
\end{array}
\] 

Genotype:  
\[ 
\begin{array}{c}
\text{for} \\
+ \\
\end{array}
\begin{array}{c}
\text{for} \\
+ \\
\end{array}
\] 

Gametes:  
\[ 
\begin{array}{c}
\text{for} \\
+ \\
\end{array}
\begin{array}{c}
\text{for} \\
+ \\
\end{array}
\] 

F1 progeny:  
\[ 
\begin{array}{c}
\text{for} \\
+ \\
\end{array}
\begin{array}{c}
\text{for} \\
+ \\
\end{array}
\] 

If \textit{for} is dominant, phenotype of F1 male is fast orienting.  
If \textit{for} is not dominant, phenotype of F1 male is normal.  

self crossed  

Gametes:  
\[ 
\begin{array}{c}
\text{for} \\
+ \\
\end{array}
\begin{array}{c}
\text{for} \\
+ \\
\end{array}
\] 

F2 progeny:  
\[ 
\begin{array}{c}
\text{for} \\
+ \\
\end{array}
\begin{array}{c}
\text{for} \\
+ \\
\end{array}
\begin{array}{c}
\text{for} \\
+ \\
\end{array}
\begin{array}{c}
\text{for} \\
+ \\
\end{array}
\] 

If \textit{for} is dominant, phenotype of F2 male is fast orienting and normal in the ratio of 1:1.  
If \textit{for} is not dominant, phenotype of F2 male is normal.  

\textbf{Test cross}  
\[ 
\begin{array}{c}
\text{for} \\
+ \\
\end{array}
\begin{array}{c}
\text{F1} \\
\text{for} \\
\end{array}
\begin{array}{c}
\text{for} \\
+ \\
\end{array}
\] 

Gametes:  
\[ 
\begin{array}{c}
\text{for} \\
+ \\
\end{array}
\begin{array}{c}
\text{for} \\
+ \\
\end{array}
\] 

Test cross progeny:  
\[ 
\begin{array}{c}
\text{for} \\
+ \\
\end{array}
\begin{array}{c}
\text{for} \\
+ \\
\end{array}
\begin{array}{c}
\text{for} \\
+ \\
\end{array}
\begin{array}{c}
\text{for} \\
+ \\
\end{array}
\] 

If \textit{for} is dominant, phenotype of test cross male progeny is fast orienting and normal in the ratio of 1:1.  
If \textit{for} is not dominant, phenotype of test cross male progeny is normal.  

Fig 8 - If the trait is digenic and X-linked (reciprocal cross)
Parents: \( \square \square for X + \square \square \)

Genotype:

\( for \quad + \)

\( for \quad + \)

Gametes:

\( for \quad , \quad + \)

F1 progeny:

\( for \quad + \)

\( + \)

If \( for \) is dominant, phenotype of F1 male is fast oriented.
If \( for \) is not dominant, phenotype of F1 male is normal.

self crossed

Gametes:

\( for \quad , \quad + \quad \times \quad for \quad , \quad + \)

F2 progeny:

\( for \quad for \quad for \quad + \)

\( for \quad + \quad + \quad + \)

If \( for \) is dominant, phenotype of F2 male is fast orienting and normal in the ratio of 3:1.
If \( for \) is not dominant, phenotype of F2 male is fast orienting and normal in the ratio of 1:3.

Test cross

\( \square \square F1 X for \quad \square \square \)

Gametes:

\( for \quad , \quad + \quad \times \quad for \)

Test cross progeny:

\( for \quad + \)

\( for \quad for \)

If \( for \) is dominant, phenotype of test cross male progeny is fast orienting.
If \( for \) is not dominant, phenotype of test cross male progeny is fast orienting and normal in the ratio of 1:1.

Fig 9 - If the trait is digenic and autosomal (direct cross)
Parents: $\text{ for } X + \text{ for }$

Genotype: $\begin{array}{c}
\text{ for } \\
\text{ for }
\end{array}$ $\begin{array}{c}
\text{ + } \\
\text{ + }
\end{array}$

Gametes: $\begin{array}{c}
\text{ for } \\
\text{ + }
\end{array}$

F1 progeny: $\begin{array}{c}
\text{ for } \\
\text{ + }
\end{array}$

If $\text{ for }$ is dominant, phenotype of F1 male is fast oriented.
If $\text{ for }$ is not dominant, phenotype of F1 male is normal.

self crossed

Gametes: $\begin{array}{c}
\text{ for } \\
\text{ + }
\end{array}$ $\times$ $\begin{array}{c}
\text{ for } \\
\text{ + }
\end{array}$

F2 progeny: $\begin{array}{c}
\text{ for } \\
\text{ for } \\
\text{ for } \\
\text{ for }
\end{array}$ $\begin{array}{c}
\text{ + } \\
\text{ + } \\
\text{ + } \\
\text{ + }
\end{array}$

If $\text{ for }$ is dominant, phenotype of F2 male is fast orienting and normal in the ratio of 3:1.
If $\text{ for }$ is not dominant, phenotype of F2 male is fast orienting and normal in the ratio of 1:3.

Test cross

$\text{ for } X \text{ for }$

Gametes: $\begin{array}{c}
\text{ for } \\
\text{ + }
\end{array}$ $\times$ $\begin{array}{c}
\text{ for }
\end{array}$

Test cross progeny: $\begin{array}{c}
\text{ for } \\
\text{ for }
\end{array}$

If $\text{ for }$ is dominant, phenotype of test cross male progeny is fast orienting.
If $\text{ for }$ is not dominant, phenotype of test cross male progeny is fast orienting and normal in the ratio of 1:1.

Fig 10 - If the trait is digenic and autosomal (reciprocal cross)
Fast orienting wildtype X normal orienting brown eye

Parents:

\[(\text{for for } ++) \times (++ \text{ bw bw})\]

Genotype:

\[
\begin{array}{cccc}
\text{for} & + & + & \text{bw} \\
+ & + & + & \text{bw} \\
\end{array}
\]

Gametes:

\[
\begin{array}{cccc}
\text{for} & \text{for} & + & + \\
+ & + & \text{bw} & \text{bw} \\
\end{array}
\]

F1 progeny: X selfing

\[
\begin{array}{cccc}
\text{for} & \text{for} & \text{bw} & \text{bw} \\
\text{bw} & \text{bw} & + & + \\
\end{array}
\]

F2 progeny:

\[
\begin{array}{cccc}
\text{for} & \text{for} & + & + \\
\text{bw} & \text{bw} & + & + \\
\text{bw} & \text{bw} & + & + \\
\end{array}
\]

Phenotypes of F2 progeny:

- normal orienting wildtype - 9
- fast orienting wildtype - 3
- normal orienting brown eye - 3
- fast orienting brown eye - 3

F2 progeny ratio - 9 : 3 : 3 : 1

Test cross ratio - 1 : 1 : 1 : 1

Fig 11 - Expected progeny when the trait is digenic and located on autosome (2nd and 3rd chromosome)
Thus, to verify the first assumption, the variant of one courtship trait selected (vide Chapter 1) was crossed with another variant of the same trait (eg. \textit{mxtp}♂ X \textit{mntp}♀). The F1 progeny was inbred and F2 progeny was obtained. To verify the second assumption, the same set of crosses was made with wild type and the possible genotypes and phenotypes for Parents, F1 and F2 were written. To know the linkage of courtship traits on a given chromosome, each of these selected lines was crossed with a mutant marker located on that chromosome. The test crosses were made in all these cases. The reciprocal crosses were also made to identify the sex linkage if any.

Following is the list of crosses done between the variants of all the traits of \textit{org k}, the mutant markers of I, II and III chromosome. The F\textsubscript{1} progeny was test crossed. The mutant and behavioral phenotypes obtained in the F\textsubscript{2} progeny of both direct, reciprocal and test crosses were scored to understand segregation/assortment/linkage. The data obtained were subjected for statistical analysis using \(\chi^2\) test.

Following are the sets of crosses conducted to know whether the courtship variants segregate or not.

a) Experiment I

| Parents             | : high line \textit{org k}♂ X low line \textit{org k}♀  
|                    | (e.g. \textit{mxtp}♂ X \textit{mntp}♀) |
| F1                  | : selfing |
| F2                  | : observation of phenotype and genotype |
| Expected phenotype  | : high line, low line |
| Expected ratio      | : 3:1 or 1:3 |
|                     | : test cross -1:1 |
b) Experiment II (Reciprocal cross)

Parents : high line org k ♀ X low line org k ♂

F1 : selfing

F2 : observation of phenotype and genotype

Expected phenotype : low line, high line

Expected ratio : 3:1 or 1:3

: test cross -1:1

c) Experiment III

Parents : courtship variant ♂ X normal (org k) ♀

F1 : selfing

F2 progeny : observation of phenotype and genotype

Expected phenotype : normal, courtship variant

Expected ratio : 3:1 or 1:3

: test cross -1:1

d) Experiment IV

Parents : courtship variant ♀ X normal (org k) ♂

F1 : selfing

F2 progeny : observation of phenotype and genotype

Expected phenotype : normal, courtship variant

Expected ratio : 3:1 or 1:3

: test cross -1:1
Following sets of crosses were made involving a wild type, one courtship variant fly with a mutant marker, and normal courtship act (eg. *forfor/++ X ++/yy*).

e) Experiment V

Parents : courtship variant ♂ X marker of I, II, III chromosome ♀
F1 : selfing
F2 progeny : observation of phenotype and genotype
Expected phenotype : wild type-wild type (normal), courtship variant-wild type,
wild type- mutant, courtship variant-mutant
Expected ratio : 9:3:3:1
: test cross -1:1:1:1

f) Experiment VI

Parents : courtship variant ♂ X marker of I, II, III chromosome ♀
F1 : selfing
F2 progeny : observation of phenotype and genotype
Expected phenotype : wild type -wild type (normal), courtship variant-wild
type, wild type- mutant, courtship variant-mutant
Expected ratio : 9:3:3:1
: test cross -1:1:1:1
2.3 Results

Figures 5 to 11 show diagrammatic representation of the possibilities of the inheritance pattern of different courtship traits. The parental chromosomal combinations, the gametes produced, F1 progeny, F2 progeny, test cross result of both direct and reciprocal crosses are shown here. The pattern of inheritance if the character is monogenic, if digenic or even if it is sex linked is all represented in these figures.

Experiment I (Direct cross): Table 1 shows the results of cross between variants of courtship traits (high line male and low line female) viz., orientation (for, sor), tapping (mxtp, mntp), wing vibration (mxwv, mnwv) and copulation duration (lcd, scd) and their test crosses. The phenotype of the flies obtained in the F1 generation, the F2 generation and test crosses are also provided in this table. The number of flies obtained in each of these crosses in F2 generation and the test cross are also shown here. If the two lines segregate, then the expected ratio in the F2 generation is 3:1 and the test cross or test cross ratio should be 1:1. The results showed that in all the crosses, the high line and low line segregated in 3:1 proportion. The test cross ratios were 1:1. The χ² values are not significant at 0.05 level.

In the cross between male of high line (for) and female of low line (sor) of orientation the F1 flies were with normal courtship behavior. The F2 flies were both fast orienting and slow orienting. Some males oriented fast and some males oriented slow. The number of flies obtained was 244 and 88 respectively and they segregated in 3:1 ratio. The χ² value was 0.402 and it was not significant at 0.05 level. In the test cross of the above combination, all the flies in F1 generation were showing normal phenotype and normal courtship behavior. In F2 generation the flies were both fast orienting and slow orienting. They segregated in 1:1 ratio and the number of flies
obtained was 197 and 189 respectively. The $\chi^2$ value was 0.166 which was not significant at 0.05 level.

