fruitless Splicing Specifies Male Courtship Behavior in Drosophila

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Summary

All animals exhibit innate behaviors that are specified during their development. Drosophila melanogaster males (but not females) perform an elaborate and innate courtship ritual directed toward females (but not males). Male courtship requires products of the fruitless (fru) gene, which is spliced differently in males and females. We have generated alleles of fru that are constitutively spliced in either the male or the female mode. We show that male splicing is essential for male courtship behavior and sexual orientation. More importantly, male splicing is also sufficient to generate male behavior in otherwise normal females. These females direct their courtship toward other females (or males engineered to produce female pheromones). The splicing of a single neuronal gene thus specifies essentially all aspects of a complex innate behavior.

Introduction

Animals are born not only with their characteristic body plan and morphology, but also a set of innate behaviors, or instincts, that are manifested as stereotyped responses to environmental stimuli (Tinbergen, 1951). Enormous progress has been made over the past several decades in elucidating the developmental processes that direct the formation of the body plan and its parts. In contrast, our understanding of how innate behaviors are specified is still rudimentary at best. It is not even clear whether the general principles gleaned from the study of morphological development also apply to the development of behavior. For example, body parts are often specified by “switch” or “selector” genes, the action of which is both necessary and sufficient to trigger the development of a complete anatomical structure (Garcia-Bellido, 1975). Might instincts be specified in a similar way? Are there behavioral switch genes that create the potential for a complex innate behavior? Or, at the other extreme, do instincts emerge diffusely from the combined actions of the vast number of genes that contribute to nervous system development and function, so that no single gene can be said to specify any particular behavior (Greenspan, 1995)?

If behavioral switch genes exist, then one place in which they are likely to be found is in the specification of sexual behaviors (Baker et al., 2001). Males and females generally have dramatically distinct and innate sexual behaviors. These behaviors are essential for their reproductive success, and so strong selective pressure is likely to have favored the evolution of genes that “hardwire” them into the brain. The initial steps of sexual differentiation have been well characterized for several model organisms, and genetic perturbations in these sex-determination hierarchies can alter all aspects of the sexual phenotype—inmate behaviors as well as gross anatomy. Several genes near the top of these sex-determination hierarchies thus qualify as developmental switch genes, but they cannot be considered specifically as behavioral switch genes. A switch gene for a sexual behavior should act to specify either male or female behavior, irrespective of the overall sexual phenotype of the animal. A candidate for such a gene is the fruitless (fru) gene of Drosophila, which is intimately linked to male sexual orientation and behavior (Baker et al., 2001).

Male courtship in Drosophila is an elaborate ritual that involves multiple sensory inputs and complex motor outputs (Hall, 1994; see Movie S1 in the Supplemental Data available with this article online). It is largely a fixed-action pattern, in which the male orients toward and follows the female, taps her with his forelegs, sings a species-specific courtship song by extending and vibrating one wing, licks her genitalia, and finally curls his abdomen for copulation. If the female is sufficiently aroused and has not recently mated, she accepts his advances by slowing down and opening her vaginal plates to allow copulation. An obvious but nonetheless remarkable aspect of this behavior is that mature males court only females, never other males, whereas females do not court at all.

Certain loss-of-function alleles of the fru gene disrupt both male courtship behavior and sexual orientation: performance of the courtship ritual is below par, and it is directed indiscriminately at either sex (Anand et al., 2001; Ito et al., 1996; Lee et al., 2001; Ryner et al., 1996; Villetta et al., 1997). Strong fru alleles completely block courtship behavior, but weaker fru alleles variously disrupt individual steps, with each step affected in some allelic combination (Anand et al., 2001; Lee et al., 2001). This suggests that fru is required for every step of the courtship ritual, not just for a single critical step. For all of these fru alleles, female morphology and behavior appear normal.

Of the many genes known to be involved in male courtship behavior (Billette et al., 2002; fru is unique in that it is sex-specifically spliced Ito et al., 1996; Ryner et al., 1996). Alternative splicing at both the 5′ and 3′ ends of the fru locus generates a complex set of transcripts, all of which encode BTB domain-containing zinc finger proteins. Most of these transcripts are not sex specific, but those initiated from the most distal (P1) promoter are spliced differently in males and females. The alleles of fru that affect male courtship are all associated with chromosomal insertions, deletions, or rearrangements that specifically disrupt these sex-specific P1 transcripts (Anand et al., 2001; Goodwin et al., 2000). This has led to the hypothesis that the male-
specific splicing of the fru P1 transcripts specifies male courtship behavior and sexual orientation (Baker et al., 2001). This is the hypothesis we test here.

