# Unattractive males can sire attractive sons in Drosophila melanogaster

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#### **1. Introduction**

In many models of sexual selection it is assumed that attractive traits are passed on from father to son and thus also help the mother attain fitness benefits, since her sons would be more likely to father even more offspring. Taylor et al. (1) showed that this is the case in Drosophila simulans, using experiments very similar to the ones we are presenting. However, Pischedda et al. (2) had previously concluded that "male fitness was not inherited by sons" in Drosophila melanogaster. Our goal was to further examine these conclusions.

#### **5.** Conclusion

Somewhat surprisingly, we observed a rather weak correlation between copulation latency and copulation frequency. Comparing our results to those of Mackay et al. (see Fig.1) it becomes clear that we did not reproduce the rank order from their experiment, i.e. their most attractive lines were not necessarily successful in our experiment. However this could be due to a number of reasons: While we used tester females from the line Canton S and observed single pairs in courtship chambers for 60 minutes, they used tester females from the line Wild Type Oregon R and observed several pairs in food vials for 2 hours.

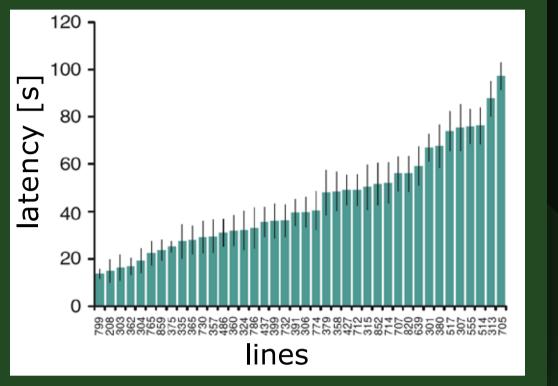
Nevertheless, we were able to identify strains with attractive males and strains producing unattractive males for a simple genetic test. Reciprocal crosses betwen an atractive and an unattractive strain should rveal any maternal or paternal genetic contributions to attractiveness.

Our results show that the male offspring from both crosses were similar in both latency and frequency to the more attractive parent line, demonstrating that fathers from an unattractive D. melanogaster population can sire atrractive sons if they mate with females from a population that produces attractive males. This result suggests an autosomal dominant heritability of attractiveness in *D. melanogaster*.

For this purpose we decided to use some of the *D. melanogaster* lines whose gene expression patterns were thoroughly characterized by Mackay et al. (3). We expect to be able to use some of the data obtained in their study in the future to hopefully explain and give further insight into our results. After obtaining results about the attractiveness of 10

of those lines, we chose two lines and repeated the experiments with offspring obtained from both recipocal crosses. These experiments provide further information about the heritability of attractiveness in Drosophila melanogaster.

Fig. 1: Variation for copulation latency (as one of the examined organismal phenotypes) among 40 wild-derived inbred lines (3).



# **Courtship Wheels**





# 2. Methods

Male virgins from 9 lines selected from the two ends of the spectrum in Fig. 1 were collected under CO<sub>2</sub> anaesthesia and housed together for 3-4 days in food vials. They were put into courtship wheels where each male was placed into a chamber with a 3-day-old female virgin from the wild type line Canton S. As a control group, virgin males from the Canton S line were also used. Each courtship wheel contained 12 chambers (see photos at center) and these were observed continuously for the duration of the experiment (60 minutes). During the experiment, the time elapsed between introduction of males and copulation for each pair was recorded as copulation latency, which served as our measure of male attractiveness. Simultaneously, the proportion of males achieving copulation was recorded as copulation frequency.

Using results from this experiment (experiment #1) we chose a strain with consistently high copulation latencies and low copulation frequencies (line 313) as an unattractive parental strain. As an attractive strain, we chose line 399, which had consistently scored high on frequencies and low on latencies (see Fig. 4). These parental strains as well as the male offspring of the reciprocal crosses between the two were then tested for copulartion latency and frequency against Canton S tester females.

To exclude spurious results due to our selection of parental strains, we will continue these experiemnts by selecting more strains for further analysis. For instance, we are currently crossing line 732 with line 360. These two lines cannot be easily classified as attractive or unattractive according to our definition, as they differ in terms of their copulation data in opposite ways (see Fig. 4).