In the cross between male of high line ($mxtp$) and female of low line ($mntp$) of tapping the phenotype of the F1 generation was normal. In the F2 generation, progeny was of parental type only. The phenotypes of the F2 generation were maximum tapping and minimum tapping. The number of flies obtained was 232 and 72 respectively and they were segregated in 3:1 ratio. The $\chi^2$ value obtained was 0.280 and it was not significant at 0.05 level. In the test cross of the above combination, all the flies in F1 generation were showing normal phenotype and normal courtship behavior. In F2 generation the observed phenotypes were maximum tapping and minimum tapping only. They segregated in 1:1 ratio and the number of flies obtained was 149 and 153 respectively. The $\chi^2$ value is 0.053 which was non-significant at 0.05 level.

In the cross between male of high line ($mxwv$) and female of low line ($mnwv$) of wing vibration, the phenotype of the F1 flies were with normal courtship behavior. The F2 progeny showed the phenotypes similar to parental type only. The phenotypes of the F2 generation were maximum wing vibration and minimum wing vibration. The number of flies obtained was 288 and 104 respectively and they were segregated in 3:1 ratio. The $\chi^2$ value was 0.490 and it was not significant at 0.05 level. In the test cross of the above combination, all the flies in F1 generation were showing normal phenotype and normal courtship behavior. In F2 generation the observed phenotypes were maximum wing vibration and minimum wing vibration only. They segregated in 1:1 ratio and the number of flies obtained was 201 and 195 respectively. The $\chi^2$ value was 0.091 which was not significant at 0.05 level.

In the cross between male of high line ($lcd$) and female of low line ($scd$) of copulation duration, the phenotype of the F1 flies were with normal courtship behavior. The F2
progeny showed the phenotype were of parental type only. The phenotype of the F2 generation was long copulation duration and short copulation duration. The number of flies obtained was 330 and 103 respectively and they were segregated in 3:1 ratio. The $\chi^2$ value obtained was 0.110 and it was not significant at 0.05 level. In the test cross of the above combination, all the flies in F1 generation were showing normal phenotype and normal courtship behavior. In F2 generation the observed phenotypes were long copulation duration and short copulation duration. They segregated in 1:1 ratio and the number of flies obtained was 187 and 171 respectively. The $\chi^2$ value was 0.684 which was not significant at 0.05 level.

**Experiment II (Reciprocal cross):** The results of the reciprocal cross of the above, involving the female of high line and the male of low line of courtship traits viz., orientation ($for$, $sor$), tapping ($mxtp$, $mntp$), wing vibration ($mxwv$, $mnwv$) and copulation duration ($lcd$, $scd$) and their test crosses are given in table 2. If there is simple segregation, expected ratio in the F2 generation is 3:1 and the test cross or test cross ratio should be 1:1 in the reciprocal cross also. The number of flies obtained in each of these crosses in F2 generation and the test cross occurred as per the expectation. The ratios of crosses of all courtship traits in the F2 generation were 3:1 and test cross was 1:1. The $\chi^2$ values were non-significant at 0.05 level. Moreover, the ratios of both direct cross and the reciprocal cross in the F2 generation and test crosses were also similar. The male female ratio in both these experiments remained equal indicating the absence of any criss-cross inheritance.

In the cross between female of high line ($for$) and male of low line ($sor$) of orientation, the phenotype of the F1 flies were normal with normal courtship behavior. The F2 progeny showed the phenotype of parental type only. The F2
generation consisted of flies with both slow orientation and fast orientation. The number of flies obtained was 268 and 76 respectively and they segregated in 3:1 ratio. The $\chi^2$ value obtained was 1.550 and it was not significant at 0.05 level. The test cross progeny consisted of flies which oriented fast as well as slow. They segregated in 1:1 ratio and the number of flies obtained was 159 and 165 respectively. The $\chi^2$ value was 0.110 which was not significant at 0.05 level.

In the cross between female of high line ($mxtp$) and male of low line ($mntp$) of tapping the F1 flies were with normal courtship behavior. In the F2 generation the flies were of the phenotype resembling parents. The phenotypes of the F2 generation were minimum tapping and maximum tapping. The number of flies obtained was 283 and 89 respectively and they segregated in 3:1 ratio. The $\chi^2$ value was 0.175 and it was not significant at 0.05 level. In the test cross of the above, the observed phenotypes were maximum tapping and minimum tapping only. They segregated in 1:1 ratio and the number of flies obtained was 139 and 147 respectively. The $\chi^2$ value was 0.224 which was insignificant at 0.05 level.

In the cross between female of high line ($mxwv$) and male of low line ($mnwv$) of wing vibration, the F1 flies were with normal courtship behavior. The F2 generation, progeny showed the phenotype which were of parental type only. The phenotypes of the F2 generation were minimum wing vibration and maximum wing vibration. The number of flies obtained was 303 and 101 respectively and they are segregated in 3:1 ratio. The $\chi^2$ value was 0.0 and it was not significant at 0.05 level. In the test cross, maximum wing vibration and minimum wing vibration segregated in 1:1 ratio and the number of flies obtained was 170 and 178 respectively. The $\chi^2$ value was 0.184 and it was insignificant at 0.05 level.
In the cross between female of high line (lcd) and male of low line (scd) of copulation duration, the phenotype of the F1 flies was normal. In the F2 generation, the progeny showed the phenotype similar to the parental type. The phenotypes of the F2 generation were short copulation duration and long copulation duration. The number of flies obtained was 305 and 107 respectively and they segregated in 3:1 ratio. The χ² value was 0.207 and it was non-significant at 0.05 level. In the test cross the two characteristics segregated in 1:1 ratio and the number of flies obtained was 208 and 182 respectively. The χ² value was 1.733 and this value was statistically insignificant.
<table>
<thead>
<tr>
<th>Crosses</th>
<th>F1 phenotype</th>
<th>F2 phenotype</th>
<th>Number of flies of F2 progeny observed</th>
<th>$\chi^2$ value</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td></td>
<td>DC</td>
<td>TC</td>
</tr>
<tr>
<td>for X sor</td>
<td>normal</td>
<td>for, sor</td>
<td>244, 88</td>
<td>197, 189</td>
</tr>
<tr>
<td>mxtp X mntp</td>
<td>normal</td>
<td>mxtp, mntp</td>
<td>232, 72</td>
<td>149, 153</td>
</tr>
<tr>
<td>mxxwv X mntwv</td>
<td>normal</td>
<td>mxxwv, mntwv</td>
<td>288, 104</td>
<td>201, 195</td>
</tr>
<tr>
<td>lcd X scd</td>
<td>normal</td>
<td>lcd, scd</td>
<td>330, 103</td>
<td>187, 171</td>
</tr>
</tbody>
</table>

*p value significant at 0.05 level

Table 1 showing the results of cross between high line male and low line female of courtship traits viz., orientation (for, sor), tapping (mxtp, mntp), wing vibration (mxxwv, mntwv) and copulation duration (lcd, scd) and their test crosses (DC=direct cross, TC=test cross).

<table>
<thead>
<tr>
<th>Crosses</th>
<th>F1 phenotype</th>
<th>F2 phenotype</th>
<th>Number of flies of F2 progeny observed</th>
<th>$\chi^2$ value</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td></td>
<td>RC</td>
<td>TC</td>
</tr>
<tr>
<td>for X sor</td>
<td>normal</td>
<td>for, sor</td>
<td>76, 268</td>
<td>159, 165</td>
</tr>
<tr>
<td>mxtp X mntp</td>
<td>normal</td>
<td>mxtp, mntp</td>
<td>89, 283</td>
<td>139, 147</td>
</tr>
<tr>
<td>mxxwv X mntwv</td>
<td>normal</td>
<td>mxxwv, mntwv</td>
<td>101, 303</td>
<td>170, 178</td>
</tr>
<tr>
<td>lcd X scd</td>
<td>normal</td>
<td>lcd, scd</td>
<td>107, 305</td>
<td>208, 182</td>
</tr>
</tbody>
</table>

*p value significant at 0.05 level

Table 2 showing the results of cross between high line female and low line male of courtship traits viz., orientation (for, sor), tapping (mxtp, mntp), wing vibration (mxxwv, mntwv) and copulation duration (lcd, scd) and their test crosses (RC=reciprocal cross, TC=test cross).
**Experiment III** (Direct cross): The crosses involving the male of high line or low line of courtship variant [viz., orientation (for, sor), tapping (mxtp, mntp), wing vibration (mxxw, mnwv) and copulation duration (lcd, scd)] with female wild type (org k) also showed segregation in the F2 progeny. The phenotype in the F1 was normal and in the F2 the different phenotypes segregated in 3:1 ratio (Table 3). Even in this case the test cross ratios were in the proportion of 1:1 showing the Mendelian pattern of inheritance. The results were non-significant in these crosses also.

In the cross between male of high line (for) and female wild type (++) of orientation the phenotype of the F1 generation flies were with normal courtship behavior. The F2 progeny showed the phenotypes resembling the parents. The phenotypes of the F2 generation were normal orientation and fast orientation. The number of flies obtained was 339 and 121 respectively and they segregated in 3:1 ratio. The $\chi^2$ value was 0.418 and it was not significant at 0.05 level. In the test cross progeny of the above, phenotypes were normal orientation and fast orientation only. They segregated in 1:1 ratio and the number of flies obtained was 205 and 171 respectively. The $\chi^2$ value was 3.074 which was not significant at 0.05 level.

In the cross between male of low line (sor) and female wild type (++) of orientation the phenotype of the F1 flies was normal. The F2 progeny showed the phenotype which was similar to parents. The phenotypes of the F2 generation were normal orientation and slow orientation. The number of flies obtained was 233 and 63 respectively and they segregated in 3:1 ratio. The $\chi^2$ value was 2.180 and it was non-significant at 0.05 level. The test cross result showed both normal orientation and slow orientation. They segregated in 1:1 ratio and the number of flies obtained was 160 and 152 respectively. The $\chi^2$ value was 0.205 which was not significant at 0.05 level.
The cross between male of high line \((mxtp)\) and female wild type \((++\)) of tapping, also showed similar results. The phenotype of the flies of F1 generation was normal tapping behavior. In the F2 generation, the progeny showed the phenotype that was similar to parental type. The phenotypes of the F2 generation were normal tapping and maximum tapping. The number of flies obtained was 258 and 94 respectively and they segregated in 3:1 ratio. The \(\chi^2\) value obtained was 0.545 which was not significant at 0.05 level. In the test cross of the above, the progeny consisted of flies with normal tapping and maximum tapping only. They segregated in 1:1 ratio and the number of flies obtained was 187 and 183 respectively. The \(\chi^2\) value was 0.043 which was not significant at 0.05 level.

The cross involving \(mntp\) male and wild type female produced the F1 progeny showing normal tapping behavior. The progeny in the F2 generation exhibited only normal tapping behavior. Obviously, the phenotypes of the F2 generation were normal tapping and minimum tapping. The number of flies obtained was 290 and 98 respectively and they are segregated in 3:1 ratio. The \(\chi^2\) value obtained was 0.014 and it was not significant at 0.05 level. The test cross of the above produced flies with normal tapping and minimum tapping only. They segregated in the proportion of 1:1 ratio and the number of flies obtained was 168 and 154 respectively. The \(\chi^2\) value was 0.608 which is not significant at 0.05 level.

In the cross between male of high line \((mxwv)\) and female wild type \((++\)) of wing vibration, the phenotype of the F1 flies were with normal courtship behavior. In the F2 generation, the flies were of parental phenotype only. The phenotypes of the F2 generation were normal wing vibration and maximum wing vibration. The number of flies obtained was 350 and 102 respectively and they segregated in 3:1 ratio. The \(\chi^2\) value obtained was 1.428 which was not significant at 0.05 level. In the
test cross, the flies showed normal wing vibration and maximum wing vibration. The number of flies obtained were 222 and 208 respectively and it was equal to 1:1 ratio and. The $\chi^2$ value was 0.456 which was not significant at 0.05 level.