We used gene targeting by homologous recombination to generate alleles of fru that are constitutively spliced in either the male or female mode. Forcing female splicing in the male results in a loss of male courtship behavior and orientation, confirming that male-specific splicing of fru is indeed essential for male behavior. More dramatically, females in which fru is spliced in the male mode behave as if they were males: they court other females. Thus, male-specific splicing of fru is both necessary and sufficient to specify male courtship behavior and sexual orientation. A complex innate behavior is thus specified by the action of a single gene, demonstrating that behavioral switch genes do indeed exist and identifying fru as one such gene.

Results

fruitless Splicing Mutants

The fru locus spans approximately 130 kb, and includes at least four promoters (P1–P4) (Figure 1A; Ito et al., 1998; Ryner et al., 1996). Transcripts from the P2–P4 promoters are not sex-specifically spliced and encode a set of common Fru isoforms that have essential functions in the development of both sexes (Figure 1B; An and et al., 2001; Ryner et al., 1996). Transcripts initiated from the distal P1 promoter include the S exon, which is sex-specifically spliced under the control of the sex-determination factors Tra and Tra-2 (Heinrichs et al., 1998; Ito et al., 1996; Ryner et al., 1996). In males, Tra is absent and the S exon is spliced at its default male-specific donor site. This results in an in-frame fusion to the exons common to all fru transcripts, adding a 101 amino acid N-terminal extension that is unique to these male-specific FruM isoforms. In females, Tra binds to fru P1 pre-mRNAs to promote splicing at a more 3′ donor site (Heinrichs et al., 1998) and to block translation of these transcripts (Usui-Aoki et al., 2000). Both mechanisms ensure that no full-length FruM proteins are produced in females.

We generated four alleles of fru by gene targeting: fruF, an allele that should prevent male-specific splicing; fruM and frustra, both of which should force male splicing; and fruC, a control allele in which splicing should be unchanged (Figures 1C and S1). In fruF, point mutations introduced at the male splice donor site of the S exon should abolish splicing at this site but not alter the coding potential of the unspliced transcripts. In fruM, the entire 1601 bp female-specific part of the S exon is deleted, while frustra contains a 261 bp deletion
that just eliminates the Tra binding sites. In fruC, the only sequence modification is the insertion of an FRT site in the intron following the S exon. This FRT insertion is a footprint of the targeting procedure and is also present in the fruD, fruM, and fruMtra alleles.

We established several independent lines for each of these four alleles and verified them by molecular, histological, and behavioral analyses. Independent derivatives of the same allele were indistinguishable in all of these assays. A single line for each allele was then backcrossed to the wild-type Canton S strain for four generations prior to more extensive behavioral tests. For all molecular, histological, and behavioral data presented here, unless otherwise stated, the fruC, fruD, fruM, and fruMtra alleles were examined in trans to fru40.

The fru40 allele results from a deletion of at least 70 kb that removes all P1 and P2 transcripts and is genetically null for the fru behavioral phenotypes [Anand et al., 2001]. Thus, any fru P1 product or activity detected in these assays can be assigned to the engineered fruC, fruD, fruM, or fruMtra allele.

PCR amplification and DNA sequencing of the entire 18 kb targeted region confirmed the predicted structure of the fru locus in each of the four alleles, and RT-PCR experiments confirmed that the predicted transcripts are indeed generated [Figure 1C; splicing at the female donor site is variable in fruM males, presumably because no Tra is present to promote use of the normal female splice site.] FruM proteins could also be detected in the brains of fruC males, and fruM and fruMtra flies of either sex, both in adults [Figure 1D] and 48 hr pupae. The distribution of FruM appears identical in each case and also matches the reported expression of FruM in wild-type males [Lee et al., 2000]. We conclude that the modifications we have introduced into the fru locus eliminate the sex differences in FruM expression but do not alter its distribution.

fru Regulates Sexual Behavior but Not Gross Sexual Anatomy

The sex determination hierarchy in Drosophila bifurcates downstream of Tra. Like fru, the doublesex (dsx) gene is also differentially spliced under the control of Tra and produces either male (Dsxx) or female (Dsxx) isoforms of a DM-domain transcription factor [Burns and Baker, 1989; Erdman and Burg, 1993; Hoshijima et al., 1991]. These Dsx proteins direct male or female morphological development, respectively, but have little influence on sexual behavior: males that lack DsxM still court, albeit at reduced levels [Villella and Hall, 1996], whereas females that produce DsxM resemble normal males but do not court [Taylor et al., 1994]. This has led to the notion that dsx regulates gross sexual anatomy, while fru regulates sexual behavior [Taylor et al., 1994].

