

RICE UNIVERSITY

***In vivo* analysis of gain-of-function mutations  
in the *Drosophila eag*-encoded K<sup>+</sup> channel.**

by

**Robert John Gunn Cardnell**

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APPROVED, THESIS COMMITTEE:



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Michael Stern, Professor  
Biochemistry and Cell Biology



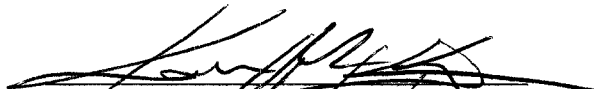
---

Richard Gomer, Professor  
Biochemistry and Cell Biology



---

Mary Ellen Lane, Assistant Professor  
Biochemistry and Cell Biology



---

Kevin MacKenzie, Assistant Professor  
Biochemistry and Cell Biology



---

Michael Kohn, Assistant Professor  
Ecology and Evolutionary Biology

HOUSTON, TEXAS

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## Abstract

Neuronal Na<sup>+</sup> and K<sup>+</sup> channels elicit currents in opposing directions and thus have opposing effects on neuronal excitability. Mutations in genes encoding Na<sup>+</sup> or K<sup>+</sup> channels often interact genetically, leading either to phenotypic suppression or enhancement for genes with opposing or similar effects on excitability respectively. For example, the effects of mutations in *Shaker* (*Sh*), which encodes a K<sup>+</sup> channel subunit, are suppressed by loss of function mutations in the Na<sup>+</sup> channel structural gene *para*, but enhanced by loss of function mutations in a second K<sup>+</sup> channel encoded by *eag*.

Here I characterize three novel mutations that suppress the effects of a *Sh* mutation on behavior and neuronal excitability. Recombination mapping localized the mutations to the *eag* locus, and I used sequence analysis to determine that two of the mutations are caused by a single amino acid substitution (G297E) in the S2-S3 linker of Eag. Because these novel *eag* mutations confer opposite phenotypes to *eag* loss of function mutations, I suggest that *eag*<sup>G297E</sup> causes an *eag* gain of function phenotype. I hypothesize that the G297E substitution may cause premature, prolonged or constitutive opening of the Eag channels by favoring the “unlocked” state of the channel. The third mutation has two amino acid substitutions in Eag (A259V and E762V) and may also be a gain of function allele of *eag*. Interestingly, these mutations appear to manifest their most obvious phenotypes under conditions that prolong the action potential.

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## List of Abbreviations

4-AP	4-amino pyridine
bEAG	bovine EAG
Ca <sup>2+</sup>	calcium ion
DmEag	Drosophila Eag
dsRNA	double-stranded RNA
ejc	excitatory junctional current
ejp	excitatory junctional potential
EMS	ethyl methane sulfonate
GAL4	transcription factor
I	current
I <sub>A</sub>	Transient K <sup>+</sup> A current
I <sub>CF</sub>	Fast Ca <sup>2+</sup> activated K <sup>+</sup> current
I <sub>CS</sub>	Slow Ca <sup>2+</sup> activated K <sup>+</sup> current
I <sub>K</sub>	Delayed rectifier K <sup>+</sup> current
K <sup>+</sup>	potassium ion
LTF	long term facilitation
mejp	spontaneous mini excitatory junctional potential
Mg <sup>2+</sup>	magnesium ion
nmj	neuromuscular junction
Na <sup>+</sup>	sodium ion
PCR	polymerase chain reaction
PNS	peripheral nervous system

rEAG	rat EAG
RFLP	restriction fragment length polymorphism
RNAi	RNA mediated interference
RT-PCR	reverse transcription PCR
SEM	standard error of the mean
TEA	tetraethylammonium
UAS	upstream activating sequence
$\overline{XX}$	attached X

## List of Genes

<i>ala</i>	<i>CamKII inhibitor peptide</i>
<i>CamKII</i>	<i>calcium/calmodulin dependent kinase II</i>
<i>Cha</i>	<i>choline acetyl transferase</i>
<i>eag</i>	<i>ether-à-go-go</i> ( $K^+$ channel subunit)
<i>elav</i>	<i>embryonic lethal abnormal visual system</i>
<i>Elk</i>	<i>eag-like</i> ( $K^+$ channel subunit)
<i>Erg</i>	<i>eag-related-gene</i> ( $K^+$ channel subunit)
<i>gli</i>	<i>gliotactin</i>
<i>Hk</i>	<i>hyperkinetic</i> ( $K^+$ channel subunit)
<i>ine</i>	<i>inebriated</i> ( $Na^+/Cl^-$ dependent neurotransmitter transporter)
<i>itpr</i>	<i>inositol-1,4,5-triphosphate receptor</i>
<i>mle<sup>nap</sup></i>	<i>male-less: no-action-potential</i>
<i>nap</i>	<i>no-action-potential</i> ; now known as <i>mle</i>
<i>pum</i>	<i>pumillio</i> (translational repressor)
<i>para</i>	<i>paralytic</i> ( $Na^+$ channel structural subunit)
<i>plc</i>	<i>phospholipase C</i>
<i>push</i>	<i>pushover</i> (also known as <i>purity of essence</i> )
<i>Rap1</i>	GTPase (also known as <i>roughened</i> )
<i>Ras1</i>	<i>Ras</i> GTPase
<i>Sh</i>	<i>Shaker</i> ( $K^+$ channel subunit)
<i>Slo</i>	<i>slow-poke</i> ( $K^+$ channel subunit)
<i>VACht</i>	<i>vesicular acetylcholine transporter</i>

# Chapter 1: Background

## 1.1 Significance

### 1.1.1 K<sup>+</sup> channel disorders

Defects in potassium (K<sup>+</sup>) channel function cause a wide range of diseases termed potassium channelopathies. These channelopathies encompass diseases such as episodic ataxia (e.g., D'ADAMO *et al.* 1999), myokymia (DEDEK *et al.* 2001), epilepsy (SCHROEDER *et al.* 1998), arrhythmia (SANGUINETTI 1999), and deafness (VAN HAUWE *et al.* 2000). Furthermore, loss of normal K<sup>+</sup> channel function can enhance tumor growth (MEYER and HEINEMANN 1998; MEYER *et al.* 1999; PARDO *et al.* 1999; SMITH *et al.* 2002; SUZUKI and TAKIMOTO 2004). K<sup>+</sup> channel gain of function mutations have been identified in patients with diseases such as familial atrial fibrillation (CHEN *et al.* 2003) and have also been associated with the low prevalence of diseases such as diastolic hypertension in some populations (FERNANDEZ-FERNANDEZ *et al.* 2004). Consequently, understanding how K<sup>+</sup> channels function, how they are regulated and how they interact with other membrane components is of substantial importance.

### **1.1.2 Drosophila neuronal excitability**

The *Drosophila* third instar larva provides a unique system to explore the effects of mutant genes upon the excitability of the motor axon. Many genes have been identified as having roles in *Drosophila* motor axon excitability and a significant proportion of these have human homologues (GANETZKY 2000). This model system thus provides an opportunity to explore possible roles for these genes in humans, with the end goal of the further understanding of human nervous system conditions such as those mentioned in chapter 1.1.1.

## **1.2 Drosophila larval peripheral nerve**

The *Drosophila* peripheral nerve contains both motor and sensory axons surrounded by peripheral glial cells, which are analogous to mammalian Schwann cells (SEPP *et al.* 2000). A second glial layer, the perineural glia (the perineurium in mammals) wraps both the axons and the peripheral glia. The perineural glia is believed to be mesodermally derived, it is absent in mutants such as *twist* that lack the mesoderm (EDWARDS *et al.* 1993).

The peripheral glia, which is a subset of the surface glia, create the *Drosophila* equivalent of the blood-brain barrier that is primarily responsible for shielding the nervous system against the high potassium levels of the hemolymph (SCHWABE *et al.*

2005). In peripheral nerves the peripheral glia form a single-cell tube that envelopes the axons and is sealed with septate junctions. These septate junctions are created and maintained at least in part by a G-protein signaling pathway in the peripheral glia. There are a number of genes that appear to be – at least in the peripheral nervous system (PNS) – expressed in only the peripheral glia; these include *gliotactin (gli)*, *moody*, and *Neuroglian (Nrg)* (AULD *et al.* 1995; BAINTON *et al.* 2005; SCHWABE *et al.* 2005)

### **1.3 The resting potential and action potential**

An axon is part of a single cell that is able to convey a uni-directional electrical signal. The resting potential is generated by differences in ionic concentrations across the axonal membrane and the selective permeability of that membrane. At rest, the inside of the axon is negatively charged with respect to outside. Whereas signaling between axons or between axons and other tissues such as muscle is usually chemical in nature, the signal within the axon – the action potential – is a result of a depolarization and subsequent repolarization of the membrane.

The resting potential, or the resting electrochemical potential of the membrane ( $E_m$ ), is the sum of all the relevant ions individual electrochemical potentials ( $I_i$ ). The electrochemical potential for each individual ionic species can be calculated using the “Nernst Equation” (Figure 1.1, equation 1). The  $E_m$  is found by combining the individual electrochemical potentials for the ionic species that contribute to the membrane potential

The electrochemical potential across a membrane for an individual ionic species:

$$E_i = (E_2 - E_1) = -\frac{RT}{zF} \ln \left( \frac{C_2}{C_1} \right) \quad \text{"Nernst Equation"} \quad (1)$$

Thus for all the ionic species important to neural activity:

$$Em = -\frac{RT}{F} \ln \left( \frac{P_K[K]_o + P_{Na}[Na]_o - P_{Cl}[Cl]_o}{P_K[K]_i + P_{Na}[Na]_i - P_{Cl}[Cl]_i} \right) \quad \text{"Goldman Constant Field Equation"} \quad (2)$$

But as  $Cl^-$  ions are distributed passively across the membrane:

$$Em = -\frac{RT}{F} \ln \left( \frac{P_K[K]_o + P_{Na}[Na]_o}{P_K[K]_i + P_{Na}[Na]_i} \right) = \frac{RT}{F} \ln \left( \frac{[Cl]_i}{[Cl]_o} \right) \quad (3)$$

If:

$$b = \frac{P_{Na}}{P_K} \quad (4)$$

Then:

$$Em = -\frac{RT}{F} \ln \left( \frac{[K]_o + b[Na]_o}{[K]_i + b[Na]_i} \right) \quad (5)$$

### Figure 1.1 The ionic basis of the membrane resting potential

The membrane potential is a consequence of an uneven balance of ions across a selectively permeable membrane. Potassium ( $K^+$ ), sodium ( $Na^+$ ), and chloride ( $Cl^-$ ) are the major ions involved. Combining their individual membrane potentials,  $E_i$ , gives the membrane potential ( $E_m$ ). Because  $Cl^-$  is distributed passively across the membrane, it can be excluded from the calculation. The introduction of  $b$ , the relative membrane permeances of  $Na^+$  to  $K^+$ , allows a simplified formula.  $C$  = concentration,  $F$  = Faraday's constant,  $P$  = permeability,  $R$  = gas constant,  $T$  = temperature,  $[X]_o$  = concentration outside,  $[X]_i$  = concentration inside,  $z$  = valence.

( $K^+$ ,  $Na^+$  and  $Cl^-$ ). The formula for  $E_m$  is called the “Goldman Constant Field Equation” (Figure 1.1, equation 2). In many species, including *Drosophila*,  $Cl^-$  ions are distributed passively across the membrane, allowing the Goldman Constant Field Equation to be simplified to include only  $K^+$  and  $Na^+$  or only  $Cl^-$  (Figure 1.1, equation 3). Introducing “ $b$ ”, the ratio of the membrane permeability of  $Na^+$  and  $K^+$  (Figure 1.1, equation 4), allows the Goldman Constant Field Equation to be simplified yet further (Figure 1.1, equation 5). At rest, the membrane is mostly impermeable to  $K^+$  and  $Na^+$ , with a higher concentration of  $K^+$  within the axon with respect to outside, and a higher concentration of  $Na^+$  outside. The unequal distribution of  $K^+$  and  $Na^+$  across the membrane is created and maintained by a  $Na^+/K^+$  ATPase pump that transports  $Na^+$  out of the axon and  $K^+$  into the axon. In the absence of the pump, the unequal ionic distribution will gradually decay to equilibrium.

A simplified action potential consists of two major components: a  $Na^+$ -driven depolarization, and a  $K^+$ -driven repolarization (Figure 1.3). The opening of  $Na^+$  channels in the membrane allows a small current of  $Na^+$  ions to enter the axon, diffusing down their electrochemical gradient (Figure 1.2, equation 2). Consequently “ $b$ ” increases (Figure 1.2, equation 1), and the relative concentrations of  $Na^+$  change. The result is a rapid increase (i.e., from a very negative potential to a positive one) of the membrane potential as computed by the Goldman Constant Field Equation (Figure 1.1, equations 2 and 6). In response to this depolarization of the membrane, voltage-gated  $K^+$  channels open, allowing a small outward current of  $K^+$  ions. This increases the membrane  $K^+$  conductance, decreasing “ $b$ ”, attenuating the depolarization and starting the

The membrane potential is a function of the internal and external concentrations of  $K^+$  and  $Na^+$ , and the relative membrane permeability ( $b$ ) to these ions. During an action potential,  $b$  increases as  $Na^+$  channels open.

$$b = \frac{P_{Na}}{P_K} \quad (1)$$

The current of an ion ( $I_i$ ) across a membrane can be computed by

$$I_i = G_i(E_m - E_i) \quad (2)$$

Where:

$$G = \frac{I}{R} \quad (3)$$

For a membrane:

$$I_m = I_c - I_i \quad (4)$$

Where:

$$I_c = C_m \frac{dV}{dt} \quad (5)$$

Voltage clamp simplifies analysis by setting:

$$\frac{dV}{dt} = 0 \quad (6)$$

Therefore:

$$\begin{aligned} I_c &= 0 \\ I_m &= I_i \end{aligned} \quad (7)$$

## Figure 1.2 The ionic basis of the action potential

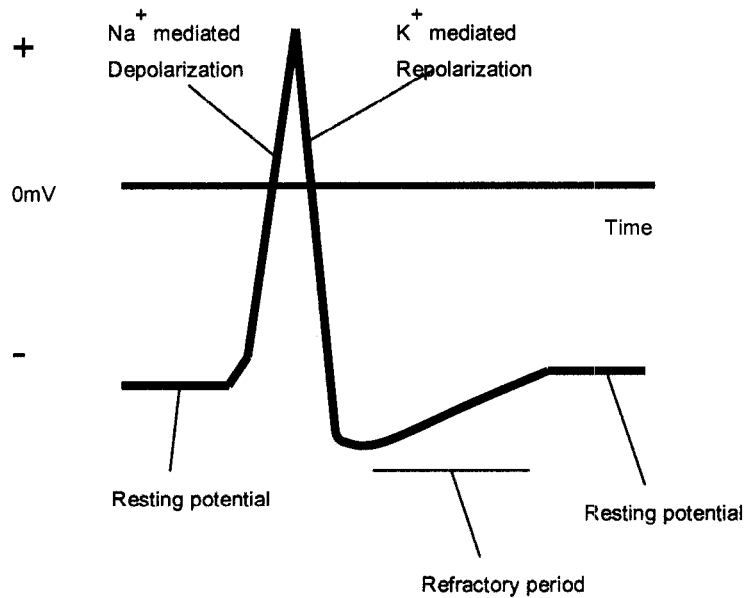
$c$  = capacitive,  $C_m$  = membrane capacitance,  $G$  = membrane conductivity,  $I$  = current,  $i$  = ionic,  $m$  = membrane,  $P$  = permeability,  $R$  = resistance,  $t$  = time,  $V$  = voltage

repolarization of the membrane. The repolarization of the membrane requires the opening and closing of a series of  $K^+$  channels that open at different rates. The transient inactivation of some channels (both  $Na^+$ - and  $K^+$ -permeant) following channel closing ensures that the wave of depolarization proceeds uni-directionally along the axon. Before a new action potential can be propagated, enough  $Na^+$  channels must recover from inactivation; this phase during which a new action potential cannot be propagated is called the refractory period.

## 1.4 Neuronal excitability and ion channel interactions

### ***K<sup>+</sup> channels.***

There are many *Drosophila*  $K^+$  channel subunits, including Shaker (Sh), Ether-á-go-go (Eag), Slowpoke (Slo), Hyperkinetic (Hk), Seizure (Sei), Elk, Ork1, Ir, Shal, Shab and Shaw, (BUTLER *et al.* 1989; ELKINS *et al.* 1986; KAPLAN and TROUT 1969; SALKOFF *et al.* 1987a; SALKOFF *et al.* 1987b; TITUS *et al.* 1997; WANG *et al.* 1997; WARMKE and GANETZKY 1994).  $K^+$  channels fall into four families: voltage gated ( $K_v$ ) (e.g., *Sh* and *eag*) (WARMKE *et al.* 1991), inward rectifier ( $K_{IR}$ ) (e.g., *Ir*) (MACLEAN *et al.* 2002), tandem pore region (e.g., *Ork1*) (GOLDSTEIN *et al.* 1996), and  $Ca^{2+}$  dependent (e.g., *slo*) (ELKINS *et al.* 1986) channels. Loss-of-function mutations in a  $K^+$  channel subunit typically result in hyperexcitability because the neuron cannot repolarize itself properly. This hyperexcitability often has behavioral phenotypes such as ether-induced leg shaking



**Figure 1.3 Annotated action potential**

A simplified action potential. Starting from the negative resting potential, the opening of  $\text{Na}^+$  channels causes a depolarization (negative to a positive membrane potential). The opening of voltage gated  $\text{K}^+$  channels reverses this depolarization by allowing  $\text{K}^+$  ions to leave the axon. The repolarization goes beyond the resting potential causing a hyperpolarization. The axon is then in a brief refractory period during which another action potential cannot be propagated.

(seen in *eag*, *Sh*, and *Hk*) (KAPLAN and TROUT 1969) and electrophysiological phenotypes such as prolonged (*Sh*) or spontaneous (*eag*) action potentials (JAN *et al.* 1977; WU *et al.* 1983). Recently, the *Sh* gene has also been suggested to play a special role in controlling *Drosophila* sleep (CIRELLI *et al.* 2005).

The loss of a  $K^+$  subunit typically results in the reduction or elimination of one of the  $K^+$  currents in the axon. As discussed in chapter 1.3,  $K^+$  currents are a major contributor to the attenuation of the action potential and the restoration of the resting potential. Electrophysiological analysis of *Drosophila* larval body wall  $K^+$  currents has revealed that the outward  $K^+$  current ( $I$ ) consists of multiple parts. These include:

- $I_A$  - transient  $K^+$  A current (WU and HAUGLAND 1985).
- $I_K$  - delayed rectifier  $K^+$  current (WU and HAUGLAND 1985).
- $I_{CF}$  - fast  $Ca^{2+}$  activated  $K^+$  current (GHO and MALLART 1986).
- $I_{CS}$  - slow  $Ca^{2+}$  activated  $K^+$  current (GHO and MALLART 1986).

### ***Na<sup>+</sup> channels.***

A number of  $Na^+$  channel subunits have been identified in *Drosophila*, including Paralytic (Para), DSC1, Ripped pocket (Rpk), and Pickpocket (Ppk) (ADAMS *et al.* 1998; DARBOUX *et al.* 1998; JACKSON *et al.* 1984; SALKOFF *et al.* 1987a; SALKOFF *et al.* 1987b; SUZUKI *et al.* 1971).  $Na^+$  channels fall into two families: voltage-gated (e.g., *para* and

*DSCI*) and ligand-gated (e.g., *ppk* and *rpk*) channels. The loss of a Na<sup>+</sup> channel subunit such as *para* confers a hypoexcitable phenotype to the neuron. For example, at non-permissive temperatures, the *para*<sup>ts</sup> allele confers a reversible paralysis phenotype (SUZUKI *et al.* 1971). Null alleles of *para* are, however, homozygous lethal (GANETZKY 1984).

### ***Reciprocal interactions between channel mutations.***

Reciprocal interactions are often observed between excitability mutations, allowing them to either enhance or suppress each others phenotypes (Table 1.1).

Combining mutations in the voltage-gated K<sup>+</sup> channel subunit genes *eag* and *Sh*, which individually confer hyperexcitability signified by ether-induced leg shaking, yields a level of hyperexcitability that is significantly increased over either single mutation. The *eag Sh* double mutant displays exaggerated ether-induced leg shaking, downturned wings, an indented thorax, and an enhancement of the *Sh*-induced electrophysiological phenotypes (GANETZKY and WU 1985; WU and GANETZKY 1986; WU *et al.* 1983). Neurotransmitter release in the double mutant is prolonged by nearly one order of magnitude as compared to either single mutant (WU *et al.* 1983). This strong synergistic interaction between *eag* and *Sh* is not always seen between other pairs of K<sup>+</sup> channel mutations. For example, only additive effects, restricted to their respective defects in I<sub>A</sub> and I<sub>CF</sub>, are observed when mutants of *Sh* and *Slo* are combined (SINGH and WU 1989).

Genotype	Enhances $Sh^{133}$	Suppresses $Sh^{133}$
$para^-$		✓
$Dp\ para^+$	✓	
$eag^-$	✓	

**Table 1.1 Genetic interactions among  $Na^+$  and  $K^+$  channel mutations**

The hypoexcitable *para* mutations suppress the  $Sh^{133}$ -induced leg shaking (STERN *et al.* 1990), whereas hyperexcitable *eag* mutations and *Dp para*<sup>+</sup> enhance the  $Sh^{133}$ -induced leg shaking (STERN *et al.* 1990). Table adapted from HUANG and STERN (2002)

Regardless of the degree of enhancement of hyperexcitability, however, combining mutations in K<sup>+</sup> channels produces a hyperexcitability greater than seen with either single mutation.

Whereas the combination of hyperexcitable or hypoexcitable mutations results in an exaggerated hyper- or hypo-excitable phenotype respectively, combining a hyperexcitable mutation (*Sh*<sup>133</sup>) with a hypoexcitable mutation (*para*<sup>63</sup>) results in suppression of the *Sh*<sup>133</sup> phenotypes (STERN *et al.* 1990). The phenotypes of the two mutations are able to counteract each other and restore nearly normal neuronal function. Interestingly combining the *Sh*<sup>133</sup> mutation with a chromosomal duplication of *para* (*Dp para*<sup>+</sup>) results in an enhancement of the *Sh* mutant-behavioral phenotypes, very similar to the behaviors seen in the *eag Sh* double mutant (STERN *et al.* 1990).

It seems that hyper- and hypo-excitable channel (and other) mutations are able to interact in an additive manner to enhance or suppress each other's phenotypes (Table 1.1). This provides a hypothesis for the interpretation of new channel mutant phenotypes.

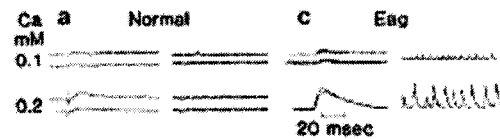
## **1.5 Function and structure of Eag**

The first *eag* mutation was identified as a mutation that gave rise to an abnormal leg-shaking phenotype, similar to that of *Sh* (KAPLAN and TROUT 1969). The *eag* locus encodes a K<sup>+</sup> channel subunit of 1174 amino acids (WARMKE *et al.* 1991). Eag is the

founding member of a family of  $K^+$  channel subunits that has three sub-families: Eag, Elk (*eag*-like  $K^+$  channel), and Erg (*eag*-related gene) (WARMKE and GANETZKY 1994).

When measuring the neurotransmitter release at the larval neuromuscular junction of *eag* mutants, it was found that excitatory junctional potentials (ejps) at low  $Ca^{2+}$  concentrations were increased in amplitude as compared to wild type and showed a high frequency of spontaneous ejps at high  $[Ca^{2+}]$  (Figure 1.4) (WU *et al.* 1983). The spontaneous ejps are similar in time-course to those evoked by nerve stimulation and are blocked by tetrodotoxin suggesting that they are due to repetitive spontaneous firing of the motor axon (WU *et al.* 1983).

Under voltage clamped conditions, it is possible to separate the outward  $K^+$  current from the inward  $Ca^{2+}$  current. The absence of extracellular  $Ca^{2+}$  eliminates the inward  $Ca^{2+}$  current and the  $Ca^{2+}$ -dependent  $K^+$  current. The resultant current is biphasic and is blocked by tetraethylammonium (TEA, a voltage-gated  $K^+$  channel blocker) as expected of a  $K^+$  current (WU *et al.* 1983). Analysis of the current-voltage relationship in larval muscles of *eag* mutants identified a large reduction in the amplitude of the  $I_K$  component and a smaller reduction in  $I_A$  (WU *et al.* 1983; ZHONG and WU 1991; ZHONG and WU 1993). Additionally, when  $I_A$  and  $I_K$  are pharmacologically blocked, the  $I_{CF}$  and  $I_{CS}$  currents are also seen to be reduced in *eag* mutant muscles (ZHONG and WU 1991). This demonstrates that Eag contributes to at least four  $K^+$  currents in *Drosophila* larval muscles, unlike Shaker and Slo, which each contribute to only one current ( $I_A$  and  $I_{CF}$  respectively) (SINGH and WU 1989; ZHONG and WU 1991). That Eag appears to contribute to a number of currents, and that none of these currents is completely



**Figure 1.4 Electrophysiological traces from *eag* mutant larvae**

Excitatory junctional potentials (ejps) obtained from larval neuromuscular junctions in normal (a) and *Eag* mutant (c) larvae at the Ca<sup>2+</sup> concentrations indicated. ejps were evoked by stimulating the segmental nerve cut close to the ganglion (left traces) or occurred spontaneously in the same preparation without stimulation (right traces). Spontaneous ejps occurred frequently in *Eag*, but only miniature ejps were seen in normal larvae. (From: WU *et al.* 1983)

eliminated in the absence of Eag, raises the possibility that the *eag* gene contributes a subunit common to a number of different K<sup>+</sup> channels.

The possibility that Eag coassembles with other K<sup>+</sup> channel subunits is supported by the observation that, in contrast to other mutations affecting K<sup>+</sup> channels, the effects of *eag* mutations upon I<sub>A</sub> and I<sub>K</sub> are temperature sensitive. At 16°C, I<sub>A</sub> and I<sub>K</sub> are reduced in *eag<sup>l</sup>*, *eag<sup>4PM</sup>* and *eag<sup>x6</sup>* with respect to wild type, but at 5°C, I<sub>A</sub> is increased and I<sub>K</sub> is unaltered in *eag<sup>l</sup>* with respect to wild type (ZHONG and WU 1993). The temperature dependency of the phenotypes indicates a modulatory effect.

### ***Oocyte Expression of eag.***

The expression of Drosophila RNA in *Xenopus* oocytes provides an opportunity to explore the action of a particular ion channel in isolation, because oocytes have no K<sup>+</sup> or Na<sup>+</sup> ion channels. It is hard to study individual channels *in vivo* as there are many channels present. Limitations of the oocyte expression technique include possible artifacts due to over-expression and possible improper assembly of channel subunits. It is important to note, for example, that although vertebrate Ca<sup>2+</sup> and Na<sup>+</sup> channels contain more than one type of subunit *in vivo*, a single subunit,  $\alpha_1$  in Ca<sup>2+</sup> channels or  $\alpha$  in Na<sup>+</sup> channels, can form active, albeit slightly abnormal, channels *in vitro* (AULD *et al.* 1988; MORI *et al.* 1991).

Expression of *eag* RNA in oocytes produces a non-inactivating voltage dependent outward current (BRUGGEMANN *et al.* 1993). Macroscopic currents recorded with conventional voltage clamping have a threshold for activation between  $-40$  and  $-30$  mV. Furthermore, the currents are biphasic with an initial fast rising phase and a second, slower rising phase. These and other observations are consistent with a highly selective  $K^+$  channel such as *Sh* (BRUGGEMANN *et al.* 1993).

An unexpected observation was that the initial slow rising phase of the *eag* channels is due to an inward  $Ca^{2+}$  current, as observed with the use of a  $Ca^{2+}$  sensitive fluorescent dye (Fluo-3) (BRUGGEMANN *et al.* 1993). Depolarization of voltage clamped oocytes expressing *eag* RNA showed an increase in intracellular fluorescence; this was shown to be quinidine sensitive but not  $CdCl_2$  sensitive. Quinidine is known to block certain  $K^+$  channels, whereas  $CdCl_2$  blocks  $Ca^{2+}$  currents. While it is possible that the Eag channel may be able to conduct  $Ca^{2+}$ , there is no suggestion that such a conductance is physiologically relevant; indeed other papers have concluded that Eag channels do not allow a  $Ca^{2+}$  flux (e.g., ROBERTSON *et al.* 1996).

It has also been reported that the *eag* encoded channel is sensitive to cAMP. The protein includes a consensus cyclic-nucleotide-binding site (GUY *et al.* 1991), and the addition of the cAMP analogs 8-Br-cAMP or 8-Br-cGMP to the extracellular solution increases the amplitude of the  $K^+$  current and shifts the activation threshold to a more negative voltage (BRUGGEMANN *et al.* 1993). Furthermore, the addition of 2mM cAMP (but not cGMP or ATP) to the extracellular bath solution significantly increases the

amplitude of the  $K^+$  current. These data are consistent with Eag being a non-inactivating, voltage dependant, cAMP sensitive  $K^+$  channel.

The expression of *eag* RNA in oocytes leads to the production of a functional channel. Given the genetic interactions between *eag* and *Sh*, and the hypothesis that Eag may form heteromultimers, it is obvious to ask if Eag and Sh can coassemble in oocytes. The hypothesis that Eag and Sh coassemble remains controversial. Initial reports indicated that the co-expression of *eag* and *Sh* RNA's produced a current greater than the sum of the currents seen for individual RNA's (non-linear summation), suggesting that a heteromultimer was formed (CHEN *et al.* 1996). Furthermore, the coexpression of Eag (non-inactivating) with Sh (inactivating) appears to significantly decrease the time constant of current decline associated with Sh N-type inactivation (CHEN *et al.* 1996).

