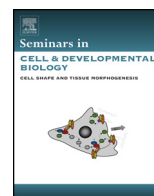




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Review

Motor axon guidance in *Drosophila*

Aref Arzan Zarin^a, Juan-Pablo Labrador^{b,c,*}

^a Howard Hughes Medical Institute, University of Oregon, Eugene, OR 97403, USA

^b Smurfit Institute of Genetics, Trinity College Dublin, Dublin, Ireland

^c Institute of Neuroscience, Trinity College Dublin, Dublin, Ireland

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ABSTRACT

The *Drosophila* motor system starts to assemble during embryonic development. It is composed of 30 muscles per abdominal hemisegment and 36 motor neurons assembling into nerve branches to exit the CNS, navigate within the muscle field and finally establish specific connections with their target muscles. Several families of guidance molecules that play a role controlling this process as well as transcriptional regulators that program the behavior of specific motor neuron have been identified. In this review we summarize the role of both groups of molecules in the motor system as well as their relationship where known. It is apparent that partially redundant guidance protein families and membrane molecules with different functional output direct guidance decisions cooperatively. Some distinct transcriptional regulators seem to control guidance of specific nerve branches globally directing the expression of groups of pathfinding molecules in all motor neurons within the same motor branch.

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* Corresponding author at: Smurfit Institute of Genetics, Trinity College Dublin, Dublin, Ireland.

E-mail address: labradoj@tcd.ie (J.-P. Labrador).

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1. Introduction

Three decades have passed since the very first molecules involved in axon guidance were discovered and insects have played a very important role in the field. Some of the very first molecules, such as Fasciclin cell adhesion molecules, were first identified in grasshopper [1,2]. Given the similarity among insect embryonic nervous systems and the power of *Drosophila* for molecular genetic analysis and genetic screens the later became the insect model organism of choice [3]. Several screens in *Drosophila* in the early 90's provided a genetic dissection of different axon guidance systems, including the motor system [4]. Since then a vast number of families of cell surface and secreted molecules directing axon guidance and their downstream signaling mechanisms have been identified [5–8].

There are several advantages that have made the *Drosophila* motor system an invaluable resource for understanding axon guidance. In addition to the *Drosophila* genetic tools available, the possibility to identify and label of individual motor neurons and the knowledge of their specific target muscles has brought the possibility of finely understanding motor neuron guidance behavior. In this review we will highlight the major families of guidance molecules that play a role in *Drosophila* motor axon guidance as well as what is known about their regulation.

2. The *Drosophila* motor system

The *Drosophila* embryo motor system is segmented into 3 thoracic and 9 abdominal segments. Each of the abdominal hemisegments A2–A7 has a stereotyped pattern of 30 muscles. The internal muscles are named dorsal acute (DA1–3), dorsal oblique (DO1–5), lateral longitudinal (LL1) ventral lateral (VL1–4) and ventral oblique (VO4–6). External muscles are named dorsal transverse (DT1), lateral oblique (LO1), lateral transverse (LT1–4), Segment border muscle (SBM), ventral transverse 1 (VT1) and ventral acute (VA1–3) [9]. These muscles are innervated by 36 different motor neurons (MNs) that project through three different main branches routes, the Intersegmental nerve (ISN), the segmental nerve (SN) and the transverse nerve (TN). TN MNs run along the segment border, innervate muscle VT1 and also establish connections with the lateral bipolar neuron (LBD), which in turn innervates alary muscles. The ISN innervates internal muscles and can be subdivided into 3 other branches innervating common groups of muscles: ISN dorsal muscles, ISNb ventral muscles (VL1–4) and ISNd a different group of ventral muscles (VO4–6). The SN is composed of 2 branches, SNa innervating LO1, LT1–4 and SMB and the SNc branch innervating VT1 and VA1–3 [10,11]. There are some specific features related to MN cell body position and muscle innervation for both main branches: The SN innervates external muscles and axons project from cell bodies present in the same segment as the muscles they innervate. The ISN innervates internal muscles and, except RP2 and VUM MNs, axons project from cell bodies positioned in the anteriorly preceding segment [12] (Fig. 1).

3. Molecular mechanisms of axon guidance in *Drosophila* motor neurons

In this section, we will discuss different families of membrane and secreted proteins playing a role in motor axon exit from the central nervous system (CNS) and proper navigation towards

their target muscles in the periphery during *Drosophila* embryonic development. We will also highlight the main signaling pathways downstream in the context of motor axon guidance.

3.1. Netrins, Frazzled and Unc-5

Netrins are secreted proteins of around 600 amino acids and are coded by two tandem functionally redundant genes in *Drosophila*, *NetA* and *NetB*. They are expressed in the midline cells of developing CNS, a subset of neurons, dorsal and ventral muscles and longitudinal epidermal patches [13,14]. Netrins signal through two different receptors: Frazzled (Fra) and Unc-5, promoting axonal attraction or repulsions depending on the receptor combination [15–17].

Genetic analysis indicates that *NetA*, *NetB* double mutant leads to significant defects in motor axon projection of all three MN pools, including the dorsally projecting intersegmental nerve (ISN), the laterally projecting segmental nerve (SN), and the ventrally projecting ISNb [13]. The repulsive Netrin receptor, Unc-5, is expressed in ISN (aCC and RP2 MNs) and SNa motor axons as well as the exit and peripheral glia along them [18,19]. Consistent with its expression pattern, *Unc-5* mutants present guidance phenotypes in both ISN and SNa MNs, where ISN inappropriately crosses the segment boundaries and one or both branches of SNa are missing [18]. Interestingly, ectopic expression of Unc-5 receptor in the CNS neurons elicits repulsion of their axons and cell bodies from the midline [17–20] (Table 1).