Consistent with this view, our fru P1 splice mutations do not generally alter external or internal sexual anatomy: fruC males have the normal male anatomy, whereas fruM and fruMtra females are anatomically normal females. The one exception is that fruM and fruMtra females have a male-specific muscle of Lawrence (MoL), and fruC males lack this muscle [Figure S2]. The MoL is a dorsal abdominal muscle that uniquely de-
Figure 2. Male Splicing of fru Is Essential for Male Courtship Behavior and Sexual Orientation

(A) Courtship indices for males of the indicated genotypes paired with wild-type virgin females. Error bars indicate SEM; n = 43–57 for each genotype. ***p < 0.0001 compared to fru^* (Kruskal-Wallis ANOVA test).

(B) Competitive mating assays in which various fru mutant males were pitted against wild-type (fru^*) males for copulation with a wild-type virgin female. The female preference index is the relative advantage of the fru mutant male over the fru^* male (i.e., the excess copulations with the fru mutant male divided by the total number of copulations), n = 43, 17, 41, and 62 for fru^C, fru^F, fru^M, and fru^stra, respectively. ***p < 0.0001; *p < 0.05, compared to fru^* (Kruskal-Wallis ANOVA test).

(C) Courtship indices for males of the indicated genotypes paired with wild-type males. n = 11–42 for each genotype. ***p < 0.0001; *p < 0.05 compared to fru^* (Kruskal-Wallis ANOVA test).

(D) Chaining indices for groups of males of the indicated genotypes. n = 4–7 groups. ***p < 0.0001 compared to fru^* (Kruskal-Wallis ANOVA test).

what more actively than do any of the control males (fru^1, fru^2, fru^M or fru^stra, Figure 2C). Comparing courtship levels in these single-pair assays is more difficult for male-male assays than for male-female assays, as courtship levels are generally much lower. A more reliable way to test for male-male courtship is to monitor chaining behavior in groups of males. If groups of fru mutant males are left on food plates for several hours or days, they begin to form courtship chains in which each male courts the one ahead of him [Hall, 1976]. It is not clear how this chaining behavior relates to normal courtship, and it probably involves environmental and social stimuli that are absent in the single-pair assays. Nevertheless, it is a robust male-male courtship behavior displayed by classical fru mutants but not wild-type males and can be readily quantified by a chaining index (Chl, the percentage of time three or more males form a chain during a 10 min observation period). Using this assay, we observed dramatically elevated levels of male-male courtship amongst fru^M males (Chl = 63%, p < 0.0001; Figure 2D and Movie S2) compared to fru^C, fru^F, fru^M, or fru^stra males (Chl < 1%). We conclude that male-specific fru splicing not only promotes male-female courtship, it also inhibits male-male courtship.

Intriguingly, in the competition assays, fru^M and fru^stra males had a slight but significant edge over their fru^C competitors, winning 71% (n = 41, p = 0.0002) and 61% (n = 62, p = 0.01) of assays, respectively (Figure 2E). This prompted us to compare individual courtship steps performed by fru^C, fru^M, and fru^stra males in single-pair assays with wild-type virgin females (Table 1). Qualitatively, courtship performed by fru^M and fru^stra males is indistinguishable from courtship by fru^C males. However, fru^M and fru^stra males initiate courtship more rapidly than fru^C males (p < 0.01 for both genotypes). Once courtship is initiated, fru^M and fru^stra males spend as much time as fru^C males performing each of the other steps (tapping, wing extension, licking, and attempted copulation; p > 0.05 for each step). Although we have not been able to detect any differences by molecular or histological means (Figure 1), it is possible that forced male splicing results in slightly elevated levels of FruM proteins in at least some cells in fru^M and fru^stra males. A tentative inference from this result is therefore that FruM is not only essential for male courtship behavior but may also contribute quantitatively to its initiation.