This concept of heteromultimerization was subsequently challenged when another group found the current from *Eag* and *Sh* coexpression to be identical to the summed individual expressions (linear summation) (TANG *et al.* 1998). This group showed that there was no statistical difference in the inactivation time constant for *Sh* expressed alone or in the presence of *Eag*, the conclusion thus being that Eag must form only homomultimers (TANG *et al.* 1998).

Subsequently, it has become apparent that the interaction between Eag and Sh subunits depends upon the expression levels of the two RNAs and how long post-injection the recordings are made (CHEN *et al.* 2000). The expression efficiency of *eag* is

greater than that of *Sh*, hence the interaction is better seen with a lower dose of *eag* RNA relative to *Sh* RNA. For example, measurement at 5 days post-injection of 0.1ng/cell *eag* and 4ng/cell *Sh* gives nonlinear summation (indicating heteromultimers) whereas injection of 0.05ng/cell *eag* and 2ng/cell *Sh* gives linear summation (indicating formation of homomultimers). Additionally the developmental time for Eag currents in oocytes is longer than for Sh; for unknown reasons it takes more time for the Eag current amplitude to develop than the Sh current. This difference in developmental time may explain, at least in part, why adequate development is important for functional interactions among co-expressed Eag and Sh subunits (CHEN *et al.* 2000). In addition to requiring adequate developmental time, the *eag* and *Sh* RNAs must be injected simultaneously for functional interaction. Sequential injection in either order fails to give rise to a functional interaction (CHEN *et al.* 2000). The need for adequate time and co-injection may be significant for *in vivo* assembly and synaptic plasticity.

I hypothesize that Eag forms both homo- and heteromultimers *in vivo*. This could partly explain the extremely diverse responses possible in the nervous system, particularly if the variability contributes to synaptic plasticity. These two types of channels would also explain the contradictory evidence described above.

### ***Regulation of Eag by extracellular $Mg^{2+}$ .***

It is known that the ion flux of many ion channels can be influenced by  $Mg^{2+}$  ions' entering and blocking the pore. For example, in neuronal tissues,  $Mg^{2+}$  blocks the NMDA-receptor at the extracellular side in a voltage dependent manner (MAYER *et al.* 1984; NOWAK *et al.* 1984).  $Mg^{2+}$  can interact with the cytoplasmic side of voltage-gated  $Na^+$  channels (PUSCH 1990), inward rectifier channels (ISHIHARA *et al.* 1989; MATSUDA *et al.* 1987), and delayed rectifier channels (LUDEWIG *et al.* 1993). Additionally,  $Ca^{2+}$  channels can be blocked at an extracellular location by  $Mg^{2+}$  (LANSMAN *et al.* 1986).

It has also been shown for most members of the Eag subfamily that the kinetics of activation are regulated by extracellular  $[Mg^{2+}]$ , an effect not observed in other types of voltage-gated  $K^+$  channels such as Shaker and Kv1.1 channels (STUHMER *et al.* 1988; TERLAU *et al.* 1996). When expressed in oocytes, rat EAG (rEAG), bovine EAG (bEAG) and Drosophila Eag (DmEag) all display  $[Mg^{2+}]$  sensitive activation kinetics, whereas channel deactivation and the steady-state current-voltage relationship are insensitive to extracellular  $[Mg^{2+}]$  (CHEN *et al.* 2000; FRINGS *et al.* 1998; SILVERMAN *et al.* 2000; TERLAU *et al.* 1996).

The slowing of rEAG channel activation by  $Mg^{2+}$  is concentration dependent; increasing  $[Mg^{2+}]$  from 0mM to 10mM causes a progressive slowing of the activation kinetics (TERLAU *et al.* 1996). Similar concentration dependency is observed for the bovine and Drosophila channels (FRINGS *et al.* 1998; TANG *et al.* 2000). The slowing of

Eag activation is more pronounced at less negative holding potentials than at more negative potentials, indicating a voltage dependency in the  $[Mg^{2+}]$ -dependent slowing of Eag activation kinetics (TERLAU *et al.* 1996).

By expressing mutant forms of DmEag in oocytes, it has been possible to determine how  $Mg^{2+}$  ions interact with the channel. It is likely that the  $Mg^{2+}$  ion is coordinated by residues D278 in S2 and D327 in S3 (two of the six transmembrane domains in each channel subunit), with D274 also being close to the binding site (SILVERMAN *et al.* 2004; SILVERMAN *et al.* 2000). The D278V mutant channel is insensitive to extracellular  $[Mg^{2+}]$  of up to 20 mM (above physiological levels), presumably due to the loss of the interaction between the ion and the negatively charged side chain (SILVERMAN *et al.* 2000). D278E channels are also insensitive to  $Mg^{2+}$ , in this case due to either steric hindrance (SILVERMAN *et al.* 2000) or to disruption of the proposed regular octahedral structure of the binding site (SILVERMAN *et al.* 2004). The neutralizing mutant D327A has the same effect as D278V and converting residue 278 to its equivalent in Sh (since it is not  $[Mg^{2+}]$  sensitive) (D278F) reduces the effect of  $Mg^{2+}$  upon activation kinetics (SILVERMAN *et al.* 2000). D327E, however, retains sensitivity to  $[Mg^{2+}]$ , indicating a greater degree of flexibility at this site than at position 278. Thus it appears that D278 and D327 coordinate the binding of the  $Mg^{2+}$  ion.

Amino acid substitutions at position 274 yield different results. The neutralizing substitution D274A has similar activation kinetics to wild-type in the presence of extracellular  $Mg^{2+}$  as does the Sh mimicking D274E substitution. The kinetics of D274E,

however, recover more slowly than wild-type following the removal of extracellular  $\text{Mg}^{2+}$ , suggesting that the glutamate side chain can reach and coordinate  $\text{Mg}^{2+}$  in a manner not seen in wild-type channels (SILVERMAN *et al.* 2000).

A variety of divalent cations (including  $\text{Zn}^{2+}$ ,  $\text{Mg}^{2+}$ ,  $\text{Mn}^{2+}$ ,  $\text{Co}^{2+}$ , and  $\text{Ni}^{2+}$ ) are able to slow the activation kinetics of Eag (TERLAU *et al.* 1996). It is likely that these ions have a common binding site. The extent to which each cation inhibits activation is proportional to its enthalpy of hydration (SILVERMAN *et al.* 2000). As seen with  $\text{Mg}^{2+}$ , the D278A channel is insensitive to  $\text{Mn}^{2+}$  and  $\text{Ni}^{2+}$ . D278E eliminates  $\text{Ni}^{2+}$  sensitivity but only reduces  $\text{Mn}^{2+}$  sensitivity (presumably by decreasing the apparent affinity of the channel for  $\text{Mn}^{2+}$ ). D327A is insensitive to  $\text{Mn}^{2+}$  but retains some sensitivity to  $\text{Ni}^{2+}$ , albeit with a reduced affinity (SILVERMAN *et al.* 2004). Both the magnitude of effect of  $\text{Mn}^{2+}$  upon Eag and the half-maximal concentration are similar to that of  $\text{Mg}^{2+}$  (SILVERMAN *et al.* 2004). It appears that  $\text{Mg}^{2+}$  and other ions enter into and bind to a pocket between S2 and S3 to regulate the activation kinetics of Eag.

It is known that in some ion channels,  $\text{Mg}^{2+}$  acts by blocking the pore. If this is the case in Eag, then the four individual subunits within each channel would not act independently with regard to  $\text{Mg}^{2+}$  inhibition. The bEAG mutant L322H (analogous to DmEag L342H) shows accelerated activation kinetics, with the channel opening at more negative potentials than wild-type. When dimeric and tetrameric constructs of wild-type and mutant subunits are co-expressed to produce channels with either 0, 1, 2, 3 or 4 mutant subunits in the tetramer, as the number of mutant subunits increases the channel

activation accelerates progressively (SCHONHERR *et al.* 1999). This is consistent with the four bEAG subunits activating independently. Analysis of dose-response data for the  $\text{Mn}^{2+}$ -dependent slowing of wild-type DmEag activation indicates that  $\text{Mn}^{2+}$  acts independently in each individual subunit to modulate gating with no co-operativity between the four binding sites (SILVERMAN *et al.* 2004). This presumably holds true for  $\text{Mg}^{2+}$  binding and is compatible with the conclusions drawn in bEAG, where the divalent cation sensitive slow gating transitions occur independently in each subunit (SCHONHERR *et al.* 1999).

In many voltage-gated channels, hyperpolarizing prepulses can be used to delay the onset of ionic current. Such pulses delay the onset, but do not affect the time course of the activation, providing evidence that such channel proteins transit through a number of closed conformations prior to opening (TANG *et al.* 2000). Like these other voltage channels, oocyte expressed DmEag displays delayed channel opening and dramatically slowed kinetics of evoked ionic currents following hyperpolarizing prepulses. This suggests that DmEag also goes through a series of closed states and that the transition between hyperpolarized states is rate limiting (TANG *et al.* 2000).

In the presence and absence of hyperpolarizing prepulses, extracellular  $\text{Mg}^{2+}$  slows the kinetics of ionic current activation (TANG *et al.* 2000). The interaction between extracellular  $\text{Mg}^{2+}$  and hyperpolarizing prepulses is complex and particularly prominent during the initial phase of activation. This interaction suggests that  $\text{Mg}^{2+}$  slows rate limiting gating transitions that occur between closed states that are populated at

hyperpolarized potentials (TANG *et al.* 2000). Furthermore, it does not appear that the final opening transition is the rate-limiting step in DmEag opening. Whereas  $Mg^{2+}$  does appear to modulate the kinetics of channel opening, channel deactivation is insensitive to  $Mg^{2+}$ , indicating that  $Mg^{2+}$  does not influence the transition between the open state and the most accessible closed state.

Analysis of DmEag gating currents when ionic currents are blocked with TEA showed that the slow component of the charge movement in ON gating is more prominent in the presence of extracellular  $Mg^{2+}$ , suggesting that the gating transitions modulated by  $Mg^{2+}$  occur slowly or involve relatively little charge or both (TANG *et al.* 2000). The effects of extracellular  $Mg^{2+}$  on gating current kinetics and opening kinetics suggest that  $Mg^{2+}$  does not act upon S4 (the voltage sensor) (TANG *et al.* 2000).

### ***$Mg^{2+}$ binds the resting channel.***

If  $Mg^{2+}$  is modulating transitions between closed states, then presumably  $Mg^{2+}$  must bind Eag when the voltage sensor (S4) is in its resting (closed) position. To determine if extracellular ions can access the binding site in closed channels, it was determined whether  $Ni^{2+}$  can access its binding site when the D274A mutant channel is closed.

At potentials of -80mV and -120mV, the probability of the D274A channel's being open is very low (the midpoint of activation is +25mV). By applying  $Ni^{2+}$  at

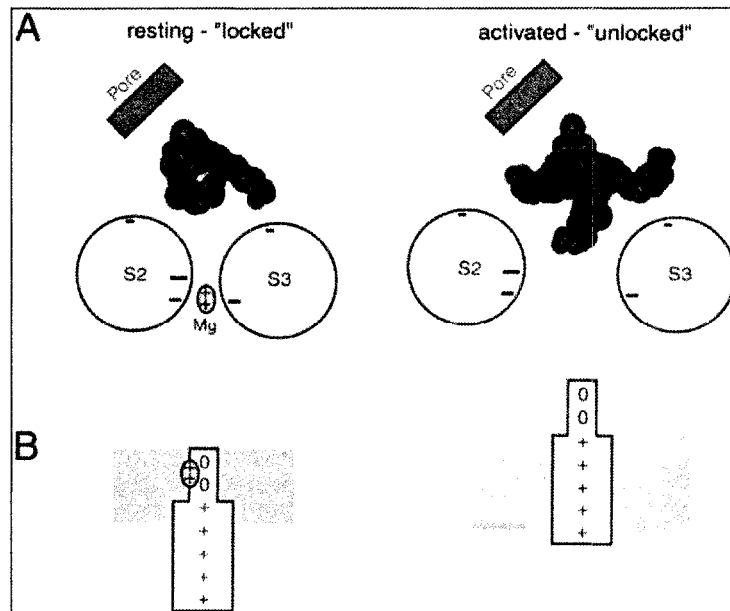
different potentials, it is apparent that  $\text{Ni}^{2+}$  is able to access its binding site from the extracellular solution when the channel is at rest (SILVERMAN *et al.* 2004). Furthermore,  $\text{Ni}^{2+}$  cannot effectively prevent the opening of the D274A channel if the voltage sensor is activated before the  $\text{Ni}^{2+}$  is added, and  $\text{Ni}^{2+}$  can also dissociate from its binding site when the channel is at rest (SILVERMAN *et al.* 2004). This suggests that the ion binding site is accessible when the channel is at rest, which is not compatible with the “paddle” model that has been proposed from the crystal structure of KvAP (the voltage-dependent  $\text{K}^+$  channel from *Aeropyrum pernix*) (JIANG *et al.* 2003a; JIANG *et al.* 2003b). Whereas  $\text{Mg}^{2+}$  coordinating residues are typically 2.7-3.4 Å apart, the paddle model has the equivalent of D278 and D327 approximately 17 Å apart, which is too far for  $\text{Mg}^{2+}$  coordination (SILVERMAN *et al.* 2004). The structure of the isolated voltage sensor (S2-S4) in the open conformation (i.e. not a conformation in which  $\text{Mg}^{2+}$  can bind) of KvAP has these residues approximately 10.8 Å apart (JIANG *et al.* 2003a; SILVERMAN *et al.* 2004). If the larger aspartic acid side chains are substituted for the corresponding valine and glycine, then, with some minor changes, these residues in the isolated voltage sensor become close enough together to conceivably bind  $\text{Mg}^{2+}$  (SILVERMAN *et al.* 2004). Interestingly, the D278 equivalent in KvAP (G101) is near a break in the secondary structure of S3 caused by P99 (P325 in DmEag). This may impart flexibility to S3 that may be important in channel opening (SILVERMAN *et al.* 2004). It thus seems likely that  $\text{Ni}^{2+}$ , and presumably all divalent cations, can bind Eag to regulate activation when the voltage sensor is at rest, and that either the paddle model is incorrect or that voltage gating mechanism of Eag is different to that of KvAP. More recent complete structures of Kv1.1

and KvAP in their open state suggest that S2 and S3 may be close enough together to allow  $Mg^{2+}$  coordination (LEE *et al.* 2005; LONG *et al.* 2005).

### ***Gating mechanism.***

It seems likely that the  $Mg^{2+}$  controlled events occur independently of and prior to the voltage-controlled events in Eag channel activation. Several gating mechanisms have been proposed for the opening and closing of Eag channels. These mechanisms involve  $Mg^{2+}$  sensitive transitions between two or more closed states that occur independently in each subunit; once all four subunits are in the most accessible closed (i.e., closest to open) all four subunits proceed simultaneously through the final voltage-dependent opening transition (SCHONHERR *et al.* 2002; SILVERMAN *et al.* 2004).

The voltage dependency of accessibility from the extracellular solution to S4 of bEAG1 is consistent with the substantial outward movement of S4 from a gating canal seen in  $Na^+$  and Sh channels (BAKER *et al.* 1998; WANG *et al.* 1999; YANG *et al.* 1996). With this mode of voltage activation in mind, it has been proposed that  $Mg^{2+}$  acts to cross-bridge S2 and S3, holding the gating canal in a narrow “locked” conformation and that for S4 to move to its activated position,  $Mg^{2+}$  must first dissociate, allowing the canal to change to a wider “unlocked” conformation (SCHONHERR *et al.* 2002). This model is shown as Figure 1.5.



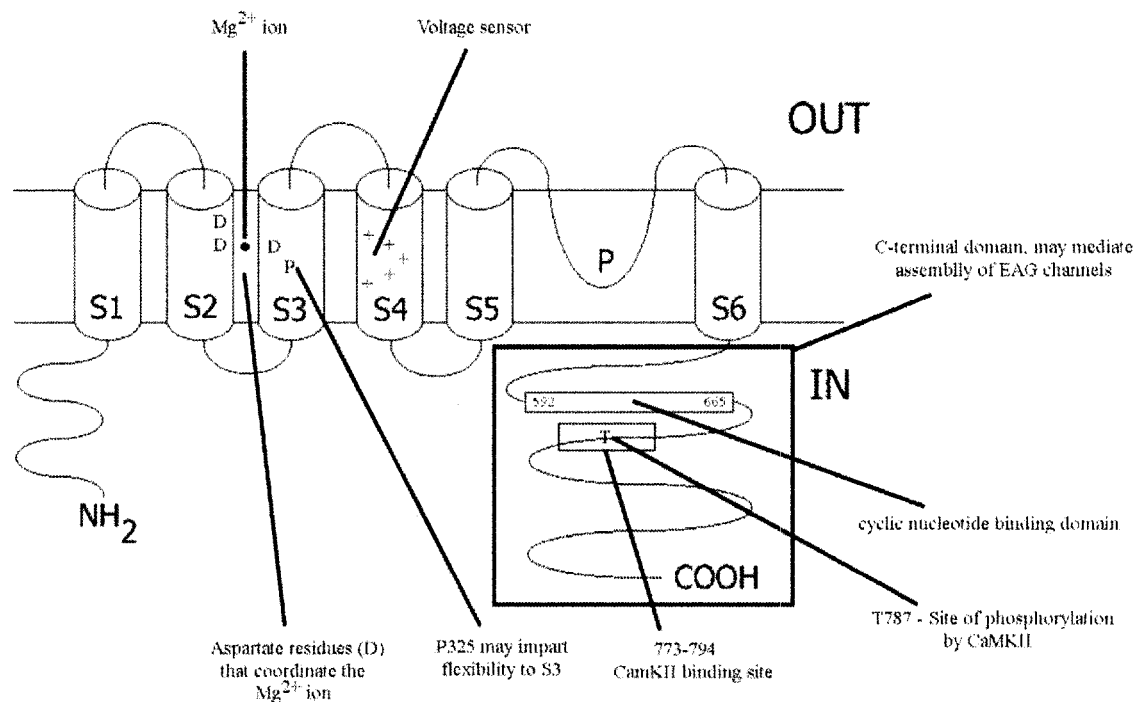
**Figure 1.5  $\text{Mg}^{2+}$ -Dependent Canal Rearrangement Proposed to Lock and Unlock S4 in the Resting State**

(Left)  $\text{Mg}^{2+}$  coordination between Eag specific negative residues in S2 and S3 (black) proposed to lock the canal in a narrow configuration. (Right) Entry of S4's wider section into the canal upon activation requires the "unlocking" motion of S2/S3 (arrows) prior to S4 activation. (A) Top view from the extracellular side shows space-filled side chains for S4's high-impact charge residues (blue) facing S2's and S3's conserved negative residues and high-impact S4's hydrophobic residues (magenta) facing the pore domain. Only high-impact residues located in the canal in the resting (left) or activated state (right) are shown. The activated topology is reached by a 9 residue helical screw motion along the pitch of the threads. (B)  $\text{Mg}^{2+}$  binding in the canal at rest and unbinding in the activated state would give the canal a constant net charge and could explain the need for stronger hyperpolarization to push S4 into the resting conformation at low  $[\text{Mg}^{2+}]$ . (Taken from: SCHONHERR *et al.* 2002).

### ***Phosphorylation of Eag.***

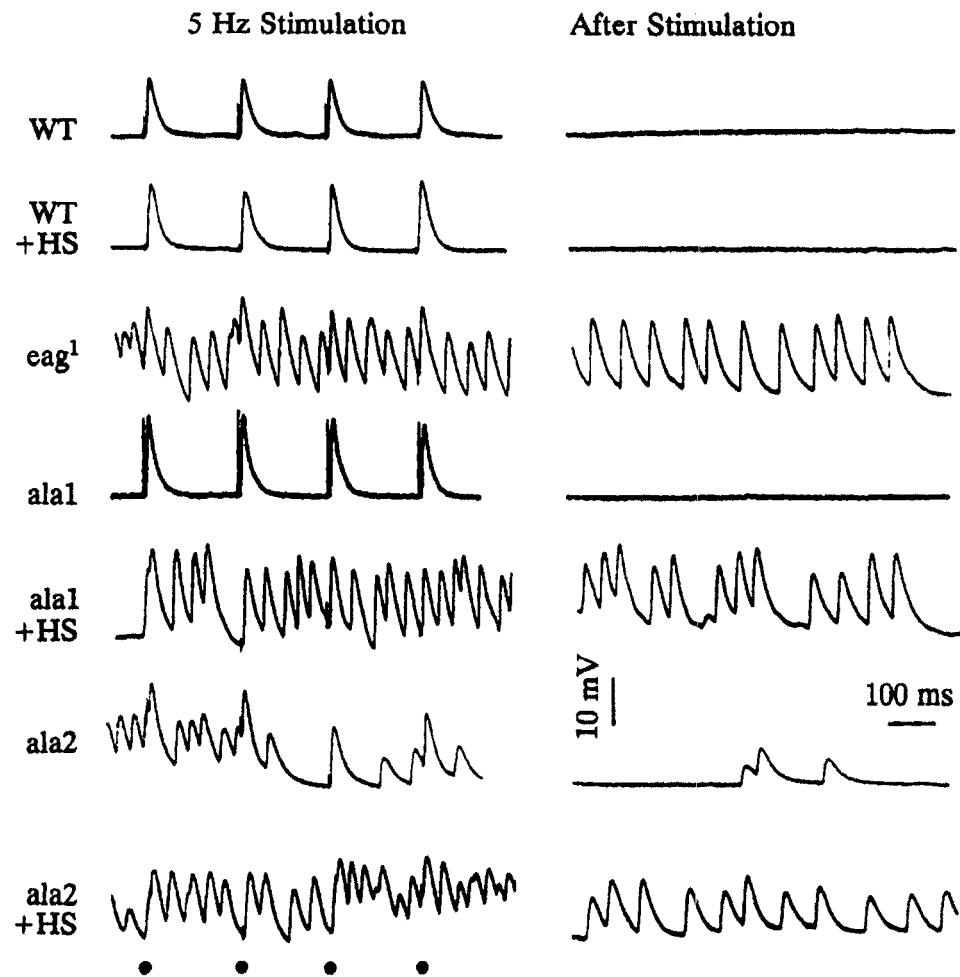
Calcium/calmodulin dependent kinase II (CaMKII) is a regulator of neuronal excitability and plasticity (GRIFFITH *et al.* 1994). Genetic interactions between *eag* and the CaMKII inhibitory peptide *ala* transgene suggest that CaMKII may regulate Eag (GRIFFITH *et al.* 1994). Biochemical and electrophysiological studies have demonstrated that current amplitude is regulated by the phosphorylation of Eag T787 by CaMKII, possibly when held in a complex with the Camguk/CASK adaptor protein (MARBLE *et al.* 2005; WANG *et al.* 2002). Conversely, there is evidence that Eag activates CaMKII in the absence of  $\text{Ca}^{2+}$ , but only when an Eag/CaMKII complex is formed (SUN *et al.* 2004). Residues 773-794 of Eag appear to be the binding site responsible for this interaction (Figure 1.6), and this direct binding of CaMKII to Eag does not appear to affect the phosphorylation of T787 (SUN *et al.* 2004). Loss of function mutations such as *eag<sup>l</sup>* appear to be phenocopied by the overexpression of *ala* (Figure 1.7), which is presumably equivalent to a reduction in CaMKII activity (GRIFFITH *et al.* 1994).

It seems possible that there is a positive feedback loop where CaMKII phosphorylates Eag to enhance its activity, which in turn activates CaMKII which again phosphorylates Eag.



**Figure 1.6 Annotated topological diagram of Eag**

Schematic depicting the topology of the Eag protein. S1 through S6 represent the six transmembrane domains, and P, the pore domain. Indicated in red are some domains and individual residues of note: the positive charges of the voltage sensor, the  $Mg^{2+}$  ion and its coordinating residues, a putative source of flexibility for gating, the site of regulation by cyclic nucleotides, CaMKII phosphorylation, and the domain important for channel assembly. Residue numbers correspond to DmEag. (GUY *et al.* 1991; LUDWIG *et al.* 1997; SILVERMAN *et al.* 2004; SUN *et al.* 2004; WANG *et al.* 2002)



**Figure 1.7 Overexpression of *ala1* phenocopies *eag*<sup>1</sup>**

EJPs recorded from larval nmjs of *eag*<sup>1</sup>, *ala1* with or without heat shock (HS), *ala2* homozygotes with or without heat shock, and Canton-S controls (wild-type, WT). Stimulus artifacts are indicated by filled circles. (Left) High-frequency supernumary discharges seen with 5-Hz stimulation in *ala* and *eag*<sup>1</sup> flies. Supernumary discharges were never observed in controls and were not seen in all heat-shocked *ala1* larvae. (Right) Continued activity after stimulation ceased. This activity could last up to 10 seconds after cessation of stimulation. (Taken from: GRIFFITH *et al.* 1994)

## 1.6 Inebriated

The *inebriated* (*ine*) gene was identified in a screen for mutations that had a behavioral interaction with the *Sh* mutation. Like the *eag Sh* double mutant, mutations in *ine* were identified for their ability to enhance *Sh*, producing downturned wings and an indented thorax in adult *Drosophila* (STERN and GANETZKY 1992). In an otherwise wild-type background, *ine* flies do not display any mutant behavioral phenotypes; they do not exhibit ether-induced leg shaking, temperature-sensitive paralysis, or sensitivity to mechanical shock (STERN and GANETZKY 1992). However, the *ine* mutation was, like the K<sup>+</sup> channel blocking agent dideoxy forskolin (DDF), able to potentiate the effects of quinidine on synaptic transmission (STERN and GANETZKY 1992).

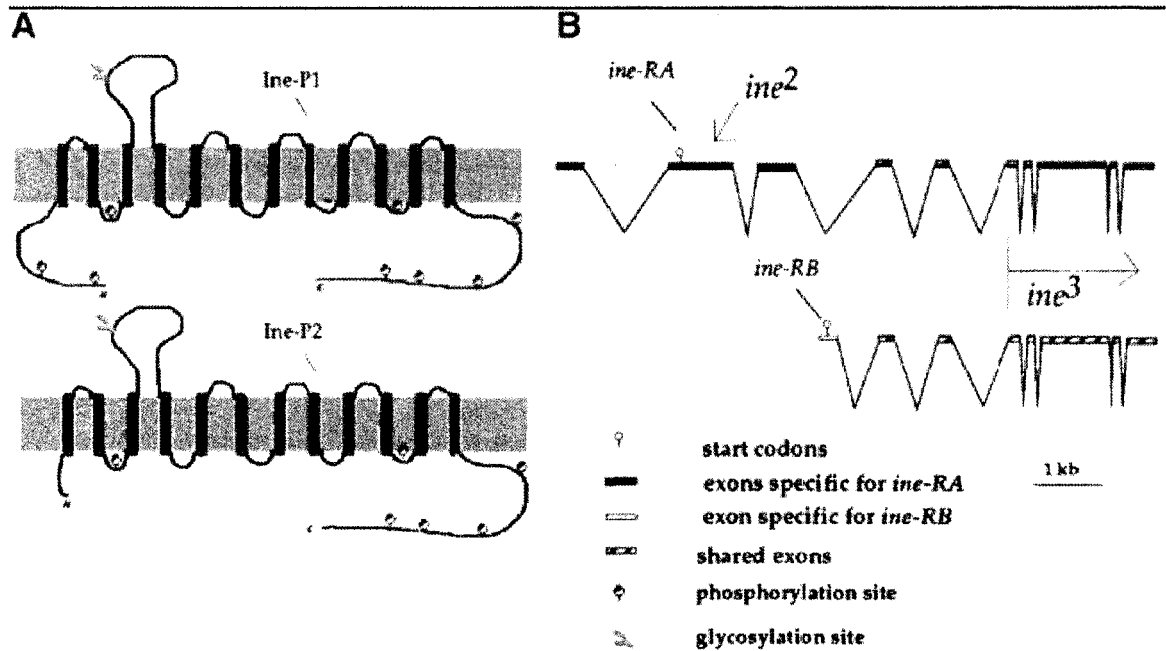
Further electrophysiological analysis showed that the *ine*<sup>1</sup> mutation increases the rate of onset of long term facilitation (LTF) (HUANG and STERN 2002), indicating that the loss of Ine increases neuronal excitability.

Mapping and cloning of the *ine* gene identified a cDNA encoding an open reading frame of 658 amino acids that bears significant similarity to members of the Na<sup>+</sup>/Cl<sup>-</sup> dependent neurotransmitter transporter family (SOEHNGE *et al.* 1996). Members of this family have been shown to catalyze the reuptake of neurotransmitters such as glycine, dopamine, 5HT, NE and, GABA, as well as metabolites or osmolytes such as taurine, betaine, β-alanine, and creatine (SOEHNGE *et al.* 1996).

Northern blot and sequence analysis showed two *ine* transcripts of 2.3kb (*ine-RB*) (SOEHNGE *et al.* 1996) and 3.6kb (*ine-RA*) (BURG *et al.* 1996). The smaller transcript encodes a protein of 658 amino acids called Ine-P2, and the longer, a protein of 943 amino acids called Ine-P1 or RosA (BURG *et al.* 1996; SOEHNGE *et al.* 1996). Ine-P1 and Ine-P2 are identical except that Ine-P1 has an additional N-terminal tail (HUANG and STERN 2002) (Figure 1.8).

Overexpression of a *UAS-ine-RA* transgene with either *gli*-GAL4 or *MZI580* (both peripheral glia GAL4 drivers) rescued both the LTF phenotype in a *ine<sup>l</sup>* background and the downturned wing phenotype in a *Sh; ine<sup>l</sup>* mutant background (HUANG and STERN 2002). The same *UAS-ine-RA* construct driven with the neuronal *elav*-GAL4 driver produced only a partial rescue of either phenotype (HUANG and STERN 2002). *MZI580* driven *UAS-ine-RB* was not able to fully rescue either the LTF or downturned wing phenotypes; only a partial rescue was observed suggesting the two isoforms of Ine have different efficiencies (HUANG and STERN 2002).