On the other hand, the attractive Netrin receptor, Fra, is expressed in aCC and RP2 MNs (ISN) as well as ventrally projecting ISNb MNs (RPs) but not in SNa MNs [18]. In the absence of *fra*, ISN shows wide range of guidance defects, including premature stall, excessive branching, segment boundary crossing and projections beyond its dorsal muscle targets. Also, the innervation of NetB expressing muscles 6/7 by ISNb MN (RP3) is significantly disrupted in *fra* mutant embryos [13,15,21]. SNa MNs do not show guidance defects in *fra* mutants while severely affected in *NetAB* double mutants, suggesting that Netrin signaling in SNa is exclusively dependent on the repulsive output of Unc-5 [15,18]. Fra's guidance output in different subsets of neurons has been shown to be dependent on several signaling molecules including, Abelson tyrosine kinase (Abl), the guanine nucleotide-exchange factor Trio, and the Abl substrate Enabled (Ena) [22,23]. In addition, targeting of ventral muscles seems mediated through two conserved domains, P1 and P3 in Fra's cytoplasmic domain [24] and the P3 domain is required for Abl signaling [25]. Abl does not seem to require its SH2 domain but rather its C-terminal region [23].

The role of Netrins and their receptors in motor axon guidance could be summarized as mediated through three different mechanisms where the repulsive effect of Netrin present in the midline and epidermal stripes may act through Unc-5 or Unc-5/Fra to promote CNS exit and prevent segment boundary crossing through (1) *Unc-5* and *fra* signaling in dorsal ISN (aCC and RP2) or (2) *Unc-5* signaling in SNa. An attractive Netrin signal in ventral muscles may signal through (3) Fra in ISNb.

3.2. Slit and Robos

The midline screen resulted in the identification of *slit* and *robo* as axon guidance genes controlling the midline crossing in embryonic CNS of *Drosophila* [26–28]. Slit, is a large extracellular matrix protein produced by midline glia in the CNS and detected by Robo

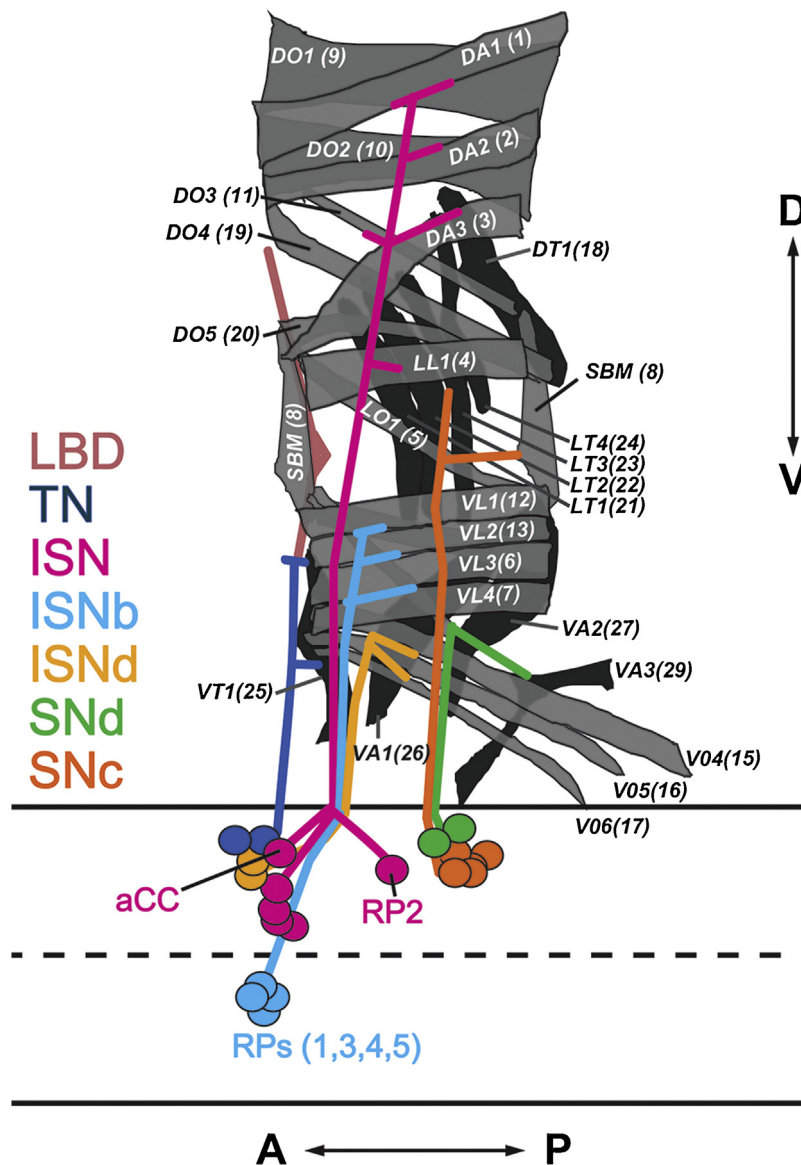


Fig 1. The *Drosophila* embryonic motor system. The *Drosophila* embryonic motor system is composed of 30 muscles labeled according to Bate 1993 [9] (First letter: D, dorsal; L, lateral; V, ventral and second letter: O, oblique; A, acute; T, transverse; L, lateral) and from 1 to 30 in brackets. Internal muscles are colored in light grey and external muscles in black. Nerve branches (TN, transverse nerve; ISN intersegmental nerve and its branches b,d and SN segmental nerve branches a and c, LBD, lateral bipolar neuron) are color coded as well as muscle projections and approximate cell body positions for motor neurons of the branch (not all neurons depicted) [10]. Two parallel lines represent the ventral nerve cord and dashed line represents the ventral midline, crossed by RP motor neurons of the ISNb). Orientation is provided by arrows: A, anterior; P, posterior; D, dorsal and V, ventral.

receptors in axonal growth cones [28]. Slit and Robo homologs have been identified in a wide range of animal taxa including vertebrates, planarians, nematodes, and insects [29–32]. In addition to the Robo receptor, critical for midline repulsion and broadly expressed throughout the VNC, there are two more Slit receptors, Robo2 and Robo3, which show diverse expression patterns and have axon guidance functions other than midline repulsion [33–38].

