# Genetic Mapping of the *bas* Mutation in *Drosophila melanogaster*

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## Abstract

In *Drosophila*, the bang-sensitive mutations cause paralysis of the fly upon mechanical shock. One specific recessive mutation from this group is in fact called "bang-sensitive" (*bas*). Ganetzky and Wu (1982) mapped this mutation to a region between the *g* (garnet) and *sd* (scalloped) mutation genes. Although *bas* has been "mapped", there are 355 possible genes in that region. We are attempting to identify the exact *bas* gene. This is to be done by the use of deletion mapping. We have used both extant deletions and deletions created using Exelixis P-element lines to narrow down the location of *bas* to the 12F1-12F4 region on the X chromosome. Mapping of *bas* is ongoing in an attempt to narrow the list of candidate genes further.

## Introduction

In a number of laboratories around the world, various behavioral characteristics of *Drosophila melanogaster* are being investigated. Among the most important of these different behavioral characteristics is a seizure behavior. Known as "bang-sensitive" mutants, these flies provide interesting model systems for research into the neural basis of seizure behavior (Lee and Wu, 2002). Studying these types of behaviors in *Drosophila* allow for insight into the mechanisms that affect seizure susceptibility in humans.

In bang-sensitive mutants, the characteristic behavior upon mechanical shock is a spasm-and-paralysis sequence. This hyperactivity is represented by intense, uncoordinated motor activity including wing flapping, leg shaking, and abdominal muscle contraction (Pavlidis and Tanouye, 1995). This is then followed by a refractory period, during which the mutant fly is no longer sensitive to mechanical disturbances (Lee and Wu, 2002). Such mutations cause *Drosophila* to become paralyzed, a symptom that resembles seizures in humans. This occurs because of the excitability from mechanical shock that the fly is exposed to. The duration of this paralysis varies with the specific mutation.

Most of the bang-sensitive mutations whose products are known, code for mitochondrial proteins. At least two of these genes, however, have yet to be identified. One gene carries the bang sensitive (*bas*) mutation, and is our gene of interest. *bas* is a recessive X-linked mutation found in the 12F region of *Drosophila melanogaster's* X chromosome. This region consists of approximately 300,000 base pairs. Flies which carry the *bas* mutation, like other bang-sensitives, are immobilized after mechanical shock. This paralysis has been found to persist for 30 to 40 seconds. The purpose of my project is to map *bas* to its exact genomic location by using both extant deletions and deletions I created using Exelixis P-element lines. Using these deletions will allow us to "knock out" the dominant wildtype copy of *bas*, allowing the mutant phenotype to be expressed. Doing so will allow us to narrow down the location of the *bas* mutation and to one day find its exact location.

## Experimental Method

During our experiment, both custom and extant deletions were used. These deletions were used to narrow down the location of *bas*.

Deletions were created using flies from the Exelixis collection housed at Harvard University School of Medicine. Two flies carrying different P-element insertions were mated together in order to create a deletion. During the mating process, the gene for an enzyme called hs-FLP (heat shock-driven FLP) is introduced into the flies of interest and is activated during heat shock. Vials containing larvae were submerged in 37°C water for an hour each day for 5 days. Once heat is delivered, the FLP enzyme cleaves specific FRT sites allowing the deletion segment to be created. In order to test paralysis of *bas* flies, "bang" was delivered to heterozygous *bas*/ deletion flies. An hour after transferring 1-8 progeny to a testing tube, the tube was vortexed for 10 seconds. The number of paralyzed flies was then counted. This would verify if the *bas* gene is in the deletion segment.

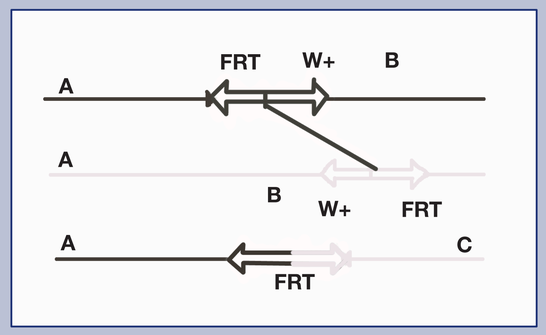


Figure 1: Sample genetic scheme for creating deletions using Exelixis P-element lines.