In the cross between male of low line ($mnwv$) and female wild type (++) of wing vibration, the F1 flies were with normal courtship behavior. In the F2 progeny, the flies had the phenotype resembling the parents. There were 290 flies which showed normal wing vibration while 98 flies showed minimum vibration. Thus they segregated in 3:1 ratio. The $\chi^2$ value was 0.014 and it was not significant at 0.05 level. The test cross progeny had flies with normal wing vibration and minimum wing vibration only. They segregated in 1:1 ratio and the number of flies obtained was 179 and 167 respectively. The $\chi^2$ value was 0.042 which was not significant at 0.05 level.

In the cross between male flies with long copulation ($lcd$) duration and wild type females (++), F1 flies were all had normal copulation duration. In the F2 generation, the flies had both long copulation duration and normal copulation duration. There were 310 flies with normal duration of copulation and 122 flies with long copulation duration with the ratio of 3:1. The $\chi^2$ value was 2.420 and it was not significant at 0.05 level. The test cross ratio was 1:1 and the number of flies with normal copulation duration and long copulation were 209 and 196 respectively. The $\chi^2$ value was 0.416 which was not significant at 0.05 level.

In the cross between male having short copulation duration ($scd$) and wild type female (++), the F1 flies had normal copulation duration. In the F2 progeny some flies had normal copulation while others had short copulation duration. The number of flies obtained was 306 and 98 respectively and they are segregated in 3:1 ratio. The $\chi^2$ value was 0.118 and it was not significant at 0.05 level. The test cross ratio was 1:1.
with 189 flies having normal copulation duration and another 182 pairs showed short copulation duration. The $\chi^2$ value was 0.132 which was in-significant at 0.05 level.

**Experiment IV** (Reciprocal cross): The results of the reciprocal crosses involving the female of high line or low line of courtship variant [viz., orientation ($for, sor$), tapping ($mxt, mnt$), wing vibration ($mxwv, mnwv$) and copulation duration ($lcd, scd$)] with male wild type ($org k$) is given in table 4. The phenotype of the flies in the F1 was normal. In the F2 generation the courtship phenotype and wild type segregated in 1:3 ratio. Even in this case the test cross ratios were in the proportion of 1:1. The $\chi^2$ values calculated for the differences between the different phenotypes of the F2 progeny from that of the expected was nonsignificant. Furthermore the result obtained in both direct cross and the reciprocal cross was also similar.

In the cross between female of high line ($for$) of orientation and wild type male ($++$), the F1 flies were with normal courtship behavior. The F2 generation consisted of flies of parental type with both normal and fast orientation. The number of flies obtained was 314 and 90 respectively and they segregated in 3:1 ratio. The $\chi^2$ value was 1.60 and it was not significant at 0.05 level. In the test cross, the progeny consisted of 204 flies showing normal orientation and 186 flies showing fast orientation. In other words, they segregated in the proportion of 1:1. The $\chi^2$ value was 0.83 which is not significant at 0.05 level.

Even the cross between involving female originated from slow orienting line ($sor$) and male wild type ($++$), gave similar results. The F1 generation had flies which oriented normally. In the F2 generation, the progeny showed behavior similar to the parental strains. There were 263 flies showing normal orientation and 77 flies showing slow orientation. The ratio of these two phenotypes was 3:1 with the $\chi^2$ value of 1.082
which was insignificant. The test cross result of this cross was also occurred as per expectation. The normal and slow orienting flies appeared in 1:1 proportion. The $\chi^2$ value was 0.790 which was insignificant at 0.05 level.

In the cross between female obtained from maximum tapping line (mxtt) and wild type with normal tapping (++), the F1 flies showed normal tapping behavior. In the F2 generation, the progeny had males with both maximum tapping and normal tapping. The number of flies obtained in the F2 was 232 and 96 respectively and they segregated in 3:1 ratio. The $\chi^2$ value was 2.341 and it was not significant at 0.05 level. In the test cross of the above combination, the phenotypes observed were normal tapping and maximum tapping which appeared in the proportion of 1:1 ratio with the number of flies obtained being 174 and 164 respectively. The $\chi^2$ value was 0.296 which was not significant at 0.05 level.

In the cross between female of low line (mntp) for tapping and male wild type (++) the phenotype of the F1 generation flies were with normal courtship behavior. In the F2 generation, the some males showed minimum tapping and some males exhibited normal level of tapping. Out of 340 flies obtained, 266 exhibited normal tapping and remaining 74 showed minimum tapping. Thus they showed segregation in the ratio of 3:1. The $\chi^2$ value obtained was 1.900 which was non-significant at 0.05 level. In the test cross of the above, males showed either normal or minimum tapping. There were 200 and 182 flies in each category of normal tapping and minimum tapping with the ratio 1:1. The $\chi^2$ value was 0.848 which was not significant at 0.05 level.

The cross involving females obtained from high line (mxwv) and male wild type (++) the phenotype of the F1 flies were with normal courtship behavior. In the F2 generation, the progeny was similar to the parental types. The phenotypes of the F2 generation were normal wing vibration and maximum wing vibration. The number of
flies obtained was 318 and 102 respectively and they segregated in 3:1 ratio. The χ² value obtained was 0.114 and it was not significant at 0.05 level. In the test cross of the above, there were 211 and 201 flies respectively with 1:1 ratio. The χ² value was 0.242 which was not significant at 0.05 level.

In the cross between female of low line (mnwv) and male wild type (++) of wing vibration, the phenotype of the F1 generation flies were with normal courtship behavior. In the F2 generation, progeny showed the phenotype similar to the parental types, i.e. with normal wing vibration and minimum wing vibration. Out of 296 male flies, 214 were normal and 82 were with minimum wing vibration. Thus they were segregated in 3:1 ratio. The χ² value was 1.153 and it was not significant at 0.05 level. In the test cross, males with normal wing vibration and minimum wing vibration appeared in 1:1 ratio and the χ² value 0.790 was not significant at 0.05 level.

In the cross between female with long copulation duration (lcd) and wild type male with normal copulation duration (++), produced the F1 progeny with normal copulation duration. The F2 progeny consisted of both long copulation duration and normal copulation duration which were obtained in the ratio of 3:1. Out of 512 pairs, 140 had long copulation duration and remaining 372 had normal copulation duration. The χ² value obtained was 1.50 which was statistically insignificant at 0.05 level. In the test cross these two phenotypic classes were obtained in the proportion of 1:1 ratio with 180 and 200 pairs respectively. The χ² value was 1.052 which was not significant at 0.05 level.

In the cross between female of copulation duration (scd) and wild type male of normal copulation duration (++), the F1 flies were with normal courtship behavior. In the F2 generation, flies with both normal copulation duration and short copulation duration were produced. In the F2 progeny, there were 270 flies with normal copulation
duration and 94 with short copulation duration. Thus the ratio of the flies of different phenotypic classes in the F2 generation was 3:1 which was statistically insignificant. The test cross result was also obtained as per expectation. The two phenotypic classes, normal and short copulation duration were obtained in the proportion of 1:1 with 204 and 178 flies respectively. The $\chi^2$ value was 1.770 which was not significant at 0.05 level.
<table>
<thead>
<tr>
<th>Crosses</th>
<th>F1 phenotype</th>
<th>F2 progeny phenotype</th>
<th>Number of flies of F2 progeny observed</th>
<th>( \chi^2 ) value</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td></td>
<td>DC</td>
<td>TC</td>
</tr>
<tr>
<td>for/for X ++</td>
<td>normal</td>
<td>for/for, ++</td>
<td>121,339</td>
<td>171,205</td>
</tr>
<tr>
<td>sor/sor X ++</td>
<td>normal</td>
<td>sor/sor, ++</td>
<td>63,233</td>
<td>152,160</td>
</tr>
<tr>
<td>mxtp/mxtp X ++</td>
<td>normal</td>
<td>mxtp/mxtp, ++</td>
<td>94,258</td>
<td>183,187</td>
</tr>
<tr>
<td>mntp/mntp X ++</td>
<td>normal</td>
<td>mntp/mntp, ++</td>
<td>98,290</td>
<td>154,168</td>
</tr>
<tr>
<td>mxvw/mxvw X ++</td>
<td>normal</td>
<td>mxvw/mxvw, ++</td>
<td>102,350</td>
<td>208,222</td>
</tr>
<tr>
<td>mntp/mntp X ++</td>
<td>normal</td>
<td>mntp/mntp, ++</td>
<td>98,290</td>
<td>167,179</td>
</tr>
<tr>
<td>lcld/lcld X ++</td>
<td>normal</td>
<td>lcld/lcld, ++</td>
<td>122,310</td>
<td>196,209</td>
</tr>
<tr>
<td>scd/scd X ++</td>
<td>normal</td>
<td>scd/scd, ++</td>
<td>98,306</td>
<td>182,189</td>
</tr>
</tbody>
</table>

*p value significant at 0.05 level

Table 3 showing the results of cross between male of courtship variants viz., orientation (for, sor), tapping (mxtp, mntp), wing vibration (mxvw, mntp) and copulation duration (lcld, scd) with female wild type strain Oregon K (++) of *D. melanogaster* and their test crosses (DC=direct cross, TC=test cross).

<table>
<thead>
<tr>
<th>Crosses</th>
<th>F1 phenotype</th>
<th>F2 progeny phenotype</th>
<th>Number of flies of F2 progeny observed</th>
<th>( \chi^2 ) value</th>
</tr>
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<tr>
<td></td>
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<td>RC</td>
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<td>for/for, ++</td>
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<td>186,204</td>
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<td>sor/sor, ++</td>
<td>77,263</td>
<td>154,170</td>
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<tr>
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<td>mxtp/mxtp, ++</td>
<td>96,232</td>
<td>164,174</td>
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<td>mntp/mntp, ++</td>
<td>74,266</td>
<td>182,200</td>
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<td>mxvw/mxvw, ++</td>
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<td>201,211</td>
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<td>mntp/mntp, ++</td>
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<td>154,170</td>
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<td>lcld/lcld X ++</td>
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<td>lcld/lcld, ++</td>
<td>140,372</td>
<td>180,200</td>
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<td>scd/scd X ++</td>
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<td>scd/scd, ++</td>
<td>94,270</td>
<td>178,204</td>
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</table>

*p value significant at 0.05 level

Table 4 showing the results of cross between female of courtship variants viz., orientation (for, sor), tapping (mxtp, mntp), wing vibration (mxvw, mntp) and copulation duration (lcld, scd) with male wild type strain Oregon K (++) of *D. melanogaster* and their test crosses (RC=reciprocal cross, TC=test cross).
Linkage Analysis:

With I chromosome marker: The results of cross between male of courtship variants viz., orientation (for, sor), tapping (mxt, mntp), wing vibration (mxwv, mnwv) and copulation duration (lcd, scd) with female of I chromosome marker (yellow body) of D. melanogaster and their test crosses (DC=direct cross, TC=test cross) are shown in table 5. When these courtship variants were crossed with a fly carrying I chromosome marker, yellow body, they assorted independently in the F2 generation in the ratio of 9:3:3:1. The test cross result showed 1:1:1:1 ratio. The reciprocal cross (Table 6) also gave similar results. The $\chi^2$ values calculated for the differences between the different phenotypes of the F2 progeny, and also the test cross progeny from that of the expected was non-significant.

Experiment V (Direct cross): In the cross involving male high line of orientation (for) and female of I chromosome marker (+y), all the F1 progeny obtained were showing wild type phenotype and normal courtship behavior. In F2 generation, four different phenotypic classes viz., wild type with normal orientation, wild type with fast orientation, yellow body mutant with normal orientation and yellow body mutant with fast orientation. The number of flies obtained in F2 generation was 213, 76, 69 and 26 respectively. All the phenotypes assorted independently in the ratio of 9:3:3:1. The $\chi^2$ value was 0.555 which was not significant at 0.05 level. In test cross also four different phenotypes were obtained as mentioned above and the number of flies observed were 106, 111, 102 and 97 respectively. The $\chi^2$ value was 1.019 which was non-significant at 0.05 level.

