

approaches in identifying new K⁺ channel genes that have not yet been isolated on the basis of sequence similarity. Finally, just as mammalian homologs have been found for *Drosophila* K⁺ channel genes in the *Sh* superfamily, we anticipate the identification of mammalian counterparts to *eag*.

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Alteration of Four Identified K⁺ Currents in *Drosophila* Muscle by Mutations in *eag*

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Voltage-clamp analysis of *Drosophila* larval muscle revealed that *ether à go-go* (*eag*) mutations affected all identified potassium currents, including those specifically eliminated by mutations in the *Shaker* or *slowpoke* gene. Together with DNA sequence analysis, the results suggest that the *eag* locus encodes a subunit common to different potassium channels. Thus, combinatorial assembly of polypeptides from different genes may contribute to potassium channel diversity.

A VARIETY OF K⁺ CHANNELS PARTICIPATE in many cellular functions and contribute to the signaling capacity of excitable cells (1). However, the genetic basis that underlies this diversity still remains to be fully explored (1–3). Studies have shown that several distinct K⁺ currents in *Drosophila* muscle are selectively affected by mutations in different genes (4–6). We investigated the effect of mutations in the *eag* gene (7) on all identified K⁺ currents in *Drosophila* larval muscle. These include the transient (*I_A*) and delayed (*I_K*) voltage-activated K⁺ currents and the fast (*I_{CF}*) and slow (*I_{CS}*) Ca²⁺-activated K⁺ currents (8–10).

A voltage-clamp analysis with two microelectrodes was performed on the body-wall muscle fibers in *Drosophila* third instar larvae (10–12). We measured the voltage-activated *I_A* and *I_K* in Ca²⁺-free saline, which eliminated the inward Ca²⁺ current (*I_{Ca}*), as well as the Ca²⁺-activated *I_{CF}* and *I_{CS}* (8–10). *I_A* and *I_K* could be separated by their kinetic differences in inactivation and recovery (11). A previous inactivating pulse to –20 mV from the holding potential (*V_H* = –80 mV) inactivated most *I_A* but left *I_K* virtually intact (Fig. 1A). The difference between corresponding traces with and without the inactivating pulse was *I_A* (11).

Current-voltage (*I-V*) relations were determined for the peak *I_A* and the maximum *I_K* at different voltages for several *eag* alleles (Fig. 1). *I_K* was reduced in *eag^{X6}* and, to a lesser extent, in *eag^{4PM}* and *eag¹* (Fig. 1C).

I_A decreased in *eag^{X6}* even though it was not significantly affected in *eag^{4PM}* and *eag¹* (13). The extreme phenotype of *eag^{X6}* is consistent with molecular data that indicate that the *eag* transcript is truncated in this mutant. Therefore, *eag^{X6}* is likely to exhibit the null phenotype (14).

Measurements of Ca²⁺-dependent currents requires the presence of Ca²⁺ in saline. As in other invertebrate species, the inward current in *Drosophila* muscle fibers is carried by Ca²⁺, which is required for contraction (15). Although it is desirable to measure isolated *I_{Ca}* with pharmacological elimination of all K⁺ currents, such experiments are prevented by the resulting contraction of all muscle fibers in the larval preparation. We instead determined the current mediated by Ca²⁺ channels by replacing Ca²⁺ with Ba²⁺, which permeates Ca²⁺ channels and blocks K⁺ channels but does not initiate muscle contraction (9, 16). These experiments indicated that the *I_{Ba}*'s in *eag^{4PM}* and *eag^{X6}* larvae were not different from that found in normal larvae (17).

The Ca²⁺-activated *I_{CF}* and *I_{CS}* were studied at a lower temperature, and the external Ca²⁺ concentration was reduced to 0.9 mM from the standard 1.8 mM (8, 11). Under these conditions, muscle contraction was minimized, but the two currents could still be measured (Fig. 2A). We removed the voltage-activated *I_A* by addition of 4-aminopyridine (18) and the voltage-activated *I_K* by addition of quinidine (10). The remaining net current was outward; the inward *I_{Ca}* was masked by the *I_{CF}* and *I_{CS}*. The inward tail currents (Fig. 2A) that followed the depolarization-induced outward currents were characteristic of Ca²⁺-activated K⁺ currents and distinct from *I_K*, which lacks inward tails at a *V_H* of –80 mV (Fig. 1C).