Temporal expression and activity of Robo receptors on axonal membranes is tightly regulated through a variety of mechanisms in *Drosophila* [39–44]. Expression of the 3 Robo receptors is very dynamic and at some stage all of them are expressed in different subsets of MNs [27,36,37]. Robo is expressed at early stages of development in aCC and RP2 MNs pioneering the ISN. However, despite its requirement in RP2 MNs to prevent its axons from crossing the midline [45], no gross abnormalities have been described on ISN guidance. Robo2 is expressed in ventrally projecting ISNb MNs and is required for their guidance and innervation of target mus-

cles, in Particular muscles 6 and 7 where *robo2* is also expressed. Interestingly, this function of Robo2 depends on its unique cytoplasmic domain that is absent in Robo and Robo3 receptors [37]. So far, only the role of Robo in midline repulsion has been shown to be dependent on Slit binding [46]. Nevertheless, misexpression of Slit in the muscle field leads to defective innervation of ventral muscles and repulsion of the ISNb [28] that may be mediated through Robo2. Finally, Robo3 is expressed early in development on the aCC MN [36] but no MN defects have been described so far. While Robo processing and signaling has been described in the midline [47–51] it is not clear if the same mechanisms are required in MN guidance (Table 1).

3.3. Semas and Plexins

Semaphorins and Plexins are another group of guidance molecules that are critical for neural circuit formation in both vertebrates and invertebrates [52–55]. In *Drosophila* there are three

Table 1
Motor axon phenotypes of relevant receptors and ligands.

Gene	Mutation/overexpression	Phenotype	Reference
<i>NetA, NetB.</i>	Double LOF	ISN dorsal segment border crossing ISNb lack of innervation of muscle 6 and 7 SNa stall near the CNS or fasciculate with the ISN	[13,18] [13,18] [18,20]
<i>NetB</i> <i>Unc-5</i>	Muscle GOF LOF	SNa stall near the CNS or fasciculate with the ISN ISN dorsal segment border crossing SNa stall near the CNS or fasciculates with the ISN, missing branches	[13,63] [18] [18]
<i>fra</i>	LOF	ISN dorsal segment border crossing ISNb lack of innervation of muscle 6 and 7	[15] [15,18,21]
<i>slit</i>	Muscle GOF	ISNb stall lack of innervation of muscle 6 and 7	[28]
<i>robo</i>	LOF	RP2 midline crossing	[45]
<i>robo2</i>	LOF	ISNb lack of innervation of muscle 6 and 7	[37]
<i>Sema-1a</i>	LOF	ISNb stall lack of innervation of muscle 6,7,12,13 SNa stall or missng branches	[61,62] [61,62]
<i>Sema-1a</i>	Muscle GOF	SNa stall or missng branches ISNb fasciculates with the ISN,lack of muscle innervation	[61] [61]
<i>Sema-2a</i>	LOF	Low penetrance ectopic muscle contact in ISNb, SNa and TN	[63]
<i>Sema-2a</i>	Muscle GOF	TN stalling (suppressed by PlexB LOF)	[58]
<i>Sema-2a, NetA, NetB</i>	Triple LOF	Suppression of ISNb lack of innervation of muscle 6 and 7 from <i>NetA, NetB</i> LOF	[63]
<i>NetA, NetB;Sema-2a</i>	Double LOF,Muscle GOF	Enhancement of ISNb lack of innervation of muscle 6 and 7 from <i>NetA, NetB</i> LOF	[63]
<i>PlexA</i> <i>PlexA</i> <i>PlexB</i>	LOF LOF LOF	ISNb stall lack of innervation of muscle 6,7,11,12 SNa abnormal branching ISNb stall lack of innervation of muscle 6,7,11,12 SNa abnormal branching	[53,58] [53,58] [58] [58]
<i>Otk</i>	LOF	ISNb stall lack of innervation of muscle 6,7,11,12 SNa abnormal branching	[65] [65]
<i>Dlar</i>	LOF	ISN dorsal truncation ISNb fasciculates with the ISN,lack of muscle innervation SNd fasciculates with the ISN,lack of muscle innervation	[128] [78,128] [78,128]
<i>Ptp69D</i>	LOF	ISNb fasciculates with the ISN,lack of muscle innervation SNa abnormal branching (low penetrance)	[79,128] [79,128]
<i>Dlar,Ptp69D</i>	Double LOF	ISN dorsal truncation (stronger than <i>Dlar</i>) ISNb defects stronger than <i>Dlar</i>	[128] [128]
<i>Ptp10D</i>	LOF	No phenotype	[80]
<i>Ptp10D,Ptp69D</i>	Double LOF	SNa abnormal branching, stronger than 69D single	[76]
<i>Ptp10D, Dlar, Ptp69D</i>	Triple LOF	ISNb fasciculates with the ISN (stronger than double)	[76]
<i>Ptp99A</i>	LOF	No phenotype	[79,128]
<i>Dlar,Ptp99A</i>	Double LOF	ISN dorsal truncation (stronger than <i>Dlar</i>) ISNb fasciculation with ISN suppressed	[128] [128]
<i>Ptp69D, Ptp99A</i>	Double LOF	ISNb fasciculates with the ISN, lack of muscle innervation, stronger than 69D single SNa abnormal branching, stronger than 69D single	[79,128] [79,128]
<i>Dlar,Ptp69D,Ptp99A</i>	Triple LOF	ISN dorsal truncation (stronger than <i>doubles</i>)	[128]
<i>Ptp10D,Dlar,Ptp69D,Ptp99A</i>	Quadruple LOF	ISN dorsal truncation suppressed	[76]
<i>Ptp52F</i>	LOF	SNa stall or missng branches	[80]
<i>Ptp52F, Dlar</i>	Double LOF	SNa stall or missng branches(stronger than <i>Ptp52F</i>)	[80]
<i>Ptp52F,Ptp10D</i>	Double LOF	ISN terminal stall phenotypes ISNb stall in ventral muscle field SNa stall or missng branches(stronger than <i>Ptp52F</i>)	[80] [80] [80]
<i>Ptp52F, Ptp69D</i>	Double LOF	ISN terminal arbor phenotypes ISNb stall in ventral muscle field SNa stall or missng branches(stronger than <i>Ptp52F</i>)	[80] [80] [80]
<i>sdc</i>	LOF	ISNb fasciculates with the ISN (low penetrance)	[83]
<i>sdc,Dlar</i>	Double LOF	ISNb fasciculates with the ISN (stronger than singles)	[83]
<i>sidestep</i>	LOF	ISN terminal stall phenotypes ISNb fasciculates with the ISN,lack of muscle innervation ISNd fails to defasciculate SNa and SNa remain fasciculated missng muscle innervation	[87] [87] [87] [87]
<i>beat Ia</i>	LOF	ISN terminal stall phenotypes ISNb fasciculates with the ISN,lack of muscle innervation (suppressed by <i>Fas2</i> LOF) ISNd fails to defasciculate SNa and SNa remain fasciculated missng muscle innervation (suppressed by <i>conn</i> LOF)	[20,86] [86] [86] [86]
<i>beat Ic</i>	LOF	TN defasciculation and ventral muscle innervation	[88]
<i>side-VI</i>	LOF	ISNb muscle 12 innervation defects (low penetrance)	[91]
<i>daw</i>	LOF	ISNb stall lack of innervation of muscle 6,7,12,13	[97,98]