In the cross involving male with slow orientation (sor) and female of I chromosome marker (+y), all the F1 progeny obtained were showing wild type phenotype and normal courtship behavior. In F2 generation four different type of phenotypes viz.,
wild type with normal orientation, wild type with slow orientation, yellow body mutant with normal orientation and yellow body mutant with slow orientation. The number of flies obtained in F2 generation was 171, 55, 60 and 18 respectively. All the phenotypes segregated independently and assorted in the ratio of 9:3:3:1. The $\chi^2$ value was 0.280 which was insignificant at 0.05 level. The test cross also yielded four different phenotypes as mentioned above and the number of flies observed was 92, 88, 90 and 86 respectively. The $\chi^2$ value obtained was 0.225 which was non-significant at 0.05 level.

In the cross involving male high line of tapping (mxtp) and female of I chromosome marker (+y), all the F1 progeny obtained were showing wild type phenotype and normal courtship behavior. In F2 generation four different phenotypic classes viz., wild type with normal tapping, wild type with maximum tapping, yellow body mutant with normal tapping and yellow body mutant with maximum tapping. The number of flies obtained in F2 generation was 150, 50, 51 and 21 respectively. All the phenotypes segregated independently and assorted in the ratio of 9:3:3:1. The $\chi^2$ value was 1.020 which was not significant at 0.05 level. In test cross four different phenotypes as mentioned above were obtained and the number of flies observed were 71, 68, 70 and 67 respectively. The $\chi^2$ value was 0.145 which was non-significant at 0.05 level.

In the cross involving male low line of tapping (mntp) and female of I chromosome marker (+y), all the F1 progeny obtained were showing wild type phenotype and normal courtship behavior. In F2 generation four different phenotypes viz., wild type with normal tapping, wild type with minimum tapping, yellow body mutant with normal tapping and yellow body mutant minimum tapping were observed. The number of flies obtained in F2 generation was 199, 69, 68 and 24 respectively. All
the phenotypes segregated independently and assorted in the ratio of 9:3:3:1. The $\chi^2$ value was 0.213 which was not significant at 0.05 level. In test cross also four different phenotypic classes as mentioned above were obtained and the number of flies observed was 106, 102, 104 and 100 respectively. The $\chi^2$ value was 0.194 which was nonsignificant at 0.05 level.

In the cross involving male high line of wing vibration ($mxwv$) and female of I chromosome marker (+y), all the F1 progeny obtained had normal body color and normal wing vibration. In F2 generation the author noticed four different type of phenotypes viz., wild type with normal wing vibration, wild type with maximum wing vibration, yellow body mutant with normal wing vibration and yellow body mutant with maximum wing vibration. The number of flies obtained in F2 generation was 203, 68, 65 and 20 respectively. All the phenotypes segregated independently and assorted in the ratio of 9:3:3:1. The $\chi^2$ value was 0.334 which was not significant at 0.05 level. In test cross also four different phenotypes were noticed as above and the number of flies observed were 105, 101, 103 and 101 respectively. The $\chi^2$ value is 0.107 which is non-significant at 0.05 level.

In the cross involving male low line of wing vibration ($mnwv$) and female of I chromosome marker (+y), all the F1 progeny obtained were showing wild type phenotype and normal courtship behavior. Four different type of phenotypes viz., wild type with normal wing vibration, wild type with minimum wing vibration, yellow body mutant with normal wing vibration and yellow body mutant with minimum wing vibration were obtained as per expectations. The number of flies obtained in F2 generation was 232, 78, 79 and 23 respectively. All the phenotypes segregated independently and assorted in the ratio of 9:3:3:1. The $\chi^2$ value was 0.341 which was not significant at 0.05 level. In test cross also four different phenotypes
were observed each with 100, 97, 99 and 98 flies respectively. The $\chi^2$ value was 0.050 which was not significant at 0.05 level.

In the cross involving male high line of copulation duration ($lcd$) and female of I chromosome marker (+y), all the F1 progeny obtained were showing wild type phenotype and normal courtship behavior. In F2 generation following four phenotypic classes were observed, wild type with normal copulation duration, wild type with long copulation duration, yellow body mutant with normal copulation duration and yellow body mutant with long copulation duration. The number of flies obtained in F2 generation was 298, 99, 102 and 37 respectively. All the phenotypes segregated independently and assorted in the ratio of 9:3:3:1. The $\chi^2$ value was 0.451 which was not significant at 0.05 level. In test cross these four phenotypes were observed with 123, 123, 120 and 118 flies respectively. The $\chi^2$ value was 0.149 which was non-significant at 0.05 level.

In the cross involving male low line of copulation duration ($scd$) and female of I chromosome marker (+y), all the F1 progeny obtained were showing wild type phenotype and normal courtship behavior. In F2 generation four different type of phenotypes viz., wild type with normal copulation duration, wild type with short copulation duration, yellow body mutant with normal copulation duration and yellow body mutant with short copulation duration. The number of flies obtained in F2 generation was 161, 53, 55 and 15 respectively. All the phenotypes segregated independently and assorted in the ratio of 9:3:3:1. The $\chi^2$ value was 0.494 which was not significant at 0.05 level. In test cross also four different phenotypes appeared with 80, 78, 79 and 69 flies respectively. The $\chi^2$ value was 1.006 which was non-significant at 0.05 level.
**Experiment VI (Reciprocal cross):** In the cross involving female high line of orientation (*for*) and male of I chromosome marker (+/y), all the F1 progeny obtained were normal with normal orientation. In F2 generation four different type of phenotypes viz., wild type with normal orientation, wild type with fast orientation, yellow body mutant with normal orientation and yellow body mutant with fast orientation. The number of flies obtained in F2 generation was 207, 69, 60 and 20 respectively. All the phenotypes segregated independently and assorted in the ratio of 9:3:3:1. The χ² value was 1.213 which was not significant at 0.05 level. In test cross also four different phenotypes as mentioned above were observed and the number of flies observed was 100, 103, 97 and 94 respectively. The χ² value was 0.456 which was nonsignificant at 0.05 level.

In the cross involving female low line of orientation (*sor*) and male of I chromosome marker (+/y), all the F1 progeny obtained were normal with normal orientation. In F2 generation there were four different type of phenotypes viz., wild type with normal orientation, wild type with slow orientation, yellow body mutant with normal orientation and yellow body mutant with slow orientation. The number of flies obtained in F2 generation was 212, 68, 71 and 25 respectively. All the phenotypes segregated independently and assorted in the ratio of 9:3:3:1. The χ² value was 0.033 which was not significant at 0.05 level. In test cross also four different phenotypes as mentioned above were observed and the number of flies observed was 80, 78, 75 and 75 respectively. The χ² value was 0.234 which is nonsignificant at 0.05 level.

In the cross involving female high line of tapping (*mxtp*) and male of I chromosome marker (+y), all the F1 progeny obtained were normal with normal courtship behavior. In F2 generation as expected four different phenotypic classes appeared viz., wild type with normal tapping, wild type with maximum tapping, yellow body
mutant with normal tapping and yellow body mutant maximum tapping. The number of flies obtained in F2 generation was 186, 61, 65 and 24 respectively. All the phenotypes assorted independently in the ratio of 9:3:3:1. The $\chi^2$ value was 0.603 which was not significant at 0.05 level. In test cross also four different phenotypes as mentioned above were observed with 94, 89, 91 and 86 flies respectively. The $\chi^2$ value was 0.378 which was nonsignificant at 0.05 level.

In the cross involving female low line of tapping (mntp) and male of I chromosome marker (+/y), all the F1 progeny obtained were showing wild type phenotype and normal courtship behavior. In F2 generation four types of flies were found, viz., wild type with normal tapping, wild type with minimum tapping, yellow body mutant with normal tapping and yellow body mutant minimum tapping. The number of flies obtained in F2 generation was 189, 65, 67 and 19 respectively. All the phenotypes assorted independently in the ratio of 9:3:3:1. The $\chi^2$ value was 0.455 which was not significant at 0.05 level. In test cross also four different phenotypic classes as mentioned above were obtained and the number of flies observed was 87, 86, 88 and 83 respectively. The $\chi^2$ value is 0.163 which is nonsignificant at 0.05 level.

In the cross involving female high line of wing vibration (mxwv) and male of I chromosome marker (+/y), all the F1 progeny obtained were with normal body color with normal courtship behavior. In F2 generation four different type of phenotypes viz., wild type with normal wing vibration, wild type with maximum wing vibration, yellow body mutant with normal wing vibration and yellow body mutant with maximum wing vibration. The number of flies obtained in F2 generation was 230, 75, 84 and 27 respectively. All the phenotypes assorted independently in the ratio of 9:3:3:1. The $\chi^2$ value was 0.683 which was not significant at 0.05 level. In test cross four different phenotypes as mentioned above were obtained and the number of flies
observed was 98, 96, 97 and 91 respectively. The $\chi^2$ value was 0.303 which was nonsignificant at 0.05 level.

In the cross involving female low line of wing vibration ($mnwv$) and male of I chromosome marker (+/y), all the F1 flies had normal body color and normal wing vibration. F2 had four different phenotypic classes, viz., wild type with normal wing vibration, wild type with minimum wing vibration, yellow body mutant with normal wing vibration and yellow body mutant with minimum wing vibration. The number of flies obtained in F2 generation was 281, 95, 97 and 31 respectively. All the phenotypes segregated independently and assorted in the ratio of 9:3:3:1. The $\chi^2$ value was 0.099 which was not significant at 0.05 level. In test cross also same phenotypic classes were observed in the proportion of 116, 117, 115 and 114 respectively. The $\chi^2$ value was 0.043 which was nonsignificant at 0.05 level.

In the cross involving female high line of copulation duration ($lcd$) and male of I chromosome marker (+/y), all the F1 progeny obtained were showing wild type phenotype and normal copulation duration. In F2 generation four different type of phenotypes viz., wild type with normal copulation duration, wild type with long copulation duration, yellow body mutant with normal copulation duration and yellow body mutant with long copulation duration. The number of flies obtained in F2 generation was 282, 91, 94 and 29 respectively. All the phenotypes assorted independently in the ratio of 9:3:3:1. The $\chi^2$ value was 0.215 which was not significant at 0.05 level. In test cross also four different phenotypes as mentioned above and the number of flies observed was 115, 112, 114 and 111 respectively. The $\chi^2$ value was 0.088 which was nonsignificant at 0.05 level.

In the cross involving female with short copulation duration ($scd$) and male of I chromosome marker (+/y), all the F1 progeny obtained were with normal body color
and normal copulation duration. In F2 generation four different type of phenotypes viz., wild type with normal copulation duration, wild type with short copulation duration, yellow body mutant with normal copulation duration and yellow body mutant with short copulation duration were obtained. The number of flies obtained in F2 generation was 211, 67, 70 and 20 respectively. The phenotypic ratio of this generation was of 9:3:3:1. The $\chi^2$ value was 0.540 which was not significant at 0.05 level. In test cross four different phenotypic classes were obtained with 90, 84, 79 and 75 flies respectively. The $\chi^2$ value was 1.536 which was nonsignificant at 0.05 level.

**With second chromosome marker:** The results of the cross involving the male of courtship variants [viz., orientation (*for*, *sor*), tapping (*mxtp*, *mntp*), wing vibration (*mxwv*, *mnwv*) and copulation duration (*lcd*, *scd*)] and female with the II chromosome marker (brown eye) of *D. melanogaster* are shown in table 7. As expected, the study showed that the flies produced in the F1 progeny in all the crosses were normal. On the contrary, the result of the F2 progeny was different from the expected. The F2 progeny of the cross involving the high line and low lines of orientation (*for* and *sor*) and the tapping (*mxtp* and *mntp*) did not show the assortment in the proportion of 9:3:3:1. The test cross result was also different from the expectation of 1:1:1:1. The $\chi^2$ test showed that the difference between different classes of phenotypes in both F2 and test cross was significant. The crosses involving wing vibration and copulation duration produced the progeny as per the expectation. The F2 progeny occurred in the proportion of 9:3:3:1 and the test cross were in the proportion of 1:1:1:1 which was non-significant through $\chi^2$ test. Similar results were obtained even in the reciprocal crosses (Table 8).
Experiment V (Direct cross): In the cross involving male high line of orientation (for) and female of II chromosome marker (+/bw), all the F1 progeny obtained were showing wild type phenotype and normal courtship behavior. In F2 generation four different type of phenotypes viz., wild type with normal orientation, wild type with fast orientation, brown eye mutant with normal orientation and brown eye mutant with fast orientation. The number of flies obtained in F2 generation was 162, 80, 76 and 34 respectively. The result obtained was different from typical di-hybrid cross and there was no independent assortment. The $\chi^2$ value was 17.57, and it was significantly different at 0.05 level. In test cross four different phenotypic classes were obtained but they were also different from the expected 1:1:1:1 ratio. The number of flies observed in the test cross was 112, 72, 69 and 111 respectively. The $\chi^2$ value was 18.53 which was significant at 0.05 level.