The overexpression of Ine-P1 (also called *Overine<sup>+</sup>*) with either *MZI580* or *gli*-GAL4 confers a number of phenotypes. First, in a *Sh* mutant background, suppression of the characteristic ether-induced leg-shaking is observed; a similar effect is seen with *para* mutations (STERN *et al.* 1990) and, more recently, with an *eag* gain-of function allele (see Chapter 3). Second, in an otherwise wild-type background, *Overine<sup>+</sup>* confers reduced excitability as assayed by the onset rate of LTF. In *Overine<sup>+</sup>* larvae, the onset rate of LTF is decreased; as in *eag<sup>84</sup>* (a gain-of-function mutation, see chapter 3), facilitation is not



**Figure 1.8 Organization of Ine and *ine***

(A) The putative membrane topology of the two Inebriated protein isoforms. The two isoforms are identical except that Ine-P1 (encoded by *ine-RA*) contains an N-terminal intracellular region that is ~300 amino acids longer than the corresponding region in Ine-P2, encoded by *ine-RB*. This 300-amino-acid extension, unlike the region common to both proteins, has no similarity to other transporters. Potential sites of N-linked glycosylation and phosphorylation are indicated. (B) Map of the *ine* region showing the exons of the two *ine* isoforms and the location of two identified mutations. The *ine<sup>2</sup>* mutation is a nonsense mutation at codon 126 of *ine-RA*, whereas *ine<sup>3</sup>* is a deletion that removes most of the open reading frame common to both transcripts and begins at codon 293 of *ine-RA*. Although *ine<sup>1</sup>* has not been localized, it was previously shown by Northern blot analysis that transcripts of both *ine* isoforms are undetectable in the *ine<sup>1</sup>* mutant (SOEHNGE *et al.* 1996). (Taken from: HUANG *et al.* 2002)

observed at 5Hz stimulation (HUANG and STERN 2002). Third, like *para*, *tipE*, and *mle<sup>nap</sup>* mutations that decrease sodium channel activity, *Overine<sup>+</sup>* causes a temperature sensitive paralysis phenotype. A synergistic relationship is observed between *Overine<sup>+</sup>* and *para<sup>63</sup>*; the double mutant displays a much stronger temperature sensitive paralysis phenotype than either single mutation. Fourth, there is an increased number of failures to evoke neurotransmitter release at the neuromuscular junction in response to nerve stimulation in *Overine<sup>+</sup>* larvae; a similar phenotype is seen in *para<sup>63</sup>* larvae. No alteration in the amplitude of spontaneous mini-excitatory junctional potentials is observed, indicating a normal muscle response to neurotransmitter and a normal quantal content of neurotransmitter.

It is known that decreasing the number of sodium channels (e.g., by mutating them as with *para<sup>63</sup>*) confers neuronal hypoexcitability and that increasing sodium channels (as in *Dp para<sup>+</sup>*) confers hyperexcitability. It has also been shown that *eag* loss-of-function mutations (e.g., *eag<sup>l</sup>*) confer neuronal hyperexcitability and that gain-of-function mutations (e.g., *eag<sup>G297E</sup>*) confer hypoexcitability. It appears that a similar effect is seen with *ine*, where loss of Ine (*ine<sup>l</sup>*) confers neuronal hyperexcitability and the over-expression of Ine-P1 (*Overine<sup>+</sup>*) confers hypoexcitability. It is thus reasonable to postulate that Ine somehow regulates sodium channels in the axonal membrane, and that the Ine-P1 isoform rather than Ine-P2 is responsible for the control of excitability.

### ***Osmotic stress response.***

There were two observations that suggested that *ine* might be involved in osmolyte transport and thereby affect the *Drosophila* stress response. First, both isoforms of Ine are robustly expressed in the kidney analogue (the Malpighian tubule, hindgut, and anal plate) (SOEHNGE *et al.* 1996); second, other members of the same transporter family as *ine* such as BGT1 transport osmolytes in the mammalian renal medulla (BURG 1995). If Ine performs osmolyte transport in the Malpighian tubules and midgut, then *ine* mutants would be defective in such transport and would be expected to be more sensitive to osmotic stress than wild-type flies (HUANG *et al.* 2002). When maintained on media with elevated [NaCl] (0.2M) for 4 days, *ine*<sup>1</sup> and *ine*<sup>3</sup> mutants exhibit significantly increased lethality than either wild-type or *ine*<sup>2</sup> mutants (HUANG *et al.* 2002). Similar results were observed with elevated sorbitol and KCl confirming that the reduced viability was due to a response to hypertonicity and not altered sensitivity to NaCl (HUANG *et al.* 2002).

The *ine*<sup>1</sup> and *ine*<sup>3</sup> mutants most likely produce null phenotypes; *ine*<sup>3</sup> is a deletion mutation that eliminates most of the ORF, and *ine*<sup>1</sup> mutants produce undetectable levels of either mRNA transcript (SOEHNGE *et al.* 1996). The *ine*<sup>2</sup> mutation is a nonsense mutation in codon 125 of the Ine-P1 isoform; this mutation is therefore expected to eliminate Ine-P1 but not Ine-P2 (HUANG *et al.* 2002).

### ***Two isoforms with different functions?***

The stress response experiments indicate that the shorter Ine-P2 isoform is mainly responsible for the transport of osmolytes in the Malphagian tubules and midgut, with Ine-P1 having very little involvement. The electrophysiological and behavioral assays suggest that absence or excess of Ine-P1 is the main mediator of the phenotypes observed. It is thus possible that the additional N-terminal region of Ine-P1 is responsible for the regulation of neuronal excitability.

## **1.7 GAL4/UAS system**

The GAL4/UAS system, adapted from yeast, uses the expression of the GAL4 gene under the control of endogenous promoters, such as *gliotactin*, *elav*, and *actin 5*, to drive the expression of the UAS-transgene (BRAND and PERRIMON 1993). The UAS promoter is only active when bound by GAL4 thus producing temporal and spatial control of transgene expression.

### ***Transgene expression.***

The *pUAST* expression vector is part of the GAL4/UAS system in *Drosophila* that allows for the selective activation of a transgene in a temporal and spatial specific manner (BRAND and PERRIMON 1993).

## ***RNAi***

For many applications dsRNA can be injected directly into cells to induce RNA mediated gene interference (RNAi). This is not, however, suitable for the heritable tissue specific silencing of a target gene. The GAL4/UAS system in *Drosophila* allows for heritable, tissue specific RNAi. Initially plasmids were created that place a gene fragment and its complement in series behind a UAS component to create a UAS-inverted repeat. Expression of the UAS-inverted repeat gives rise to a hairpin dsRNA molecule (KENNERDELL and CARTHEW 2000). Subsequent improvements involved the creation of cDNA-genomic combinations to avoid problems with homologous recombination within the construct (KALIDAS and SMITH 2002). Finally a vector was created whereby RNAi is triggered by the symmetrical transcription of a transgene (GIORDANO *et al.* 2002).

## **Chapter 2: Materials and Methods**

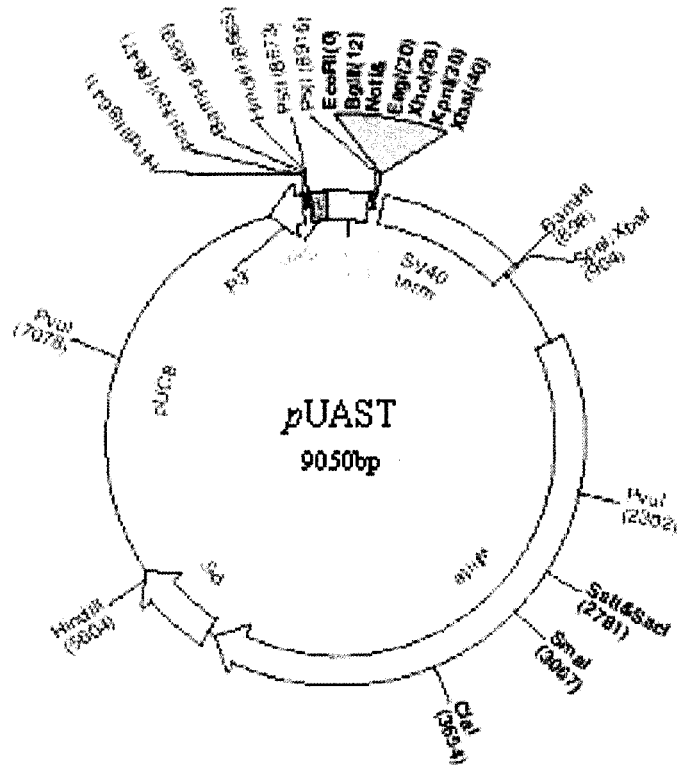
### **2.1 Drosophila genetics**

All fly stocks were maintained on standard cornmeal/agar *Drosophila* media at room temperature in either half pint bottles or vials. Vials were transferred approximately every four weeks.

Fly husbandry was performed as described previously (GREENSPAN 1997).

### **2.2 pUAST expression vector**

The *pUAST* expression vector (BRAND and PERRIMON 1993) (Figure 2.1) contains 5 UAS (GAL4 binding) sites followed by the *hsp70* TATA box and a transcriptional start site. This region is followed by a polylinker containing restriction sites for EcoRI, BglII, NotI, XhoI, KpnI and XbaI which is followed by a polyadenylation site. The vector also contains P3' and P5' p-element insertion sites, and the *mini-white* gene to act as a heritable *in vivo* marker. *pUAST* is based upon the pUC vector which provides ampicillin resistance and an origin of replication for selection and replication in *Escherichia coli*.



**Figure 2.1 pUAST expression vector**

pUAST consists of five tandemly arrayed optimized GAL4 binding sites (red) followed by the *hsp70* TATA box and transcriptional start (blue), a polylinker (green) containing unique restriction sites for EcoRI, BglII, NotI, Xho, KpnI and XbaI and the SV40 small t intron and polyadenylation site. These features are included in a P-element vector (pCaSpeR3) containing the P element ends (P3' and P5') and the white gene which acts as a marker for successful incorporation into the *Drosophila* genome (BRAND and PERRIMON 1993).

Image from: <http://www.gurdon.cam.ac.uk/~brandlab/reagents/pUAST.html>

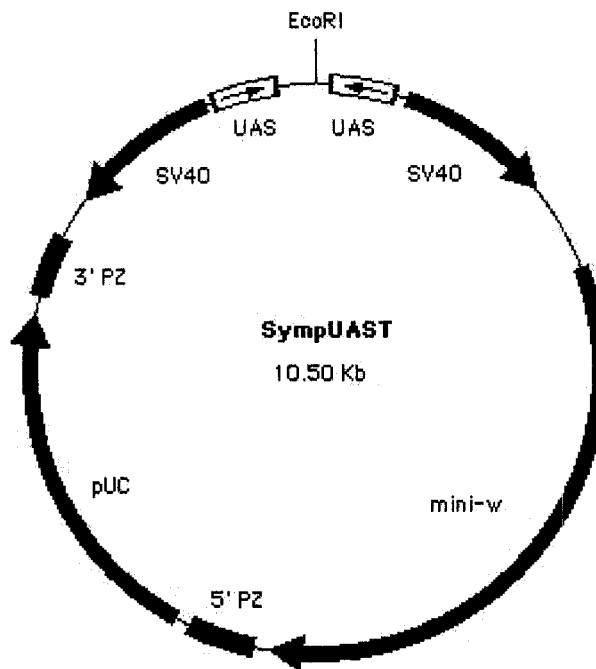
### 2.3 *sym-pUAST* RNAi vector

The symmetrical transcription plasmid (*sym-pUAST*) (Figure 2.2) contains two UAS arrays and two SV40 polyadenylation sites. This arrangement drives the transcription of a single insert corresponding to the target gene in two directions, giving both the sense and anti-sense strands. Thus the dsRNA molecule can be made by the cell.

### 2.4 Making *sym-pUAST-eag*

To make a UAS RNAi transgene targeting the *eag* K<sup>+</sup> channel, a 509nt fragment of genomic DNA corresponding to the 5'UTR and most of exon 1 of *eag* was amplified by PCR (forward primer: ATATAAGAATTCGAAAGAGAGTGAGACAGC, reverse primer: ATATAAAGATCTGCATGATGATGTTCTCCGAGG). The PCR product was TA-cloned into the pGEM-T vector (Promega). An EcoRI/BglII double digest was then used to transfer the PCR product into the *sym-pUAST* plasmid. The new plasmid, named *sym-pUAST-eag*, was sequenced to ensure accurate cloning prior to being micro-injected into *Drosophila* embryos.

The fragment of *eag* used as the trigger for RNAi shows no significant homology to other genes as determined by a BLAST search of all *Drosophila* sequences.



**Figure 2.2** *sym-pUAST* RNAi vector

Contains an EcoRI site for the insertion of the trigger fragment. The *mini-w* gene is a selectable marker for following insertion into the fly genome. pUC carries an Amp<sup>R</sup> gene for selection in E.coli. 3'PZ and 5'PZ are p-element insertion sites. UAS (upstream activation sequence) is a promoter and the SV40 is a polyA terminator (GIORDANO *et al.* 2002).

All other *sym-pUAST* plasmids (see chapter 7.3) were created in a similar manner to *sym-pUAST-eag*. Primer details are included in chapter 7.3.

## **2.5 Sequencing of *eag***

As recombination and RFLP mapping had demonstrated that the suppressor mutations were within the *eag* locus, I undertook the sequencing of all 15 exons from the three suppressors and appropriate controls. PCR primers (listed in table 2.1) were designed at the beginning and end of either each exon, or pair of exons. If an individual exon was too large to easily amplify it was amplified in two parts.

Genomic PCR products were separated by gel electrophoresis and the appropriate band excised and gel extracted using the Montage DNA Gel Extraction Kit (Millipore, MA) as per the manufacturer's instructions. The extracted band was purified using the QIAquick PCR Purification Kit (Qiagen, MD) as per the manufacturer's instructions. The PCR product was then sequenced using both PCR primers and occasionally with additional internal primers. Putative mutations were resequenced from repeat PCR reactions as confirmation.

Name	Direction	Sequence (5'→3')
eag exon 1F	F	GAAAGAGAG TGAGACAGC
eag exon 1F-2	F	GGGAGAAAGAGAGTGAGACAGCATC
eag exon 1R	R	GGATGATGTTCTCGAGG
RC-EAG-EX1R	R	TTGAACTTGGTACACC
eag exon 1R-2	R	CCGGATGATGTTCTCGAGGAATGTG
RC-EAG-EX2F	F	GGTGAAGAGGTGAATC
RC-EAG-EX2R	R	CGATTATTGAAACGC
RC-EAG-EX3F	F	GCATTCTGGCATT
RC-EAG-EX3F-3	F	TCTTCTGGCATCTCCTG
RC-EAG-EX3R-2	R	CTTTTGCATAGCAGG
RC-EAG-EX3R-3	R	CGACTTTGATTTGGGTATAGC
RC-EAG-EX4F	F	CACCAGCGAGTATC
RC-EAG-EX4R	R	CCAAGACACGTTAG
4R-2	R	CCAAGACACGAATCG
RC-EAG-EX5F	F	GCATCTCTGGTGTTC
RC-EAG-EX5R	R	TTCATCAGGCAACC
EX6F	F	GTGTGCGTGTACCC
RC-EAG-EX6F	F	CTAAAGGATCCCACGAAGCAGTCCAATTTGGC
RC-EAG-EX7R	R	GTTGCATACCTCGAC
RC-EAG-EX8F	F	TTCCAGGTGCCATAC
RC-EAG-EX9R	R	CCCATTATCCGCATCG
RC-EAG-EX10F	F	GATCCAATACAGCTG
10F-2	F	CGATGCGGATAATGG
EX11R	R	CTGCAATGATCATC
RC-EAG-11R-2	R	CACCTGCAATGATGATCATC
RC-EAG-IN11F-1	F	AAAGCTAGGCCATCC
IN11F-2	F	CGTGAGAAAACCTGCC
RC-EAG-IN11R-1	R	CGTGAGAAAATGCC
MF-EAG-EX12F	F	CTCTGCTGTATGCC
12F-2	F	GCTCTGCTGTATGCC
EAG-EX12F	F	CTCTGCTGTATGCCACGATCTTTGGTCACG
MF-EAG-EX12R	R	CTTCTCGGTATCCAG
12R-2	R	CCTTCTCGGTATCCAG
EAG-EX12R	R	CTTGGTCATGGCCCAGGTGGAGACGACATAGTCC
RC-EAG-EX13F	F	GGTACTAAACTATTGTCCG
RC-EAG-EX13R	R	CCAATATTGCCAC
RC-EAG-EX14F	F	TTACAGGCAAGGG
RC-EAG-14F-2	F	CAGTAAGGAGCTCGTC
RC-EAG-EX14R	R	CTTAGTTCGCTCCACC
RC-EAG-IN14R	R	CAACGAGCATAAGTCAC
ex15F	F	GATAACCATTTTCATCGCC
RC-EAG-EX15F-2	F	CATCCGCATCTCC
RC-EAG-15F-3	F	CACACCCACAACACAGG
ex15R	R	TTCATCCAAAACCTCCACTAC
RC-EAG-EX15R-2	R	GATCCTGATGCTCC
RC-EAG-15R-3	R	GCGATTGATCTGCCG

**Table 2.1 Primers used in genomic sequencing of *eag***

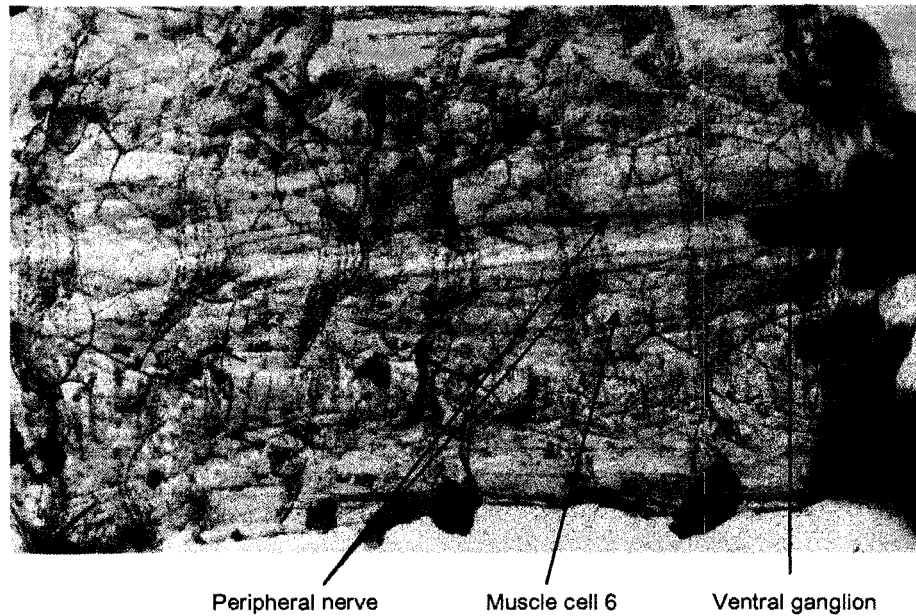
Primers used for PCR amplification and/or sequencing of PCR products. All sequences presented 5'→3'.

Some regions that proved difficult to amplify from genomic DNA were amplified from cDNAs and sequenced as above. The cDNAs were created by extracting RNA from adult flies using the TRIzol Reagent protocol (GibcoBRL) and performing RT-PCR (Superscript III First-Strand Synthesis System for RT-PCR (Invitrogen)). PCR reactions were subsequently performed on the cDNA, and were analyzed as above.

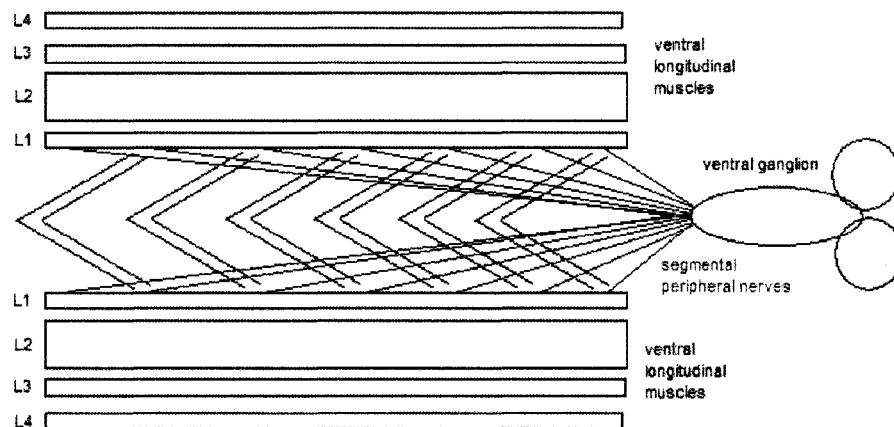
## **2.6 Larval micro-dissection**

Wandering third instar larvae were grown in uncrowded half pint bottles and collected 1 or 2 days after the appearance of the first wandering third instar larva. Larval dissections and muscle recordings were made as described previously (GANETZKY and WU 1982; HUANG *et al.* 2002; JAN and JAN 1976; STERN *et al.* 1995; STERN and GANETZKY 1989). Ventral lateral longitudinal peripheral nerves that innervate the body wall muscles were cut immediately posterior to the ventral ganglion (see Figure 2.3) and were captured and stimulated using a suction electrode (see Figure 2.4). Intracellular muscle recordings were made using a microelectrode pulled on a Flaming/Brown micropipette puller to tip resistances of 30-60 M $\Omega$  and filled with 3M KCl. All dissections and recordings were performed at room temperature in standard saline solution (JANs buffer) (0.128M NaCl, 2.0mM KCl, 4.0mM MgCl<sub>2</sub>, 0.34M sucrose, 5.0mM Hepes pH 7.1 and CaCl<sub>2</sub> as specified in the text) unless otherwise indicated. Ventral longitudinal muscle cell 6 (also known as muscle L2) was used for the recording

A.



B.



**Figure 2.3 Wandering 3<sup>rd</sup> instar larval preparation**

A. Light micrograph of a filleted wandering third instar larva. B. Schematic of a filleted wandering third instar larva. The ventral lateral longitudinal peripheral nerves (red) are cut immediately posterior of the ventral ganglion. Each peripheral nerve innervates the section of longitudinal muscle posterior to where the nerve contacts the muscle. Muscle cell 6 (L2) is used for recordings where the amplitude or duration of the response will be assayed.

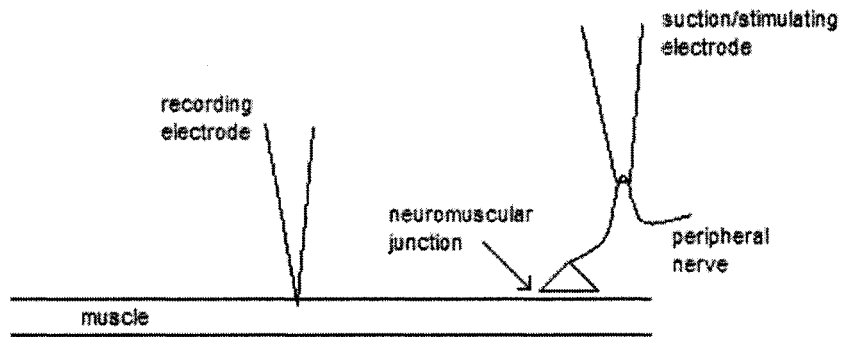
of all electrophysiological parameters. Quinidine, 4-Aminopyridine (4-AP) and tetraethylammonium (TEA) were applied following dissection as described previously (JAN *et al.* 1977; SINGH and WU 1989).

## **2.7 ejp and mejp recordings**

The mean amplitude and duration was typically calculated from 5 evoked excitatory junctional potentials (ejps) for each larva and data was collected from at least 3 larvae for each genotype under each set of conditions. The number of larvae tested is presented as the n-value. Duration of the ejp was measured as the interval from half-maximal response to half-maximal response. The amplitude of spontaneous mejps was determined similarly.

## **2.8 Voltage clamping and ejc recordings**

To voltage clamp, larvae were dissected as for ejp recordings and a nerve was captured as before. Two electrodes were introduced into muscle cell 6, one to act as the current electrode the second as the voltage electrode (see Figure 2.5). To obtain voltage a variable current is applied through the current electrode to hold the muscle at the desired holding potential (-60 mV in my experiments). The muscle potential is monitored by the voltage electrode.



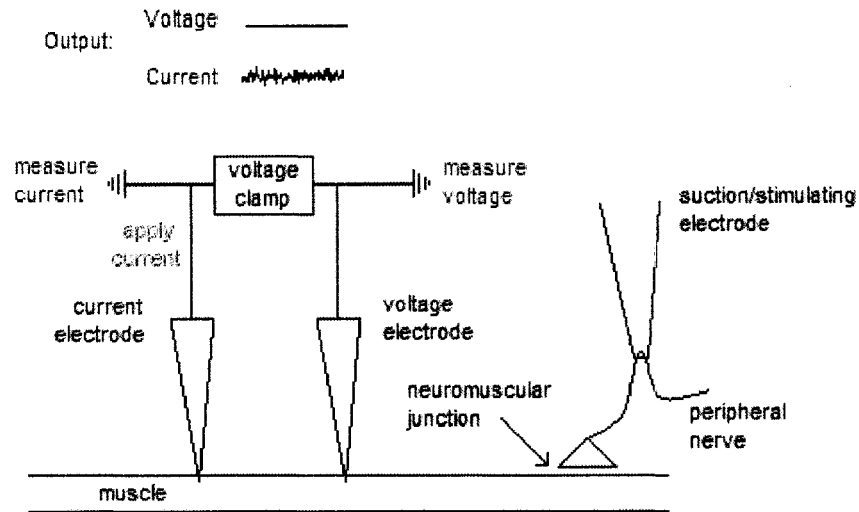
### Figure 2.4 Standard larval nmj preparation

A loop of peripheral nerve is captured with a suction electrode. The electrode is then positioned such that no strain is placed upon the nerve. An intracellular recording electrode is then inserted into a muscle cell (typically muscle cell 6). The nerve is then stimulated through the suction electrode at the desired frequency. The muscle response is recorded via the recording electrode and digitized.

An excitatory junctional current (ejc) is the change in the current applied to maintain the muscle potential at -60mV in response to an evoked action potential in the innervating nerve. Several ejcs were recorded per larva and the average ejc amplitude was calculated for each larva.

## **2.9 Long term facilitation**

LTF, also known as augmentation, is a phenomenon exhibited at the *Drosophila* larval nmj. Following repetitive stimulation at frequencies typically between 3 and 10 Hz, an excitation threshold is reached, and subsequent stimulations elicit a facilitated response of increased magnitude and duration (JAN and JAN 1978; WANG *et al.* 1994). Certain mutations that decrease neuronal excitability (such as *para* (MIKE STERN, UNPUBLISHED DATA)) result in delayed onset of LTF; those that increase excitability (such as *Dp para*<sup>+</sup>, *Hk*, *frq* and *pumilio* (RIVOSECCHI *et al.* 1994; SCHWEERS *et al.* 2002; STERN *et al.* 1995; STERN and GANETZKY 1989)) result in faster onset of LTF.



**Figure 2.5 Larval nmj voltage clamp setup**

As shown in Figure 2.4, a nerve is captured and stimulated. To voltage clamp the muscle, two intracellular electrodes are introduced into the same muscle cell. The voltage electrode monitors the muscle potential, as described in Figure 2.4. The output from the voltage electrode is recorded and also feeds into the voltage clamp. The current electrode applies a current. The current applied to maintain the desired muscle potential is recorded simultaneously to the muscle potential (voltage).

## Chapter 3: Suppressors of *Shaker*

### 3.1 Mutagenesis

To identify novel mutations that suppress the leg-shaking phenotype of *Sh*-mutants, males carrying *Sh*<sup>133</sup> were mutagenized with EMS, crossed to  $\overline{XX}$ <sub>yw<sup>f</sup></sub> females, and their sons scored for an absence of leg-shaking. Of 35,000 sons tested, nine failed to shake their legs when etherized. Five of these suppressor mutations have previously been shown to be new alleles of *para*, which encodes a sodium channel subunit (STERN *et al.* 1990).

#### *Five alleles of para.*

The characterization of these alleles provides the basis for my hypotheses for the characterizing of the remaining suppressors. The new alleles of *para* are known as 60, 63, 74, 103 and 141. The allele *para*<sup>74</sup> has been characterized molecularly to be a methionine to isoleucine substitution within the third S6 domain (PITTENDRIGH *et al.* 1997).

#### *The remaining 4 suppressors.*

One of these lines was lost with time leaving only three (*Sup*<sup>39</sup>, *Sup*<sup>84</sup> and *Sup*<sup>146</sup>) to be further characterized.