FruM Inhibits Female Reproductive Behaviors

We next examined the sexual behaviors of females for each of the fru splicing mutants, focusing first on female reproductive behaviors (Figure 3). fru^C and fru^F females are as fertile as fru^C controls (>99%), but less than 25% of fru^M and fru^stra females are fertile (Figure 3A). We could not detect any gross morphological abnormalities in the genitalia or reproductive organs of these females, including their innervation, suggesting that the reduced fertility might be due to behavioral rather than anatomical defects (L. Tirian and B.J.D., unpublished data). We therefore examined two female behaviors critical for reproduction: mating receptivity and egg laying.

In mating assays in which a single virgin test female was paired with a wild-type male, fru^C and fru^F females almost always copulated within 60 min (>94%), but less than 16% of fru^M and fru^stra females copulated (Figure 3B). Similarly, in competition assays in which a wild-type male was offered a choice of two virgin females, one fru mutant and one wild-type, the fru^C and fru^F females competed equally with the wild-type females but fru^M and fru^stra females were never chosen (Figure 3C).

We took the females that did mate in the single-pair
Table 1. Comparison of Courtship by fruC Males and fruM and frustra Males and Females

<table>
<thead>
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<th>fruC Male</th>
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<td>n</td>
<td>13</td>
<td>10</td>
<td>11</td>
<td>21</td>
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<td>All courtship steps (CI)</td>
<td>72.94 ± 3.41</td>
<td>89.75 ± 2.87</td>
<td>81.86 ± 4.23</td>
<td>42.40 ± 3.58**</td>
<td>45.76 ± 3.55*</td>
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<td>Courtship latency (s)</td>
<td>50.00 ± 15.23</td>
<td>6.90 ± 2.64*</td>
<td>10.27 ± 3.62*</td>
<td>48.86 ± 10.57</td>
<td>41.73 ± 7.72</td>
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<td>Tapping (s)</td>
<td>51.23 ± 10.28</td>
<td>73.00 ± 8.95</td>
<td>56.09 ± 6.79</td>
<td>86.67 ± 9.49*</td>
<td>147.20 ± 18.02***</td>
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<td>Wing extension (s)</td>
<td>128.77 ± 16.66</td>
<td>181.30 ± 19.63</td>
<td>153.36 ± 22.08</td>
<td>105.57 ± 16.14</td>
<td>86.20 ± 12.87</td>
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<td>Licking</td>
<td>3.77 ± 0.76</td>
<td>5.60 ± 0.62</td>
<td>9.09 ± 3.03</td>
<td>0.62 ± 0.22*</td>
<td>0.27 ± 0.12*</td>
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<td>Attempted copulation</td>
<td>1.54 ± 0.29</td>
<td>2.40 ± 0.65</td>
<td>3.36 ± 1.06</td>
<td>0 ± 0**</td>
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Courtship assays for fruC males and fruM and frustra males and females paired with wild-type virgin females were recorded at higher magnification to monitor individual courtship steps. Values are mean ± SEM. For tapping and wing extension, the total time engaged in these steps was recorded; for licking and attempted copulation, it was the total number of events. *p < 0.01; **p < 0.001; ***p < 0.0001 compared to fruC males (Kruskal-Wallis ANOVA test). p > 0.05 for all other comparisons.

assays and counted the number of eggs they laid over each of the next 3 days. Mated fruC and fruF females laid on average over 65 eggs during this period, whereas the fruM or frustra females laid on average less than two eggs [Figure 3D]. By mating fruM and frustra females to males whose sperm are labeled by GFP (djGFP) [Santel et al., 1997], we confirmed that sperm are transferred and stored in the spermathecae of ~30% of these females (L. Tirián and B.J.D., unpublished data). At least some of these sperm are used, as we often observed fully developed embryos in the uterus of a mated fruM female and occasionally even witnessed a “live birth” as a larva attempted to crawl out through the vagina. Thus, male specific fru products inhibit at least two female reproductive behaviors: copulation and egg laying.

Females Behaving Like Males

If fru is a behavioral switch gene, then fruM and frustra females should not only lose female reproductive behaviors, they should also gain male behaviors. Specifically, they should court other females. We tested this prediction in single-pair courtship assays and in chaining assays [Figure 4].