In the cross involving male low line of orientation (sor) and female of II chromosome marker (+/bw), all the F1 progeny obtained were of wild type phenotype and normal courtship behavior. In F2 generation four different type of phenotypes viz., wild type with normal orientation, wild type with slow orientation, brown eye mutant with normal orientation and brown eye mutant with slow orientation. The number of flies obtained in F2 generation was 152, 77, 79 and 40 respectively. There was no independent assortment and there was no ratio of 9:3:3:1. The $\chi^2$ value was 30.10 and it was significantly different for the di-hybrid ratio at 0.05 level. In test cross also four different phenotypes appeared as per expectation but the ratio was different. A total of 101, 53, 95 and 51 respectively were observed and the ratio deviated from the expected 1:1:1:1. The $\chi^2$ value was 28.48 and it was significantly different at 0.05 level.
In the cross involving male high line of tapping (*mxtp*) and female of II chromosome marker (+/bw), all the F1 progeny obtained showed wild type phenotype and normal courtship behavior. In F2 generation four different phenotypic classes were obtained, viz., wild type with normal tapping, wild type with maximum tapping, brown eye mutant with normal tapping and brown eye mutant maximum tapping. The number of flies obtained in F2 generation was 212, 80, 83 and 41 respectively. There was no independent assortment in this generation. The $\chi^2$ value was 11.31 for the expected ratio of 9:3:3:1 which was significant at 0.05 level. In test cross, four different phenotypes were produced with 113, 54, 94 and 63 flies respectively which was also different from the expected ratio of 1:1:1:1. The $\chi^2$ value was 27.73 and it was significant at 0.05 level.

In the cross involving male low line of tapping (*mntp*) and female of II chromosome marker (+/bw), all the F1 progeny obtained were showing wild type phenotype and normal courtship behavior. In F2 generation four different phenotypic classes viz., wild type with normal tapping, wild type with minimum tapping, brown eye mutant with normal tapping and brown eye mutant minimum tapping were observed. The number of flies obtained in F2 generation was 202, 98, 106 and 26 respectively. There was no independent assortment in the expected 9:3:3:1 ratio. The $\chi^2$ value was 18.23 and it was significant at 0.05 level. The test cross result gave four different phenotypes as expected but the ratio was different from the expected 1:1:1:1 with 131, 62, 114 and 65 respectively. The $\chi^2$ value was 44.19 and it was significant at 0.05 level.

In the cross involving male high line of wing vibration (*mxwv*) and female of II chromosome marker (+/bw), all F1 flies had normal eye color (red) and wing vibration. In F2 generation four different phenotypes viz., wild type with normal
wing vibration, wild type with maximum wing vibration, brown eye mutant with normal wing vibration and brown eye mutant with maximum wing vibration appeared. The number of flies obtained in F2 generation was 159, 80, 87 and 22 respectively. All the phenotypes assorted independently in the ratio of 9:3:3:1. The \( \chi^2 \) value was 1.777 which was insignificant at 0.05 level. In test cross four different phenotypes as above appeared with 112, 108, 110 and 106 flies respectively. The \( \chi^2 \) value was 0.183 which was nonsignificant at 0.05 level.

In the cross involving male low line of wing vibration (\( mnwv \)) and female of II chromosome marker (+/bw), all the F1 progeny had normal eye color and normal wing vibration. In F2 generation four different phenotypes viz., wild type with normal wing vibration, wild type with minimum wing vibration, brown eye mutant with normal wing vibration and brown eye mutant with minimum wing vibration were obtained. The number of flies obtained in F2 generation was 250, 83, 86 and 29 respectively. These four phenotypes assorted independently in the ratio of 9:3:3:1. The \( \chi^2 \) value was 0.111 which was not significant at 0.05 level. In test cross also four different phenotypic classes were observed as mentioned above and the number of flies observed was 107, 103, 106 and 104 respectively. The \( \chi^2 \) value was 0.095 which was nonsignificant at 0.05 level.

In the cross involving male with long copulation duration (\( lcd \)) and female carrying II chromosome marker brown eye (+/bw), the F1 flies were red eyed (normal) and normal copulation duration. In F2 generation four different type of phenotypes viz., wild type with normal copulation duration, wild type with long copulation duration, brown eye with normal copulation duration and brown eye with long copulation duration. The number of flies obtained in F2 generation was 165, 54, 56 and 13 respectively. All the phenotypes assorted independently with a ratio of 9:3:3:1. The
χ² value was 1.517 which was not significant at 0.05 level. In test cross also the same four phenotypes were observed, with 86, 82, 83 and 73 flies respectively. The χ² value was 1.160 which was nonsignificant at 0.05 level.

In the cross involving male with short copulation duration (scd) and female of II chromosome marker (+/bw), all the F1 progeny obtained were showing normal red eye and normal copulation duration. In F2 generation four different phenotypes viz., wild type with normal copulation duration, wild type with short copulation duration, brown eye mutant with normal copulation duration and brown eye mutant with short copulation duration. The number of flies obtained in F2 generation was 175, 53, 56 and 20 respectively. All the phenotypes segregated independently and assorted in the ratio of 9:3:3:1. The χ² value was 0.444 which was not significant at 0.05 level. In test cross also four different phenotypes were observed each with 71, 70, 68 and 67 flies respectively. The χ² value was 0.145 which was nonsignificant at 0.05 level.

**Experiment VI (Reciprocal cross):** In the cross involving female high line of orientation (for) and male with II chromosome marker (+/bw), all the F1 progeny obtained showed wild type phenotype and normal courtship behavior. In F2 generation four different phenotypes viz., wild type with normal orientation, wild type with fast orientation, brown eye mutant with normal orientation and brown eye mutant with fast orientation were obtained with 192, 96, 87 and 41 flies respectively. There was no independent assortment because the progeny did not occur in the ratio of 9:3:3:1. The χ² value was 19.74 which was significant at 0.05 level. In test cross also the same four phenotypes were observed each with 103, 73, 85 and 49 flies respectively and the ratio was 1:1:1:1. The χ² value was 19.86 and it was significant at 0.05 level.
In the cross involving female low line of orientation (sor) and male with II chromosome marker (+/bw), all the F1 progeny obtained were showing wild type phenotype and normal courtship behavior. In F2 generation four different type of phenotypes viz., wild type with normal orientation, wild type with slow orientation, brown eye mutant with normal orientation and brown eye mutant with slow orientation were observed. The number of flies obtained in F2 generation was 175, 81, 82 and 30 respectively. There was no independent assortment. The result obtained did not fit into the usual dihybrid ratio of 9:3:3:1. The $\chi^2$ value was 11.61 and it was significantly different from the expected at 0.05 level. In test cross also four different phenotypic classes were observed with 102, 42, 100 and 40 flies respectively. There was deviation in the number of flies obtained from the typical test cross ratio 1:1:1:1. The $\chi^2$ value was 50.76 and it was significant at 0.05 level.

In the cross involving female high line of tapping (mxtp) and male with II chromosome marker (+/bw), all the F1 progeny obtained were wild type phenotype with normal tapping. In F2 generation four different type of phenotypes viz., wild type with normal tapping, wild type with maximum tapping, brown eye mutant with normal tapping and brown eye mutant with maximum tapping were obtained. The number of flies obtained in F2 generation was 224, 96, 98 and 46 respectively. In this experiment also the different phenotypic classes did not assort independently. The $\chi^2$ value was 16.57 and it was significant at 0.05 level. The same four phenotypic combinations were noticed in the test cross with 97, 51, 93 and 47 flies respectively. There was deviation in the test cross ratio also from the usual 1:1:1:1. The deviation in this ratio was also statistically significant at 0.05 level because the $\chi^2$ value was 29.61.
In the cross involving female low line of tapping (mntp) and male with II chromosome marker (+/bw), all the F1 progeny obtained were normal eyed and normal tapping. In F2, four different type of phenotypes viz., wild type with normal tapping, wild type with minimum tapping, brown eye mutant with normal tapping and brown eye mutant with minimum tapping were observed. The number of flies obtained in F2 generation was 245, 107, 112 and 48 respectively. However, there was no independent assortment in the ratio of 9:3:3:1. The $\chi^2$ value was 18.35 and it was significant at 0.05 level. In test cross also the same four different phenotypes as mentioned above appeared with 134, 94, 120 and 90 flies respectively and they did not assort in the ratio of 1:1:1:1. The $\chi^2$ value of 12.16 was significant at 0.05 level.

The cross between female of maximum wing vibration line (mxwv) and male with II chromosome marker brown eye (+/bw) yielded F1 progeny with normal eye color and normal wing vibration. In F2 generation four different phenotypic classes viz., wild type with normal wing vibration, wild type with maximum wing vibration, brown eye mutant with normal wing vibration and brown eye mutant with maximum wing vibration appeared with 212, 73, 72 and 23 flies respectively. All the phenotypes assorted independently in the ratio of 9:3:3:1. The $\chi^2$ value was 0.089 which was not significant at 0.05 level. Test cross also yielded four different phenotypes as mentioned above and the number of flies observed was 100, 101, 101 and 100 respectively. The test cross ratio of 1:1:1:1, which was nonsignificant at 0.05 level with the $\chi^2$ value is 0.010.

In the cross involving female low line of wing vibration (mnwv) and male with II chromosome marker (+/bw), all the F1 progeny obtained were wild type with normal wing vibration. In F2 generation four different phenotypes viz., wild type with normal wing vibration, wild type with minimum wing vibration, brown eye mutant with normal wing vibration, brown eye mutant with minimum wing vibration, brown eye mutant
with normal wing vibration and brown eye mutant with minimum wing vibration were observed. The number of flies obtained in F2 generation was 240, 78, 80 and 26 respectively. These phenotypic classes were in the proportion of 9:3:3:1. The $\chi^2$ value was 0.050 which was not significant at 0.05 level. In test cross also four different phenotypes as mentioned above were observed and the number of flies observed was 106, 92, 100 and 90 respectively and they were in the ratio of 1:1:1:1. The $\chi^2$ value was 1.690 which was nonsignificant at 0.05 level.

In the cross involving female high line of copulation duration ($lcd$) and male with II chromosome marker (+/bw), F1 progeny had only wild type phenotype with normal copulation duration. In F2, four different phenotypes viz., wild type with normal copulation duration, wild type with long copulation duration, brown eye mutant with normal copulation duration and brown eye mutant with long copulation duration. Here 200, 69, 70 and 25 flies appeared. There was independent assortment with the ratio of 9:3:3:1. The $\chi^2$ value is 0.386 which was not significant at 0.05 level. In test cross also four different phenotypes as mentioned above and the number of flies observed was 78, 79, 77 and 72 respectively and they were in the ratio of 1:1:1:1. The $\chi^2$ value was 0.379 which was nonsignificant at 0.05 level.