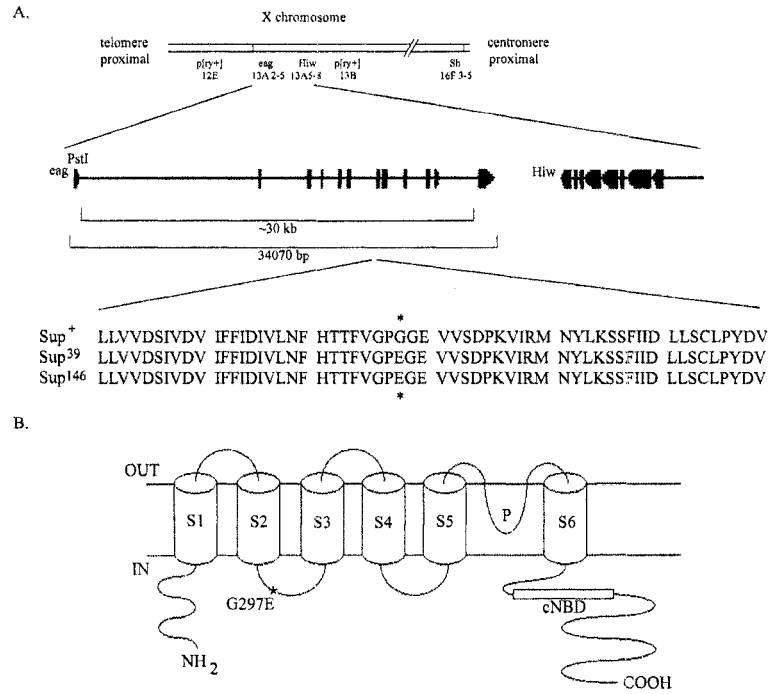
### 3.2 Mapping: recombination and RFLP

Initial recombination mapping, by Mike Stern, using the leg-shaking phenotype placed *Sup*<sup>39</sup>, *Sup*<sup>84</sup> and *Sup*<sup>146</sup> between the *garnet* (12B4-6) and *scalloped* (13F) loci and then to a region between two P[ry<sup>+</sup>]-elements at positions 12E and 13B/C.

Damian Dalle Nogare used restriction fragment length polymorphism (RFLP) analysis to localize *Sup*<sup>146</sup> centromere-proximal to a PstI polymorphism in exon 1 of *ether-a-go-go* (*eag*). The frequency of cross-over between the leg-shaking suppression phenotype and the RFLP suggested that *Sup*<sup>146</sup> is approximately 30Kb from *eag* exon 1, which would place it within the *eag* locus (see Figure 3.1A).

### 3.3 Genomic sequencing

To test the possibility that *Sup*<sup>39</sup>, *Sup*<sup>84</sup> and *Sup*<sup>146</sup> are new alleles of *eag*, I sequenced genomic DNA from the 15 exons of *eag* from the suppressor mutations as well as from isogenic *Sup*<sup>+</sup> flies. The *eag* sequence of *Sup*<sup>39</sup> yielded only a single amino acid substitution: a glycine to glutamate change at position 297 (G297E, see Figure 3.1B). Interestingly, the *eag* sequence from *Sup*<sup>146</sup> flies showed the identical G297E mutation as well as two additional mutations (A1088T and I1142T). To test the possibility that these



**Figure 3.1 Map position of the *Sup*<sup>39</sup> and *Sup*<sup>146</sup> mutations**

(A) Mapping of the suppressor mutations between P[ry<sup>+</sup>]-elements at positions 12E and 13B. Direct genomic sequencing of *Sup*<sup>39</sup> and *Sup*<sup>146</sup> identified the substitution of a glutamate for a glycine at position 297, indicated by the pair of asterisks. *Sup*<sup>+</sup> represents sequence from *eag*<sup>+</sup> *para*<sup>63</sup> and *eag*<sup>+</sup> *para*<sup>141f</sup>. *para*<sup>63</sup> and *para*<sup>141</sup> are siblings of *Sup*<sup>39</sup> and *Sup*<sup>146</sup>, respectively generated by mutagenesis from the same isogenic wildtype X chromosome. (B) Schematic depicting the topology of the Eag protein. S1 through S6 represent the 6 transmembrane domains, P the pore domain and cNBD the cyclic nucleotide binding domain. The asterisk indicates the location of the G297E substitution identified in *Sup*<sup>39</sup> and *Sup*<sup>146</sup>. Having shown *Sup*<sup>39</sup> and *Sup*<sup>146</sup> to be mutations in *eag*, I have subsequently renamed them *eag*<sup>G297E</sup>.

two additional mutations were generated after the mutagenesis, while the fly line was being maintained, I sequenced these regions from a second *Sup*<sup>146</sup> stock, which was split off from the first stock about 6 months after *Sup*<sup>146</sup> was obtained. I found that the G297E mutation was retained in this second *Sup*<sup>146</sup> stock, but that the two additional mutations were absent. I conclude that *Sup*<sup>146</sup>, like *Sup*<sup>39</sup>, is a G297E mutation in *eag*; I shall now refer to them as *eag*<sup>G297E</sup>. I am not aware of any previous study that has assigned a function to G297.

Genomic sequencing of *Sup*<sup>84</sup> revealed two substitutions: A259V and E762V (Figure 3.1B); I have renamed this allele *eag*<sup>84</sup>. It remains unclear as to whether one or both of these substitutions is responsible for the phenotypes observed.

### 3.4 Gain-of-function hypothesis

Previous studies have shown that *eag* loss of function mutations enhance the phenotypes of *Sh*<sup>133</sup> mutation (WU *et al.* 1983). In contrast *eag*<sup>G297E</sup> and *eag*<sup>84</sup> suppress the phenotypes of the *Sh*<sup>133</sup> mutation. I thus hypothesize that *eag*<sup>G297E</sup> is a gain of function allele (Table 3.1). *eag*<sup>84</sup> may also be a gain of function allele of *eag*.

An alignment of the Eag protein sequence from several species (Figure 3. 2) indicates that position 297 and the surrounding residues are highly conserved in all members of the Eag channel sub-family, but not in the Eag-like (Elk) or Eag-related

Genotype	Enhances $Sh^{133}$	Suppresses $Sh^{133}$
$para^-$		✓
$Dp\ para^+$	✓	
$eag^-$	✓	
$eag^{G297E}$		✓
$eag^{84}$		✓

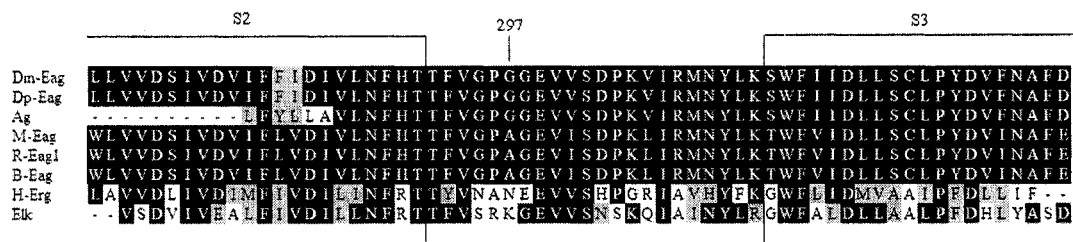
**Table 3.1 Genetic interactions among  $Na^+$  and  $K^+$  channel mutations**

The hypoexcitable *para* mutations suppress the  $Sh^{133}$ -induced leg shaking (STERN *et al.* 1990), whereas hyperexcitable *eag* mutations and *Dp para*<sup>+</sup> enhance the  $Sh^{133}$ -induced leg shaking (STERN *et al.* 1990). *eag*<sup>G297E</sup> and *eag*<sup>84</sup> suppress the  $Sh^{133}$ -induced leg shaking, leading me to hypothesize that *eag*<sup>G297E</sup> and *eag*<sup>84</sup> are gain of function mutations. Table adapted from HUANG AND STERN (2002)

(Erg) sub-families. Interestingly this region of Eag is close to the site at which  $Mg^{2+}$  ions interact with the channel to regulate its activity, a phenomenon not seen in either the Elk or Erg sub-families (TANG *et al.* 2000).

### 3.5 Suppression of the $Sh^{133}$ -induced ejp by $eag^{G297E}$ at low $[CaCl_2]$

In  $Sh^{133}$  mutants, motor axon excitability is increased, which leads to action potential triggered  $Ca^{2+}$  influx in the nerve terminal that is larger and more prolonged than in wild-type (JAN *et al.* 1977). This increased  $Ca^{2+}$  influx, in turn, leads to increased neurotransmitter release from the motor neuron and subsequent muscle depolarization that is increased in amplitude and duration compared to wild type. I hypothesize that  $eag^{G297E}$  suppresses the  $Sh^{133}$ -induced leg shaking phenotype by reducing neuronal excitability, which would compensate for the increased excitability conferred by  $Sh^{133}$ . If so, then  $eag^{G297E}$  might suppress the increased neurotransmitter release conferred by  $Sh^{133}$ . To test this possibility I used the larval neuromuscular junction (nmj) preparation (JAN *et al.* 1977) to compare synaptic transmission at the larval nmj in  $eag^{G297E} Sh^{133}$  and  $eag^+ Sh^{133}$ . With this preparation an action potential is induced in the motor axon and the consequent neurotransmitter release at the nmj elicits a depolarization in the muscle called an excitatory junctional potential (ejp) which is monitored with an intracellular recording electrode.



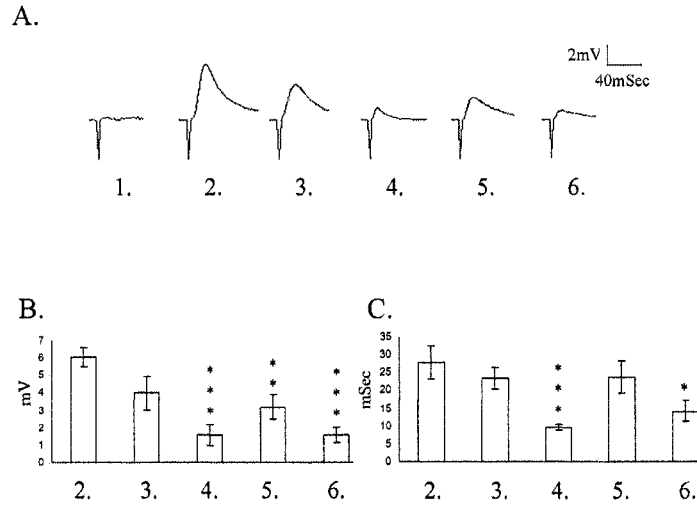
**Figure 3.2 Sequence conservation in the S2-S3 loop of Eag**

An alignment of the amino acid sequences corresponding to the S2 domain, the S3 domain and the S2-S3 loop of Eag from a number of species. The S2 and S3 domains are boxed. Also indicated is Dm-Eag position 297. Dm-Eag, *Drosophila melanogaster* (WARMKE *et al.* 1991); Dp-Eag, *Drosophila pseudoobscura* (RICHARDS *et al.* 2005); M-Eag, Mouse (WARMKE and GANETZKY 1994); R-Eag1 (LUDWIG *et al.* 1994), Rat; B-Eag, *Bos Taurus* (Bovine) (FRINGS *et al.* 1998); Ag-Eag, *Anopheles gambiae* (mosquito) (MONGIN *et al.* 2004), H-Erg, Human Eag related gene (WARMKE and GANETZKY 1994); Elk, Human Eag like K<sup>+</sup> channel (WARMKE and GANETZKY 1994). The Eag family has three branches – Eag, Erg and Elk, all with slightly different properties. At the position indicated within the S2-S3 linker, a residue with a small, non-polar side chain is conserved with the Eag sub-family.

As neurotransmitter release is dependent upon  $\text{Ca}^{2+}$  influx into the nerve terminal, at low external  $[\text{Ca}^{2+}]$  (such as 0.1mM) at most only a single quantum of neurotransmitter is released into a wild-type neuromuscular junction following nerve stimulation. As a consequence, only failures or low amplitude ejps are observed (JAN and JAN 1976). The  $Sh^{133}$  mutant exhibits a prolonged nerve terminal depolarization, leading to prolonged neurotransmitter release and an ejp of increased duration and amplitude even at low  $[\text{Ca}^{2+}]$  (JAN *et al.* 1977).

To determine if  $eag^{G297E}$  can suppress the defects in synaptic transmission conferred by the  $Sh^{133}$  mutation, I compared ejps from  $eag^+ Sh^{133}$  with ejps from  $eag^{G297E} Sh^{133}$  (Figure 3.3). I found that the  $eag^{G297E}$  allele from either the  $Sup^{39}$  or  $Sup^{146}$  lines partially suppress the  $Sh^{133}$  phenotype in a dosage dependent manner. Significant decreases in both ejp amplitude ( $p < 0.001$ ) and duration ( $p < 0.001$  for  $eag^{G297E}$  from  $Sup^{39}$  and  $p < 0.05$  for  $Sup^{146}$ ) were observed when the suppressor mutations were homozygous. When heterozygous, a moderate decrease in the  $Sh^{133}$ -induced ejp amplitude, but not ejp duration, was observed ( $p < 0.02$  for  $Sup^{146}$ , Figure 3.3). The smaller suppressive effect in the heterozygotes indicates that dosage of  $eag^{G297E}$  controls the degree of suppression observed.

Similar suppression of  $Sh^{133}$ -induced phenotypes has been observed previously by mutations in *para* and *mle<sup>nap</sup>*, which decrease the number of  $\text{Na}^+$  channels (GANETZKY and WU 1985; STERN *et al.* 1990) and thus create hypoexcitable neurons. These



**Figure 3.3 Dosage dependent suppression of *Sh*<sup>133</sup> by *eag*<sup>G297E</sup>**

(A) Averaged intracellular muscle recordings from larvae of the indicated genotypes in response to nerve stimulation. (B) Average amplitudes of eejps evoked by nerve stimulation in the presence of low bath [Ca<sup>2+</sup>] (0.1mM) in larvae of the genotypes indicated. Under these low [Ca<sup>2+</sup>] conditions most successful wild type eejps result from the release of at most a single vesicle of neurotransmitter. (C) Average duration of evoked eejps. Values are presented as the mean ± SEM, data collected from at least 5 larvae for each genotype.

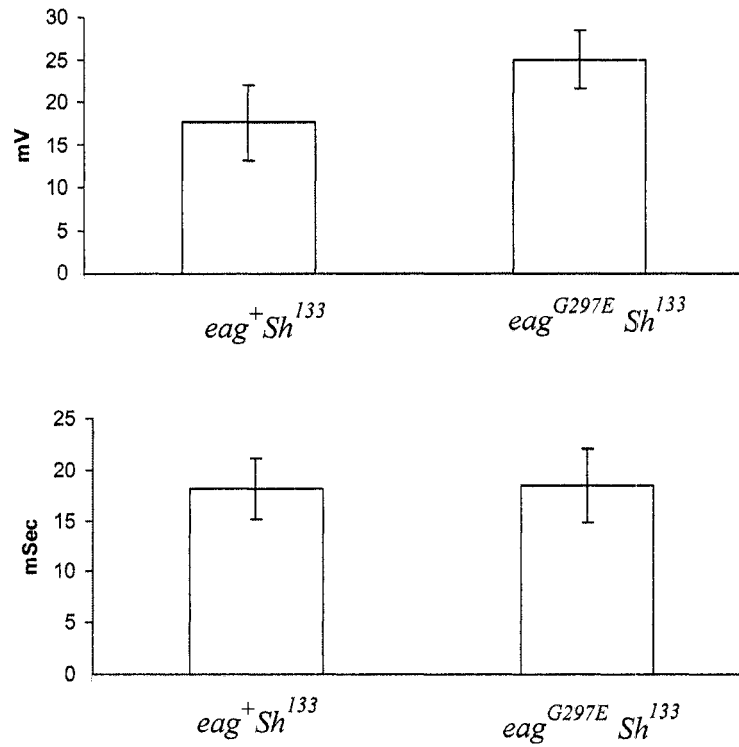
1. *eag*<sup>+</sup> *Sh*<sup>+</sup>; 2. *eag*<sup>+</sup> *Sh*<sup>133</sup>; 3. *eag*<sup>G297E</sup> (from *Sup*<sup>39</sup>) *Sh*<sup>133</sup> / *eag*<sup>+</sup> *Sh*<sup>133</sup>; 4. *eag*<sup>G297E</sup> (from *Sup*<sup>39</sup>) *Sh*<sup>133</sup>; 5. *eag*<sup>G297E</sup> (from *Sup*<sup>146</sup>) *Sh*<sup>133</sup> / *eag*<sup>+</sup> *Sh*<sup>133</sup>; 6. *eag*<sup>G297E</sup> (from *Sup*<sup>146</sup>) *Sh*<sup>133</sup>.

\*p<0.05 by student's t-test, \*\*p <0.02 by student's test, \*\*\*p <0.01 by student's t-test versus *eag*<sup>+</sup> *Sh*<sup>133</sup>.

observations support the hypothesis that *eag*<sup>G297E</sup> reduces neuronal excitability, a phenomenon that is presumably the result of conferring a gain of function phenotype on the Eag channels. A suppression of *Sh*<sup>133</sup> could possibly be produced by increasing the number of Eag channels in the neuronal membrane; similar to the enhancement of *Sh*<sup>133</sup> seen with *Dp para*<sup>+</sup> (table 3.1). An alternative possibility is that this gain of function phenotype is the result of premature, prolonged or constitutive opening of the Eag channels.

### **3.6 No suppression of the *Sh*<sup>133</sup>-induced ejp by *eag*<sup>G297E</sup> at higher [CaCl<sub>2</sub>]**

When performed at higher [CaCl<sub>2</sub>] (0.4mM), *eag*<sup>G297E</sup> does not decrease the amplitude or duration of *Sh*<sup>133</sup> mutant ejps (Figure 3.4). This result is not unexpected as the evoked ejp at this [CaCl<sub>2</sub>] is not significantly different in *Sh* mutants as compared to wild type (JAN *et al.* 1977). The absence of an effect by *eag*<sup>G297E</sup> in the presence of high [CaCl<sub>2</sub>] does suggest that muscle is not impaired in its response to neurotransmitter at the nmj.



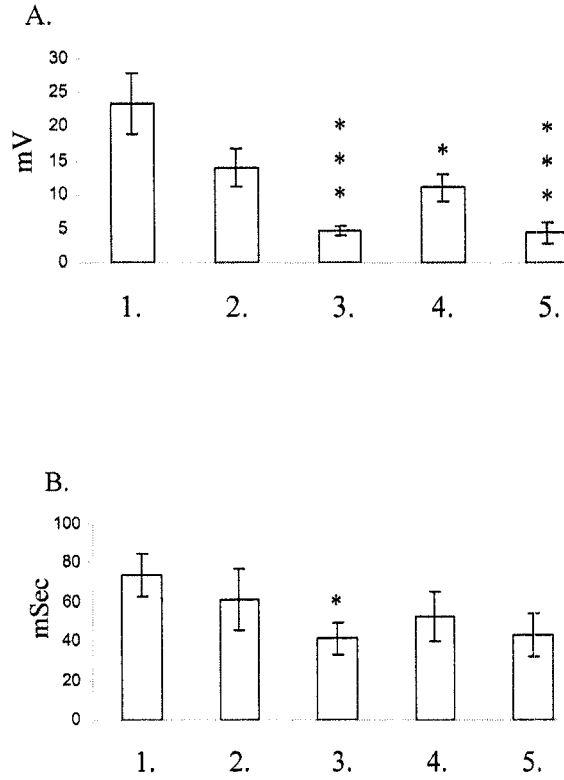
**Figure 3.4 No suppression of *Sh<sup>133</sup>* at high [CaCl<sub>2</sub>]**

Mean amplitudes and durations of excitatory junctional potentials (ejps) evoked by nerve stimulation in the presence of high bath [Ca<sup>2+</sup>] (0.4mM) in larvae of the genotypes indicated. Values are presented as the mean  $\pm$  SEM, data collected from at least 4 larvae for each genotype.

### 3.7 Suppression of the quinidine enhanced $Sh^{133}$ -induced increase in neurotransmitter release by $eag^{G297E}$

The addition to the extracellular bath of 0.1mM quinidine, a drug that selectively blocks  $I_K$  in *Drosophila* larval muscles (SINGH and WU 1989), enhances the amplitude and duration of the action potential-evoked ejp in  $Sh^{133}$  mutant larvae (WU *et al.* 1989). To determine if  $eag^{G297E}$  is able to suppress this enhancement of the  $Sh^{133}$  phenotype, ejp recordings were performed at 0.1mM  $[Ca^{2+}]$  and in the presence of 0.1mM [quinidine]. As shown in Figure 3.5, when homozygous  $eag^{G297E}$  is able to partially suppress the quinidine enhanced  $Sh^{133}$  ejp phenotype.

If 0.1mM [quinidine] blocks  $I_K$  completely, how can  $eag^{G297E}$  reduce the sensitivity of the motor neuron to quinidine? There are several possible explanations. First, while it is known that 0.1mM [quinidine] nearly eliminates  $I_K$  in *Drosophila* larval body wall muscles (SINGH and WU 1989), it is not clear if it blocks  $I_K$  specifically and completely in the motor neuron. Second, the G297E mutation might render Eag less sensitive to quinidine than  $eag^+$ . This possibility is supported by the observation that mutations in human Eag can alter the binding characteristics of quinidine and other antiarrhythmic agents (GESSNER *et al.* 2004). Third, the  $K^+$  channels distinct from  $I_K$  in which Eag participates ( $I_A$ ,  $I_{CS}$  &  $I_{CF}$  (GANETZKY and WU 1983; WARMKE *et al.* 1991; WU *et al.* 1983; ZHONG and WU 1991)) are not sensitive to quinidine, and it is possible that  $Eag^{G297E}$  exerts its effects through one of these channels.



**Figure 3.5 Suppression of the  $Sh^{133}$ -induced increase in neurotransmitter release by  $eag^{G297E}$ : effects of quinidine**

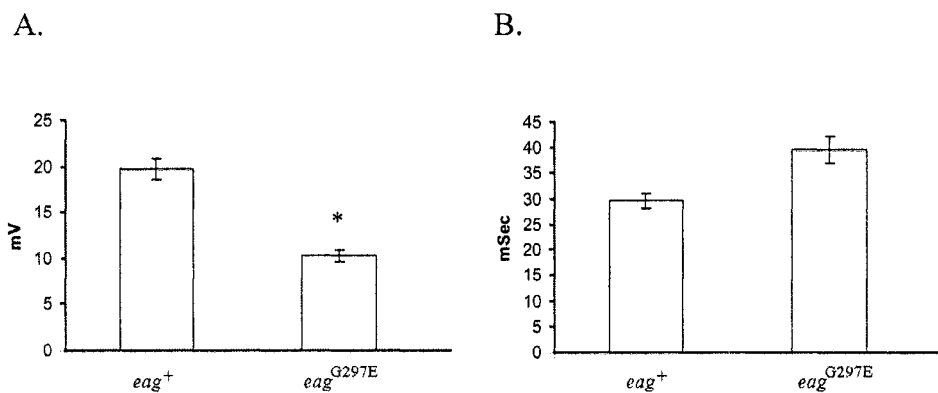
Mean amplitudes and durations of excitatory junctional potentials (ejps) evoked by nerve stimulation in the presence of low bath  $[Ca^{2+}]$  (0.1mM) and 0.1mM [quinidine] in larvae of the genotypes indicated. Values are presented as the mean  $\pm$  SEM, data collected from at least 4 larvae for each genotype.

1.  $eag^+ Sh^{133}$ ; 2.  $eag^{G297E}$  (from  $Sup^{39}$ )  $Sh^{133} / eag^+ Sh^{133}$ ; 3.  $eag^{G297E}$  (from  $Sup^{39}$ )  $Sh^{133}$ ; 4.  $eag^{G297E}$  (from  $Sup^{146}$ )  $Sh^{133} / eag^+ Sh^{133}$ ; 5.  $eag^{G297E}$  (from  $Sup^{146}$ )  $Sh^{133}$ . \* $p < 0.05$ , \*\*\* $p < 0.01$  versus  $eag^+ Sh^{133}$ .

### 3.8 Suppression of the $Sh^{133}$ -induced ejp by $eag^{G297E}$ is not allele specific

The  $eag^{G297E}$  mutation does not appear to produce any obvious behavioral abnormality in an otherwise wild type background. No temperature sensitive paralysis is observed, the flies appear well coordinated and flight appears normal. To determine if  $eag^{G297E}$  confers a defect in synaptic transmission in an otherwise wild type background, I made measurements of ejp amplitude and duration at 0.15mM  $[CaCl_2]$ . No significant decrease in either ejp amplitude or duration was observed (data not shown). Similarly, the onset rate of long term facilitation (JAN and JAN 1978) was also unaffected by  $eag^{G297E}$  (see chapter 3.12). The observation that  $eag^{G297E}$  conferred no detectable excitability phenotype in a  $Sh^+$  background raised the possibility that the suppression of  $Sh^{133}$  by  $eag^{G297E}$  might be an allele-specific restoration of Sh function. This possibility is supported by the observation that Eag and Sh subunits can co-assemble in a channel complex (CHEN *et al.* 1996; CHEN *et al.* 2000). To test this possibility I examined the effects of  $eag^{G297E}$  on the hyperexcitability conferred by the  $K^+$  channel blocking drug 4-aminopyridine (4-AP) which is a specific Sh channel blocker (GANETZKY and WU 1983; YAMAMOTO and SUZUKI 1989).

I found that the amplitude of ejps evoked at 0.1mM  $[CaCl_2]$  and 2mM [4-AP] was significantly suppressed by  $eag^{G297E}$  (Figure 3.6). This suppression of the increased ejp conferred by 4-AP suggests that the G297E mutation is increasing the activity of the



**Figure 3.6 Suppression of *Sh*<sup>133</sup> by *eag*<sup>G297E</sup> is not allele specific**

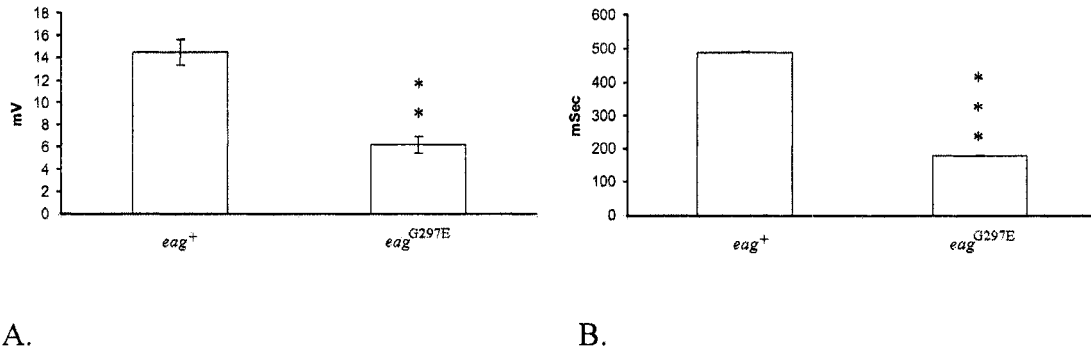
Mean amplitudes and durations of excitatory junctional potentials (ejps) evoked by nerve stimulation in the presence of low bath [Ca<sup>2+</sup>] (0.1mM) and 2mM [4-AP] in larvae of the genotypes indicated. Values are presented as the mean  $\pm$  SEM, data collected from at least 5 larvae for each genotype. \*p<0.05, versus *eag*<sup>+</sup>.

voltage-gated  $K^+$  channels that remain active following the addition of 4-AP, and thus that the suppression of the *Sh*-induced increased ejp is not allele specific.

### 3.9 *eag*<sup>G297E</sup> suppresses the effect of TEA

Having shown that *eag*<sup>G297E</sup> suppresses the effect of 4-AP on synaptic transmission, I tested the effects of *eag*<sup>G297E</sup> on the hyperexcitability conferred by a second  $K^+$  channel blocking drugs tetraethylammonium (TEA), which is a more general voltage-gated  $K^+$  channel blocker (GANETZKY and WU 1983; YAMAMOTO and SUZUKI 1989).

I found that the large amplitude and prolonged ejp's evoked at 0.1mM  $[CaCl_2]$  by addition of 10mM [TEA] were easily evoked in all wild type larvae; in contrast in *eag*<sup>G297E</sup> larvae it was possible to evoke such an ejp in only about half of the larvae tested (data not shown). Furthermore as shown in Figure 3.7, even when an ejp was successfully elicited, *eag*<sup>G297E</sup> reduced the amplitude and duration of the ejp in comparison to *eag*<sup>+</sup>. This suppression of the increased ejp conferred by TEA further suggests that the G297E mutation is increasing the activity of the voltage-gated  $K^+$  channels that remain active following the addition of either 4-AP or TEA. Interestingly, it appears that *eag*<sup>G297E</sup> manifests its most obvious phenotypes under conditions that prolong the action potential.

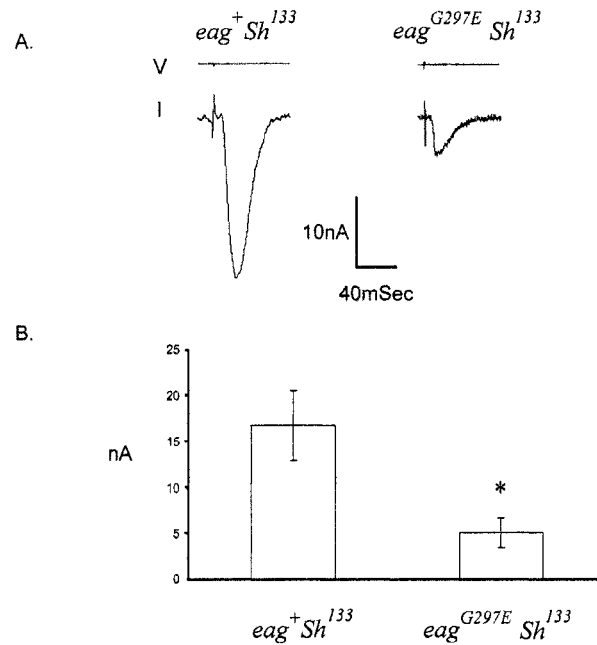


**Figure 3.7** *eag*<sup>G297E</sup> suppresses the effect of TEA

Mean amplitudes and durations of excitatory junctional potentials (ejps) evoked by nerve stimulation in the presence of low bath [Ca<sup>2+</sup>] (0.1mM) and 10mM [TEA] in larvae of the genotypes indicated. Values are presented as the mean ± SEM, data collected from at least 4 larvae for each genotype. \*\*p<0.02, \*\*\*p<0.01 versus *eag*<sup>+</sup>.