Table 1 (Continued)

Gene	Mutation/overexpression	Phenotype	Reference
<i>babo</i>	LOF	SNa stall or missng branches ISNb stall lack of innervation of muscle 6,7,12,13	[97,98] [97,98]
<i>put</i>	LOF	SNa stall or missng branches ISNb stall lack of innervation of muscle 6,7,12,13	[97,98] [97,98]
<i>Fas2</i> <i>Fas2</i>	LOF GOF	SNa stall or missng branches No phenotype Increased faciculation preventing ISNb, SNa muscle targetting, ISN misrouting	[97,98] [20,86] [102]
<i>Fas2,Sema-1a</i> <i>conn</i> <i>conn</i>	Doube LOF LOF GOF	Suppression of ISNb stall present in <i>Sema-1a</i> LOF No phenotype Repulsive for ISNb and ISNd axons, attractive homophilic for Sna axons	[62] [103] [103,104]
<i>Sema-1a, Fas2, conn</i>	GOF	SNa axons stall near the CNS or fasciculate with the ISN, stronger than single GOF	[63]
<i>nrg</i>	LOF	ISN dorsal truncation inappropriate contact with trachea ISNb stall, lack of innervation of muscle 6 and 7 ISNd fails to defasciculate SNa and SNaC stal of fail to defasciculate missng muscle innervation	[20,106] [106] [106] [106]
<i>nrg,Unc-5</i>	Double LOF	ISN dorsal segment border crossing from <i>Unc-5</i> enhanced	[20]
<i>nrg, beat 1a</i> <i>Unc-5, beat 1a</i> <i>nrg, Unc-5, beat 1a</i>	Double LOF Double LOF Triple LOF	ISN dorsal truncation enhanced ISN dorsal truncation enhanced ISN dorsal truncation very severe	[20] [20] [20]

LOF: Loss of function, GOF:gain of function.

transmembrane Semaphorins (Sema-1a, Sema-1b, and Sema-5c), two secreted Semaphorins (Sema-2a and Sema-2b), and two Plexins (Plexin A and Plexin B) [56]. Sema-1b and Sema-5c are not expressed in embryonic CNS, and do not seem to have a role in neural development [57]. Plexin B (PlexB) binds and detects the secreted Semas and Plexin A (PlexA) transmembrane Semas [53,58]. Sema-1a acts as a ligand for PlexA but it can also act as a receptor in reverse signaling [59,60].

Sema-1a has been reported to mediate motor axon defasciculation [59] through reverse signaling. Embryos lacking *Sema-1a* show defects in axon pathfinding of ISNb, ISNd and SNa motor nerves [61,62]. Following Sema-1a stimulation its cytoplasmic domain recruits two major antagonistic regulators of the Rho1 GTPase, pebble (Pbl), the activator and RhoGAP p190, the inhibitor. Pbl is a Rho guanine nucleotide exchange factor (GEF) that facilitates the exchange of bound GDP with GTP activating Rho1. Thus, the GEF and GAP activities of Pbl and RhoGAP, respectively play opposing roles in Sema-1a reverse signaling controlling defasciculation of motor axons at specific choice points and target muscle recognition. Pbl triggers axon–axon repulsion and defasciculation activating Rho1, while p190-RhoGAP inhibits Rho1 leading to axonal attraction [59]. *pbl* mutant embryos in *Drosophila* show defasciculation defects in all three motor axon roots (ISN, SNa, ISNb), while RhoGAP p190 mutations only affect the ISNb [59]. Whether Sema-2a and Sema-2b behave as ligands in the motor system in the same way they do in the CNS midline [60] has not been explored yet. However *Sema-2a* mutants present low penetrance ectopic muscle contact in ISNb, SNa and TN branches and its misexpression in muscles presents phenotypes in the TN that can be suppressed by partial elimination of PlexB [58,63].