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Further simple physiological separation of I_{CF} and I_{CS} is not yet feasible. However, as indicated by studies involving genetic elimination of I_{CF} (6, 10), I_{CF} contributes mainly to the early outward transient current, and I_{CS} contributes to the delayed plateau (Fig. 2A).

The I - V relations for the plateau at the end of pulses (Fig. 2B) and for the transient peak (Fig. 2C) were determined. Because I_{Ca} does not appear to be affected by various *eag* alleles, the differences between normal and mutant currents represent reductions in I_{CF} and I_{CS} . Both I_{CF} and I_{CS} were reduced in *eag*¹ and *eag*^{X6} larvae, whereas only I_{CS} was decreased in *eag*^{APM} larvae (Fig. 2).

Our results demonstrate that all K⁺ currents in larval muscle were affected by *eag* mutations, unlike *Sh* (*Shaker*) and *slowpoke* (*slo*) mutations, which specifically eliminate I_A and I_{CF} , respectively (4-6, 8-10). This observation raises the possibility that the *eag* gene contributes a subunit common to different K⁺ channels. Indeed, sequence analysis of *eag* shows that this gene defines a putative K⁺ channel polypeptide that is related to but distinct from the I_A channel proteins encoded by the *Sh* superfamily (14). Recombinant heteromultimeric K⁺ channels have been expressed in *Xenopus* oocytes from the assembly of different splicing products of the *Sh* locus or of the products of genes in the *Sh* family (19, 20). We suggest that a combinatorial assembly of polypeptides from

different genes contributes to K⁺ channel diversity in vivo (see also 3, 8, 20).

None of the *eag* alleles examined completely eliminated any of the K⁺ currents in *Drosophila* larval muscle. The severity of the defects in *eag*^{X6} larvae likely represents the null phenotype of this locus. Similar defects have been seen in a different allele, *eag*^{sc29}, which also truncates *eag* transcripts and is thus also likely to cause a null phenotype (14). The fact that none of the currents were eliminated even in *eag* null alleles and that individual species of *Sh* transcripts can produce I_A -like currents in the oocyte expression system (21) indicate either that the *eag* product is not essential to channel activation or that different channels can form with other channel subunits substituted for the *eag* subunit.

The notion that the *eag* protein participates directly in channel operation is strengthened by its allele-dependent effects. The mutation *eag*¹ affected I_{CF} and I_{CS} to the same extent as did the null allele *eag*^{X6} but left I_A intact (Figs. 1 and 2). In *eag*^{APM}, only I_{CS} was substantially reduced (Figs. 1 and 2). Furthermore, allele-specific interactions that could result from physical contact between two gene products (22) were observed in *eag Sh* double-mutant combinations; defects of I_A not seen for either the *eag* or *Sh* allele alone were detected in certain