Remarkably, fruM and frustra females court wild-type females, with courtship indices over 40% in single-pair assays [Figures 4A and 4B and Movie S3]. Placed together on food plates, groups of fruM and frustra females also form courtship chains similar to those formed by fruF males [Figure 4C and Movie S4]. In these assays, fruM and frustra females had chaining indices of over 40%. Neither fruC nor fruF females show any female-female courtship, either in single-pair assays (CI < 0.1%) or in chaining assays (CI < 0.1%).

Qualitatively, courtship of wild-type virgin females by fruM and frustra females resembles normal male courtship, as shown for example by fruC females [Table 1]. fruM and frustra females perform all steps of the courtship ritual, with the obvious exception of copulation, which is anatomically impossible, as well as abdominal bending in attempt to copulate, which may be inhibited by the much larger abdomen of the female. There are also some quantitative differences in the individual courtship steps performed by fruM or frustra females and fruC females. For example, fruM and frustra females copulate with wild-type males at higher frequencies than fruC females; fruM females and frustra females also copulate more frequently than fruC females. This suggests that fruM and frustra females are able to overcome the reproductive inhibition caused by fru expression in order to successfully copulate with wild-type males.

Figure 3. Male Splicing of fru Suppresses Female Reproductive Behaviors

(A) Fertility of females of the indicated genotypes. n = 100-128, ***p < 0.0001 (x² test).
(B) Receptivity of females of the indicated genotypes. n = 39, 54, 93, and 66, respectively. ***p < 0.0001 (x² test).
(C) Competitive mating assays in which various fru mutant females were pitted against wild-type (fruF) females for copulation with a wild-type male. The male preference index is the relative advantage of the fru mutant female over the fru+ female (i.e., the excess copulations with the fru mutant female divided by the total number of copulations). n = 33-31. ***p < 0.0001 (Kruskal-Wallis ANOVA test).
(D) Eggs laid by single mated females of the indicated genotype for each of the first three days after copulation with a wild-type male. The three bars for each genotype indicate the average number of eggs laid on the first, second, and third days, respectively. Error bars indicate SEM. n = 89, 69, 22, and 30 for fruC, fruF, fruM, and frustra, respectively. ***p < 0.0001 (Kruskal-Wallis ANOVA test).
Development endows an animal with the morphology and instinctive behaviors characteristic for its species, preparing it for survival and reproduction in the environment into which it is likely to be born. An animal’s instinctive behaviors are just as stereotyped and just as characteristic for its species as its morphology, and so one might expect to find a similar logic underlying the genetic programs that specify morphology and behavior. Yet, whereas morphological development has now largely succumbed to the attack of classical forward genetics in a few model organisms, the same approach has made only modest inroads into the developmental origins of complex innate behaviors. Does this reflect a fundamental difference in the ways behavior and morphology are specified during development or just a lack of attention to the problem of behavioral development?

One of the lessons from the genetic analysis of morphological development is that anatomical features are often specified by switch genes, the action of which is both necessary and sufficient to direct the formation of a particular feature. A striking example of such a morphological switch gene is the eyeless gene of Drosophila, which is both necessary and sufficient for eye development. If analogous genetic principles guide the emergence of both morphology and behavior, then we should also expect that at least some innate behaviors are specified by switch genes.
The action of such a behavioral switch gene would be both necessary and sufficient to hardwire the potential for the behavior into the nervous system. Until now, such behavioral switch genes have been elusive. Here, we have demonstrated that the fruitless (fru) gene of Drosophila is a switch gene for a complex innate behavior: the elaborate ritual of male courtship.

fru as a Switch Gene for Male Courtship Behavior

fru has long been known to be required for male courtship behavior (Gill, 1963). In this regard, however, fru is not particularly unusual. Many other genes have also been implicated in male courtship behavior, and in one way or another, a substantial fraction of the genome is likely to be required for a male to be capable of and inclined to court a female. fru only assumed its more prominent position when it was molecularly characterized, revealing that some of its transcripts are spliced differently in males and females (To et al., 1996; Ryner et al., 1996). This led to the hypothesis that splicing of fru specifies male courtship behavior (To et al., 1996; Ryner et al., 1996). Although widely discussed (e.g., Baker et al., 2001), this hypothesis has remained untested for almost a decade. We have now confirmed the key predictions of this hypothesis by showing that male splicing is indeed necessary for male courtship behavior (Figure 2) and is also sufficient to generate male behavior by an otherwise normal female (Figure 4).