In addition to its function as a receptor in reverse signaling, Sema-1a acts as a ligand for PlexA in forward signaling and is also required for motor axon defasciculation [64]. *PlexA* mutants present SNa and ISNb guidance defects where these nerves fail to reach their target muscles [53]. Two other components of this signaling complex are transmembrane proteins, Off-track (OTK) that associates with PlexA, and a receptor guanylyl cyclase (Gyc76C). *Otk* mutants present motor axon phenotypes resembling those of *PlexA* and *Sema-1a* [65] consistent with its role as a PlexA coreceptor. *Gyc76C* interacts genetically and physically with the Sema-1a/PlexA

complex during motor axon guidance [66,67]. Guanylyl cyclases catalyze the conversion of GTP to cGMP modulating different cellular and physiological processes [68], including axonal and dendritic guidance [69–72]. Sema-1a/PlexA mediated repulsive guidance is also modulated by an extracellular matrix proteoglycan called Perlecan, highly abundant in motor axon trajectories and pathway choice points. Perlecan increases Sema-1a induced dephosphorylation of focal adhesion kinase (FAK) and shows antagonistic relationship with integrin adhesive functions, thereby leading to motor axon defasciculation [64]. MICAL, a cytosolic oxidoreductase belonging to family of flavoprotein monooxygenases interacts with the PlexA and is necessary for Sema-1a mediated cytoskeletal alterations leading to axon repulsion. MICAL interacts with actin, intermediate filaments, and cytoskeletal-associated adaptor proteins [73].

Finally, PlexB is required for motor axon guidance of ISNb and SNa [58]. *PlexB* mutants present strikingly similar phenotypes to those of *PlexA* where ISNb fails to innervate ventral muscles 6, 7, 11, 12 and 13 and SNa stops short of its target muscle 24 indicating that both cooperate on their guidance. In fact, the both interact through their intracellular domains and although *PlexA* can partially substitute for *PlexB*, the opposite does not happen [58]. Despite a high degree of conservation between PlexA and PlexB they can both signal through specific downstream effectors. PlexB interacts with the small GTPase Rac enhancing RhoA signaling, but PlexA does not [73–75]. In addition, PlexB does not interact with MICAL, although it is required downstream for some of its guidance functions [58,60] (Table 1).

3.4. Receptor protein phosphatases and heparan sulfate proteoglycans

The receptor tyrosine phosphatase family (RPTPs) is another group of molecules playing a role in motor axon guidance. There are 8 identified RPTs but only six: DLAR, DPTP69D, DPTP99A, DPTP4E, DPTP10D and DPTP52F with defined roles in axon guidance [76]. These RPTPs contain a variable number of FN-III repeats and can be structurally classified into two groups depending on whether they have one (4E, 10D and 52F) or two (DLAR, 69D and 99A) PTP domains in their cytoplasmic region [77].

While *Dlar*, *Ptp69D* and *Ptp52F*, mutants present clear motor axon phenotypes the rest show only mild phenotypes but their function is complementary to the other phosphatases. In *Dlar* mutants ISNb axons do not innervate their target muscles and instead remain fasciculated to the ISN. In addition SNd axons fail to innervate its target muscles 15–17 fasciculating with the ISN and making aberrant contact with lateral or dorsal muscles [78]. *Ptp69D* mutants also present a bypass phenotype on the ISNb and low penetrance defects on the SNa branch. However, these phenotypes are exacerbated in *Ptp69D*, *Ptp99A* double mutants. *Ptp99A* deficient embryos do not show any obvious phenotype in the motor system [79]. Mutations in *Ptp52F* result in specific defects on the SNa where it fails to bifurcate, has extra branches or stalls at the branching point [80]. *Ptp52F* has low penetrance phenotypes on the ISN where it stops prematurely; this phenotype can be enhanced by further removal of *Ptp10D* and *Ptp69D*, which have no ISN phenotype on their own. *Ptp52F* also seems to be required in combination with *Ptp10D* and *Ptp69D* in ISNb guidance as double mutants present strong stalling phenotypes [80]. Analysis of double, triple and quadruple *Ptp10D*, *Dlar*, *Ptp69D* and *Ptp52F* mutants reveals a complex interaction among these PTPs: *Ptp10D* is required for SNa outgrowth in combination with *Dlar* and *Ptp69D*. *Ptp10D* also works together with *Dlar*, *Ptp69D* and *Ptp99A* in ISNb defasciculation. Finally, mutations on *Ptp10D* suppress ISN truncation phenotypes of *Dlar*, *Ptp69D*, *Ptp99A* mutants [76].

Signaling downstream RPTPs has been thoroughly studied in DLAR and several molecules have been identified. The cytoplasmic tyrosine kinase Abl and its substrate Enabled (Ena) interact with DLAR and both are downstream effectors required for ISNb guidance [81]. Genetic interaction between *Trio*, a GEF for small GTPases, and *Dlar* reveal that both work together in multiple axonal pathways including ISNb [82] (Table 1).

Two Heparan Sulfate Proteoglycans, Syndecan (Sdc) and Dally-like (Dlp) have been identified as ligands for DLAR in the nervous system. Sdc and DLAR bind to each other in vivo. *sdc* and *Dlar* interact genetically in trans presenting ISNb bypass phenotypes, a strong indication of their interaction [83]. In addition Dlp also interacts with LAR and together with Sdc control different aspect of synaptic function [84]. Interactome studies have also detected homophilic interactions for the extracellular domain of DPTP99A, raising the possibility of a trans interaction of this phosphatase in two opposing cellular surfaces [85].