In the cross involving female low line of copulation duration ($scd$) and male with II chromosome marker (+/bw), all the F1 progeny obtained were wild type phenotype and normal copulation duration. In F2 generation four different phenotypes viz., wild type with normal copulation duration, wild type with short copulation duration, brown eye mutant with normal copulation duration and brown eye mutant with short copulation duration were obtained with 156, 48, 50 and 18 flies respectively. These flies occurred in the ratio of 9:3:3:1. The $\chi^2$ value was 0.314 which was nonsignificant at 0.05 level. In test cross also four different phenotypes appeared with
82, 79, 80 and 67 flies respectively and they were in the ratio of 1:1:1:1. The $\chi^2$ value was 1.792 which was nonsignificant at 0.05 level.

**With III chromosome marker:** Table 9 shows the results of cross between male of courtship variants viz., orientation ($for$, $sor$), tapping ($mxtp$, $mntp$), wing vibration ($mxvw$, $mnwv$) and copulation duration ($lcd$, $scd$) with female of III chromosome marker (ebony body) of *D. melanogaster* and their test crosses (DC= direct cross, TC= test cross). Independent assortment was noticed in the crosses involving orientation and the marker as well as tapping and the marker. The F2 progeny consisted of different phenotypic classes in the proportion of 9:3:3:1 and the test cross progeny in the proportion of 1:1:1:1. The $\chi^2$ test also showed that the difference between different phenotypic classes is nonsignificant. Even the reciprocal crosses and their test crosses also showed independent assortment. The crosses involving the courtship traits, wing vibration and copulation duration on the other hand did not show independent assortment. The phenotypic classes both in the direct cross and the test cross were different from the expectation of 9:3:3:1 and 1:1:1:1. Being significant at 0.05 level, the $\chi^2$ test also confirmed that the progeny of these two traits and the markers did not occur as per Mendelian dihybrid ratio. The reciprocal crosses also showed similar results (Table 10).

**Experiment V (Direct cross):** In the cross involving male high line of orientation ($for$) and female with III chromosome marker (+/e), F1 progeny consisted of flies with normal body color and normal orientation. In F2 generation four different type of phenotypes viz., wild type with normal orientation, wild type with fast orientation, ebony body mutant with normal orientation and ebony body mutant with fast orientation appeared. The number of flies obtained in F2 generation was 222, 79, 78
and 29 respectively. All the phenotypes assorted independently in the ratio of 9:3:3:1. The $\chi^2$ value was 2.233 which was not significant at 0.05 level. In test cross also four different phenotypes similar to that of F2 generation appeared with 127, 125, 124 and 126 flies respectively which were in the ratio of 1:1:1:1. The $\chi^2$ value was 0.040 which was nonsignificant at 0.05 level.

In the cross involving male low line of orientation (sor) and female with III chromosome marker (+/e), all the F1 progeny obtained were having normal body color with normal orientation. In F2 generation four different type of phenotypes viz., wild type with normal orientation, wild type with slow orientation, ebony body mutant with normal orientation and ebony body mutant with slow orientation were observed. The number of flies obtained in F2 generation was 176, 63, 59 and 22 respectively. All the phenotypes segregated independently and assorted in the ratio of 9:3:3:1. The $\chi^2$ value was 0.455 which was not significant at 0.05 level. In test cross also four different phenotypes as mentioned above appeared with 97, 96, 95 and 94 flies respectively which was in the ratio 1:1:1:1. The $\chi^2$ value was 0.052 which was nonsignificant at 0.05 level.

In the cross involving male high line of tapping (mxtp) and female with III chromosome marker (+/e), the F1 progeny obtained consisted of normal body color and normal tapping. In F2 generation four different phenotypic classes appeared viz., wild type with normal tapping, wild type with maximum tapping, ebony body mutant with normal tapping and ebony body mutant maximum tapping. The number of flies obtained in F2 generation was 229, 73, 77 and 21 respectively and they occurred in the ratio of 9:3:3:1. The $\chi^2$ value was 0.818 which was not significant at 0.05 level. In test cross the same four different phenotypes as mentioned above appeared with
103, 98, 101 and 100 flies respectively and they were in the ratio of 1:1:1:1. The $\chi^2$ value was 0.130 which was nonsignificant at 0.05 level.

In the cross involving male low line of tapping ($mntp$) and female with III chromosome marker (+/e), the F1 progeny had all flies with normal body color and normal tapping behavior. F2 progeny consisted of four different phenotypes viz., wild type with normal tapping, wild type with minimum tapping, ebony body mutant with normal tapping and ebony body mutant with minimum tapping. The number of flies obtained in F2 generation was 140, 50, 52 and 22 respectively with a phenotypic ratio of 9:3:3:1. The $\chi^2$ value was 2.450 which was not significant at 0.05 level. In test cross also four different phenotypes appeared with 76, 74, 70 and 64 flies respectively and they were in the ratio of 1:1:1:1. The $\chi^2$ value was 1.183 which was nonsignificant at 0.05 level.

In the cross involving male high line of wing vibration ($mxwv$) and female with III chromosome marker (+/e), all the F1 progeny obtained were showing normal body color and normal wing vibration. In F2 generation four different phenotypes viz., wild type with normal wing vibration, wild type with maximum wing vibration, ebony body mutant with normal wing vibration and ebony body mutant with maximum wing vibration were obtained. The number of flies obtained in F2 generation was 211, 104, 97 and 48 respectively. There was no independent assortment and the ratio deviated from the usual 9:3:3:1. The $\chi^2$ value was 22.53 and it was significant at 0.05 level. In test cross also four different phenotypes appeared but the ratio was different from the usual 1:1:1:1 and the number of flies obtained was 108, 60, 103 and 57 respectively. The $\chi^2$ value was 27.15 and it was significant at 0.05 level.

In the cross involving male low line of wing vibration ($mnwv$) and female with III chromosome marker (+/e), all the F1 flies produced were with normal body color and
normal wing vibration. In F2 generation four different phenotypic classes appeared, viz., wild type with normal wing vibration, wild type with minimum wing vibration, ebony body mutant with normal wing vibration and ebony body mutant with minimum wing vibration. The number of flies obtained in F2 generation was 168, 86, 73 and 45 respectively. These phenotypes did not assort independently and the $\chi^2$ value was 32.42 and it was significant at 0.05 level. The test cross also was although the same four phenotypes appeared. The test cross progeny had 116, 68, 71 and 101 flies respectively which was not in the ratio of 1:1:1:1. The $\chi^2$ value was 18.40 and it was significant at 0.05 level.

In the cross involving male high line of copulation duration ($l_{cd}$) and female with III chromosome marker (+/e), all the F1 progeny obtained were with normal body color and normal copulation duration. In F2 generation there were phenotypic classes, viz., wild type with normal copulation duration, wild type with long copulation duration, ebony body mutant with normal copulation duration and ebony body mutant with long copulation duration. The number of flies obtained in F2 generation was 221, 95, 92 and 40 respectively. There was no independent assortment and the ratio was different from 9:3:3:1. The $\chi^2$ value was 11.16 which was significant at 0.05 level. In test cross also four different phenotypic classes appeared but the ratio was different. There were 136, 82, 132 and 78 flies respectively. The $\chi^2$ value for test cross ratio was 27.40 and it was significant at 0.05 level.

In the cross involving male low line of copulation duration ($s_{cd}$) and female with III chromosome marker (+/e), all the F1 progeny obtained were normal bodied and normal copulation duration. In F2 generation four different phenotypes appeared viz., wild type with normal copulation duration, wild type with short copulation duration, ebony body mutant with normal copulation duration and ebony body mutant with normal copulation duration and ebony body mutant with
short copulation duration. The number of flies obtained in F2 generation was 181, 79, 84 and 40 respectively. Although four phenotypic classes were observed, there was no independent assortment. There was deviation in the ratio of F2 progeny from 9:3:3:1. The $\chi^2$ value for the deviation was 19.02 which were significant at 0.05 level. In test cross also four different phenotypes appeared with 135, 83, 128 and 82 flies respectively. The test cross ratio was deviated from the classical 1:1:1:1 ratio and the $\chi^2$ value was 82.68 which was significant at 0.05 level.

**Experiment VI (Reciprocal cross):** The reciprocal crosses also gave similar results. In the cross involving female high line of orientation ($for$) and male with III chromosome marker (+/e), all the F1 progeny obtained were wild type and normal courtship behavior. In F2 generation four different phenotypes appeared viz., wild type with normal orientation, wild type with fast orientation, ebony body mutant with normal orientation and ebony body mutant with fast orientation. The number of flies obtained in F2 generation was 271, 90, 88 and 23 respectively. All the phenotypes assorted independently in the ratio of 9:3:3:1. The $\chi^2$ value was 1.574 and it was nonsignificant at 0.05 level. In test cross also four different phenotypes as mentioned above appeared and the number of flies observed was 113, 115, 114 and 114 respectively and the values in the ratio of 1:1:1:1. The $\chi^2$ value was 0.015 which was nonsignificant at 0.05 level.

In the cross involving female low line of orientation ($sor$) and male with III chromosome marker (+/e), all the F1 progeny obtained had normal body color and normal courtship behavior. In F2 generation four different type of flies appeared viz., wild type with normal orientation, wild type with slow orientation, ebony body mutant with normal orientation and ebony body mutant with slow orientation. The
number of flies obtained in F2 generation was 281, 94, 92 and 29 respectively. The four phenotypic classes were assorted independently in the ratio of 9:3:3:1. The $\chi^2$ value was 0.165 which was not significant at 0.05 level. In test cross also four different phenotypes appeared with 63, 66, 64 and 63 flies respectively with typical Mendelian test cross ratio of 1:1:1:1. The $\chi^2$ value was 0.094 which was nonsignificant at 0.05 level.

In the cross involving female high line of tapping (mxtp) and male with III chromosome marker (+/e), all the F1 progeny obtained were normal bodied and normal tapping. In F2 generation four different phenotypes viz., wild type with normal tapping, wild type with maximum tapping, ebony body mutant with normal tapping and ebony body mutant with maximum tapping appeared. The number of flies obtained in F2 generation was 220, 76, 77 and 23 respectively. These four phenotypic classes assorted independently in the ratio of 9:3:3:1. The $\chi^2$ value was 0.240 which was nonsignificant at 0.05 level. In test cross also four different phenotypes as mentioned above appeared and the number of flies observed was 90, 88, 89 and 81 respectively and in the ratio of 1:1:1:1. The $\chi^2$ value was 0.574 which was nonsignificant at 0.05 level.

In the cross involving female low line of tapping (mntp) and male with III chromosome marker (+/e), all the F1 progeny obtained were normal and normal courtship behavior. In F2 generation four different type of phenotypes viz., wild type with normal tapping, wild type with minimum tapping, ebony body mutant with normal tapping and ebony body mutant with minimum tapping appeared with 157, 48, 49 and 18 flies respectively. All the phenotypes assorted independently in the ratio of 9:3:3:1. The $\chi^2$ value was 0.418 which was nonsignificant at 0.05 level. In test cross also four different phenotypes as mentioned above and the number of flies observed
was 84, 82, 80 and 76 flies respectively and they were the ratio of 1:1:1:1. The $\chi^2$ value was 0.435 which was nonsignificant at 0.05 level.

In the cross involving female high line of wing vibration ($mxwv$) and male with III chromosome marker (+/e), the F1 progeny produced had normal body color and normal wing vibration. In F2 generation four different phenotypes viz., wild type with normal wing vibration, wild type with maximum wing vibration, ebony body mutant with normal wing vibration and ebony body mutant with maximum wing vibration appeared with 185, 82, 80 and 45 flies respectively. However, there was no independent assortment in the ratio of 9:3:3:1. The $\chi^2$ value was 24.43 which were significant at 0.05 level. In test cross also four different phenotypes as mentioned above were produced with 122, 76, 119 and 71 flies respectively. The test cross ratio was also different from expectation of 1:1:1:1. The $\chi^2$ value was 22.95 which was significant at 0.05 level.