Male courtship behavior performed by fruM and fruMΔmales is a remarkable mimic of courtship by wild-type or control fru males. Some courtship steps, such as initiation, orientation, following, and wing extension, are indistinguishable in fruM and fruMΔmales. Other steps are clearly abnormal. fruM females do not, for obvious reasons, copulate. But licking, which should be anatomically possible, is also significantly reduced. Qualitatively, this pattern of courtship resembles that of dsex males (Villella and Hall, 1996). This is perhaps not surprising, as fruM females resemble dsex males in that they lack male-specific Dsx isoforms (DsxM) and hence are anatomically female, yet they express the male-specific Fru isoforms (FruM).

The distinct roles of fru and dsex in sexual development are clearly illustrated by the differences between animals that produce either only FruM or only DsxM. Animals that express DsxM but not FruM (either fruF males or dsexF females) resemble normal males but do not court (Figure 2A; Taylor et al., 1994). Conversely, animals that express FruM but not DsxM (either fruF males or dsexF males) do court, even though they resemble normal females (Figure 2B; Villella and Hall, 1996). Thus, FruM is both necessary and sufficient for male courtship, whereas DsxM is neither necessary nor sufficient. The role of DsxM in courtship may simply be to provide the gross male anatomy needed for its optimal execution. This anatomical contribution of DsxM includes the formation of male reproductive organs and external genitalia (Burtis and Baker, 1989), the generation of the neurons that innervate these organs (Taylor and Truman, 1992), and the formation of male-specific taste sensilla on the legs that may house pheromone-detecting neurons (Bray and Amrein, 2003).

An open question is whether fru specifies male-like behavioral patterns more generally or is exclusively involved in male courtship behavior. We have focused our study on courtship behavior because this is the most dramatic, most robust, and best understood of the sexually dimorphic behaviors in Drosophila. But other behavioral patterns, such as aggression (Chen et al., 2002; Nilsen et al., 2004), are also sexually dimorphic, and it will be interesting to determine to what extent these behaviors depend on fru.

How Does fru Specify Male Courtship Behavior?

A behavioral switch gene such as fru must act through the relevant neural circuits. In the accompanying paper (Stockinger et al., 2005), we begin the anatomical and functional characterization of the neurons in which FruM is expressed and present evidence that they form a neural circuit that is largely dedicated to male courtship behavior. As the same circuit seems to be present in the female, we reason that FruM most likely exerts its effect by modulating the function rather than the assembly of this circuit. Nevertheless, the critical period for FruM to do so is evidently during development, as adult males begin courting soon after eclosion, without any prior exposure to another fly. Moreover, experiments involving conditional expression of fra have suggested that male behavior is irreversibly programmed during the early- to midpupal stages (Arthur et al., 1998), coincident with the onset of FruM expression in increasing numbers of neurons in the male nervous system (Lee et al., 2000).

By analogy to other members of the BTB-zinc finger family, FruM proteins are thought to be transcription factors and as such would specify sexual behavior by regulating the expression of one or more target genes. In the simplest scenario, fru may regulate one and the same target gene in all of the neurons in which it is expressed—acting merely as a switch that sets another switch. Alternatively, fru might directly regulate a large number of target genes, with different targets in different neurons. Several observations favor this latter scenario. The set of FruM proteins includes isoforms with at least four different DNA binding domains, which are likely to homo- and heterodimerize through their common BTB domain. FruM may also interact with other BTB-domain-containing zinc finger transcription factors such as Lola, which itself has at least 20 different DNA binding domains (Gecke et al., 2003; Horiuchi et al., 2003). Thus, FruM has the potential to form a large set of distinct regulatory complexes, as might be expected if it is to regulate different genes in different neurons. That at least some of this potential is utilized is suggested by the fact that we could not rescue a fru mutant with cDNAs encoding just a single isoform (even when using fruGAL4, Stockinger et al., 2002) to drive expression in the correct neurons; D. Kvitkow and B.J.D., unpublished data) and that we have already isolated mutations in two different DNA binding domains in an ongoing screen for revertants of the gain-of-function fruΔmales phenotype (L. Tirián and B.J.D., unpublished data).