3.5. Beat and Sidestep families in motor axon guidance

Two genes, *sidestep* (*side*) and *beaten path* (*beat*, later renamed *beat la*), were identified in the MN screens of the early 90's presenting very similar phenotypes where all branches within the ISN and SN nerves are affected [4,86,87]. Both were just the founding members of large families with 14 *beats* and 8 *sides*. [88,89]. Despite their highly similar phenotypes they were not initially identified as interacting partners [85,90]. Both families belong to the immunoglobulin (Ig) superfamily of proteins. Sides have 5 Ig domains and a fibronectin type III (FN-III) fold in their extracellular region and all seem to be transmembrane proteins [91]. Beat proteins have 2 Ig domains but are more diverse and can interact with membranes through transmembrane domains or glycosphosphatidylinositol links [88].

Beat la behaves as a receptor present in axons and interacts with Sidestep present in cellular membranes across its path. In *beat la* mutants the ISN is often truncated and its ventral branches ISNb and ISNd fail to defasciculate resulting in defective innervation of their ventral muscle targets. The segmental nerve is also affected as SNc remains fasciculated with SNa and their branches do not extend into their muscle domains [86]. The Beat family of proteins comprises 14 members and most of them have nervous system

expression. Among the *beat I* subgroup *beat Ic* presents defects where the transverse MN defasciculates and occasionally innervates ventral muscles [88]. Among the Beat V group Beat Va and Beat Vb are expressed in aCC and RP2 dorsal MNs suggesting a role for these receptors in ISN guidance [91] (Table 1).

Sidestep is expressed in a highly dynamic pattern in the CNS, PNS and muscles during embryogenesis and functions as a target-derived attractant [87,90]. Side expressing cells down regulate its expression upon contact with Beat-expressing axons [90]. Mutants for *side* present striking similarity with *beat la* one and both of them are interacting pairs [85,90]. In addition to Sidestep most of remaining 7 Side proteins have been identified as interactors of Beat family ones and some of them present specific expression in neurons such as Side IV and side VII suggesting they may behave as guidance receptors [91]. Interactome networks have been well characterized and although there is some degree of promiscuity in their interactions it seems restricted within Beat subfamilies. For example Beat vs seem to specifically interact with Side VI [85,91]. Nevertheless, the role of other individual Beat/Side pairs in motor axon guidance has not been studied yet.

3.6. Other guidance molecules

3.6.1. Transforming growth factor-beta family

The TGF- β superfamily in *Drosophila* is composed of three structurally and functionally distinct subfamilies: Activins, TGF- β s and Bone Morphogenetic Proteins (BMPs) [92]. They are involved in different functions in the nervous system, including neural induction and patterning, and control of neuronal differentiation and synaptogenesis [93–96]. Two independent studies have shown the requirement of a cell signaling pathway initiated by Activin-like protein Dawdle (Daw) in motor axon guidance [97,98]. Elimination of *daw* results in stalling of the ISNb within the ventral muscle field. SNa is also affected in these mutants stalling or missing branches [97,98]. Daw, is produced in muscle and glia, signaling through a heteromeric receptor complex of Baboon (Babo), the type-I receptor, and Punt (Put), the type-II; both expressed on motor axons. Importantly, *daw* mutations are phenocopied by zygotic mutants of these two receptors [97,98]. A further component of the system is a secreted enzyme, the metalloprotease tolloid-related (Tlr), also called Tolkin (Tok) [98]. Tok processes Daw's pro-domain and enhances signaling mediated by this ligand. Tok is a circulatory enzyme produced in muscles and subset of CNS neurons and is secreted to hemolymph where it acts in a cell non-autonomous manner to process various extracellular matrix components including Daw ligand. Mutations in *tok* also lead to the same ISNb and SNa defects, further confirming the relevance of this whole pathway in motor axon guidance [98,99]. Further metalloproteases are likely to play a role in motor axon guidance as matrix metalloprotease 2 (Mmp2) seems to regulate the BMP signaling pathway through one of its substrates, faulty attraction (Frac) and both are required for ISNb and SNa guidance [100,101] (Table 1).

3.6.2. Cell adhesion molecules

Cell adhesion molecules (CAMs) were the first ones proposed to play a role in axon guidance. They belong to the Ig superfamily of proteins have been generally understood to play a role promoting adhesion through homophilic interactions. Most of the cell adhesion molecule mutants seem to have rather mild phenotypes, if any, in the neuromuscular system. Nevertheless, misexpression studies and compound mutations mutants reveal distinct roles for these molecules. *Fasciclin II* (*Fas2*), for example, lacks any overt neuromuscular phenotype in mutant embryos; however, when misexpressed in neurons it leads to increased fasciculation of virtually all motor nerve branches preventing them from reaching their targets [102]. Compound mutants of *Sema-1a* and *Fas2* reveal