In the cross involving female low line of wing vibration ($mnwv$) and male with III chromosome marker (+/e), all the F1 progeny obtained were with normal color and normal wing vibration. In F2 generation four different phenotypes viz., wild type with normal wing vibration, wild type with minimum wing vibration, ebony body mutant with normal wing vibration and ebony body mutant with minimum wing vibration appeared. The number of flies obtained in F2 generation was 172, 85, 72 and 39 respectively. There was no independent assortment because; the ratio was different from 9:3:3:1. The $\chi^2$ value was 20.88 which was significant at 0.05 level. In test cross also the four different phenotypic classes appeared which was 112, 65, 108 and 63 respectively and they are not in the ratio of 1:1:1:1. The $\chi^2$ value was 24.44 which was significant at 0.05 level.
In the cross involving female high line of copulation duration (\textit{lcd}) and male with III chromosome marker (+/e), the F1 progeny obtained had flies with normal body color and normal copulation duration. In F2 generation, following four different types of flies were obtained, viz., wild type with normal copulation duration, wild type with long copulation duration, ebony body mutant with normal copulation duration and ebony body mutant with long copulation duration. The number of flies obtained in F2 generation was 208, 93, 97 and 38 respectively. There was no independent assortment and the ratio was different from 9:3:3:1. The $\chi^2$ value was 14.29 which were significant at 0.05 level. In test cross also same four different phenotypes appeared with 128, 85, 122 and 77 flies respectively and the ratio was different from 1:1:1:1. The $\chi^2$ value was 19.28 and it was significant at 0.05 level.

In the cross involving female low line of copulation duration (\textit{scd}) and male with III chromosome marker (+/e), all the F1 progeny obtained were normal bodied and with normal copulation duration. In F2 generation following four different phenotypes viz., wild type with normal copulation duration, wild type with short copulation duration, ebony body mutant with normal copulation duration and ebony body mutant with short copulation duration were obtained. The number of flies obtained in F2 generation was 229, 102, 109 and 44 respectively. There was no independent assortment and the phenotypic ratio was different from 9:3:3:1. The $\chi^2$ value was 19.83 and it was significant at 0.05 level. In test cross also four different phenotypes as mentioned above appeared and the number of flies observed was 141, 93, 135 and 85 respectively. These values were different from the ratio of 1:1:1:1 with $\chi^2$ value of 21.60 which was significant at 0.05 level.
<table>
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<tr>
<th>Crosses</th>
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<th>F2 progeny phenotype</th>
<th>Number of flies of F2 progeny</th>
<th>χ² value for F2 progeny</th>
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</table>

* χ² value significant at 0.05 level

Table 5 showing the results of cross between male of courtship variants viz., orientation (*for, sor*), tapping (*mxt, mnt*), wing vibration (*mwv, mnr*) and copulation duration (*lcd, scd*) with female of I chromosome marker (yellow body) of *D. melanogaster* and their test crosses (DC=direct cross, TC=test cross).
<table>
<thead>
<tr>
<th>Crosses</th>
<th>F1 phenotype</th>
<th>F2 progeny phenotype</th>
<th>Number of flies of F2 progeny</th>
<th>$\chi^2$ value for F2 progeny</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td></td>
<td>RC</td>
<td>TC</td>
</tr>
<tr>
<td>$for^{f+}$ X $+/y$</td>
<td>normal</td>
<td>$+/+, for^{f+}, +/y, for^{f+}$</td>
<td>207, 69, 60, 20</td>
<td>100, 103, 97, 94</td>
</tr>
<tr>
<td>$sor^{f} X +/y$</td>
<td>normal</td>
<td>$+/+, sor^{f}, +/y, sor^{f}y$</td>
<td>212, 68, 71, 25</td>
<td>80, 78, 75, 75</td>
</tr>
<tr>
<td>$mxtp^{f+} X +/y$</td>
<td>normal</td>
<td>$+/+, mxtp^{f+}, +/y, mxtp^{f+}$</td>
<td>186, 61, 65, 24</td>
<td>94, 89, 91, 86</td>
</tr>
<tr>
<td>$mntp^{f+} X +/y$</td>
<td>normal</td>
<td>$+/+, mntp^{f+}, +/y, mntp^{f+}$</td>
<td>189, 65, 67, 19</td>
<td>87, 86, 88, 83</td>
</tr>
<tr>
<td>$mxwv^{f+} X +/y$</td>
<td>normal</td>
<td>$+/+, mntp^{f+}, +/y, mntp^{f+}$</td>
<td>230, 75, 84, 27</td>
<td>98, 96, 97, 91</td>
</tr>
<tr>
<td>$mnwv^{f+} X +/y$</td>
<td>normal</td>
<td>$+/+, mnwv^{f+}, +/y, mnwv^{f+}$</td>
<td>281, 95, 97, 31</td>
<td>116, 117, 115, 114</td>
</tr>
<tr>
<td>$lcd^{f+} X +/y$</td>
<td>normal</td>
<td>$+/+, lccd^{f+}, +/y, lccd^{f+}$</td>
<td>282, 91, 94, 29</td>
<td>115, 112, 114, 111</td>
</tr>
<tr>
<td>$sccd^{f+} X +/y$</td>
<td>normal</td>
<td>$+/+, sccd^{f+}, +/y, sccd^{f+}$</td>
<td>211, 67, 70, 20</td>
<td>90, 84, 79, 75</td>
</tr>
</tbody>
</table>

*p value significant at 0.05 level

Table 6 showing the results of cross between female of courtship variants viz., orientation ($for, sor$), tapping ($mxtp, mntp$), wing vibration ($mxwv, mnwv$) and copulation duration ($lcd, sccd$) with male of 1 chromosome marker (yellow body) of *D. melanogaster* and their test crosses (RC=reciprocal cross, TC=test cross).
<table>
<thead>
<tr>
<th>Crosses</th>
<th>F1 phenotype</th>
<th>F2 progeny phenotype</th>
<th>Number of flies of F2 progeny</th>
<th>$\chi^2$ value for F2 progeny</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td></td>
<td>DC, TC</td>
<td>DC, TC</td>
</tr>
<tr>
<td>for/+ X +/bw</td>
<td>normal</td>
<td>+/-, for/,+/,+/-bw, for/bw</td>
<td>162, 80, 76, 34</td>
<td>112, 72, 69, 111</td>
</tr>
<tr>
<td>sor/+ X +/bw</td>
<td>normal</td>
<td>+/-, sor/,+/,+/-bw, sor/bw</td>
<td>152, 77, 79, 40</td>
<td>101, 53, 95, 51</td>
</tr>
<tr>
<td>mxtp/+ X +/bw</td>
<td>normal</td>
<td>+/-, mxtp/,+/,+/-bw, mxtp/bw</td>
<td>212, 80, 83, 41</td>
<td>113, 54, 94, 63</td>
</tr>
<tr>
<td>mntp/+ X +/bw</td>
<td>normal</td>
<td>+/-, mntp/,+/,+/-bw, mntp/bw</td>
<td>202, 98, 106, 26</td>
<td>131, 62, 114, 65</td>
</tr>
<tr>
<td>mxwv/+ X +/bw</td>
<td>normal</td>
<td>+/-, mxwv/,+/,+/-bw, mxwv/bw</td>
<td>159, 80, 87, 22</td>
<td>112, 108, 110, 106</td>
</tr>
<tr>
<td>mnwv/+ X +/bw</td>
<td>normal</td>
<td>+/-, mnwv/,+/,+/-bw, mnwv/bw</td>
<td>250, 83, 86, 29</td>
<td>107, 103, 106, 104</td>
</tr>
<tr>
<td>lcd/+ X +/bw</td>
<td>normal</td>
<td>+/-, lcd/,+/,+/-bw, lcd/bw</td>
<td>165, 54, 56, 13</td>
<td>86, 82, 83, 73</td>
</tr>
<tr>
<td>scd/+ X +/bw</td>
<td>normal</td>
<td>+/-, scd/,+/,+/-bw, scd/bw</td>
<td>175, 53, 56, 20</td>
<td>71, 70, 68, 67</td>
</tr>
</tbody>
</table>

*p value significant at 0.05 level

Table 7 showing the results of cross between male of courtship variants viz., orientation (for, sor), tapping (mxtp, mntp), wing vibration (mxwv, mnwv) and copulation duration (lcd, scd) with female of II chromosome marker (brown eye) of *D. melanogaster* and their test crosses (DC=direct cross, TC=test cross).
<table>
<thead>
<tr>
<th>Crosses</th>
<th>F1 phenotype</th>
<th>F2 progeny phenotype</th>
<th>Number of flies of F2 progeny</th>
<th>$\chi^2$ value for F2 progeny</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td></td>
<td>RC</td>
<td>TC</td>
</tr>
<tr>
<td>$for^+/X+/bw$</td>
<td>normal</td>
<td>$+/+, \ for^+/+, +/bw; for/bw$</td>
<td>192, 96, 87, 41</td>
<td>103, 73, 85, 49</td>
</tr>
<tr>
<td>$sor^+/X+/bw$</td>
<td>normal</td>
<td>$+/+, \ sor^+/+, +/bw; sor/bw$</td>
<td>175, 81, 82, 30</td>
<td>102, 42, 100, 40</td>
</tr>
<tr>
<td>$mxt^+/X+/bw$</td>
<td>normal</td>
<td>$+/+, \ mxt^+/+, +/bw; mxt/bw$</td>
<td>224, 96, 98, 46</td>
<td>97, 51, 93, 47</td>
</tr>
<tr>
<td>$mnt^+/X+/bw$</td>
<td>normal</td>
<td>$+/+, \ mnt^+/+, +/bw; mnt/bw$</td>
<td>245, 107, 112, 48</td>
<td>134, 94, 120, 90</td>
</tr>
<tr>
<td>$mxx^+/X+/bw$</td>
<td>normal</td>
<td>$+/+, \ mxx^+/+, +/bw; mxx/bw$</td>
<td>212, 73, 72, 23</td>
<td>100, 101, 101, 100</td>
</tr>
<tr>
<td>$mxx^+/X+/bw$</td>
<td>normal</td>
<td>$+/+, \ mxx^+/+, +/bw; mxx/bw$</td>
<td>240, 78, 80, 26</td>
<td>106, 92, 100, 90</td>
</tr>
<tr>
<td>$lxd^+/X+/bw$</td>
<td>normal</td>
<td>$+/+, \ lxd^+/+, +/bw; lxd/bw$</td>
<td>200, 69, 70, 25</td>
<td>78, 79, 77, 72</td>
</tr>
<tr>
<td>$sxd^+/X+/bw$</td>
<td>normal</td>
<td>$+/+, \ sxd^+/+, +/bw; sxd/bw$</td>
<td>156, 48, 50, 18</td>
<td>82, 79, 80, 67</td>
</tr>
</tbody>
</table>

* p value significant at 0.05 level

Table 8 showing the results of cross between female of courtship variants viz., orientation ($for$, $sor$), tapping ($mxt$, $mnt$), wing vibration ($mxx$, $mxx$) and copulation duration ($lxd$, $sxd$) with male of II chromosome marker (brown eye) of *D. melanogaster* and their test crosses (RC = reciprocal cross, TC = test cross).
<table>
<thead>
<tr>
<th>Crosses</th>
<th>F1 phenotype</th>
<th>F2 progeny phenotype</th>
<th>Number of flies of F2 progeny</th>
<th>$\chi^2$ value for F2 progeny</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td></td>
<td>DC</td>
<td>TC</td>
</tr>
<tr>
<td>for/+ X +/e</td>
<td>normal</td>
<td>+/-, for/+ , +/e, for/e</td>
<td>222, 79, 78, 29</td>
<td>127, 125, 124, 126</td>
</tr>
<tr>
<td>sor/+ X +/e</td>
<td>normal</td>
<td>+/-, sor/+ , +/e, sor/e</td>
<td>176, 63, 59, 22</td>
<td>97, 96, 95, 94</td>
</tr>
<tr>
<td>mxtp/+ X +/e</td>
<td>normal</td>
<td>+/-, mxtp/+ , +/e, mxtp/e</td>
<td>229, 73, 77, 21</td>
<td>103, 98, 101, 100</td>
</tr>
<tr>
<td>mnip/+ X +/e</td>
<td>normal</td>
<td>+/-, mnip/+ , +/e, mnip/e</td>
<td>140, 50, 52, 22</td>
<td>76, 74, 70, 64</td>
</tr>
<tr>
<td>mxwv/+ X +/e</td>
<td>normal</td>
<td>+/-, mnip/+ , +/e, mnip/e</td>
<td>211, 104, 97, 48</td>
<td>108, 60, 103, 57</td>
</tr>
<tr>
<td>mnwv/+ X +/e</td>
<td>normal</td>
<td>+/-, mnwv/+ , +/e, mnwv/e</td>
<td>168, 86, 73, 45</td>
<td>116, 68, 71, 101</td>
</tr>
<tr>
<td>lcd/+ X +/e</td>
<td>normal</td>
<td>+/-, lcd/+ , +/e, lcd/e</td>
<td>221, 95, 92, 40</td>
<td>136, 82, 132, 78</td>
</tr>
<tr>
<td>scd/+ X +/e</td>
<td>normal</td>
<td>+/-, scd/+ , +/e, scd/e</td>
<td>181, 79, 84, 40</td>
<td>135, 83, 128, 82</td>
</tr>
</tbody>
</table>