### 3.10 *eag*<sup>G297E</sup> acts presynaptically to suppress *Sh*<sup>133</sup>

The suppression of the *Sh*<sup>133</sup>-induced increased amplitude ejp conferred by *eag*<sup>G297E</sup> could be a consequence of a suppression of the increased neurotransmitter release of *Sh*<sup>133</sup> mutants, of reduced sensitivity of the muscle membrane glutamate receptors to the neurotransmitter L-glutamate, or increased voltage-dependent or voltage-independent K<sup>+</sup> currents in the muscle membrane. To distinguish among these possibilities I monitored synaptic transmission while holding the muscle membrane potential to -60mV with a voltage clamp, which prevents the opening of voltage-gated ion channels such as Eag and Sh in the muscle membrane. If the *eag*<sup>G297E</sup>-dependent suppression of the *Sh*<sup>133</sup>-induced increase in ejp size is due to suppression of the increased neurotransmitter release, then I expect that excitatory junctional currents (ejcs) of reduced amplitude will be observed in *eag*<sup>G297E</sup> *Sh*<sup>133</sup> compared with *eag*<sup>+</sup> *Sh*<sup>133</sup>. In contrast, if the suppression of the ejp amplitude phenotype is a result of altered muscle voltage-dependent K<sup>+</sup> currents then ejc amplitude in *eag*<sup>G297E</sup> *Sh*<sup>133</sup> is expected to be the same as *eag*<sup>+</sup> *Sh*<sup>133</sup>. Figure 4 shows that the ejc in *eag*<sup>G297E</sup> *Sh*<sup>133</sup> is significantly smaller than in *eag*<sup>+</sup> *Sh*<sup>133</sup>, which is consistent with the notion that *eag*<sup>G297E</sup> acts pre-synaptically to suppress *Sh*<sup>133</sup> phenotypes by decreasing the amount of neurotransmitter released. The proportional reduction in ejc amplitude (69%) is similar to the proportional reduction in ejp amplitude (73%).



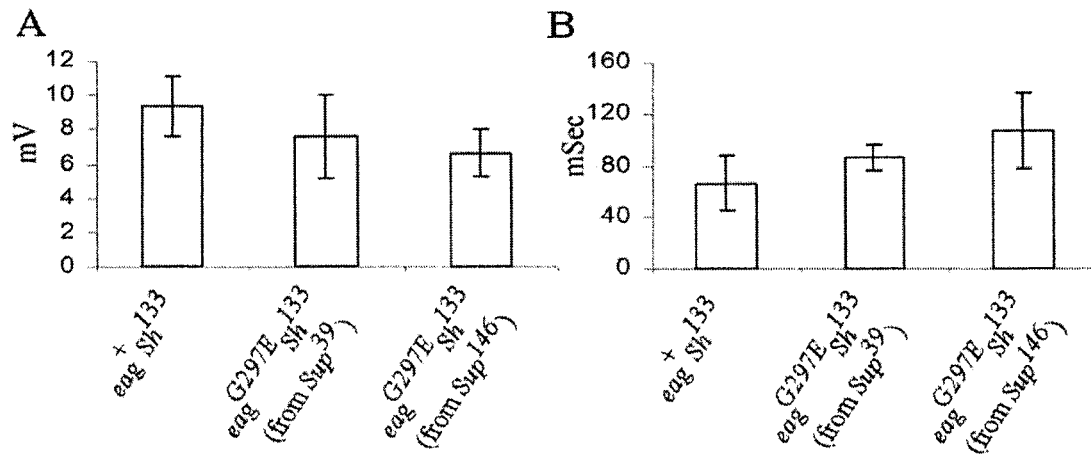
**Figure 3.8 The *eag<sup>G297E</sup>* mutation acts pre-synaptically to suppress the phenotypes of *Sh<sup>133</sup>***

(A) Typical excitatory junctional currents (ejcs) in response to nerve stimulation in the presence of 0.1mM [ $\text{Ca}^{2+}$ ]. Holding potential was -60mV. Simultaneous intracellular recording of voltage (V) and current (I) were performed. (B) Average amplitude of evoked ejcs. *eag<sup>G297E</sup>* from *Sup<sup>39</sup>*. Values presented as mean  $\pm$  SEM, n = 4. \*p<0.05 by student's t-test.

To exclude the possibility that an altered voltage-independent current or altered sensitivity to L-glutamate is responsible for the suppression of the ejp phenotypes I compared the amplitude of spontaneous miniature ejps (mejp) in  $eag^+ Sh^{133}$  and  $eag^{G297E} Sh^{133}$ . If the  $eag^{G297E}$ -dependent suppression of the  $Sh^{133}$ -induced increased ejp amplitude is due to decreased muscle response to the neurotransmitter L-glutamate or increased voltage-independent  $K^+$  currents, then mejps of reduced amplitude will be observed in  $eag^{G297E} Sh^{133}$  compared to  $eag^+ Sh^{133}$ . I found that the mejp amplitudes recorded in  $eag^{G297E} Sh^{133}$  and  $eag^+ Sh^{133}$  are almost identical ( $0.79\text{mV} \pm 0.11$  and  $0.81\text{mV} \pm 0.14$  respectively), suggesting  $eag^{G297E}$  does not affect voltage-independent currents or the muscle response to L-glutamate. I conclude that  $eag^{39}$  acts pre-synaptically to suppress the effects of  $Sh^{133}$ .

### **3.11 Suppression by $eag^{G297E}$ of the $Sh^{133}$ -induced increase in neuronal excitability requires extracellular $Mg^{2+}$**

The S2 and S3 transmembrane domains of Eag contain three aspartic acid residues that coordinate the binding of a  $Mg^{2+}$  ion when the channel is in its closed state (SCHONHERR *et al.* 2002; SILVERMAN *et al.* 2000; TANG *et al.* 2000).  $Mg^{2+}$  ions slow channel activation in a concentration- and voltage-dependent manner in bovine, mouse and Drosophila Eag (SCHONHERR *et al.* 1999; SILVERMAN *et al.* 2000; TANG *et al.* 2000; TERLAU *et al.* 1996). The observation that the G297E substitution falls within the highly



**Figure 3.9 Suppression of the *Sh*<sup>133</sup>-induced increase in neurotransmitter release by *eag*<sup>39</sup> and *eag*<sup>146</sup> requires extracellular Mg<sup>2+</sup>**

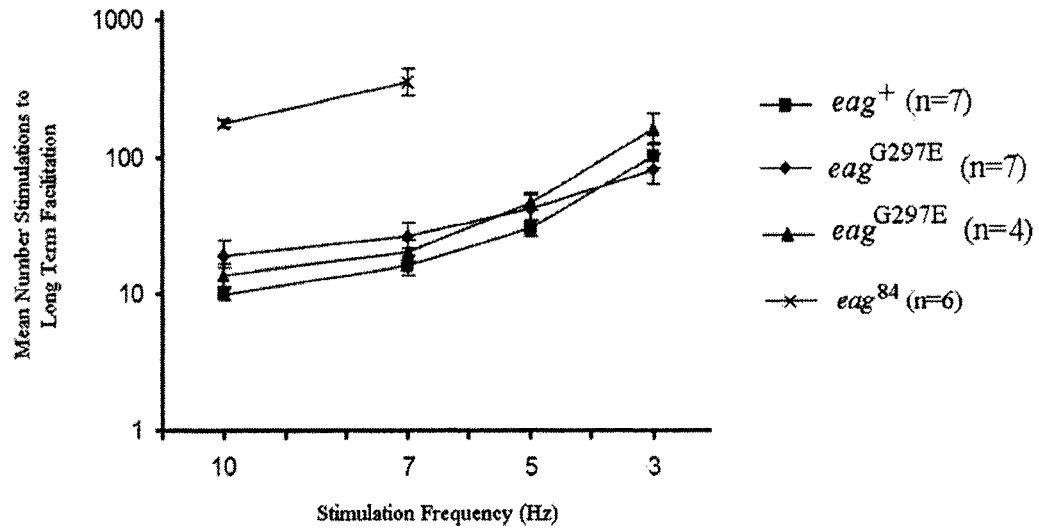
Mean amplitudes and durations of ejps evoked by nerve stimulation in the absence of extracellular MgCl<sub>2</sub> and in the presence of low bath [Ca<sup>2+</sup>] (0.1mM) in larvae of the genotypes indicated. Values are presented as the mean ± SEM, data collected from at least 4 larvae for each genotype.

conserved S2-S3 linker raised the possibility that G297E acts by eliminating or reducing the effect of  $Mg^{2+}$ . If so, then in the absence of extracellular  $Mg^{2+}$ , neuronal excitability is predicted to be the same in  $eag^{G297E}$  and  $eag^+$ . To test this possibility, ejp recordings were performed in  $eag^{G297E} Sh^{133}$  and  $eag^+ Sh^{133}$  at low  $[Ca^{2+}]$  in the absence of extracellular  $Mg^{2+}$  (table 4). Table 4 shows that the ejp amplitude and duration are not significantly different in  $eag^+ Sh^{133}$  as in  $eag^{G297E} Sh^{133}$ . This observation supports the hypothesis that the regulatory effects of  $Mg^{2+}$  upon Eag have been lost in  $eag^{G297E}$  and is consistent with the possibility that  $eag^{G297E}$  increases Eag activity by reducing the affinity of Eag for  $Mg^{2+}$ .

The model of  $Mg^{2+}$  action upon Eag proposed by Schönherr et al. (2002) suggests that  $Mg^{2+}$  is involved in the switch between the resting (“locked”) and activated (“unlocked”) states (Figure 1.5). I suggest that the G297E mutation alters the configuration of the channel such that it favors the “unlocked” over the “locked” state. Studies of this mutant channel in oocytes would be required to test this possibility.

### **3.12 $eag^{84}$ , but not $eag^{G297E}$ , produces a hypoexcitable LTF phenotype**

Like  $eag^{G297E}$ ,  $eag^{84}$  does not confer decreased ejp amplitude in an otherwise wild-type background. Similarly, no temperature sensitive paralysis or other behavioral phenotypes are observed. However, unlike  $eag^{G297E}$ , the rate of onset of LTF in  $eag^{84}$  is decreased as compared to wild-type (Figure 3.10). Delayed facilitation was observed



**Figure 3.10 *eag*<sup>84</sup> delays the onset of long term facilitation**

Average number of stimulations required to elicit the facilitative response at the stimulation frequencies tested (10, 7, 5 and 3 Hz). No facilitation observed in *eag*<sup>84</sup> at 5 or 3 Hz stimulation. Both *eag*<sup>G297E</sup> alleles from *Sup*<sup>146</sup>. Values presented as mean  $\pm$  SEM, n-values as indicated.

following stimulation at 10Hz and 7Hz, but no facilitation was seen in *eag*<sup>84</sup> larvae at 5Hz or 3Hz, unlike wild-type that facilitated at all frequencies tested. This indicates a significant decrease in neuronal excitability in *eag*<sup>84</sup>.

### **3.13 *eag*<sup>84</sup> suppresses the effects of 4-AP and TEA on motor neuron excitability**

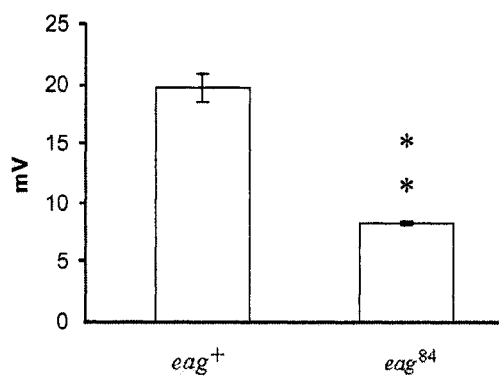
To determine if *eag*<sup>84</sup> could suppress the hyperexcitability conferred by 4-AP, I compared the amplitude and duration evoked ejps in the presence of 4-AP in *eag*<sup>84</sup> and *eag*<sup>+</sup> larvae. Like *eag*<sup>G297E</sup>, *eag*<sup>84</sup> significantly reduced the amplitude of ejps evoked at 0.1mM [CaCl<sub>2</sub>] and 2mM [4-AP] in an otherwise wild-type background (Figure 3.11). This suggests that *eag*<sup>84</sup> is also likely to suppress the *Sh*<sup>133</sup>-induced ejp.

I was unable to elicit the typical TEA-induced exaggerated response seen in wild-type larvae in any of the *eag*<sup>84</sup> larvae tested (n=4). This indicates that *eag*<sup>84</sup> is increasing the activity of K<sup>+</sup> channels that retain activity in the presence of either 4-AP or TEA.

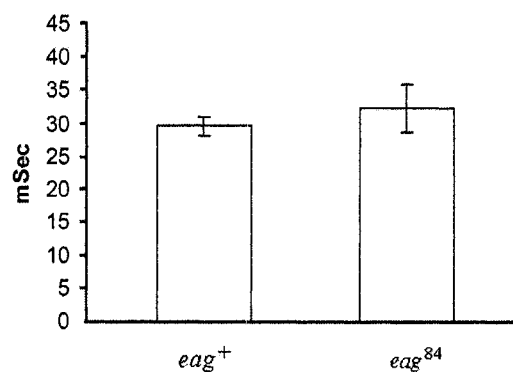
### **3.14 Aberrant phosphorylation hypothesis**

I suggested in chapter 1.5 that there is a positive feedback loop in which CaMKII phosphorylates Eag to enhance its activity, which in turn further activates CaMKII. I

A.



B.



### Figure 3.11 Suppression of the effects of 4-AP by *eag*<sup>84</sup>

Mean amplitudes and durations of excitatory junctional potentials (ejps) evoked by nerve stimulation in the presence of low bath  $[Ca^{2+}]$  (0.1mM) and 2mM [4-AP] in larvae of the genotypes indicated. Values are presented as the mean  $\pm$  SEM, data collected from at least 4 larvae for each genotype. \*\* $p < 0.02$ , versus *eag*<sup>+</sup>.

hypothesize that as one of the substitutions in *eag*<sup>84</sup> (E762V) is close to the CaMKII phosphorylation site (T787) and the CaMKII binding site (residues 773-794), the gain-of-function characteristics of *eag*<sup>84</sup> are due to aberrant phosphorylation. A mutation that makes Eag easier to phosphorylate would cause an increased level of Eag phosphorylation and thus an increased level of Eag activity. Additionally, altering a phosphorylation mechanism may explain why *eag*<sup>84</sup> produces a LTF phenotype where *eag*<sup>G297E</sup> does not.

### **3.15 Phenocopying of *eag*<sup>G297E</sup> and *eag*<sup>84</sup> with a UAS transgene**

To show that the identified mutations are truly responsible for the phenotypes observed, I attempted to create UAS-*eag* transgenes carrying the mutations. Previous attempts to create UAS-*eag* transgenes have been unsuccessful; my strategy was to create a transgene with no UTRs as this had not previously been tried. While obtaining a cDNA I learnt that another group had made transgenic flies carrying the wild-type construct that I was trying to make (LESLIE GRIFFITH, PERSONAL COMMUNICATION). As this group has not been able to make the transgene functionally express, there is no purpose served in creating the mutant transgenes. A potential solution is to use homologous recombination to replace the wild-type gene in control line with a mutant copy.

### 3.16 Conclusions

*eag*<sup>G297E</sup>

The results shown here demonstrate that the leg-shaking and electrophysiological phenotypes caused by the *Sh*<sup>l33</sup> mutation are suppressed in a dosage dependent manner by *eag*<sup>G297E</sup>. Because phenotypes of *eag*<sup>G297E</sup> are opposite to those of *eag* loss-of-function mutants (BRUGGEMANN *et al.* 1993; WARMKE *et al.* 1991; WU *et al.* 1983) I propose that these new mutations confer a gain-of-function phenotype to the Eag channels. Thus, *eag* activity regulates neuronal excitability: reduction in *eag* activity confers a hyperexcitable neuron, whereas increases in *eag* activity confer a hypoexcitable neuron. A similar phenomenon occurs with the *para*-encoded Na<sup>+</sup> channel: decreasing or increasing channel number produces hypoexcitable or hyperexcitable neurons respectively (STERN *et al.* 1990). Given that *eag*<sup>G297E</sup> acts pre-synaptically, I hypothesize that the neuronal hypoexcitability effect is mediated by the premature, prolonged or constitutive opening of the Eag channels in the motor neuron membrane, resulting in an attenuation of the action potential. Furthermore, the experiments raise the possibility that the reduction or elimination of the response to extracellular Mg<sup>2+</sup> may be responsible for this gain of function phenotype of *eag*<sup>G297E</sup>.

Polymorphisms such as *eag*<sup>G297E</sup>, if they exist in humans, might be of particular therapeutic importance because an individual carrying such a polymorphism might exhibit no overt abnormalities, and yet show an aberrant sensitivity to particular

therapeutic drugs. The identification of a gain of function mutation in a K<sup>+</sup> channel gene that can be further studied both *in vivo* and *in vitro* provides a unique opportunity to obtain new knowledge in K<sup>+</sup> channel regulation.

### *eag*<sup>84</sup>

I propose that *eag*<sup>84</sup> also confers a gain of function phenotype to Eag channels. The mode of action of *eag*<sup>84</sup> appears to be different to *eag*<sup>G297E</sup>. It seems possible that the gain of function phenotype may be conferred through a phosphorylation dependent mechanism, although this hypothesis remains to be tested. Like *eag*<sup>G297E</sup>, it appears that the phenotypes of *eag*<sup>84</sup> are best observed under conditions that prolong the action potential such as in the presence of drugs such as quinidine and 4-AP.

## 3.17 Future Work

Future experiments that may be considered either in the Stern lab or in other labs include: analysis of the current voltage relationship in larval muscles, oocyte expression and single channel analysis of channel activation kinetics and Mg<sup>2+</sup> dependence, biochemical analysis of channel phosphorylation, and the replacing of wild-type *eag* with mutant forms *in vivo* using homologous recombination.

## Chapter 4: Tissue specificity of *eag*

### 4.1 Introduction

Neuronal function is in large part regulated by  $K^+$  ion channels. The loss of a  $K^+$  channel such as the *Drosophila* *eag*-encoded voltage gated  $K^+$  channel results in increased neuronal excitability, that is, an increase in the propensity for a neuron to generate and propagate an action potential in response to synaptic activity. Loss of function mutations in  $K^+$  channel subunit genes such as *eag*, *Sh*, and *Hk* confer electrophysiological phenotypes such as spontaneous or prolonged action potentials, which lead to behavioral phenotypes such as ether-induced leg shaking (GANETZKY and WU 1983; WARMKE *et al.* 1991; WU *et al.* 1983; ZHONG and WU 1991). For example, the first *ether-à-go-go* (*eag*) mutation was identified by its ether-induced leg shaking phenotype (KAPLAN and TROUT 1969); these were later found to be caused by spontaneous action potentials (WU *et al.* 1983).

While many of the characteristics of Eag have been studied *in vivo* and in heterologous systems, no definitive data exist to confirm in which tissues the normal function of Eag is necessary for correct neuronal function. Recent work using a truncated, dominant negative, *eag* transgene has shown that the expression of this transgene in motor neurons is sufficient to replicate the degree of ether-induced leg shaking observed in *eag<sup>l</sup>* mutant flies (BROUGHTON *et al.* 2004). It has not, however, been determined if this dominant negative transgene can also recapitulate the other phenotypes of *eag*

mutations, such as the observation of spontaneous ejps at the larval neuromuscular junction or the enhancement of the *push<sup>1</sup>*-induced thickening of the larval perineural glia. Concern also remains that the dominant negative transgene is producing a phenotype via some secondary mechanism rather than by only preventing the proper formation of channels containing the Eag subunit.

The aims of this study are to confirm that the loss of Eag function in neuronal tissues is sufficient to confer neuronal hyper-excitability, to demonstrate that the UAS-*eag<sup>A932</sup>* transgene disrupts Eag function and not some other intracellular process, and to determine in which tissue(s) the loss of Eag function acts to enhance the *push<sup>1</sup>*-induced thickening of the perineural glia.

## 4.2 Methods

**Drosophila stocks:** All fly stocks were maintained on standard cornmeal/agar *Drosophila* media at room temperature. The *push<sup>1</sup>* allele is a recessive *push* allele described previously (RICHARDS *et al.* 1996; YAGER *et al.* 2001) that causes neurophysiological defects, sterility, and a thickening of the perineural glia. The UAS-*eag<sup>A932</sup>* line carries a truncated form of *eag* that produces a dominant negative effect that behaviorally mimics the *eag<sup>1</sup>* mutation (BROUGHTON *et al.* 2004).

**UAS-*eag*<sup>RNAi</sup> transgenic flies:** The RNAi transgene targeting the *eag*-encoded K<sup>+</sup> channel was created by amplifying a 509bp fragment of genomic DNA corresponding to the 5'UTR and most of exon 1 of *eag* was amplified by PCR (primers: forward: ATATAAGAATTC-GAAAGAGAGTGAGACAGC; reverse: ATATAAAGATCT-GCATGATGATGTTCTCCGAGG). The PCR product was TA-cloned into the pGEM-T vector (Promega). An *EcoRI*/*Bgl*II double digest was then used to transfer the PCR product into the *sym-pUAST* plasmid (GIORDANO *et al.* 2002). Finally, the transgene was introduced into *Drosophila* using P-element mediated transformation. The fragment of *eag* used as the trigger for RNAi shows no significant homology to other *Drosophila* genes as determined by a BLAST search of all *Drosophila* sequences.

**Behavioral tests:** *Leg-shaking:* Ether-induced leg shaking was assayed by exposing young adult flies to ether for about 10 seconds. Under these conditions, wild-type flies are immobilized except for occasional tarsal twitches; *Sh*<sup>133</sup>-mutant flies exhibit a rapid shaking of all six legs.

**Electrophysiology:** Larval dissections and muscle recordings were performed as described previously (GANETZKY and WU 1982; HUANG and STERN 2002; JAN and JAN 1976; STERN *et al.* 1995; STERN and GANETZKY 1989). Ventral lateral longitudinal peripheral nerves that innervate the body wall muscles were cut immediately posterior to the ventral ganglion and were stimulated using a suction electrode. Intracellular muscle recordings were made using a microelectrode pulled on a Flaming/Brown micropipette puller to tip resistances of 30-60 MΩ and filled with 3M KCl. All dissections and

recordings were performed at room temperature in standard saline solution (0.128M NaCl, 2.0 mM KCl, 4.0 mM MgCl<sub>2</sub>, 0.34 M sucrose, 5.0 mM HEPES pH 7.1 and CaCl<sub>2</sub> as specified in the text). Quinidine was applied following dissection as described previously (JAN *et al.* 1977; SINGH and WU 1989)

**Semi-quantitative PCR:** Semi-quantitative PCR was performed on RNA extracted from the heads of 20 flies. Flies were manually decapitated, and RNA was extracted using the TRIzol® Reagent Protocol (GIBCOBRL). Oligo(dT)<sub>20</sub>-primed cDNAs were prepared using the SuperScript III First-Strand Synthesis System (Invitrogen).

**Western blotting:** Western blots were performed on total protein extracted from heads of 20 flies. The flies were decapitated as described above and protein extracted using standard methods and probed using an anti-Eag antibody.

**Transmission electron microscopy:** Tissue sections were prepared as described previously (YAGER *et al.* 2001). Wandering third instar larvae were grown in uncrowded half-pint bottles at room temperature and were collected 1-2 days after the first third instar larva appeared. Larvae were dissected, fixed with glutaraldehyde and paraformaldehyde, stained with both 0.5% OsO<sub>4</sub> and 2% uranyl acetate, and embedded in an eponate 12-araldite mixture. Ultrathin cross-sectional slices (pale gold, 75-125 nm thick) were captured, poststained with uranyl acetate and Reynolds lead citrate, and analyzed using a transmission electron microscope. The thickness of the perineural glial layer for a given nerve was determined by averaging the distance from the edge of the

nerve to the boundary of the axon containing lumen at 8 different positions equally spaced around the nerve. Measurements were not taken when a perineural glial cell nucleus was encountered.

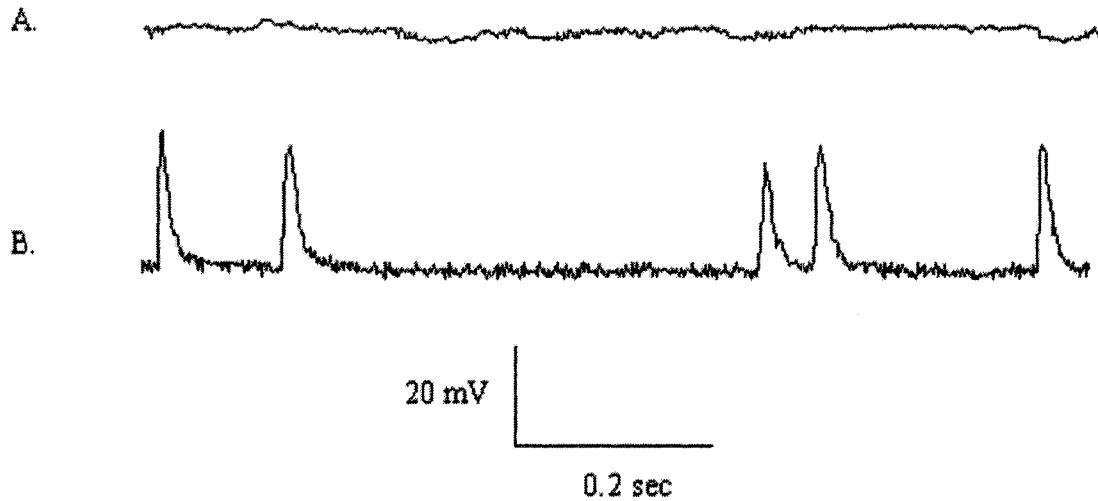
## 4.3 Results

An RNAi transgene targeting the *ether-à-go-go* (*eag*) gene was created for use in the GAL4/UAS system (BRAND and PERRIMON 1993) to create larvae and adults with increased neuronal excitability. Enhancer trap GAL4 lines were used to drive the expression of the RNAi transgene (UAS-*eag*<sup>RNAi</sup>, see methods) to enhance neuronal excitability. The GAL4 lines were chosen for their particular expression patterns in regions previously implicated in Eag function. The tissues tested by these GAL4 lines include post-mitotic neurons (*elav*-GAL4 (SCHUSTER *et al.* 1996)) and motor neurons (D42 (YEH *et al.* 1995)).

### 4.3.1 Neuronal expression of UAS-*eag*<sup>RNAi</sup> confers neuronal excitability

The overexpression of a novel, dominant negative, truncated *eag* K<sup>+</sup> channel in motor neurons enhances their excitability (BROUGHTON *et al.* 2004). To determine if the knockdown of the *eag* transcript by RNAi could also enhance neuronal excitability, we made intracellular muscle recordings in third instar larvae of the genotypes *elav*-GAL4/Y; *eag*<sup>RNAi/+</sup>, *act5C*-GAL4/UAS-*eag*<sup>RNAi</sup> and *elav*-GAL4/Y; UAS-*eag*<sup>RNAi</sup>.

Spontaneous ejps in the presence of 0.4 mM [CaCl<sub>2</sub>], characteristic of *eag* mutants (WU *et al.* 1983), were only observed in the *elav*-GAL4/Y; UAS-*eag*<sup>RNAi</sup> larvae (Figure 4.1), indicating that with two copies of the RNAi transgene, the knockdown of *eag* in neurons is sufficient to phenocopy loss-of-function mutations in *eag*. Similarly, *elav*-GAL4/Y; UAS-*eag*<sup>RNAi</sup> adults displayed ether-induced leg shaking, whereas a single copy of the RNAi transgene driven by either *elav*-GAL4 or *act5C*-GAL4 was unable to do so. This provides independent verification of the finding that the loss of Eag function in motor neurons is sufficient to elicit the characteristic *eag* mutant behavioral phenotype (BROUGHTON *et al.* 2004) and indicates that the effect of the dominant negative transgene is to disrupt Eag function specifically.



**Figure 4.1 RNAi knockdown of neuronal *eag* elicits spontaneous ejps**

Example intracellular recordings obtained from larval neuromuscular junctions in A. wild-type and B. *elav-GAL4/y; UAS-eag<sup>RNAi</sup>* larvae in the presence of 0.4 mM [CaCl<sub>2</sub>]. Spontaneous ejps are observed in *elav-GAL4/Y; UAS-eag<sup>RNAi</sup>* larvae (B.), whereas only miniature ejps were observed in wild-type larvae (A.).

## **4.4 Future work**

### **4.4.1 Is disruption of *eag* in motor neurons sufficient to phenocopy *eag*<sup>l</sup>?**

To show that the dominant negative and RNAi constructs confer the same affect upon neuronal excitability, recordings should be made at the larval nmj of *elav*-GAL4; UAS-*eag*<sup>4932</sup> larvae in the presence of 0.4 mM [CaCl<sub>2</sub>]; spontaneous ejps will confirm the existing data. If driving the dominant negative transgene with D42, which drives transgene expression in motor neurons, produces the same result, then the effect can be considered specific to motor neurons.

### **4.4.2 Are mRNA and protein levels decreased in *elav*-GAL4; UAS-*eag*<sup>RNAi</sup> heads?**

To determine the efficiency of the disruption of *eag* expression, I propose to compare *eag* mRNA and Eag protein levels in adult heads from *elav*-GAL4; UAS-*eag*<sup>RNAi</sup> and wild-type flies. The *eag* mRNA levels in adult heads will be assayed by semi-quantitative PCR. Protein levels will be measured using Western blotting with an anti-Eag antibody.

#### 4.4.3 Does neuronally driven *eag*<sup>A932</sup> enhance *push*<sup>I</sup> nerve thickness?

Whereas the *eag*<sup>I</sup> mutation alone has no effect upon the thickness of the perineural glia in the third instar larval peripheral nervous system, the *eag*<sup>I</sup> mutation confers a significant enhancement of the *push*<sup>I</sup>-induced increase in perineural glial thickness (YAGER *et al.* 2001). I propose to determine in which tissue(s) the loss of Eag function is sufficient to affect perineural glial thickness. Since two copies of the UAS-*eag*<sup>RNAi</sup> construct are needed to produce a neurophysiological phenotype, and only one copy of the UAS-*eag*<sup>A932</sup> transgene is sufficient to mimic the *eag*<sup>I</sup> mutation (BROUGHTON *et al.* 2004), I propose to use the dominant-negative transgene rather than the RNAi transgene. I predict that neuronal expression of the UAS-*eag*<sup>A932</sup> transgene will produce an enhancement of the *push*<sup>I</sup>-induced thickening of the perineural glial layer.