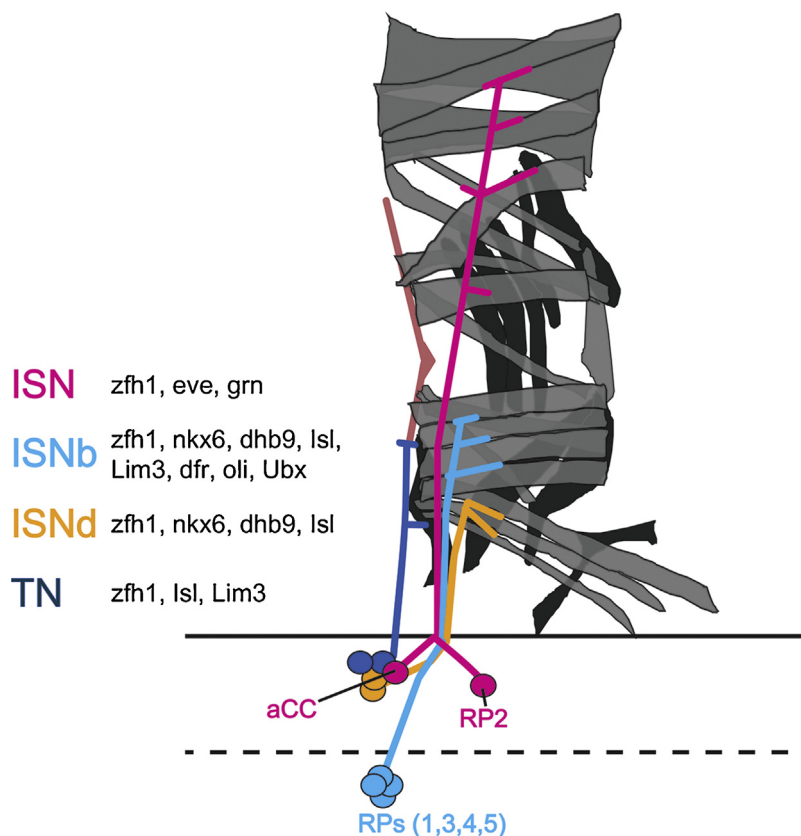


Fig. 2. Expression of transcriptional regulators in the transverse nerve and intersegmental nerve branches. Transcriptional regulators expressed in the transverse nerve (TN), intersegmental nerve (ISN) and branches (b, d). *zinc finger homeodomain 1 (zfh1)* *even-skipped (eve)*, *grain (grn)*, *exex (hb9)*, *nkx6*, *Islet (Isl)*, *Lim3*, *Oli* (Olig family), *drifter (dfr)* and *Ultrabithorax (Ubx)*.

opposing roles for both genes as elimination of *Fas2* leads to a suppression of the ISNb phenotype present in *Sema-1a* mutants [62]. Connectin (Conn), another cell adhesion molecule expressed on the SNa and the muscles it innervates does not present any MN defect when its gene is mutated but misexpression studies show that it can work as a homophilic adhesion molecule [103,104]. Triple compound mutants *Sema-1a*, *Fas2*, *conn* again reveal the role of cell adhesion molecules as SNa phenotypes present in *Sema-1a* are suppressed in triple mutants [62]. Neuroglian (Nrg) is the Drosophila homolog of the L1 cell adhesion molecule and it is expressed throughout the nervous system including MNs [105]. *nrg* mutants maybe an exception to the rule of lack of motor nerve guidance phenotypes on individual mutants of cell adhesion molecules as they show stalling of ISN and ISNb axons [106] (Table 1).

4. Transcriptional specification of motor neuron guidance

Guidance molecules control how growth cone steer on their path but their expression must be regulated on individual neurons. One of the main levels of regulation is transcriptional. In this chapter we will discuss the different transcriptional regulators that have been show to play a role in motor axon guidance and the pathfinding molecules they may regulate.

While there are transcriptional regulators specifically expressed by subgroups of MNs one is expressed by all of them, *Zfh1*. *Zfh1* is a zinc finger homeobox protein required for proper motor axon guidance of both ISN and SN nerves. In the absence of *zfh1*, ISN and SN MNs fail to exit the CNS or have truncated axons and present severe defects in branching and innervation of target muscles [107]. Interestingly, ectopic expression of *zfh1* in different CNS interneurons redirects their axons away towards the muscle field away from the

CNS indicating that it may be regulating CNS exit, a general function shared by all MNs [20,107]. Several guidance genes have been identified downstream *zfh1*, namely *Unc-5*, *beat 1a* and *Fas2* [20]. However, these cannot account for all *zfh1* targets as, except *Fas2*, they have restricted expression in MNs. Interestingly *zfh1* does not specify MN identity as all MNs seem to be present in *zfh1* mutants [107].

In addition to *Zfh1*, the pan-MN transcription factor, Drosophila MNs that exit the CNS and project axons via common routes, share some transcriptional regulators. Unique codes seem be required for specifying the guidance of each distinct MN subclass and the expression of different set of cell surface receptors on them.

4.1. Dorsal ISN motor route

This motor branch is pioneered by the aCC and RP2 MNs and innervates the dorsal muscles of the body wall (Section 2). MNs in this branch express the homeodomain transcription factor *Even-skipped (Eve)* and the GATA family transcription factor *Grain*, both of which are necessary for correct motor pathfinding [108–110]. In *eve* mutants aCC and RP2 fail to exit the CNS and innervate their target muscles [108], a phenotype shared by *grain (grn)* deficient embryos [110]. There are complex interactions among *zfh1*, *grn* and *eve* that are dependent on individual MNs; and *eve* regulates the expression of *grn* and *zfh1* in aCC but not RP2 [110].

A study of mRNA isolated from aCC and RP2 dorsal projecting MNs (dMNs) identified multiple axon guidance genes that are transcriptionally regulated by *eve* [20]. Genes coding for two cell surface receptors (*Unc-5* and *beat 1a*) and two cell adhesion molecules (*Fas2* and *Neuroglian*, *Nrg*) are among its downstream effectors. *Unc-5*, *beat 1a*, *fas2*, and *nrg* show significant down regulation in