* p value significant at 0.05 level

Table 9 showing the results of cross between male of courtship variants viz., orientation (for, sor), tapping (mxtp, mnip), wing vibration (mxwv, mnwv) and copulation duration (lcd, scd) with female of III chromosome marker (ebony body) of D melanogaster and their test crosses (DC=direct cross, TC=test cross).
<table>
<thead>
<tr>
<th>Crosses</th>
<th>F1 phenotype</th>
<th>F2 progeny phenotype</th>
<th>Number of flies of F2 progeny</th>
<th>$\chi^2$ value for F2 progeny</th>
</tr>
</thead>
<tbody>
<tr>
<td>$for/+ \times +/e$</td>
<td>normal</td>
<td>$+/-, for/+ , +/e, for/e$</td>
<td>271, 90, 88, 23 113, 115, 114, 114</td>
<td>1.574 0.015</td>
</tr>
<tr>
<td>$sor/+ \times +/e$</td>
<td>normal</td>
<td>$+/-, sor/+ , +/e, sor/e$</td>
<td>281, 94, 92, 29 63, 66, 64, 63</td>
<td>0.165 0.094</td>
</tr>
<tr>
<td>$mxtp/+ \times +/e$</td>
<td>normal</td>
<td>$+/-, mxtp/+ , +/e, mxtp/e$</td>
<td>220, 76, 77, 23 90, 88, 89, 81</td>
<td>0.240 0.574</td>
</tr>
<tr>
<td>$mnlp/+ \times +/e$</td>
<td>normal</td>
<td>$+/-, mnlp/+ , +/e, mnlp/e$</td>
<td>157, 48, 49, 18 84, 82, 80, 76</td>
<td>0.418 0.435</td>
</tr>
<tr>
<td>$mxwv/+ \times +/e$</td>
<td>normal</td>
<td>$+/-, mnwv/+ , +/e, mnwv/e$</td>
<td>185, 82, 80, 45 122, 76, 119, 71</td>
<td>24.43* 22.95*</td>
</tr>
<tr>
<td>$mnwv/+ \times +/e$</td>
<td>normal</td>
<td>$+/-, mnwv/+ , +/e, mnwv/e$</td>
<td>172, 85, 72, 39 112, 65, 108, 63</td>
<td>20.88* 24.44*</td>
</tr>
<tr>
<td>$lcmd/+ \times +/e$</td>
<td>normal</td>
<td>$+/-, lcmd/+ , +/e, lcmd/e$</td>
<td>208, 93, 97, 38 128, 85, 122, 77</td>
<td>14.29* 19.28*</td>
</tr>
<tr>
<td>$scd/+ \times +/e$</td>
<td>normal</td>
<td>$+/-, scd/+ , +/e, scd/e$</td>
<td>229, 102, 109, 44 141, 93, 135, 85</td>
<td>19.83* 21.60*</td>
</tr>
</tbody>
</table>

* p value significant at 0.05 level

Table 10 showing the results of cross between female of courtship variants viz., orientation ($for, sor$), tapping ($mxtp, mnlp$), wing vibration ($mxwv, mnwv$) and copulation duration ($lcmd, scd$) with male of III chromosome marker (ebony body) of $D. melanogaster$ and their test crosses (RC=reciprocal cross, TC=test cross).
2.4 Discussion

As per the Mendelian laws of inheritance if a character is controlled by a single gene with its alleles, a cross involving a dominant and a recessive phenotype are segregated in the proportion of 3:1 ratio in the F2 generation and 1:1 in the test cross. The present studies (Table 1 and 2) show that the cross involving the high line (for, mxtp, mxwv and lcd) and low line (sor, mntp, mnwv and scd) courtship traits are segregated in the normal Mendelian pattern. However, the crosses involving the high line (for, mxtp, mxwv and lcd) and the wild type (org k) or low line (sor, mntp, mnwv and scd) and the wild type (org k) also showed segregation. Therefore it is unlikely that these courtship traits are monogenic in inheritance. Moreover, if a character is controlled by different alleles of the same gene, it is possible to isolate the pure breeding (homozygous) stock of that mutation in the second generation. This is possible because of simple segregation of these alleles. It has already been shown in chapter I that to obtain the pure breeding variant stocks of any one of these courtship traits requires selection for at least 12 generations. Although the general scrutiny of the results in the present study appears that these courtship variants are controlled by segregating alleles, the results of chapter I and the contradicting results of experiments 1-4 (similar results in both the sets of experiments) in this chapter does not support the idea that they are segregating alleles of the same gene. The fact that the selection requires at least 12 generations confirms the polygenic inheritance of these courtship traits.

Since the results of both direct and the reciprocal crosses were the same it can be concluded that these traits are not sex linked (Tables 3 and 4). It is surprising to note that even wing vibration, the trait performed only by males to produce the courtship song does not show any sign of sex linkage. Collins and Hewitt (1984) have
demonstrated that the male specific traits such as wing vibration, attempting copulation and copulation characters show some i-type epistatic variation. They have also shown that the first element of courtship sequence, orientation showed a different pattern of inheritance with again low additive genetic variation but directional dominance for low levels of orientation (Collins and Hewitt; 1984). The present study also confirms the observations of Collins and Hewitt (1984) because of the dominance of high line in certain crosses and wild type in others.

In a precise acoustic study of *Drosophila* courtship songs, Ewing (1969, 1970) demonstrated that the genes controlling the song patterns are located on the X-chromosome, while quantitative features of it are controlled by autosomal genes. As the authors have not studied the song patterns, the first part of the observation of Ewing (1969, 1970) could not be verified. However the present study definitely confirms the autosomal control of this trait. Moreover, the wing vibration was quantified and counted in the present study as bouts in the present study which would further confirm the observation of Ewing (1969, 1970).

The linkage analysis further demonstrates the non-association of these courtship traits on sex chromosome. The experiments involving the flies carrying the high line or low line of courtship traits to the yellow bodied flies (I chromosome maker) showed the independent assortment with the occurrence of the four phenotypic classes in the proportion of 9:3:3:1. Moreover, the test cross progeny obtained were also in the proportion of 1:1:1:1. Both the direct and reciprocal crosses showed similar results. This confirms that the courtship traits studied are not linked on the X chromosome.

The crosses involving *for/sor* and *mxtp/mntp* along with wild type crossed with the brown eyed flies (II chromosome marker) did not show independent assortment. Even the test cross result was different from that of 1:1:1:1 ratio (Tables 7 and 8).
The $\chi^2$ test showed that the difference between different classes of phenotypes in both F2 and test cross was significant. The classical linkage experiments of Morgan (1910) have demonstrated the absence of independent assortment of linked genes. He has also demonstrated that equal proportions of different phenotypic classes occur only if the two genes are unlinked. Since the test cross ratio in the present study is different from 1:1:1:1 it is evident that there is no independent assortment. In the present study since for/sor and mxtp/mntp showed association with brown eyed mutation, it could be concluded that these two characteristics (orientation and tapping) are located on the second chromosome.

The other two traits, wing vibration and copulation duration must be located on the third chromosome because these two traits did not show independent assortment with reference to the yellow or ebony body colors which served as first and third chromosome markers respectively. Even here the F2 progeny as well as the test cross progeny obtained were significantly different from the expected (by $\chi^2$ test; p value at 0.05 level). The remaining combination of crosses showed the typical independent assortment with respect to these marker genes.

One interesting feature of the present study is the occurrence of equal proportions of parental combination and recombination in certain crosses which is unexpected in linkage experiments. As per the linkage theory of Morgan (1910) when ever two genes are linked with each other, the number of recombinants that would occur is always less than the parental combination. Morgan's (1910) assumption is correct if these traits are controlled by single genes. The discrepancy noticed in the present study thus may be because the courtship traits studied are polygenic in inheritance and crossovers which occur at different points on the chromosome must have altered the ratio.
Although we provide evidence for autosomal linkage of these courtship traits, the important role X chromosome in sexual behavior cannot be ruled out. For example, Volkova et al (2007) have demonstrated that genes which control the male sexual activity (SA), female sexual receptivity (SR) and copulation latency (CL) of D. melanogaster are determined by the interactions of X-linked and autosomal genes. Regarding the copulation duration (CD), Volkova et al (2007) are of the opinion that the major gene controlling this trait in Drosophila is located in the X-chromosome and several modifier genes are located in autosomes. Moehring (2006) mapped at least three QTL affecting discrimination of D. santomea females against D. yakuba males, one X-linked and one autosomal QTL affecting the likelihood of copulation, and a second X chromosome QTL affecting copulation latency. They also have demonstrated that there are three autosomal QTL affecting mating success of D. yakuba males with D. santomea. Thus from the above studies it is clear that the genes controlling different elements of courtship in Drosophila are located on the autosomes, and different loci responsible for actual mating and sexual isolation appear to be linked with both autosomes and sex chromosomes.

Drosophila mojavensis from the Sonora region and Baja California show asymmetrical sexual isolation in the laboratory: males from Sonora mate equally frequently with Sonora and Baja females, while the mating success of Baja males with Sonora females is reduced. This failure has been localized to three separate behavioral landmarks occurring during courtship. Genetic analysis was conducted using reciprocal F1 hybrids of Sonora and Baja strains to examine inheritance patterns of the responsible courtship behaviors. Mating success and propensity of F1 males were similar to Sonora males. F1 females mated with males of Sonora and Baja races equally, although mating propensity of F1 females was intermediate between that of
Sonora and Baja females. Males of Baja strains presented with F1 females showed a relatively high level of failure at attempted intromission. Genes for mating behaviors are located in the autosomes, but different loci responsible for the sexual isolation appear to act in males and females (Krebs, 1990).

The effect of variation in gene density per centimorgan on quantitative trait locus (QTL) mapping studies using data from the *Drosophila melanogaster* genome project and documented regional rates of recombination. There is tremendous variation in gene density per centimorgan across this genome, and we observe that this variation can cause systematic biases in QTL mapping studies. Specifically, in our simulated mapping experiments of 50 equal-effect QTL distributed randomly across the physical genome, very strong QTL are consistently detected near the centromeres of the two major autosomes, and few or no QTL are often detected on the X chromosome. This pattern persisted with varying heritability, marker density, QTL effect sizes, and transgressive segregation. Our results are consistent with empirical data collected from QTL mapping studies of this species and its close relatives, and they explain the "small X-effect" that has been documented in genetic studies of sexual isolation in the *D. melanogaster* group (Noor et al., 2001).

### 2.5 Summary

The present study clearly shows that the selected four courtship traits polygenic in inheritance. The study also shows that these courtship traits are autosomal linked although the enactment of any one of these traits is limited to particular sex. Out of the four traits, the genes which control orientation and tapping are linked on to the second chromosome while wing vibration and copulation duration are linked on to the third chromosome.