## Chapter 5: A dominant-negative *inebriated* transgene

### 5.1 Introduction

The control of neuronal excitability, the propensity for a neuron to generate and propagate an action potential in response to synaptic activity, is in large part regulated by ion channels, that themselves are affected by other proteins and neurotransmitters. Such affects can be direct, as in the enhancement and suppression of the  $Sh^{133}$  mutation by mutations in other ion channels (CARDNELL *et al.* 2006; STERN *et al.* 1990), or indirect, as observed with the *in vivo* manipulation of the *Drosophila* neurotransmitter transporter encoded by *inebriated* (*ine*) (HUANG and STERN 2002).

The *ine* mutation was first identified for its increased neuronal excitability that enhanced the  $Sh^{133}$ -mutant behavioral phenotypes (STERN and GANETZKY 1992). Flies defective in both *ine* and *Sh*, which encodes a voltage gated  $K^+$  channel subunit, display a downturned wing and indented thorax phenotype, a phenotype identical to that seen in *eag Sh* double mutants (STERN *et al.* 1990). Two isoforms of *ine* are transcribed in *Drosophila*, a long form (*ine-RA*) and a short form (*ine-RB*) (BURG *et al.* 1996; SOEHNGE *et al.* 1996). These two isoforms encode two proteins that differ only at the N-terminus, at which the long form (Ine-P1) has an additional domain that is not present in the short form (Ine-P2); this N-terminal extension of Ine-P1 bears no significant homology to any other known protein domains.

Whereas the *UAS-ine-RA* construct was able to fully rescue the excitability phenotypes of *ine<sup>l</sup>*, *UAS-ine-RB* was only able to partially rescue the phenotypes (HUANG and STERN 2002). These results suggest that the unique N-terminal domain of Ine-P1 is important for some aspects of neuronal excitability regulation. I hypothesize that the over expression of the N-terminal 313 amino acids of the long isoform of Inebriated will create a dominant negative phenotype conferring neuronal hyper-excitability by preventing the N-terminal domain of endogenous full-length Ine-P1 from interacting with its intracellular partners.

## 5.2 Methods

**Drosophila stocks:** All fly stocks were maintained on standard cornmeal/agar *Drosophila* media at room temperature, except where indicated for viability assays. The *Sh<sup>l33</sup>* allele is a dominant *Sh* allele described previously (JAN *et al.* 1977; KAPLAN and TROUT 1969) that produces a rapid leg-shaking phenotype when under ether anesthesia. The *push<sup>l</sup>* allele is a recessive *push* allele described previously (RICHARDS *et al.* 1996; YAGER *et al.* 2001) that causes neurophysiological defects, sterility, and a thickening of the perineural glia.

**UAS-*inePI<sup>l-313</sup>* transgenic flies:** The truncated UAS-*inePI<sup>l-313</sup>* transgene was created by amplifying a 939bp genomic fragment starting at the ATG start codon of *ine-RA* with PCR (primers: forward: GAATTC-ATGGCGGAGAACAAAGCAG, reverse:

GGTACC-TGGTGGCGTCTGCGATTG). This fragment of *ine-RA* was cloned into pGEM-T. We then used the *EcoRI* and *KpnI* restriction sites to transfer this fragment into *pUAS-T*. Finally, the transgene was introduced into *Drosophila* using P-element mediated transformation.

**Behavioral tests:** *Leg-shaking*: Ether-induced leg shaking was assayed by exposing young adult flies to ether for about 10 seconds. Under these conditions, wild-type flies are immobilized except for occasional tarsal twitches; *Sh*<sup>l33</sup>-mutant flies exhibit a rapid shaking of all six legs.

**Electrophysiology:** Larval dissections and muscle recordings were performed as described previously (GANETZKY and WU 1982; HUANG and STERN 2002; JAN and JAN 1976; STERN *et al.* 1995; STERN and GANETZKY 1989). Ventral lateral longitudinal peripheral nerves that innervate the body wall muscles were cut immediately posterior to the ventral ganglion and were stimulated using a suction electrode. Intracellular muscle recordings were made using a microelectrode pulled on a Flaming/Brown micropipette puller to tip resistances of 30-60 MΩ and filled with 3M KCl. All dissections and recordings were performed at room temperature in standard saline solution (0.128 M NaCl, 2.0 mM KCl, 4.0 mM MgCl<sub>2</sub>, 0.34 M sucrose, 5.0 mM HEPES pH 7.1, and CaCl<sub>2</sub> as specified in the text). Quinidine was applied following dissection as described previously (JAN *et al.* 1977; SINGH and WU 1989)

**Viability assays on hypertonic media:** Flies were grown in uncrowded half-pint bottles and collected during the first four days following the initial eclosions. Following etherization, flies were aliquoted into groups of 20 and placed into vials for 1 day to allow recovery from the etherization. The flies were then transferred into vials containing instant medium (Carolina) prepared according to the manufacturer's instructions, except that salt solutions of the appropriate concentrations were substituted for water. Fly manipulations and assays were performed at 18°C and 70% relative humidity, and fly viability on salt media was assayed every day for 10 days.

**Transmission electron microscopy:** Tissue sections were prepared as described previously (YAGER *et al.* 2001). Wandering third instar larvae were grown in uncrowded half-pint bottles at room temperature and were collected 1-2 days after the first third instar larva appeared. Larvae were dissected, fixed with glutaraldehyde and paraformaldehyde, stained with both 0.5% OsO<sub>4</sub> and 2% uranyl acetate, and embedded in an eponate 12-araldite mixture. Ultrathin cross-sectional slices (pale gold, 75-125 nm thick) were captured, poststained with uranyl acetate and Reynolds lead citrate, and analyzed using a transmission electron microscope. The thickness of the perineural glial layer for a given nerve was determined by averaging the distance from the edge of the nerve to the boundary of the axon containing lumen at 8 different positions equally spaced around the nerve. Measurements were not taken when a perineural glial cell nucleus was encountered.

## 5.3 Results

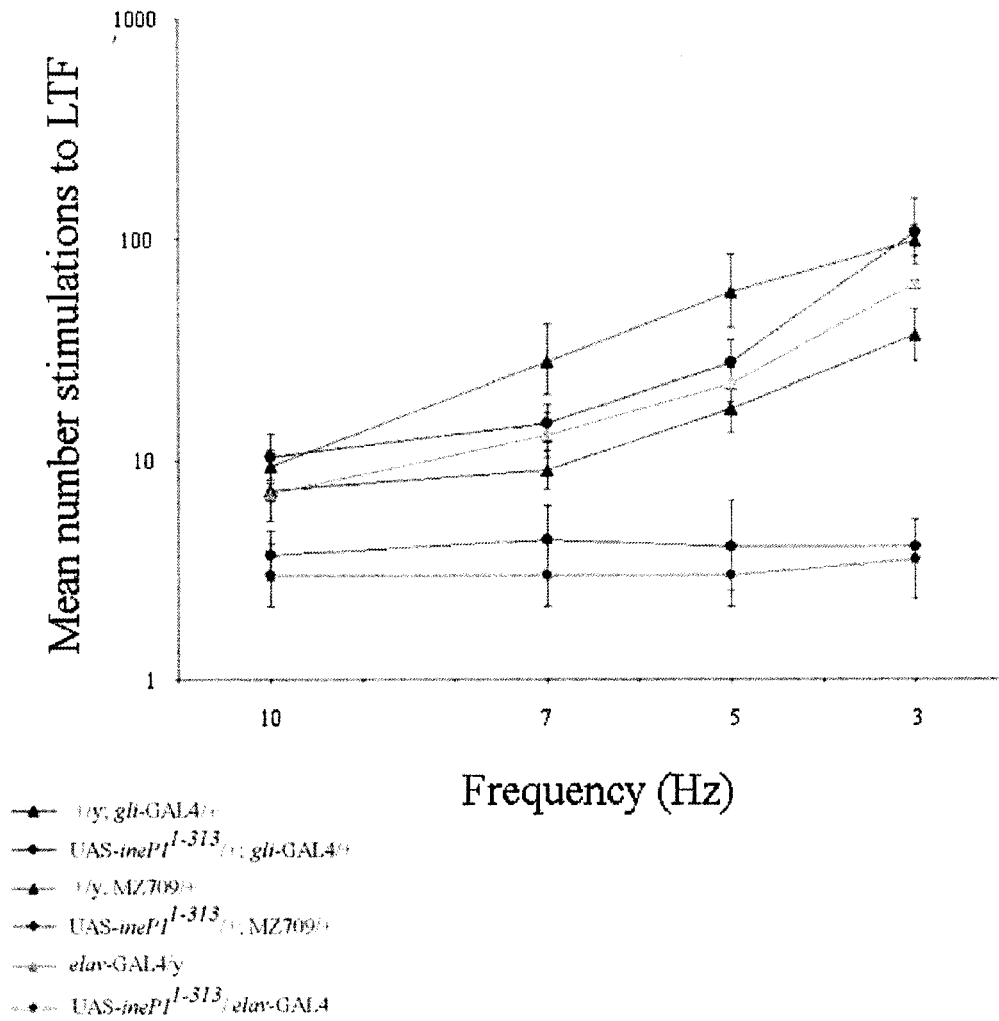
A transgene based upon the *inebriated* (*ine*) gene was created for use in the GAL4/UAS system (BRAND and PERRIMON 1993) to create larvae and adults with increased neuronal excitability. Five enhancer-trap GAL4 lines were used to drive the expression of a novel truncated *ine* transgene (UAS-*inePI*<sup>1-313</sup>; see methods) to enhance neuronal excitability. The GAL4 lines were chosen for their particular expression patterns in regions previously implicated in Ine function. The tissues tested by these GAL4 lines include post-mitotic neurons (*elav*-GAL4 (SCHUSTER *et al.* 1996)), motor neurons (D42 (YEH *et al.* 1995)), and peripheral glia (*gli*-GAL4 and MZ709 (ITO *et al.* 1995; SEPP and AULD 1999)), alongside a GAL4 line expressed in all tissues at all times (*act5C*-GAL4 (PIGNONI and ZIPURSKY 1997)).

### 5.3.1 Neuronal expression of UAS-*inePI*<sup>1-313</sup> confers neuronal hyperexcitability

The loss of Ine function confers a number of phenotypes, including a neuronal excitability phenotype manifested at the neuromuscular junction (nmj) of wandering third instar larvae. Wild-type *Drosophila* larvae nmjs exhibit a phenomenon termed long term facilitation (LTF), also known as augmentation. Following repetitive stimulation at frequencies typically between 3 and 10 Hz, an excitation threshold is reached, and subsequent stimulations elicit a facilitated response of increased magnitude and duration (JAN and JAN 1978; WANG *et al.* 1994). Certain mutations that decrease neuronal excitability (such as *para* (MIKE STERN, UNPUBLISHED DATA) and *eag*<sup>84</sup> (ROBERT

CARDNELL, UNPUBLISHED DATA)) result in delayed onset of LTF; those that increase excitability (such as *Dp para*<sup>+</sup>, *Hk*, *frq* and *pumilio* (RIVOSECCHI *et al.* 1994; SCHWEERS *et al.* 2002; STERN *et al.* 1995; STERN and GANETZKY 1989)) result in faster onset of LTF. The *ine*<sup>1</sup> mutation also confers an increased rate of onset of LTF that is rescued by the expression of a UAS-*ine-RA* transgene.

To determine if the overexpression of the N-terminal domain of Ine-P1 could increase neuronal excitability, we made measurements of the onset rate of LTF in the presence of 0.15 mM [CaCl<sub>2</sub>] and 0.1 mM [quinidine]. Figure 5.1 shows that the rate of onset of LTF is dramatically increased when the truncated *ine* transgene is expressed in neurons. Unexpectedly, despite both being considered peripheral glia drivers, *gli*-GAL4 and MZ709 driven UAS-*inePI*<sup>1-313</sup> gave different outcomes. MZ709 driven expression of the transgene gave a rate of onset of LTF similar to that of the neuronal driver suggesting that MZ709 expresses GAL4 in neurons in addition to the peripheral glia.



**Figure 5.1** Neuronally driven UAS-*ineP1*<sup>l-313</sup> increases the rate of onset of LTF

Average number of stimulations required to elicit the facilitative response at the stimulation frequencies tested (10, 5, 7 and 3 Hz). An accelerated rate of onset of facilitation is observed in larvae when UAS-*ineP1*<sup>l-313</sup> is driven by *elav*-GAL4 or MZ709. Values presented as mean  $\pm$  SEM,  $n \geq 2$ .

## 5.4 Future work

### 5.4.1 Does neuronal expression of UAS-*inePI*<sup>1-313</sup> truly confer neuronal hyperexcitability?

The n-values for the data presented in Figure 5.1 must be increased to confirm the phenotypes observed. Additionally, the rate of onset of LTF should be determined when the UAS-*inePI*<sup>1-313</sup> construct is expressed in motor neurons (D42) and when constitutively expressed (*act5C*-GAL4).

### 5.4.2 Does neuronal expression of UAS-*inePI*<sup>1-313</sup> enhance the *Sh* mutant behavioral phenotype?

The *ine*<sup>1</sup> mutation was isolated in a mutant screen in which it enhanced the ether-induced leg shaking behavior of *Sh*<sup>133</sup> adults to produce exaggerated leg shaking, down-turned wings and an indented thorax (STERN and GANETZKY 1992). Since many factors can increase the rate of LTF onset, to confirm that the increased neuronal excitability seen with neuronally expressed UAS-*inePI*<sup>1-313</sup> is due to the loss of Ine function, I will express the UAS-*inePI*<sup>1-313</sup> in the presence of the *Sh*<sup>133</sup> mutation. The observation of exaggerated ether-induced leg shaking, down-turned wings and an indented thorax in the presence of the *Sh*<sup>133</sup> mutation (i.e., a phenocopy of the *Sh*<sup>133</sup>; *ine*<sup>1</sup> double mutant) would indicate that the loss of Ine function is responsible for the observed neuronal hyperexcitability.

I predict that expression of UAS-*ineP1*<sup>1-313</sup> in the motor neurons will enhance *Sh*<sup>133</sup> to produce down-turned wings, and an indented thorax, showing that the expression of the dominant negative transgene in motor neurons is sufficient to phenocopy the neuronal excitability phenotypes of the *ine*<sup>1</sup> mutation.

#### **5.4.3 Does the UAS-*ineP1*<sup>1-313</sup> transgene affect osmotic tolerance?**

Both isoforms of Ine are expressed in the *Drosophila* kidney analogue (the Malpighian tubule and midgut) (SOEHNGE *et al.* 1996) and other members of the same transport family, such as BGT1, perform osmolyte transport in the mammalian renal medulla (BURG 1995). As would be expected of an osmolyte transporter, *ine* mutants display reduced tolerance of hypertonicity. The *ine*<sup>1</sup> and *ine*<sup>3</sup> null mutations that produce neither isoform of Ine confer significantly increased lethality when maintained on media with elevated [NaCl] (HUANG *et al.* 2002). The *ine*<sup>2</sup> mutation, which is expected to eliminate only Ine-P1 and not Ine-P2, also confers an increased sensitivity to hypertonicity. All the *ine* mutations can be rescued by the overexpression of Ine-P2, raising the question as to whether or not the N-terminal domain of Ine-P1 is involved in osmoregulation. To test the possibility that the N-terminal domain of Ine-P1 is not important for the osmotic stress response, I propose to assess the viability of flies expressing the UAS-*ineP1*<sup>1-313</sup> transgene on hypertonic media. I predict that when driven by *elav*-GAL4 or *gli*-GAL4 the transgene will have no effect upon osmotolerance. When expressed ubiquitously with *act5C*-GAL4, if the N-terminal domain does play a role in

the osmotic stress response, then decreased viability in response to hypertonicity will be observed.

#### **5.4.4 Does neuronal expression of the UAS-*ineP1*<sup>1-313</sup> transgene phenocopy the enhancement of perineural glial growth observed in *ine*<sup>1</sup> mutants?**

Whereas the *ine*<sup>1</sup> mutation alone has no effect upon the thickness of the perineural glia in the third instar larval peripheral nervous system, it does confer a significant enhancement of the *push*<sup>1</sup>-induced increase in perineural glial thickness (YAGER *et al.* 2001). Since this enhancement of the *push*<sup>1</sup> thickened perineural glia is rescued by the overexpression of Ine-P1, and since a similar enhancement is produced by the *eag*<sup>1</sup> mutation (YAGER *et al.* 2001), I propose to test the possibility that the overexpression of UAS-*ineP1*<sup>1-313</sup> might also affect perineural glial thickness. I predict that neuronal expression of the UAS-*ineP1*<sup>1-313</sup> transgene will produce an enhancement of the *push*<sup>1</sup>-induced thickening of the perineural glial layer, mimicking that produced with *ine*<sup>1</sup>.

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## Chapter 7: Appendices

### 7.1 FlyBase Report: Alleles of Gene *eag*

#### Alleles

Symbol	Allele class	Phenotype includes	Mutagen	Stocks	Molec. info.
1	hypomorph	chemical sensitive	ethyl methanesulfonate	2	yes
24	--	behavioral	--	--	--
101	--	behavioral   conditional ts	ethyl methanesulfonate	--	--
102	--	hyperactive	ethyl methanesulfonate	--	--
4PM	--	neurophysiology defective	ethyl methanesulfonate	--	--
EY00714	--	--	P-element activity	1	--
f06369	--	--	piggyBac transposase	--	--
hd14	--	chemical sensitive   recessive	PM hybrid dysgenesis	--	yes
hd15	--	olfaction defective   recessive	PM hybrid dysgenesis	--	yes
hd15r1	--	--	PM hybrid dysgenesis	--	yes
hd15r2	--	--	PM hybrid dysgenesis	--	yes
hd15r3	--	--	PM hybrid dysgenesis	--	yes
sc29	amorph	olfaction defective   recessive	--	1	--
unspecified	--	--	--	--	--
X6	amorph	olfaction defective   recessive	$\gamma$ ray	--	--
$\Delta$ 932.Scer\UAS	--	neurophysiology defective   conditional ts with Scer\GAL4 <sup>hs.PB</sup>	in vitro construct   deletion	--	yes

Sixteen mutant alleles in a addition to the wild-type allele of *eag* are recorded in the FlyBase database. All of the mutant alleles confer a decrease in Eag function. The mutant phenotypes are summarized below. Stocks refer to the number of stocks of that allele held in publicly available stock centers such as Bloomington.

#### Summary of Allele Phenotypes

Phenotype manifest in	Allele
leg	<i>eag</i> <sup>1</sup>
neuromuscular junction, synapse	<i>eag</i> <sup>1</sup>
synapse	<i>eag</i> <sup>1</sup>

<http://flybase.bio.indiana.edu/bin/fbidq.html?content=allele-table&FBgn0000535>

## 7.2 Amino acid translation sequence from *Sup*<sup>39</sup>, *Sup*<sup>146</sup>, *Sup*<sup>84</sup>, *para*<sup>141</sup> and *para*<sup>63</sup>

Translation of sequence derived from genomic sequencing. Also shown is a consensus sequence for wild-type Eag (WARMKE and GANETZKY 1994).

		10	20	30	40
	..... .....	..... .....	..... .....	..... .....	
consensus	MPGGRRGLVA	PQNTFLENII	RRSNSQPDSS	FLLANAQIVD	
para141f	MPGGRRGLVA	PQNTFLENII	RRSNSQPDSS	FLLANAQIVD	
Sup39 Sh133	MPGGRRGLVA	PQNTFLENII	RRSNSQPDSS	FLLANAQIVD	
Sup146 Sh133	MPGGRRGLVA	PQNTFLENII	RRSNSQPDSS	FLLANAQIVD	
Sup84	MPGGRRGLVA	PQNTFLENII	RRSNSQPDSS	FLLANAQIVD	
para63	~~~~~	~~~~~	~~~~~	~~~~~	
		50	60	70	80
	..... .....	..... .....	..... .....	..... .....	
consensus	FPIVYCNESE	CKISGYNRAE	VMQKSCRYVC	GFMYGELTDK	
para141f	FPIVYCNESE	CKISGYNRAE	VMQKSCRYVC	GFMYGELTNK	
Sup39 Sh133	FPIVYCNESE	CKISGYNRAE	VMQKSCRYVC	GFMYGELTDK	
Sup146 Sh133	FPIVYCNESE	CKISGYNRAE	VMQKSCRYVC	GFMYGELTDK	
Sup84	FPIVYCNESE	CKISGYNRAE	VMQKSCRYVC	GFMYGELTNK	
para63	~~~~~	~~~~~	~~~~~	~~~~~	
		90	100	110	120
	..... .....	..... .....	..... .....	..... .....	
consensus	ETVGRLEYTL	ENQQQDQFEI	LLYKKNNLQC	GCALSQFGKA	
para141f	ETVGRLEYTL	ENQQQDQFKI	LLYKKNNLQC	GCALSQFGKA	
Sup39 Sh133	ETVGRLEYTL	ENQQQDQFEI	LLYKKNNLQC	GCALSQFGKA	
Sup146 Sh133	ETVGRLEYTL	ENQQQDQFEI	LLYKKNNLQC	GCALSQFGKA	
Sup84	ETVGRLEYTL	ENQQQDQFKI	LLYKKNNLQC	GCALSQFGKA	
para63	~~~~~	~~~~~	~~~~~	~~~~~	
		130	140	150	160
	..... .....	..... .....	..... .....	..... .....	
consensus	QTQETPLWLL	LQVAPIRNER	DLVVLFLLT	RDITALKQPI	
para141f	QTQETPLWLL	LQVAPIRNER	DLVVLFLLT	RDITALKQPI	
Sup39 Sh133	QTQETPLWLL	LQVAPIRNER	DLVVLFLLT	RDITALKQPI	
Sup146 Sh133	QTQETPLWLL	LQVAPIRNER	DLVVLFLLT	RDITALKQPI	
Sup84	QTQETPLWLL	LQVAPIRNER	DLVVLFLLT	RDITALKQPI	
para63	~~~~~	~~~~~	~~~~~	~~~~~	
		170	180	190	200
	..... .....	..... .....	..... .....	..... .....	
consensus	DSEDTKGVLG	LSKFAKLARS	VTRSRQFSAH	LPTLKDPTKQ	
para141f	DSEDTKGVLG	LSKFAKLARS	VTRSRQFSAH	LPTLKDPTKQ	
Sup39 Sh133	DSEDTKGVLG	LSKFAKLARS	VTRSRQFSAH	LPTLKDPTKQ	
Sup146 Sh133	DSEDTKGVLG	LSKFAKLARS	VTRSRQFSAH	LPTLKDPTKQ	
Sup84	DSEDTKGVLG	LSKFAKLARS	VTRSRQFSAH	LPTLKDPTKQ	
para63	~~~~~	~~~~~	~~~~~	~~~~~	

	210	220	230	240
	.... ....	.... ....	.... ....	.... ....
consensus	SNLAHMMSLS	ADIMPQYRQE	APKTPPHILL	HYCAFKAIWD
para141f	SNLAHVMSLS	ADIMPQYRQE	APKTPPHILL	HYCAFKAIWD
Sup39 Sh133	SNLAHVMSLS	ADIMPQYRQE	APKTPPHILL	HYCAFKAIWD
Sup146 Sh133	SNLAHVMSLS	ADIMPQYRQE	APKTPPHILL	HYCAFKAIWD
Sup84	SNLAHVMSLS	ADIMPQYRQE	APKTPPHILL	HYCAFKAIWD
para63	~~~~~	~~~~~	~~~~~	~~~~~

	250	260	270	280
	.... ....	.... ....	.... ....	.... ....
consensus	WVILCLTFYT	AIMVPYNVAF	KNKTSEDVSL	LVVDSIVDVI
para141f	WVILCLTFYT	AIMVPYNVAF	KNKTSEDVSL	LVVDSIVDVI
Sup39 Sh133	WVILCLTFYT	AIMVPYNVAF	KNKTSEDVSL	LVVDSIVDVI
Sup146 Sh133	WVILCLTFYT	AIMVPYNVAF	KNKTSEDVSL	LVVDSIVDVI
Sup84	WVILCLTFYT	AIMVPYNVAF	KNKTSEDVSL	LVVDSIVDVI
para63	~~~~~	~~~VPYNVAF	KNKTSEDVSL	LVVDSIVDVI

	290	300	310	320
	.... ....	.... ....	.... ....	.... ....
consensus	FFIDIVLNFH	TTFVGPGEV	VSDPKVIRMN	YLKSWFIIDL
para141f	FFIDIVLNFH	TTFVGPGEV	VSDPKVIRMN	YLKSWFIIDL
Sup39 Sh133	FFIDIVLNFH	TTFVGPGEV	VSDPKVIRMN	YLKSWFIIDL
Sup146 Sh133	FFIDIVLNFH	TTFVGPGEV	VSDPKVIRMN	YLKSWFIIDL
Sup84	FFIDIVLNFH	TTFVGPGEV	VSDPKVIRMN	YLKSWFIIDL
para63	FFIDIVLNFH	TTFVGPGEV	VSDPKVIRMN	YLKSWFIIDL

	330	340	350	360
	.... ....	.... ....	.... ....	.... ....
consensus	LSCLPYDVFN	AFDRDEDGIG	SLFSALKVVR	LLRLGRVVRK
para141f	LSCLPYDVFN	AFDRDEDGIG	SLFSALKVVR	LLRLGRVVRK
Sup39 Sh133	LSCLPYDVFN	AFDRDEDGIG	SLFSALKVVR	LLRLGRVVRK
Sup146 Sh133	LSCLPYDVFN	AFDRDEDGIG	SLFSALKVVR	LLRLGRVVRK
Sup84	LSCLPYDVFN	AFDRDEDGIG	SLFSALKVVR	LLRLGRVVRK
para63	LSCLPYDVFN	AFDRDEDGIG	SLFSALKVVR	LLRLGRVVRK

	370	380	390	400
	.... ....	.... ....	.... ....	.... ....
consensus	LDRYLEYGAA	MLILLLCFYM	LVAHWLACIW	YSIGRSDADN
para141f	LDRYLEYGAA	MLILLLCFYM	LVAHWLACIW	YSIGRSDADN
Sup39 Sh133	LDRYLEYGAA	MLILLLCFYM	LVAHWLACIW	YSIGRSDADN
Sup146 Sh133	LDRYLEYGAA	MLILLLCFYM	LVAHWLACIW	YSIGRSDADN
Sup84	LDRYLEYGAA	MLILLLCFYM	LVAHWLACIW	YSIGRSDADN
para63	LDRYLEYGAA	MLILLLCFYM	LVAHWLACIW	YSIGRSDADN

	410	420	430	440
	.... ....	.... ....	.... ....	.... ....
consensus	GIQYSWLWKL	ANVTQSPYSY	IWSNDTGPEL	VNGPSRKSMY
para141f	GIQYSWLWKL	ANVTQSPYSY	IWSNDTGPEL	VNGPSRKSMY
Sup39 Sh133	GIQYSWLWKL	ANVTQSPYSY	IWSNDTGPEL	VNGPSRKSMY
Sup146 Sh133	GIQYSWLWKL	ANVTQSPYSY	IWSNDTGPEL	VNGPSRKSMY
Sup84	GIQYSWLWKL	ANVTQSPYSY	IWSNDTGPEL	VNGPSRKSMY
para63	G~~~~~	~~~~~	~~~~~	~~~~~

	450	460	470	480
	.... ....	.... ....	.... ....	.... ....
consensus	VTALYFTMTC	MTSVGFGNVA	AETDNEKVFT	ICMMIIAALL
para141f	VTALYFTMTC	MTSVGFGNVA	AETDNEKVFT	ICMMIIAALL
Sup39 Sh133	VTALYFTMTC	MTSVGFGNVA	AETDNEKVFT	ICMMIIAALL
Sup146 Sh133	VTALYFTMTC	MTSVGFGNVA	AETDNEKVFT	ICMMIIAALL
Sup84	VTALYFTMTC	MTSVGFGNVA	AETDNEKVFT	ICMMIIAALL
para63	~~~~~	~~~~~	~~~~~	~~~~~

	490	500	510	520
	.... ....	.... ....	.... ....	.... ....
consensus	YATIFGHVTT	IIQQMTSATA	KYHDMLENNVR	EFMKLHEVVK
para141f	YATIFGHVTT	IIQQMTSATA	KYHDMLENNVR	EFMKLHEVVK
Sup39 Sh133	YATIFGHVTT	IIQQMTSATA	KYHDMLENNVR	EFMKLHEVVK
Sup146 Sh133	YATIFGHVTT	IIQQMTSATA	KYHDMLENNVR	EFMKLHEVVK
Sup84	YATIFGHVTT	IIQQMTSATA	KYHDMLENNVR	EFMKLHEVVK
para63	~~~~~	~~~~~	~~~~~	~~~~~

	530	540	550	560
	.... ....	.... ....	.... ....	.... ....
consensus	ALSERVMDYV	VSTWAMTKGL	DTEKVLNYCP	KDMKADICVH
para141f	ALSERVMDYV	VSTWAMTKGL	DTEKVLNYCP	KDMKADICVH
Sup39 Sh133	ALSERVMDYV	VSTWAMTKGL	DTEKVLNYCP	KDMKADICVH
Sup146 Sh133	ALSERVMDYV	VSTWAMTKGL	DTEKVLNYCP	KDMKADICVH
Sup84	ALSERVMDYV	VSTWAMTKGL	DTEKVLNYCP	KDMKADICVH
para63	~~~~~	~~~~~	~~~~~	~~~~ADICVH