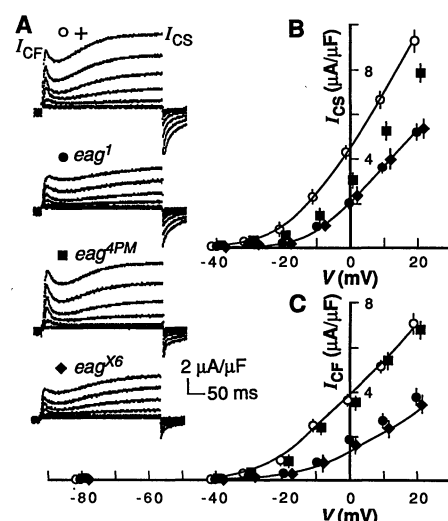
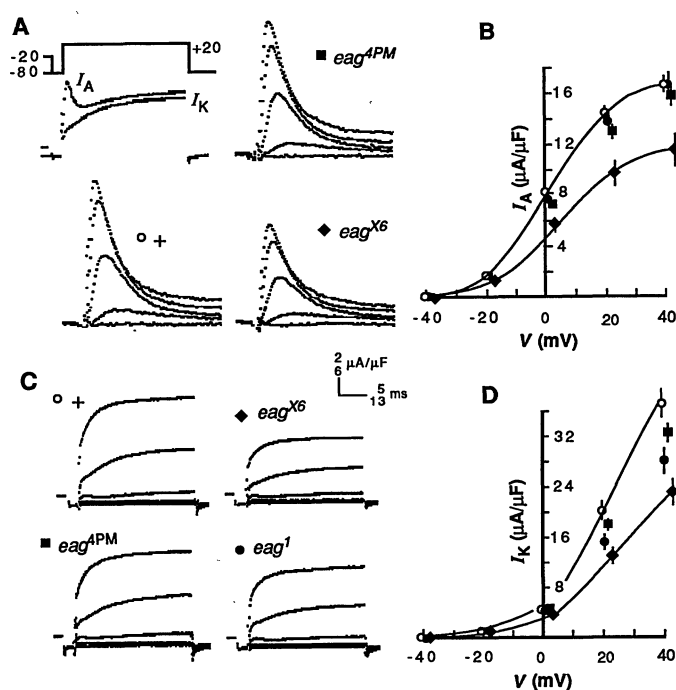


Fig. 2. Effects of *eag* mutations on I_{CF} and I_{CS} . Families of currents were recorded in saline containing Ca^{2+} , 4-aminopyridine, and quinidine (12) at 5°C. (A) The traces represent Ca^{2+} -activated outward I_{CF} and I_{CS} , which masked the inward I_{Ca} . (B) I - V relations at the I_{CS} plateau determined at the end of the 400-ms test pulse. (C) I - V relations at the I_{CF} peak. I - V relations were determined without subtraction of I_{Ca} . The number of fibers was 10, 10, 8, and 8 from three to five larvae for +, *eag*¹, *eag*^{APM}, and *eag*^{X6}, respectively.

Fig. 1. Effects of *eag* mutations on I_A and I_K in *Drosophila* larval muscle.



(A) The voltage-clamp traces demonstrate I_A and I_K and the isolated I_A . As shown in the inset (top left), a conditioning pulse (2 s) to -20 mV inactivated I_A but left I_K intact (11). Without the pulse, both I_A and I_K were activated by the test pulse (60 ms). The families of traces demonstrate I_A extracted from the currents with and without the conditioning pulse. (B) I - V relations of I_A for normal (+) and mutant alleles. (C) Traces of I_K from normal and mutant alleles. I_A was inactivated by the conditioning pulse. (D) I - V relations for I_K in normal and mutant alleles. All experiments were performed at 16°C, in Ca^{2+} -free saline (11). The number of fibers was 10, 9, 8, and 8 from three to six larvae for +, *eag*¹, *eag*^{APM}, and *eag*^{X6}, respectively. Scale bars, 2 $\mu A/\mu F$ (vertical), 5 ms (horizontal) for I_A ; 6 $\mu A/\mu F$ and 13 ms for I_K . For this figure and Fig. 2, data were collected from muscle fibers 6 and 12 in abdominal segments 3 to 5 (11) at a V_H of -80 mV. In both figures, traces represent current density (normalized to membrane capacitance in microamperes per microfarad) averaged from the number of fibers specified for each allele, error bars in I - V relations indicate SEM, and curves are fit by eye to data from normal and *eag*^{X6} fibers.

double-mutant combinations (23). Such phenotypes might arise from the compounding effects of structural alterations in the *Sh* and *eag* polypeptides in the I_A channel. The allele-dependent effects on individual K⁺ currents may reflect the association of specific domains with the function of a particular channel. In *Paramecium*, separate domains of calmodulin are responsible for the activation of two different currents, and mutants associated with different domains demonstrated allele-dependent effects on the currents (24).

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