# **3. Attractive and unattractive** males

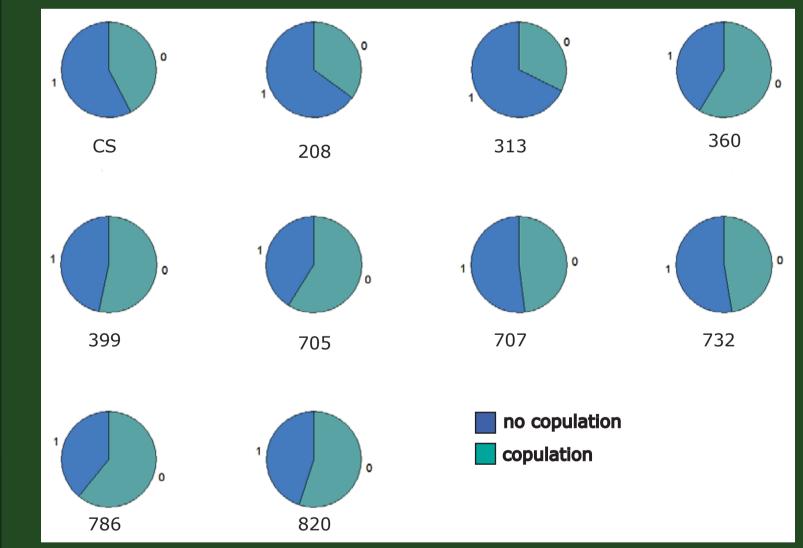
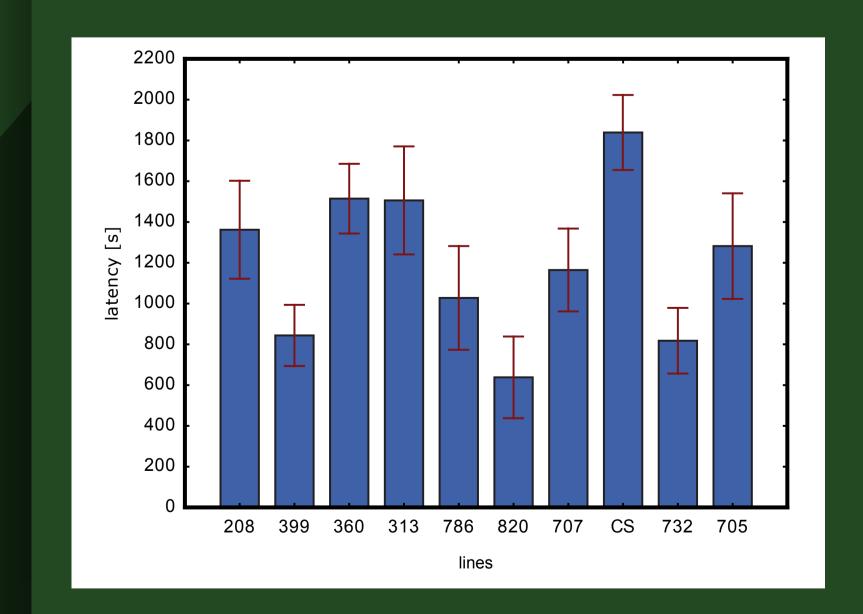
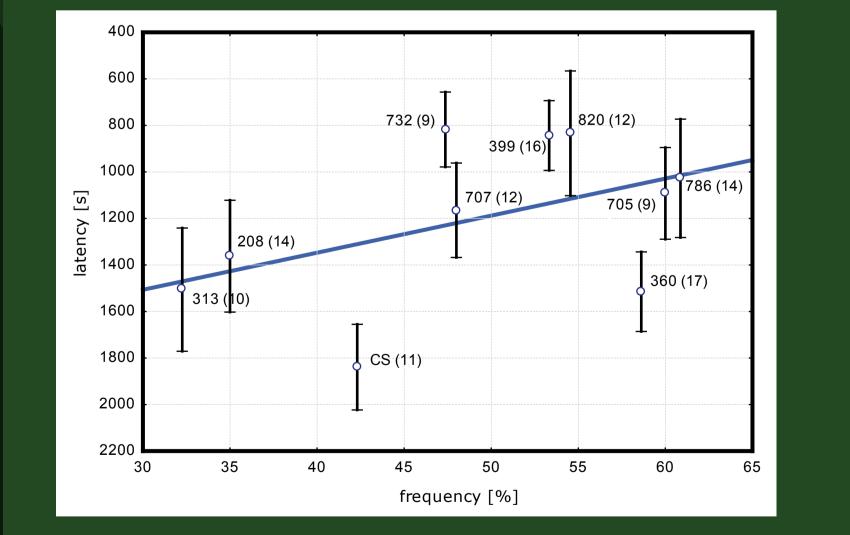


Fig. 2: Copulation Frequency for each tested line from experiment #1.



### 4. Offspring of reciprocal crosses are all attractive



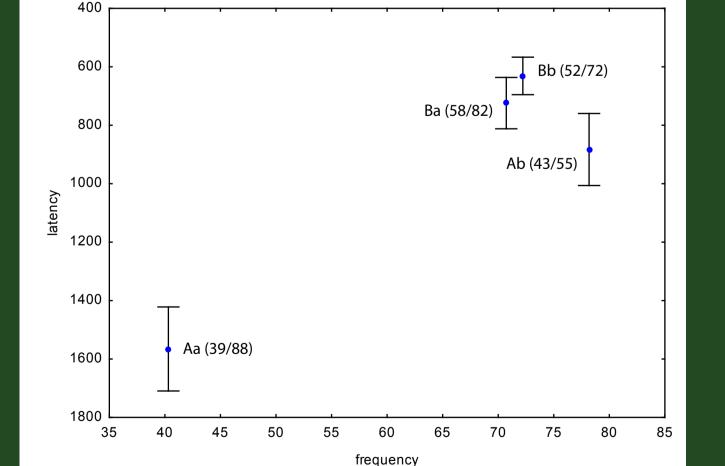


Fig. 3: Relationship of latency and frequency scores from experiment #1 for male offspring of the ten tested line. Based on this data the lines for experiment #2 (313, 399) were chosen.

Fig. 4: Relationship of latency and frequency scores from experiment #2 for male offspring of reciprocal crossbreeds and the parent lines (313~Aa; 399~Bb). A,B: maternal genes *a,b: paternal genes* 

> Fig. 3: Copulation Latency for each tested line from experiment #1.

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