	570	580	590	600
	.... ....	.... ....	.... ....	.... ....
consensus	LNRKVFNEHP	AFRLASDGCL	RALAMHFMMS	HSAPGDLLYH
para141f	LNRKVFNEHP	AFRLASDGCL	RALAMHFMMS	HSAPGDLLYH
Sup39 Sh133	LNRKVFNEHP	AFRLASDGCL	RALAMHFMMS	HSAPGDLLYH
Sup146 Sh133	LNRKVFNEHP	AFRLASDGCL	RALAMHFMMS	HSAPGDLLYH
Sup84	LNRKVFNEHP	AFRLASDGCL	RALAMHFMMS	HSAPGDLLYH
para63	LNRKVFNEHP	AFRLASDGCL	RALAMHFMMS	HSAPGDLLYH

	610	620	630	640
	.... ....	.... ....	.... ....	.... ....
consensus	TGESIDSLCF	IVTGSLEVIQ	DDEVVAILGK	GDVFGDQFWK
para141f	TGESIDSLCF	IVTGSLEVIQ	DDEVVAILGK	GDVFGDQFWK
Sup39 Sh133	TGESIDSLCF	IVTGSLEVIQ	DDEVVAILGK	GDVFGDQFWK
Sup146 Sh133	TGESIDSLCF	IVTGSLEVIQ	DDEVVAILGK	GDVFGDQFWK
Sup84	TGESIDSLCF	IVTGSLEVIQ	DDEVVAILGK	GDVFGDQFWK
para63	TGESIDSLCF	IVTGSLEVIQ	DDEVVAIL~	~~~~~

	650	660	670	680
	.... ....	.... ....	.... ....	.... ....
consensus	DSAVGQSAAN	VRALTYCDLH	AIKRDKLLEV	LDFYSAFANS
para141f	DSAVGQSAAN	VRALTYCDLH	AIKRDKLLEV	LDFYSAFANS
Sup39 Sh133	DSAVGQSAAN	VRALTYCDLH	AIKRDKLLEV	LDFYSAFANS
Sup146 Sh133	DSAVGQSAAN	VRALTYCDLH	AIKRDKLLEV	LDFYSAFANS
Sup84	DSAVGQSAAN	VRALTYCDLH	AIKRDKLLEV	LDFYSAFANS
para63	DSAVGQSAXN	VRALTYCDLH	AIKRDKLLEV	LDFYSAFANS

		690	700	710	720
		.... ....	.... ....	.... ....	.... ....
consensus		FARNLVLTYN	LRHRLIFRKV	ADVCREKELA	ERRKNPQLP
para141f		FARNLVLTYN	LRHRLIFRKV	ADVCREKELA	ERRKNPQLP
Sup39 Sh133		FARNLVLTYN	LRHRLIFRKV	ADVCREKELA	ERRKNPQLP
Sup146 Sh133		FARNLVLTYN	LRHRLIFRKV	ADVCREKELA	ERRKNPQLP
Sup84		FARNLVLTYN	LRHRLIFRKV	ADVCREKELA	ERRKNPQLP
para63		FARNLVLTYN	LRHRLIFRKV	ADVCREKELA	ERRKNPQLP
		730	740	750	760
		.... ....	.... ....	.... ....	.... ....
consensus		QNQDHLVRKI	FSKFR RTPQV	QAGSKELVGG	SGQSDVEKGD
para141f		QNQDHLVRKI	FSKFR RTPQV	QAGSKELVGG	SGQSDVEKGD
Sup39 Sh133		QNQDHLVRKI	FSKFR RTPQV	QAGSKELVGG	SGQSDVEKGD
Sup146 Sh133		QNQDHLVRKI	FSKFR RTPQV	QAGSKELVGG	SGQSDVEKGD
Sup84		QNQDHLVRKI	FSKFR RTPQV	QAGSKELVGG	SGQSDVEKGD
para63		QNQDHLVRKI	FSKFR RTPQV	QAGSKELVGG	SGQSDVEKGD
		770	780	790	800
		.... ....	.... ....	.... ....	.... ....
consensus		GEVERTKVFP	KAPKLQASQA	TLARQDTIDE	GGEVDSSPPS
para141f		GEVERTKVFP	KAPKLQASQA	TLARQDTIDE	GGEVDSSPPS
Sup39 Sh133		GEVERTKVFP	KAPKLQASQA	TLARQDTIDE	GGEVDSSPPS
Sup146 Sh133		GEVERTKVFP	KAPKLQASQA	TLARQDTIDE	GGEVDSSPPS
Sup84		GEVERTKVFP	KAPKLQASQA	TLARQDTIDE	GGEVDSSPPS
para63		GEVERTK~P	KAPKLQASQA	TLARQDTIDE	GGEVDSSPPS
		810	820	830	840
		.... ....	.... ....	.... ....	.... ....
consensus		RDSRVVIEGA	AVSSATVGPS	PPVATTSSAA	AGAGVSGGPG
para141f		RDSRVVIEGA	AVSSATVGPS	PPVATTSSAA	AGAGVSGGPG
Sup39 Sh133		RDSRVVIEGA	AVSSATVGPS	PPVATTSSAA	AGAGVSGGPG
Sup146 Sh133		RDSRVVIEGA	AVSSATVGPS	PPVATTSSAA	AGAGVSGGPG
Sup84		RDSRVVIEGA	AVSSATVGPS	PPVATTSSAA	AGAGVSGGPG
para63		RDSRVVIEGA	AVSSATVGPS	PPVATTSSAA	AGAGVSGGPG
		850	860	870	880
		.... ....	.... ....	.... ....	.... ....
consensus		SGGTVVAIVT	KADRNLALER	ERQIEMASSR	ATTSDTYDTG
para141f		SGGTVVAIVT	KADRNLALER	ERQIEMASSR	ATTSDTYDTG
Sup39 Sh133		SGGTVVAIVT	KADRNLALER	ERQIEMASSR	ATTSDTYDTG
Sup146 Sh133		SGGTVVAIVT	KADRNLALER	ERQIEMASSR	ATTSDTYDTG
Sup84		SGGTVVAIVT	KADRNLALER	ERQIEMASSR	ATTSDTYDTG
para63		SGGTVVAIVT	KADRNLALER	ERQIEMASSR	ATTSDTYDTG
		890	900	910	920
		.... ....	.... ....	.... ....	.... ....
consensus		LRETPPTLAQ	RDLIATVLDM	KVDVRLELQR	MQQRIGRIED
para141f		LRETPPTLAQ	RDLIATVLDM	KVDVRLELQR	MQQRIGRIED
Sup39 Sh133		LRETPPTLAQ	RDLIATVLDM	KVDVRLELQR	MQQRIGRIED
Sup146 Sh133		LRETPPTLAQ	RDLIATVLDM	KVDVRLELQR	MQQRIGRIED
Sup84		LRETPPTLAQ	RDLIATVLDM	KVDVRLELQR	MQQRIGRIED
para63		LRETPPTLAQ	RDLIATVLDM	KVDVRLELQR	MQQRIGRIED

		930	940	950	960
		.... ....	.... ....	.... ....	.... ....
consensus		LLGELVKRLA	PGAGSGGNAP	DNSSGQTTPG	DEICAGCGAG
para141f		LLGELVKRLA	PGAGSGGNAP	DNSSGQTTPG	DEICAGCGAG
Sup39 Sh133		LLGELVKRLA	PGAGSGGNAP	DNSSGQTTPG	DEICAGCGAG
Sup146 Sh133		LLGELVKRLA	PGAGSGGNAP	DNSSGQTTPG	DEICAGCGAG
Sup84		LLGELVKRLA	PGAGSGGNAP	DNSSGQTTPG	DEICAGCGAG
para63		LLGELVKRLA	PGAGSGGNAP	DNSSGXTXPG	DXICAGCGAG
		970	980	990	1000
		.... ....	.... ....	.... ....	.... ....
consensus		GGGTPTTQAP	PTSAVTSPVD	TVITISSPGA	SGSGSGTGAG
para141f		GGGTPTTQAP	PTSAVTSPVD	TVITISSQGT	SGSGSGTGAG
Sup39 Sh133		GGGTPTTQAP	PTSAVTSPVD	TVITISSPGA	SGSGSGTGAG
Sup146 Sh133		GGGTPTTQAP	PTSAVTSPVD	TVITISSPGA	SGSGSGTGAG
Sup84		GGGTPTTQAP	PTSAVTSPVD	TVITISSPGA	SGSGSGTGAG
para63		GGGTPTTXAP	PTSAVTSPVD	TVITISSPGA	SGSGSGTGAG
		1010	1020	1030	1040
		.... ....	.... ....	.... ....	.... ....
consensus		AGSAVAGAGG	AGLLNPGATV	VSSAGGNGLG	PLMLKKRRSK
para141f		AGSAVAGAGG	AGLLNPGATV	VSSAGGNGLG	PLMLKKRRSK
Sup39 Sh133		AGSAVAGAGG	AGLLNPGATV	VSSAGGNGLG	PLMLKKRRSK
Sup146 Sh133		AGSAVAGAGG	AGLLNPGATV	VSSAGGNGLG	PLMLKKRRSK
Sup84		AGSAVAGAGG	AGLLNPGATV	VSSAGGNGLG	PLMLKKRRSK
para63		AGSAVAGAGG	AGLLNPGATV	VSSAGGNGLG	PLMLKKRRSK
		1050	1060	1070	1080
		.... ....	.... ....	.... ....	.... ....
consensus		SRKAPAPPKQ	TLASTAGTAT	AAPAGVAGSG	MTSSAPASAD
para141f		SRKAPAPPKQ	TLASTAGTAT	AAPAGVAGSG	MTSSAPASAD
Sup39 Sh133		SRKAPAPPKQ	TLASTAGTAT	AAPAGVAGSG	MTSSAPASAD
Sup146 Sh133		SRKAPAPPKQ	TLASTAGTAT	AAPAGVAGSG	MTSSAPASAD
Sup84		SRKAPAPPKQ	TLASTAGTAT	AAPAGVAGSG	MTSSAPASAD
para63		SRKAPAPPKQ	TLASTAGTAT	AAPAGVAGSG	MTSSAPASAD
		1090	1100	1110	1120
		.... ....	.... ....	.... ....	.... ....
consensus		QQQQHQSTAD	QSPTTPGAEL	LHLRLLEEDF	TAAQLPSTSS
para141f		QQQQHQSAAD	QSPTTPGAEL	LHLRLLEEDF	TAAQLPSTSS
Sup39 Sh133		QQQQHQSAAD	QSPTTPGAEL	LHLRLLEEDF	TAAQLPSTSS
Sup146 Sh133		QQQQHQSTAD	QSPTTPGAEL	LHLRLLEEDF	TAAQLPSTSS
Sup84		QQQQHQSAAD	QSPTTPGAEL	LHLRLLEEDF	TAAQLPSTSS
para63		QQQQHQSAAD	QSPTTPGAEL	LHLRLLEEDF	TAAQLPSTSS
		1130	1140	1150	1160
		.... ....	.... ....	.... ....	.... ....
consensus		GGAGGGGGSG	SGATPTTPPP	TIAGGSGSGT	PTSTTATTTT
para141f		GGAGGGGGSG	SGATPTTPPP	TIAGGSGSGT	PTSTTATTTT
Sup39 Sh133		GGAGGGGGSG	SGATPTTPPP	TIAGGSGSGT	PTSTTATTTT
Sup146 Sh133		GGAGGGGGSG	SGATPTTPPP	TIAGGSGSGT	PTSTTATTTT
Sup84		GGAGGGGGSG	SGATPTTPPP	TIAGGSGSGT	PTSTTATTTT
para63		GGAGGGGGSG	SGATPTTPPP	TIAGGSGSGT	PTTPQPXHPT

	1170	1180	1190	1200
consensus	.... ....	.... ....	.... ....	.... ....
para141f	TGSGTATRGK	LDFL		
Sup39 Sh133	TGSGTATRGK	LDFL*PTTIG	KERRGEGDTS	SSEQ*YKNWG
Sup146 Sh133	TGSGTATRGK	LDFL*PTTIG	KERRGEGDTS	SSEQ*YKNWG
Sup84	TGSGTATRGK	LDFL*PTTIG	KERRGEGDTS	SSEQ*YKNWG
para63	GSG			

	1210	1220	1230	1240
consensus	.... ....	.... ....	.... ....	.... ....
para141f	K*GPSHAHSQ	AYAYA*LVYI	LKIQL*PQLD	TETRSSISNT
Sup39 Sh133	K*GPSHAHSQ	AYXYA*LVYI	LKIQL*PQLD	TETRSSISNT
Sup146 Sh133	K*GPXHAHSQ	AYAYA*LVYI	LKIQL*PQLD	TETXSSISNT
Sup84	K*GPSHAHSQ	AYAYA*LVYI	LKIQL*PQLD	TETRSSISNT
para63				

	1250	1260	1270	1280
consensus	.... ....	.... ....	.... ....	.... ....
para141f	LKVHCNVFIR	R*RKAFRKKI	V*KRF*KSDF	*KFKSRVQRE
Sup39 Sh133	LKVHCNVFIR	R*RKAFRKKI	V*KRF*KSDF	*KFKSRVQRE
Sup146 Sh133	LKVHCNVFIR	R*RKAFRKKI	V*KRF*KXDF	*KFISRVQRE
Sup84	LKVHCNVFIR	R*RKAFRKKI	V*KRF*KSDF	*KFKSRVQRE
para63				

	1290	1300	1310	1320
consensus	.... ....	.... ....	.... ....	.... ....
para141f	TFKYS*YGTQ	SI*DCN*LKI	MN*YLI*RLE	NMNIIYLHLS
Sup39 Sh133	TFKYS*YGTQ	SI*DCN*LKI	MN*YLI*RLE	NMNIIYLHLS
Sup146 Sh133	TFKYS*YGTQ	SI*DCN*LKI	MN*YLI*RLE	NMNIIYLHLS
Sup84	TFKYS*YGTQ	SI*DCN*LKI	MN*YLI*RLE	NMNIIYLHLS
para63				

	1330	1340	1350	1360
consensus	.... ....	.... ....	.... ....	.... ....
para141f	SIQILFS*YL	*ALW*YS*YL	YITNN*FMIF	FKGKRLLLSF
Sup39 Sh133	SIQILFS*YL	*ALW*YS*YL	YITNN*FMIF	FKGKRLLLSF
Sup146 Sh133	SIQILFS*YL	*ALW*YS*YL	YITNN*FMIF	FKGKRLLLSF
Sup84	SIQILFS*YL	*ALW*YS*YL	YITNN*FMIF	FKGKRLLLSF
para63				

	1370
consensus	.... ....
para141f	VSLNH
Sup39 Sh133	VSLNH
Sup146 Sh133	VSLNH
Sup84	VSLNH
para63	

### 7.3 Amino acid alignment of Dm-Eag, Dp-Eag, M-Eag, R-EAG1, B-EAG, Ag-Eag, H-Erg and Elk

Amino acid sequence alignment Dm-Eag, *Drosophila melanogaster* (WARMKE *et al.* 1991); Dp-Eag, *Drosophila pseudobscura* (RICHARDS *et al.* 2005); M-Eag, Mouse (WARMKE and GANETZKY 1994); R-EAG1 (LUDWIG *et al.* 1994), Rat; B-EAG, *Bos Taurus* (Bovine) (FRINGS *et al.* 1998); Ag-Eag, *Anopheles gambiae* (mosquito) (MONGIN *et al.* 2004), H-Erg, Human Eag related gene (WARMKE and GANETZKY 1994); Elk, Human Eag like K<sup>+</sup> channel (WARMKE and GANETZKY 1994).

Dm-Eag	-----	--MPGGRRGL	VAPQNTFLEN	TIIRRSNSQPD	GSFLLANAQI
Dp-Eag	MSVSVSVSVS	MSMPCDASAW	FA-HVTCLOP	YNVER-V-PD	GSFLLANAQI
M-Eag	-----	MTMAGGRRGL	VAPQNTFLEN	IVRRSN----	TNEVLGNAQI
R-Eag1	-----	MTMAGGRRGL	VAPQNTFLEN	IVRRSN----	TNEVLGNAQI
B-Eag	-----	MTMAGGRRGL	VAPQNTFLEN	IVRRSN----	TNEVLGNAQI
Ag	-----	-----	-----	-----	-----
H-Erg	-----	--MP-VRRGH	VAPQNTFLDT	TIIRKFEGQSR	-KFLIANARV
Elk	-----	--MP-AR-GL	VAPQNTFLDT	TATKFDG-TH	SNEVLGNAQA
Dm-Eag	VDFTPIVYCNE	SFCKTSGYNR	AEVMQKSCRY	VCGFMYGELT	DKETVGRLEY
Dp-Eag	VDFTPIVYCNE	SFCKTSGYNR	AEVMQKSCR-	-CGFMYGELT	DKETVGRLEY
M-Eag	VDWPTVYSND	GFCKTSGYHR	AEVMQKSS--	ACSEFMYGELT	DKDTVEKVRQ
R-Eag1	VDWPTVYSND	GFCKTSGYHR	AEVMQKSSA-	-CSEFMYGELT	DKDTVEKVRQ
B-Eag	VDWPTVYSND	GFCKLSGYHR	AEVMQKSS--	TUSEFMYGELT	DKDTTEKVRQ
Ag	-----	-----	-----	-----	-----
H-Erg	ENCAVTYCND	GFCELCGYSR	AEVMORPC--	TODELHGPRP	QRRAAAQIAQ
Elk	NGNPPIVYCS	GFVDLTGYSR	AQIMQKGC--	SCHFLYGPDT	KELEHKQOIER
Dm-Eag	TLENQQQDQF	EILLYKKNNL	QCGCALSQFG	KAQTQETPLW	LLLOVAPTRN
Dp-Eag	TLENQQQDQF	EILLYKKNNV	QCGCALSQFG	KAQTQETPLW	LLLOVAPTRN
M-Eag	TFENYEMNSF	EILMYKKNR-	-----	TPVW	FFVKIAPTRN
R-Eag1	TFENYEMNSF	EILMYKKNR	-----	TPVW	FFVKIAPTRN
B-Eag	TFENYEMNSF	EILMYKKNR	-----	TPVW	FFVKIAPTRN
Ag	-----	-----	-----	-----	-----
H-Erg	ALLGAFERKV	ETAFYRND--	-----	-----GSCFL	CLVDVVLVKN
Elk	SLSNKMELKL	EVTFYKKE--	-----	-----GAPFW	CLFDIVPIKN
Dm-Eag	ERDLVVLFL	TERDITALK-	-----	-----	-----
Dp-Eag	ERDLVVLFL	TERDITALK-	-----	-----	-----
M-Eag	EQDKVVLFLC	TFSDITAFK-	-----	-----	-----
R-Eag1	EQDKVVLFLC	TFSDITAFK-	-----	-----	-----
B-Eag	EQDKVVLFLC	TFSDITAFK-	-----	-----	-----
Ag	-----	-----	-----	-----	-----
H-Erg	EDGAVIMFIL	NIEVVMKEDM	VGSPAHD TNH	RGPPTSWLAP	GRAKTFRLKL
Elk	EKRDVVLFLA	SHKDIHTTSM	LEMNVN EEC	-----	-----

Dm-Eag	-----	QPI DSEDT	KG-----V	-----	-----L
Dp-Eag	-----	QPI DSEDT	KCAVNLFPLV	-----	-----L
M-Eag	-----	QPIEDDSC	K-----	-----	-----
R-Eag1	-----	QPIEDDSC	K-----	-----	-----
B-Eag	-----	QPIEDDSC	K-----	-----	-----
Ag	-----	-----	-----	-----	-----
H-Erg	PALLALTARE	SSVRS GGAGG	AG-----A	PGAVVVDVDL	TPAAPSSSESI
Elk	-SVFALTAAL	LGARFRAGSN	AGM-----	-----	-----L
Dm-Eag	GLSKFAKLAR	SVT-----	-----	-----	-----
Dp-Eag	GLSKFAKLAR	SVT-----	-----	-----	-----
M-Eag	GWGKFARLTR	ALT-----	-----	-----	-----
R-Eag1	GWGKFARLTR	ALT-----	-----	-----	-----
B-Eag	GWGKFARLTR	ALT-----	-----	-----	-----
Ag	-----	-----	-----	-----	-----
H-Erg	AIDEVTAMDN	HVAGLGPAEE	RRALVGP GSP	PRSAPGQLPS	PRAHSLNPDA
Elk	GTGGLPGIGG	PAASDGDTE-	-----	-----	--AGEGNNLD
Dm-Eag	-----	RSR-----	-----	-----	-----
Dp-Eag	-----	RSR-----	-----	-----	-----
M-Eag	-----	SSR-----	-----	-----	-----
R-Eag1	-----	SSR-----	-----	-----	-----
B-Eag	-----	SSR-----	-----	-----	-----
Ag	-----	-----	-----	-----	-----
H-Erg	SGSSCSLART	RSRESCASVR	RASSADDIEA	MRAGVLPPPP	RHASTGAMHP
Elk	VPAGCNMGRR	RSR-----	-----	-----	-----
Dm-Eag	-----	-----	QFSAHL	PTLKD-----	-----
Dp-Eag	-----	-----	QFSAHL	PTLKD-----	-----
M-Eag	-----	-----	GVLQQLAPSV	QKGEN-----	-----
R-Eag1	-----	-----	GVLQQLAPSV	QKGEN-----	-----
B-Eag	-----	-----	GVLQQLAPSV	QKGEN-----	-----
Ag	-----	-----	-----	-----	-----
H-Erg	LRSGLLNSTS	DSDLVRYRTI	SKLPQTLNLF	VDLRGDPFLA	SPTSDREIIA
Elk	-----	-----	AVLYQLSGHY	KPEKG-----	-----
Dm-Eag	-----PTKQ	S-NLAHVMMSL	SADI-MPQYR	QEAPKTPPHI	LLHYCAFKAI
Dp-Eag	-----PTKQ	S-NLAHVMMSL	SADI-MPQYR	QEAPKTPPHI	LLHYCAFKAI
M-Eag	-----VHKH	S-RLAEVLQL	GSDI-LPQYK	QEAPKTPPHI	LLHYCVFKTT
R-Eag1	-----VHKH	S-RLAEVLQL	GSDI-LPQYK	QEAPKTPPHI	LLHYCVFKTT
B-Eag	-----VHKH	S-RLAEVLQL	GSDI-LPQYK	QEAPKTPPHI	LLHYCVFKTT
Ag	-----	-----	-----	-----	-----
H-Erg	PKIKERTINV	TEKVTQVLSI	GADV-LPEYK	LCAPRIHRWT	LLHYSPFKAV
Elk	-----GVNT	KLKLGNNFMH	STEAPFTEYK	TQSIKKSRLI	LLHYGVFKGI
Dm-Eag	WDWVILCLTF	YTAIMVPYNV	AFKNKTSFDV	-----	-SLLVVDSTV
Dp-Eag	WDWVILCLTF	YTAIMVPYNV	AFKNKTSFDV	-----	-SLLVVDSTV
M-Eag	WDWILILITF	YTAIVVPYNV	SEKTR-QNNV	-----	-AWLVVDSTV
R-Eag1	WDWILILITF	YTAIVVPYNV	SEKTR-QNNV	-----	-AWLVVDSTV
B-Eag	WDWILILITF	YTAIVVPYNV	SEKTR-QNNV	-----	-AWLVVDSTV
Ag	-----	-----	-----	-----	-----
H-Erg	WDWILILIVI	YTAVFTTYSA	AFLLKETE EG	PPATECGYAC	QPLAVVDLIV
Elk	WDWVILVAPF	YVALMVPYNA	AFKADROTK	-----	---VSDVIV

Dm-Eag	DVIFFDIVL	NEHTTFVGP	GEVVSDFKVI	RMNYLKSWFI	IDLLSCLPYD
Dp-Eag	DVIFFDIVL	NEHTTFVGP	GEVVSDFKVI	RMNYLKSWFI	IDLLSCLPYD
M-Eag	DVIFFDIVL	NEHTTFVGP	GEVVSDFKLI	RMNYLKTWFI	IDLLSCLPYD
R-Eag1	DVIFFDIVL	NEHTTFVGP	GEVVSDFKLI	RMNYLKTWFI	IDLLSCLPYD
B-Eag	DVIFFDIVL	NEHTTFVGP	GEVVSDFKLI	RMNYLKTWFI	IDLLSCLPYD
Ag	--LFFLLAVI	NEHTTFVGP	GEVVSDFKVI	RMNYLKSWFI	IDLLSCLPYD
H-Erg	DIMFIVDILI	NFRTTYVNAN	EEVVSHEGR	AVHYFKGWFI	IDMVAATPFD
Elk	EALFIVDILI	NFRTTFVSRK	GEVVSNSKQI	AINYIRGWFI	LDLHAALIFD
Dm-Eag	VFNADF----	-----	-----	---RDEGIG	SLESAIKVVR
Dp-Eag	VFNADF----	-----	-----	---RDEGIG	SLESAIKVVR
M-Eag	VINAFENVDE	VSAFMGDPGK	IGFADQIPPP	LEGRESQGIS	SLESSIKVVR
R-Eag1	VINAFENVDE	-----	-----	-----GIS	SLESSIKVVR
B-Eag	VINAFENVDE	VSAFMGDPGK	IGFADQIPPP	LEGRESQGIS	SLESSIKVVR
Ag	VFNADF----	-----	-----	---HDEDVN	-----
H-Erg	LLIF-----	-----	-----	---GSCSE	ELIGLIKTKAR
Elk	HLIASILY--	-----	-----	---DCED	SHIHLVKLTR
Dm-Eag	LLRLGRVVRK	LDRYLEYGAA	MLILILCFYM	LVAHWLACIW	YSIG-----R
Dp-Eag	LLRLGRVVRK	LDRYLEYGAA	MLILILCFYM	LVAHWLACTW	YSIG-----R
M-Eag	LLRLGRVVRK	LDHYLEYGAA	VLVLVCFVFC	LAHWMACIW	YSIGDYEIFD
R-Eag1	LLRLGRVVRK	LDHYLEYGAA	VLVLVCFVFC	LAHWMACIW	YSIGDYEIFD
B-Eag	LLRLGRVVRK	LDHYLEYGAA	VLVLVCFVFC	LAHWMACIW	YSIGDYEIFD
Ag	-----	-----	-----	-----	-----
H-Erg	LLRLGRVVRK	LDRYSEYGAA	VLFLIMCTFA	LVAHWLACIW	YALGNMEQPH
Elk	LLRLARLLQK	LDRYSOHTAM	ILTLIMFSFT	LAHWLACIW	YVIAVKIYEW
Dm-Eag	SDADNGIQYS	WIKLANVTQ	SPYSYIWSND	TGPELVNGPS	RKSMYVTALY
Dp-Eag	SDADNGIQYS	WIKLANVTQ	SPYSYIWSND	TGPELVNGPS	RKSMYVTALY
M-Eag	EDTKTIRNNS	WLYQLALDIG	TPYQF--NGS	GSCKWEGGPS	KNSVYISSLY
R-Eag1	EDTKTIRNNS	WLYQLALDIG	TPYQF--NGS	GSCKWEGGPS	KNSVYISSLY
B-Eag	EDTKTIRNNS	WLYQLALDIG	TPYQF--NGS	GSCKWEGGPS	KNSVYISSLY
Ag	-----	-----	-----	-----	-----
H-Erg	MDSR-----IG	WIHNLGDQIG	KPYN-----	--SSGLGGPS	IKDKYVTALY
Elk	FPESN1---G	WLQLLAERKN	ASVAILTAE	T-----	---YSTALY
Dm-Eag	FTMTCTMTSVG	FGNVAAETDN	EKVFTICMMI	IAALLYATIF	GNVTTTFQOM
Dp-Eag	FTMTCTMTSVG	FGNVAAETDN	EKVFTICMMI	IAALLYATIF	GNVTTTFQOM
M-Eag	FTMTSLTSVG	FGNIAPSTDI	EKIFAVAIMM	IGSLLYATIF	GNVTTTFQOM
R-Eag1	FTMTSLTSVG	FGNIAPSTDI	EKIFAVAIMM	IGSLLYATIF	GNVTTTFQOM
B-Eag	FTMTSLTSVG	FGNIAPSTDI	EKIFAVAIMM	IGSLLYATIF	GNVTTTFQOM
Ag	-----	-----	-----	-----	-----
H-Erg	FTFSSILTSVG	FGNVSNITNS	EKIFSIQVME	IGSLMYASIF	GNVSAITQRL
Elk	FTFSSILTSVG	FGNVSANITA	EKVFTIIMMI	IGALMHAVVF	GNVTATTORM
Dm-Eag	TSATAPKYHDM	LNNVREFMKT	HEVPKALSER	VMDYVSTWA	MSRGIDTEKV
Dp-Eag	TSATAPKYHDM	LNNVREFMKT	HEVPKALSER	VMDYVSTWA	MSRGIDTEKV
M-Eag	YANTNRYHEM	LNSVRDFLKL	YQVPKGLSER	VMDYVSTWS	MSRGIDTEKV
R-Eag1	YANTNRYHEM	LNSVRDFLKL	YQVPKGLSER	VMDYVSTWS	MSRGIDTEKV
B-Eag	YANTNRYHEM	LNSVRDFLKL	YQVPKGLSER	VMDYVSTWS	MSRGIDTEKV
Ag	-----	-----	-----	-----	-----
H-Erg	YSGTARYITQ	MLRVREFIRF	HOIINPLROR	LEEFQHAWW	YINCHDMNAV
Elk	YSRRSLYESK	WRDLKDFVAL	INMIREIKOR	IEDYFQTSW	LEHGIDDIYET