The fru target genes themselves are unknown, as are, for the most part, their effects. The few cellular func-
tions so far ascribed to fru are the regulation of the number or size of synaptic terminals in specific glomeruli of the antennal lobe [Stockinger et al., 2005] and at the MoL [Billeter and Goodwin, 2004], as well as the production of serotonin in certain male-specific neurons of the abdominal ganglion [Lee and Hall, 2001]. A fascinating question for the future is whether profound differences in sexual behavior arise as the sum of many subtle differences such as these, or are instead primarily due to a still unknown action of FruM in a few key “decision” neurons.

Single Genes and Complex Behaviors
Complex behaviors require the actions of vast numbers of genes, and so it is quite easy to isolate mutations in single genes that disrupt a particular behavior. Almost all of these mutations are relatively uninformative as to the genetic basis of that behavior or indeed the relationship between genes and behavior more generally. More useful are genes for which different allelic states result in different manifestations of the behavior. Several fascinating examples of such genes have been found, and all have provided important insights into the behaviors they influence. This includes, for example, the npr-1 neuropeptide receptor gene in the control of social feeding in C. elegans [de Bono and Bargmann, 1998], the foraging cGMP-dependent protein kinase gene in Drosophila social feeding behavior [Osborne et al., 1997], the vasopressin 1a receptor gene in affiliative behavior in voles [Lim et al., 2004; Young et al., 1999], and, more controversially, the serotonin transporter gene in human depression [Ogilvie et al., 1996]. Importantly, fru differs from “behavior genes” such as these in one critical aspect: it does not influence a behavior as it happens, but rather acts during development to create the potential for a behavior [Baker et al., 2001].

Might there be other behavioral switch genes like fru, and if so, how will we find them? The lack of obvious candidates is no reason to doubt that other behavioral switch genes exist. Indeed, in many ways it is almost fortuitous that this function of fru has been discovered at all. Mutations that eliminate all fru function are lethal and hence uninformative as regards to fru’s role in male courtship. This role only came to light through the isolation of relatively rare alleles that disrupt specific transcripts [Gill, 1963]. Even then, it was not until its molecular cloning that fru acquired any particular significance [Ito et al., 1996; Ryner et al., 1996] and only now, through precise gene manipulations, that its role as a switch gene has been established. Classical forward genetics might not be the most effective way to search for behavioral switch genes, particularly if, like fru, the genes also have essential but unrelated functions during development.

Perhaps even more challenging will be recognizing a behavioral switch gene when we find one. Formally, this requires a sufficiency experiment, which involves asking if ectopic expression can specify a novel behavioral pattern in an otherwise normal animal. It is difficult to envision how such an experiment might be performed for anything other than a sexually dimorphic behavior. Hence, if we are to identify switch genes for behaviors that are not sex specific, then we must relax this strict criterion. What other features of fru could serve as a guide in assessing other candidate switch genes? Four aspects of fru stand out. First, as already noted, it acts during development to create the potential for the behavior, rather than directly influencing the behavior itself. Second, it appears to be involved in most or all aspects of the behavior, not just a single component. Third, loss-of-function mutations do not result in a general impairment of neural function, but a specific behavioral deficit. Fourth, it is required in a diverse set of neurons with little in common except their role in this behavior, to which they may also be dedicated. Candidate vertebrate genes that fulfill at least some of these criteria have been linked to behaviors at opposite extremes of complexity: the ETS transcription factor genes Er81 and Pea3 in the spinal stretch reflex [Lin et al., 1998] and, more speculatively, the forkhead-domain transcription factor gene FoxP2 in human language ability [Vargha-Khadem et al., 2003].

Finally, the concept that a switch gene can specify an entire innate behavior in no way denies the critical role of complex gene networks, just as the concept of a morphogenetic switch does not deny the existence of complex regulatory networks among the genes it regulates. These networks add both detail and robustness to the behavioral or morphological pattern initially laid down by the switch gene at the top of the hierarchy. The notion of a behavioral switch gene does, however, imply that at least some instinctive behaviors develop according to the familiar genetic logic of morphological development. Given the appropriate genetic tools, behavioral instincts should ultimately succumb to the same kind of molecular genetic analysis that has so successfully revealed the principles of morphological development.