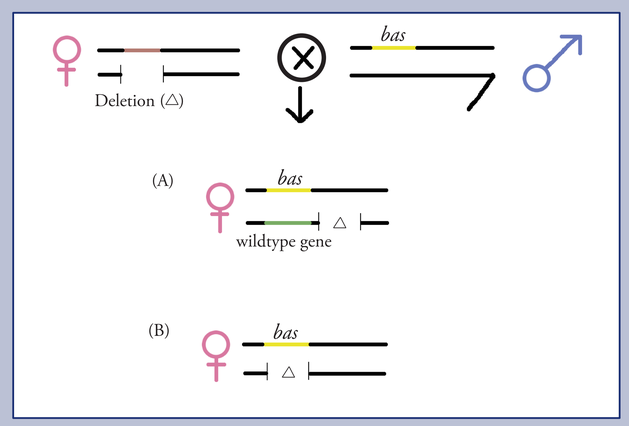


Figure 2: How deletion mapping works. *(A) bas* phenotype is not expressed because the deletion does not delete the dominant "wildtype" copy of *bas*. *(B) bas* phenotype is expressed because the deletion removes all (or part) of the dominant "wildtype" copy of *bas*.

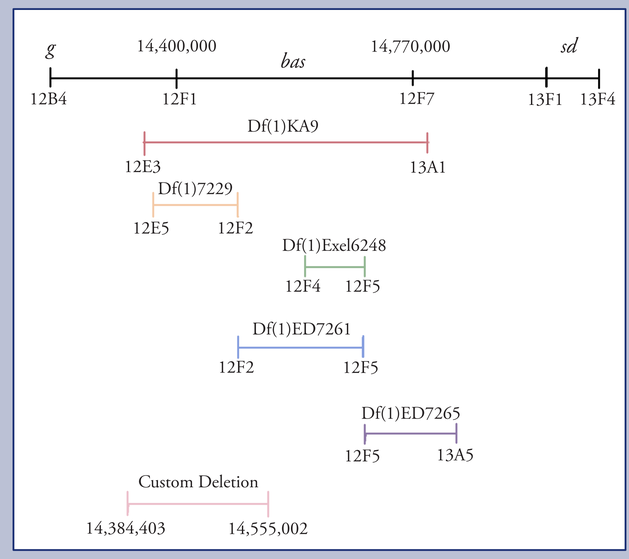


Figure 3: Deletion map of the *bas* region. Shown above are the different deletions used to map the position of the *bas* gene. If *bas* is in their region, progeny will fall paralyzed, as described in figure 2.

## Results and Discussion

After experimentation, the location of *bas* has been narrowed down to region 12F1-12F4. Testing of heterozygous $\frac{bas}{\triangle}$ progeny allowed us to reach this conclusion. A "bang" was delivered to all progeny and a record was made of how many flies fell paralyzed after each test. From Table 1, we see that of the 61 heterozygous *bas*/ Df(1)ED7265 flies that were tested, one fell paralyzed. This allowed us to eliminate the region of 12F5-13A5. Of the other heterozygous $\frac{bas}{\triangle}$ progeny flies that were tested, excluding heterozygous *bas*/Df(1)Exel6248, more than half fell paralyzed. This data allows us to conclude that the *bas* mutation is in the region of 12F1-12F3; however, further tests must be run.

Table 1: Percent Paralysis of Heterozygous $\frac{bas}{\triangle}$ Progeny

| | Number of Flies Paralyzed | Total Flies Tested | Fraction Paralyzing |
|---|---|---|---|
| $\frac{bas}{Df(1)ED7261}$ | 36 | 60 | 60 |
| $\frac{bas}{Df(1)KA9}$ | 17 | 22 | 77 |
| $\frac{bas}{Df(1)ED7265}$ | 1 | 61 | 1.6 |
| $\frac{bas}{Df(1)7229}$ | 11 | 12 | 92 |
| $\frac{bas}{Df(1)7229}$ | 0 | 8 | 0 |

Tests remain ongoing. Still to be tested is the deletion that I have created. That region covers the base pair region of 14,384,403-14,555,002, or 12E11-12F2.

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## References

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