Dm-Eag	LNYCPKDMKA	DTCVHLNRKV	FNEHPAFRLA	SDGCLRALAM	HEMMSHSAPG
Dp-Eag	LNYCPKDMKA	DTCVHLNRKV	FNEHPAFRLA	SDGCLRALAM	HEMMSHSAPG
M-Eag	LQICPKDMRA	DTCVHLNRKV	FKEHPAFRLA	SDGCLRALAM	EFQTVHCAPG
R-Eag1	LQICPKDMRA	DTCVHLNRKV	FKEHPAFRLA	SDGCLRALAM	EFQTVHCAPG
B-Eag	LQICPKDMRA	DTCVHLNRKV	FKEHPAFRLA	SDGCLRALAM	EFQTVHCAPG
Ag					
H-Erg	LKGFPECLQA	DICLHLNRSL	LQHCKPFRGA	TKGCLRALAM	KFKITHAPPG
Elk	LREFPEELRG	DVSMITHREI	L-QLPIFEAA	SGGCKLISL	LIKTNFCAPG
Dm-Eag	DLLYHTGESI	DSLCFIVTGS	LEVIQDDEVV	ATLGKGDVFG	DQFW-----
Dp-Eag	DLLYHTGESI	DSLCFIVTGS	LEVIQDDEVV	ATLGKGDVFG	DQFW-----
M-Eag	DLLYHAGESV	DSLCFVVSGS	LEVIQDDEVV	ATLGKGDVFG	DVFW-----
R-Eag1	DLLYHAGESV	DSLCFVVSGS	LEVIQDDEVV	ATLGKGDVFG	DVFW-----
B-Eag	DLLYHAGESV	DSLCFVVSGS	LEVIQDDEVV	ATLGKGDVFG	DVFW-----
Ag					
H-Erg	DTLVHAGDLL	TALYFISRG	IFILRGDVVV	ATLGKNDLFG	EPLNLY----
Elk	EYLIHKGDAL	NYIYYLCNGS	MEVIKDDMVV	ATLGKGDVFG	SDINVHLVAT
Dm-Eag	-----	--KDSAVGQS	AANVRALTYC	DLHAIKRDKI	LEVLDIFYSAF
Dp-Eag	-----	--KDSAVGQS	AANVRALTYC	DLHAIKRDKI	LEVLDIFYSAF
M-Eag	-----	--KEATLAQS	CANVRALTYC	DLHVIKRDAL	QKVLEFYTAI
R-Eag1	-----	--KEATLAQS	CANVRALTYC	DLHVIKRDAL	QKVLEFYTAI
B-Eag	-----	--KEATLAQS	CANVRALTYC	DLHVIKRDAL	QKVLEFYTAI
Ag					
H-Erg	-----	---ARPCKE	NGDVRALTYC	DLIKTHRDIL	LEVLDIMYPEI
Elk	SNGQMTATTN	SAGQDVVVR	SSDIKALTYC	DLKCIHMGGL	MEVIRLYPEY
Dm-Eag	ANSFARNL--	VLTYNLRH--	-----R	LIFRKVADV	REKELAE--
Dp-Eag	ANSFARNL--	VLTYNLRH--	-----R	LIFRKVADV	REKELAE--
M-Eag	SHSFSRNL--	LLTYNLRK--	-----R	IVFRKISDV	REEFERMK--
R-Eag1	SHSFSRNL--	LLTYNLRK--	-----R	IVFRKISDV	REEFERMK--
B-Eag	SHSFSRNL--	LLTYNLRK--	-----R	IVFRKISDV	REEFERMK--
Ag					
H-Erg	NDHWSSELE	LTENLRDTE	-NMIPGSPGS	TELEGGFSRQ	RKRKLSFRRR
Elk	QQQFANDIQH	DLTCNLREGY	ENQSDIGPS	FPLPSISEDD	ENREEALEGG
Dm-Eag	--RKNEPOLP	QNQDHLVRKI	FSKFRRTPOV	QAGSKELV--	G--SGQSDVE
Dp-Eag	--RKNEPOLP	QNQDHLVRKI	FSKFRRTPOV	QAGSKDLVGG	GT--SGQSDVE
M-Eag	--RKNEAPLI	LPPDHPVRR	FORFRQOKEA	RLAAERGG--	R-DLDDLDVE
R-Eag1	--RKNEAPLI	LPPDHPVRR	FORFRQOKEA	RLAAERGG--	R-DLDDLDVE
B-Eag	--RKNEAPLI	LPPDHPVRR	FORFRQOKEA	RLAAERGG--	R-DLDDLDVE
Ag					
H-Erg	TDKDTEQFGE	VSALGPGRAG	AGPSSNGRPG	GPWGSPS--	S--PSSPESP
Elk	KGEKENGGGP	PSGASPLHNI	SNSPLHATRS	PLGGMGSP--	R-NQRLHQRG
Dm-Eag	KGDGEYERIK	-V---FPAKAP	KL-----	-----QAS	QAILARQDTI
Dp-Eag	KGDGEYERVK	SL---YPAKKI	LI-----	-----QAS	QAILARQDTI
M-Eag	KGNALTDHTS	-ANHSIVKAS	VVTVRESPTAT	PVST--QAAT	TSIMSDIAKI
R-Eag1	KGNALTDHTS	-ANHSIVKAS	VVTVRESPTAT	PVST--QAAT	TSIMSDIAKI
B-Eag	KGSVITFHS-	--HIGLAKAS	VVTVRESPTAT	PVAI--PAAA	APAGLDIARI
Ag					
H-Erg	EDEGPRSSSS	P-LRLVDFSS	PRPPGEPTGG	EPLMEDCEKS	SDICNPLSGA
Elk	RSLITLREIN	-KRIRTLNAA	CSLDNGSFEE	PEPLEEES	GKRPSSLERL

Dm-Eag	DEGG-----	-EVDSSPPSR	DSRVV-----	EGAA-----	--VSSATVGP
Dp-Eag	DEGG-----	-EVDSSPPSR	DSRIV-----	D-----	-----
M-Eag	HAPGSECLGP	KAVSCDPAKR	KGWAK-----	KDACCKGEDW	NKVSKAESME
R-Eag1	HAPGSECLGP	KAGGGDPAKR	KGWAK-----	KDACCKGEDW	NKVSKAESME
B-Eag	QAPGATGLGP	KAGGADCAKR	KGWAK-----	KDACGQAEIW	SKVSKAESME
Ag					
H-Erg	FSQVSNIF--	-----SFWG	DSRGRQYQEL	PRCPAPTSL	LNIPPLSSPGR
Elk	DSQVSTLHQD	VAQLAEVRN	AISALQEMT	TSNAMTSHSS	LKFPPARSIP
Dm-Eag	SPI-VAITSS	AAAGAGVSGG	PGSGGTVAI	VTKADRNIAL	ERERQIEMAS
Dp-Eag	-----	-----	---CGAAS--	-TTGERNLAL	ERERQIEMAS
M-Eag	TLP-ERTKAP	GEATLKKTDS	CDSG-----	ITKSDLRLD	-----NVGETR
R-Eag1	TLP-ERTKAS	GEATLKKTDS	CDSG-----	ITKSDLRLD	-----NVGEAR
B-Eag	TLP-ERTKAA	GEATLKKTDS	CDSG-----	ITKSDLRLD	-----NVGEAR
Ag					
H-Erg	RPRGDVESRL	DALQRQLNRL	ETRLSADMAT	VLQLLQRQMT	LVPPPAYSAVT
Elk	NISGVAGTRR	GVAVEHGLMG	GVLAALAA	MQRSSSHPE	VWGRDVOLPT
Dm-Eag	SRATTSDTYD	TGLRETPPT-	-----	-----	AQRDLIATVL
Dp-Eag	SRATTSDTYD	TGLRETPPT-	-----	-----	AQRDLIATVL
M-Eag	SPQDRSPIL-	AEVKHSFYF-	-----	-----	PEQTLQATVL
R-Eag1	SPQDRSPIL-	AEVKHSFYF-	-----	-----	PEQTLQATVL
B-Eag	SPQDRSPILA	EVKHSFYF--	-----	-----	PEQTLQAAYL
Ag					
H-Erg	TTPGPGTSTS	PLLPVSTLPT	LTLDSLSQVS	QFMACEELPP	GAPELPQEGP
Elk	SNTASAKAPS	PVEPKKMTS	RSSQTDYRI	DFPTFERFVL	ANPRVLGLI
Dm-Eag	DMKVDVRLEI	ORMOOR----	-----	IGRIEDLLGE	LVKRLAP--G
Dp-Eag	DMKVDVRLEI	ORMOOR----	-----	IGRIEDLLGE	LVKRLGP---
M-Eag	EVKVELKEDI	KALNAK----	-----	MTSIEKQLSE	ILRLIMSRGS
R-Eag1	EVKVELKEDI	KALNAK----	-----	MTSIEKQLSE	ILRLIMSRGS
B-Eag	EVKVELKEDI	KALSTK----	-----	MTSIEKQLSE	ILRLITSRRS
Ag					
H-Erg	TRRLSLPGQI	GALTSOPLHR	HGSDPGS		
Elk	GIEPATKNFM	DLLOOKQTLQ	ISPLNTIDEC	VSPSDHNLAS	SKERLITSSA
Dm-Eag	AGSGG-----	-----	-----NAPDN	SSGOTTPGDE	ICAGC---G-
Dp-Eag	QD---G-----	-----	-----G-DN	SSGOTTPGDE	ICAGCGASGV
M-Eag	AQSPQ-----	-----	-----ETGLI	SRPQSPESDR	DIFGAS
R-Eag1	SQSPQ-----	-----	-----DTCEV	SRPQSPESDR	DIFGAS
B-Eag	SQSPQ-----	-----	-----ELFEI	SRPQSPESER	DIFGAS
Ag					
H-Erg					
Elk	VPTFCRIYPP	LDDENSNDFR	WTMKHSASHH	SCCKSTDALL	SPEEQ---P-
Dm-Eag	-A---GG--GG	TPTTQAPPTS	AV-----	---TSPVDTV	PTISSPGTSG
Dp-Eag	AAGPGAGPAP	GGPGIGTGTP	GPGTPTTPAT	VTVTTPVDTV	PTISSPTSA
M-Eag					
R-Eag1					
B-Eag					
Ag					
H-Erg					
Elk	-P---IS-IL	PVDATPAISV	QE-----	---VRSSKRS	IRKPTSGNS

Dm-Eag	SGSGT	GAGAG	SAVAGAGGA	LLNPGATVVS	SAGGNGLGPI	MLKKRRSKSR
Dp-Eag	AP-	GAGAGAG	S-----G	LLNPGVPVVS	SAGGNGLGPI	MLKKRRSKSR
M-Eag						
R-Eag1						
B-Eag						
Ag						
H-Erg						
Elk	SLSSSSSSSN	SCLVSQSTGN	ITTTN	ASVHC	SNSSQSVASV	ATTRASWKL

Dm-Eag	KAPAPPKQTL	A-STAGTATA	APAGVAGSGM	TSSAPASADQ	QQQHQSAAEQ
Dp-Eag	KAPAPPKQTL	ALAGAASTTT	TLT	AAGSG-	ITS-R-RFN
M-Eag					TA-APAAAR
R-Eag1					
B-Eag					
Ag					
H-Erg					
Elk	QHSRSGEYRR	L-SEATAEYS	PPA-----K	TPLPVAGVSY	GGDEEESVEL

Dm-Eag	SPTTPCAELL	HRLLEEDFT	AAQLPSTSSG	GAGGGGSGS	GATTTTPPT
Dp-Eag	GLYGPAAA	----LDTDSH	DPDIVGHAGG	QRHAGGQQR	SKGRQTGVPL
M-Eag					
R-Eag1					
B-Eag					
Ag					
H-Erg					
Elk	LPRRNSRPI	LGVSQNGQ	GQAMNFRFSA	GDADKLEKGL	RGLSTRSLR

Dm-Eag	IAGGS	GSGTP	TSTTATTTPT	GSG-TATRCK	LDFL-
Dp-Eag	AQDSVAASVE	GSGFGLSFGF	GFSEERGEHE	HGAIK	
M-Eag					
R-Eag1					
B-Eag					
Ag					
H-Erg					
Elk	DPSSK				

## **7.4 Control of perineural glial growth and neuronal excitability: axon-glia signalling**

Communication between the axon and the glia (or Schwann cell) has been studied in many systems other than *Drosophila*, such as squid, frog and crayfish. For example, in response to 100Hz stimulation of the squid giant axon, the surrounding Schwann cell exhibits a hyper-polarization of its membrane potential (VILLEGAS 1974).

Like the *Drosophila* motor axon, the squid giant axon is glutamatergic. A series of pharmacological experiments identified the mechanism that underlies the hyper-polarization. The principal components are acetylcholine (ACh), a neuropeptide related to VIP and PACAP, octopamine (a stress hormone) and the intracellular messengers IP<sub>3</sub>, PLC and cAMP, all of which are produced in the Schwann cell (EVANS *et al.* 1992a; EVANS *et al.* 1992b; EVANS *et al.* 1985; EVANS *et al.* 1986; EVANS and VILLEGAS 1988). These molecules act either as internal messengers or are released to feedback onto other Schwann cells further along the axon. The hyper-polarization is associated with an increase in K<sup>+</sup> selectivity by the Schwann cell membrane that most likely results from the activation of K<sup>+</sup> channels (VILLEGAS 1974).

Experiments using crayfish satellite cells, which are analogous to glia or Schwann cells, have shown that membrane hyper-polarization can be achieved by exogenous addition of ACh, carbachol or nicotine (LIEBERMAN *et al.* 1981). These results suggest that the hyper-polarization is mediated by ACh acting upon a nicotinic ACh receptor.

Additional experiments using the crayfish medial giant axon have shown that electrical stimulation of the nerve results in a change in the membrane potential of the periaxonal glia (LIEBERMAN *et al.* 1994). Furthermore, this change in the membrane potential is blocked by a non-NMDA glutamate receptor antagonist and is enhanced by a non-specific glutamate transporter inhibitor indicating that the signal from the axon to the glia is glutamatergic (LIEBERMAN *et al.* 1994).

Electrical stimulation of the *Rana pipiens* frog motor nerve, or the application of exogenous ACh to the perisynaptic Schwann cell (PSC) results in an increase in intracellular calcium concentration in the Schwann cell (JAHROMI *et al.* 1992). Further analysis in the absence of extracellular  $\text{Ca}^{2+}$  or presence of extracellular EGTA failed to eliminate the PSC response to ACh suggesting that the calcium is released from intracellular stores (JAHROMI *et al.* 1992). More recently experiments using immunofluorescence to label IP3 receptors and Xestospongin C (an IP3 receptor blocker) have indicated that IP3 is involved in the liberation of the  $\text{Ca}^{2+}$  in the PSC (CASTONGUAY and ROBITAILLE 2001; CASTONGUAY and ROBITAILLE 2002).

The conclusions about axon-glia communication that can be drawn from these other systems are that the initial signal from the neuron to the glia is glutamatergic; the glia may feedback onto itself using ACh; the release of intracellular  $\text{Ca}^{2+}$  stores is key; IP3 probably mediates the release of intracellular  $\text{Ca}^{2+}$ ; and that the glial response is also affected by a neuropeptide.

Considering the evidence from these non-Drosophila systems and the intracellular signaling pathways the Stern lab has elucidated in the Drosophila peripheral nerve, I decided to explore the roles of a number of genes in axon-glia signaling, neuronal excitability and perineural glial growth.

To address these questions I created a number of transgenic lines carrying RNAi constructs targeting a number of genes. *Ras1* and *push* were chosen for their proven roles in perineural glial growth (YAGER *et al.* 2001). *VACHT*, *PLC* and *itpr* were chosen as they have been implicated in axon-glia signalling in other species. *Rap1* was chosen as it is suspected to antagonize *Ras1* in intracellular signalling (HARIHARAN *et al.* 1991). *RyR* was chosen as this is an alternative to IP3 signaling for the release of intracellular Ca<sup>2+</sup> stores.

### **7.3.1 RNAi vectors**

RNAi vectors were created in a similar manner to that targeting *eag* (described in Chapter 2). Details of the trigger fragment introduced into the *sym-pUAST* vector are listed below.

***sym-pUAST-itpr.***

RNAi trigger fragment targeting *itpr* of 336nt created using forward primer:  
AGATCTACATAACGAGGTCGAC, reverse: GAATTCAGTGTGCTCAAGAAACC.

***sym-pUAST-PLC.***

RNAi trigger fragment targeting *PLC* of 251nt created using forward primer:  
GCATAGATCTCGTCAAATTCTCGACAAGGAGG, reverse: GGAATTCGAAAAA-  
CCTATACGGGCGTGCC.

***sym-pUAST-Push.***

RNAi trigger fragment targeting *push* of 316nt created using forward primer:  
GCATAGATCTACCATTTCGCTGTCTTCGC, reverse: GAATTCTGCTATCCGTG-  
GACTTG.

***sym-pUAST-Ras1.***

RNAi trigger fragment of 310nt targeting *Ras1* created using forward primer:  
TAAGAATTCACCGACCAACACGCTCCCAC, reverse: TAAGAATTCATACATTG-  
AGACATCCGCC.

***sym-pUAST-VAcHt.***

RNAi trigger fragment of 260nt targeting *VAcHt* created using forward primer: GGAATTCGTTGACTCTATGTGCGTAT, reverse: GGAATTCCGATATGACGGA-GCTTAGGTCCGAC.

***sym-pUAST-Rap1.***

RNAi trigger fragment of 271nt targeting *Rap1* created using forward primer: ATTTAGAATTCATACCAGCCACATCCCACACAC, reverse: ATTAGATCTTGGG-ATTGACACGACAGTTTAG.

***sym-pUAST-RyR.***

RNAi trigger fragment of 309nt targeting *RyR* created using forward primer: TATTGAATTCTGCCACGACGACGACTTTCTGC, reverse: AAATTAGATCTAGG-CTGCTGCACTTGCGG.

**7.3.2 Preliminary data**

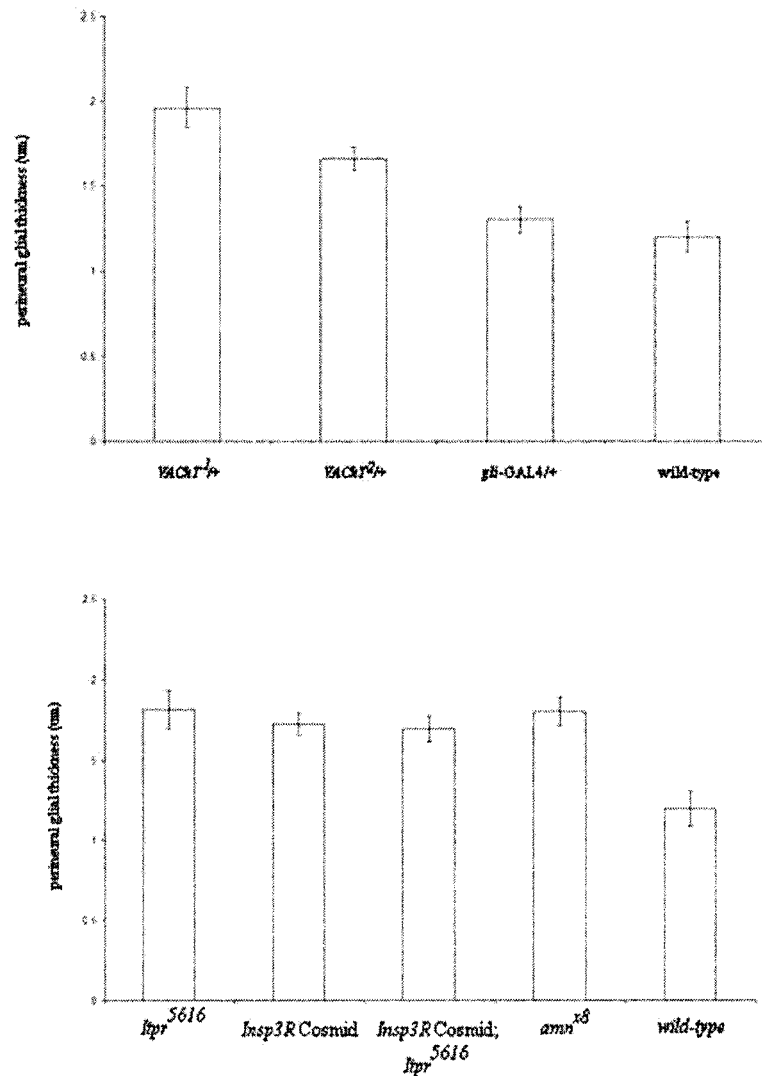
***itpr* hypomorph.**

To determine if larvae from a hypomorphic allele of *itpr* could affect perineural glial growth, larvae from the hypomorphic line (*itpr*<sup>5616</sup>) ( $1.81\mu\text{m} \pm 0.12$ ), from a line

carrying a rescue construct (*Insp3R Cosmid*) ( $1.72\mu\text{m} \pm 0.07$ ), and from a rescue cross (*Insp3R Cosmid;itpr<sup>5616</sup>*) ( $1.690\mu\text{m} \pm 0.08$ ) were measured. All these perineural glial thicknesses are similar to that of the *amn<sup>x8</sup>* mutant (Figure 7.1). None of these values are statistically significantly different from each other, all of them being at around  $1.7\mu\text{m}$ , which is significantly thicker than wild type ( $1.3\mu\text{m}$ ).

To determine if the *itpr<sup>5616</sup>* hypomorph has an effect upon neuronal excitability, the rate of onset of LTF was also determined for *itpr<sup>5616</sup>*, *Insp3R Cosmid*, and from *Insp3R Cosmid;itpr<sup>5616</sup>* (Figure 7.2). It appears that both the hypomorphs and the rescue are moderately hypoexcitable, whereas the cosmid alone has a similar excitability to wild-type.

Ras signaling is involved in the regulation of perineural glial growth. To determine if there is a relationship between Ras and IP3, the perineural glial thickness of the genotype *gli-GAL4/UAS-Ras<sup>v12</sup>(II); itpr<sup>5616</sup>/itpr<sup>90B.0</sup>* was measured and shown to be  $2.083\mu\text{m} \pm 0.135$ . This may be showing an enhancement of *gli-GAL4/UAS-Ras<sup>v12</sup>(II)* which has been previously shown to be  $1.4\mu\text{m} \pm 0.069$ . This value is also thicker than that of *itpr<sup>5616</sup>* which is  $1.81\mu\text{m} \pm 0.12$ . These enhancements are, however, most likely not meaningful.



**Figure 7.1 Preliminary perineurial glial thickness data**

Perineurial glia thickness data from two *VACHT* hypomorphs an IP3 receptor hypomorph and a rescue of the IP3 hypomorph. Nerves from larvae carrying the IP3-R hypomorphic (*itpr<sup>5616</sup>*) allele, larvae carrying only the rescue cosmid (*Insp3R Cosmid*), and larvae from a rescue cross (*Insp3R Cosmid ; itpr<sup>5616</sup>*) were photographed using electron microscopy. *VACHT<sup>1/+</sup>* and *VACHT<sup>2/+</sup>* heterozygote larvae were also measured. Values for *amn<sup>x8</sup>*, and *wt* (YAGER *et al.* 2001), *gli-GAL4/+* (MIKE STERN, UNPUBLISHED DATA).

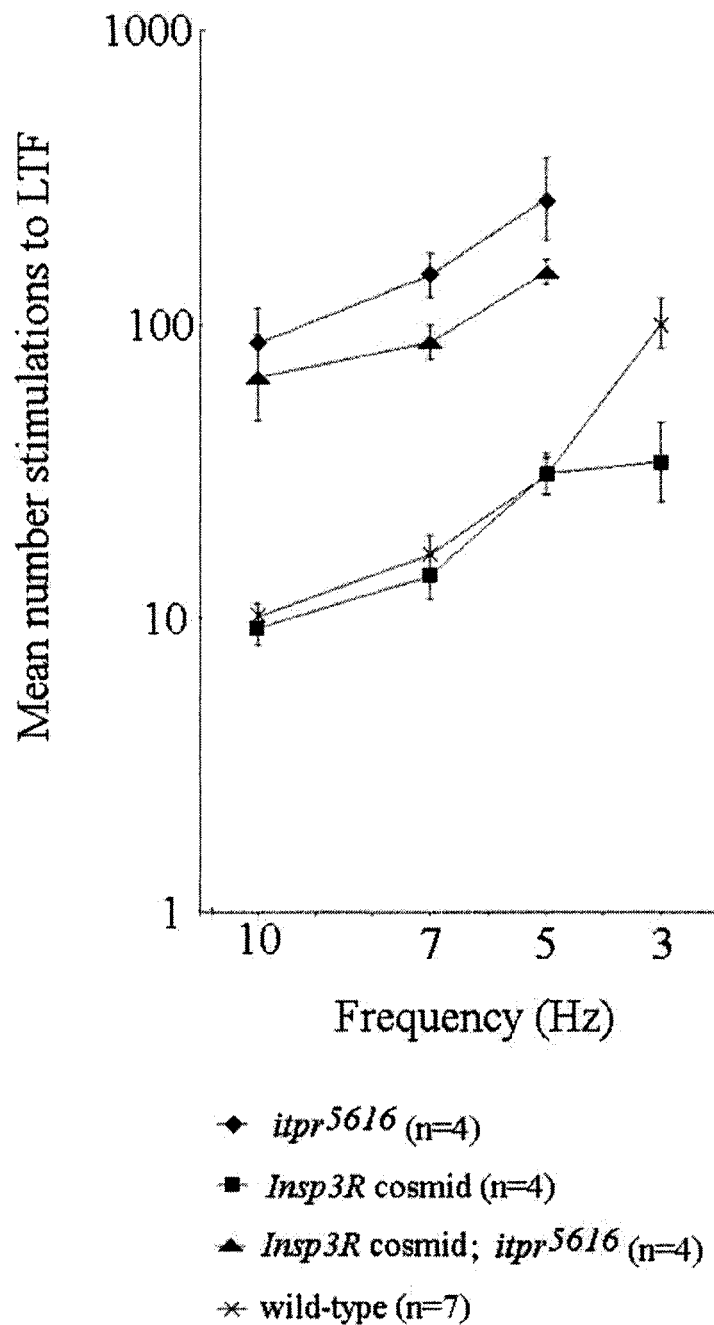
### ***VACHT* hypomorphs.**

Two hypomorphic alleles of *VACHT* were acquired from Paul Salvaterra (KITAMOTO *et al.* 2000). These are each lethal when homozygous. Similar to the homozygotes, the trans-heterozygote (*VACHT<sup>1</sup>/VACHT<sup>2</sup>*) fails to mature to third instar larvae. As such I was only able to collect heterozygote 3<sup>rd</sup> instar larvae.

To determine if the the *VACHT* alleles affected perineural glial growth we measured the perineural glial thickness in *VACHT<sup>1</sup>/+* and *VACHT<sup>2</sup>/+*. The data collected showed a slight, but not significant, thickening of the perineural glial (Figure 7.1) that was greater in *VACHT<sup>1</sup>/+* ( $1.957\mu\text{m} \pm 0.117$ ) than *VACHT<sup>2</sup>/+* ( $1.661\mu\text{m} \pm 0.122$ ). This fits with previous characterizations of these *VACHT* hypomorphs, where *VACHT<sup>1</sup>* had a stronger mutant phenotype than *VACHT<sup>2</sup>* (KITAMOTO *et al.* 2000).

### ***VACHT* RNAi.**

*Cha*-GAL4 is a GAL4 insertion in the *Choline acetyltransferase* gene that is essential for the production of Acetyl Choline (ACh). As *VACHT* is an essential gene, we crossed the *VACHT* RNAi construct to *Cha*-GAL4. The heterozygous combination of the *Cha*-GAL4 driver and the RNAi construct produced adult flies. As *VACHT* is known to be an essential gene, no adult survivors were expected to be seen. As with *eag<sup>RNAi</sup>*, it is possible that a single copy of the RNAi transgene is not sufficient to produce a phenotype.



**Figure 7.2** *itpr* hypomorphs may confer neuronal hypoexcitability

Average number of stimulations required to elicit the facilitative response at the stimulation frequencies tested (10, 7, 5 and 3 Hz). Values presented as mean  $\pm$  SEM, n-values as indicated. Wild-type is *Sup<sup>+</sup>f*, as used in Figure 3.10.

### ***Ras1 RNAi.***

To determine if the loss of *Ras1* can affect perineural glial thickness, we tested perineural glial thickness of UAS-*Ras1*<sup>RNAi</sup>/y; *gli*-GAL4/+ and determined the thickness to be 1.77μm ±0.068. This value is not significantly different from *gli*-GAL4/+. Again, it may be necessary for there to be two copies of the transgene for a *Ras1* loss of function phenotype.

Unexpectedly, F1 flies from the cross UAS-*Ras1*<sup>RNAi</sup> x *gli*-GAL4 did not produce an equal number of male and female progeny; there were approximately twice as many females (UAS-*Ras1*<sup>RNAi</sup>/X; *gli*-GAL4/+) than males (UAS-*Ras1*<sup>RNAi</sup>/y; *gli*-GAL4/+). This observation suggests that there may be a reduction in viability when the RNAi construct is homozygous. This is not unexpected as null alleles of *Ras1* are lethal, as is *gli*-GAL4 driven UAS-Ras<sup>v12</sup> (a constitutively active transgene). An alternative hypothesis is that the effect of the loss of *Ras1* is more profound in males than in females.

UAS-*Ras1*<sup>RNAi</sup>/y; *gli*-GAL4/+ larvae were also examined for an electrophysiological phenotype; there did not appear to be an LTF phenotype.

### ***PLC RNAi.***

To determine if PLC plays a role in the control of perineural glial growth, nerves from larvae of the genotype  $\text{UAS-PLC}^{\text{RNAi}}/\text{gli-GAL4}$  were measured. Larvae of the genotype  $\text{UAS-PLC}^{\text{RNAi}}/\text{gli-GAL4}$  have a perineural glial thickness of  $1.844\mu\text{m} \pm 0.126$ .