Experimental Procedures

Generation of fru Splicing Mutants
Gene targeting by homologous recombination was performed essentially as described by Rong and Golic [2000] and illustrated in Figure S1. Four “5′ half” donor elements were used to derive targeted lines containing one of each of the desired modifications in the 5′ part of the fru locus, followed by the FRT insertion. Similarly, a single “3′ half” donor construct was used to derive targeted lines consisting of an FRT insertion and the 3′ part of the fru locus. Targeted lines were selected by mobilizing and linearizing the original donor using hsFLP and bal-SceI and crossing these virgin females to eyFLP [Newsome et al., 2001] males so that reintegration can be detected in the progeny by the stable expression of the white* reporter. Between two and ten independent lines were obtained from each of the original donor elements. We selected two independent 3′ lines and recombined each with one of two different 5′ lines (for each of the four alleles), using hsFLP to induce recombination at the FRT site. This generated two completely independent lines for each allele. For genomic sequencing, PCR was used to amplify nine overlapping fragments of 1.1–5.1 kb, which were directly sequenced. For RT-PCR, files were frozen and passed through a sieve to isolate heads, legs, and wings, which were then homogenized and used to prepare mRNA using the Quick Prep Micro mRNA purification kit (Amersham Biosciences). Random hexamers were used for first strand synthesis, and gene-specific primers were used for second strand synthesis.

Behavioral Assays
Flies were raised on semidefined medium [Backhaus et al., 1984] at 25°C in a 12hr:12hr light:dark cycle and aged for 5–7 days after
eclosure. Test flies were collected shortly after eclosure and aged individually in small food vials. Flies used as courtship objects were aged in pools of 30–50 in large food vials, with the exception of the naïve males used in the oo-GAL4/US-α-tra experiments, which were aged individually. The oo-GAL4 line is line C described in [Ferveut et al. (1997)](#).

### Single-Pair Courtship

Single-pair courtship assays [Villela et al., 1997] were performed using a round chamber of 10 mm diameter and 4 mm height containing a white nitrocellulose filter. For same-sex courtship assays, genotypes were distinguished by applying a terra cotta color marker to the thorax of one fly at the time of initial collection. In control experiments, the marker did not influence the courtship vigor of either the marked or unmarked flies.

### Chaining

Chaining assays [Villela et al., 1997] were performed using groups of eight flies placed in a 35 mm × 10 mm petri dish containing food. Flies were left undisturbed for one day and observed for 10 min on the second day.

### Competitive Mating

In the competitive mating assays [Bray and Amrein, 2003], a terra cotta marker was used to distinguish flies of the same sex. For each pair of genotypes, the marker was applied to each genotype in approximately half the assays. No difference in outcome was observed between the two sets of assays for a given pair of genotypes, and the data were therefore pooled.

### Fertility

Single virgin males or females were placed in food vials with five wild-type virgin females or eight males, respectively, and scored as sterile if the flies were still alive but there was no progeny after 20 days.

### Receptivity

In receptivity tests [Aligaki et al., 1991], females were scored as receptive if they mated within 60 min.

### Egg Laying

Single virgin females were paired with three wild-type males in a food vial. After copulation, the female was removed and transferred every 24 hr to a new food vial. The number of eggs in each vial was counted.

### Histochemistry

Staining of pupal and adult brains was performed as described in [Stockinger et al. (2005)](#). Dorsal abdominal muscles were stained with rhodamine-labeled phallolidin as described in [Taylor (1992)](#).

### Supplemental Data

Supplemental Data include three figures and four movies and can be found with this article online at [http://www.cell.com/cgi/content/full/121/7/785/DC1](http://www.cell.com/cgi/content/full/121/7/785/DC1).

### Acknowledgments

We thank Eric Buchner, Jean-François Ferveur, Kent Golio, Rolf Nöthiger, and Barbara Taylor for providing valuable reagents, Duda Kvtisiani for help and advice on behavioral assays and statistical analysis, Petra Stockinger for anti-FnuM4, László Tírián for unpublished data, Angela Graf and Karin Piahsa for technical support, and Kim Nasmyth, Silvia Arber, László Tírián, and Frank Schnorrer for critical comments on the manuscript.

Received: January 30, 2005

Revised: March 28, 2005

Accepted: April 13, 2005

Published: June 2, 2005

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