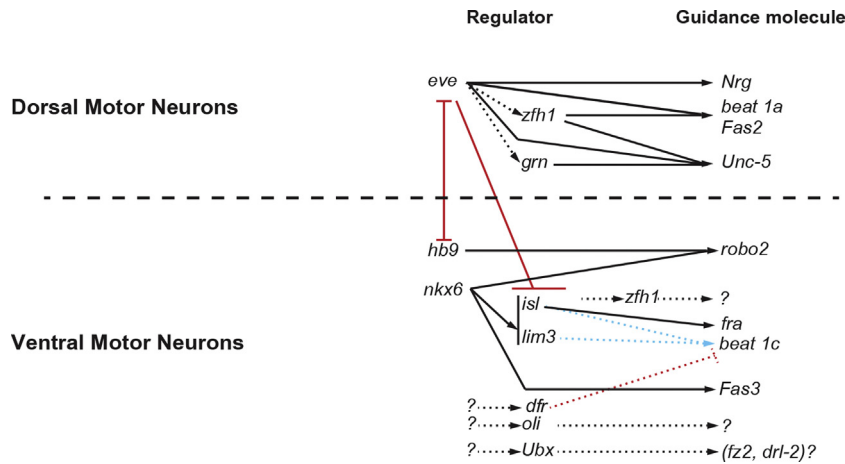


Fig. 3. Transcriptional regulation of guidance in ventral versus dorsal motor neurons. Transcriptional regulators in dorsal and ventral motor neurons and their hierarchy is represented from left to right. Dorsal motor neurons (intersegmental nerve, ISN): *even-skipped (eve)* regulates expression of two other transcription factors in dorsal motor neurons, *zinc finger homeodomain 1 (zfh1)* *even*-and *grain (grn)* in aCC but not in RP2 (indicated by dotted lines). Different combinations of transcription factors regulate the expression of pathfinding molecules. Only *eve* is required for *Neuroglian (Nrg)* expression; both *eve* and *zfh1* for *Fasciclin 2 (Fas2)* and *beaten path 1a (beat 1a)* and the three of them for *Unc-5* expression. Ventral motor neurons: determinants for these neurons are *nrx6* and *hb9*. *Nrx6* regulates the expression of *Isl* and *lim3* but *hb9* and *nrx6* do not regulate each other. The dorsal determinant *eve* represses *Isl* and *lim3* and in addition there is a crossrepressive activity between *eve* and *hb9* indicated by red lines. *zfh1* is expressed in all motor neurons, including ventral motor neurons, it is likely downstream *nrx6*, *lim3* and *Isl* (this uncertainty is signified by dotted lines). *drifter (dfr)*, *Olig* family (*Oli*) and *Ultrabithorax* are also expressed in ventral motor neurons. *nrx6* regulates expression of the cell adhesion molecule *Fasciclin 3 (Fas3)* and together with *hb9* the expression of the guidance receptor *robo2*. *Isl*, but not *lim3* regulates the expression of the guidance receptor *frazzled (fra)* and both *lim3* and *Isl* probably regulate *beat 1c* in the transverse nerve and they interact genetically (indicated by cyan dashed lines). *dfr* may represses *beat 1c* expression in the ISNb. *Oli* and *Ubx* are expressed in ventral motor neurons and contribute to its guidance, but the genes they regulate have not been identified in these neurons (indicated by the ? sign).

dMNs in the absence of *eve*. Individual mutants for these cell surface molecule leads to milder motor guidance defects compared with *eve* but compound mutants closely resemble its phenotype. Another interesting finding is the different transcriptional regulator requirement for the expression of these genes in dMNs. *grn* and *zfh1* cooperate with *eve* for the expression of these genes in dMNs and, interestingly, also in interneurons where they are mis-expressed. *zfh1* is required for *Unc-5*, *beat 1a* and *Fas2* expression in dMNs, while *grn* is only required for *Unc-5* expression [19,20].

4.2. ISNb and ISNd motor branches

ISNb and ISNd motor branches share common regulators with the TN therefore all these branches will be discussed together. ISNb MNs are 4 MNs RP1, 3–5 that innervate a group of ventral muscles (Section 2). RPs coexpress the transcription factors Hb9 (Exex), Nrx6, Isl (Isl or Tup), Lim3, Oli (Olig family), Drifter (Dfr) and Ultrabithorax (Ubx). ISNd MN express Isl but do not express Dfr, setting a differential code of transcriptional regulators within these ventral ISN branches (Lim3 and Hb9 expression has not been unequivocally determined in these MNs). TN MNs express Isl and Lim3. These conserved proteins are required for terminal aspects of MN differentiation including axon guidance [111–120] (Fig. 2).

Isl and *Lim3* deficient embryos present phenotypes where ISNb it fails to innervate ventral muscles. In *Lim3* mutants ISNb MN are redirected towards ISNd target muscles. Interestingly *Lim3* misexpression leads to ISNd redirection towards ISNb ventral muscles likely upregulating effectors responsible for ISNb guidance [111,112]. *hb9* mutants have ventral muscle innervation defects in the ISNb [113,116] and *hb9*, *Isl* compound mutants show stronger effects on ISNb targeting than each single mutant, indicating they work in parallel [21]. In *nrx6* mutants both ISNb and ISNd are defective as they fail to exit the CNS [114]. Reduction of *dfr* together with *lim3* or *Isl* leads to defects in ISNb targeting as well but also redirect TN MN towards ventral muscles suggesting they work together in ISNb and TN pathfinding [117]. In *oli* mutants muscles 12 and 13 fail to be innervated by ISNb and TN NM targets ventral muscles and these defects are enhanced in *oli*, *hb9* double mutants [119].

Ubx mutants ISNb presents defects on muscle 12 innervation and is occasionally misrouted making contacts with the TN [120].

The regulatory network among these transcription factors is complex. While *hb9* and *nrx6* do not regulate each other, *nrx6* seems to be upstream all the others. *nrx6* regulates expression of *Isl* and *lim3* [114]. *Isl*, *lim3*, *dfr* and *oli* do not seem to be transcriptional targets of each other although they can work in combination [119]. *hb9* does not seem to be downstream *Ubx* as it is clearly detected in *Ubx* mutant RPs [120].

Few targets have been identified downstream these transcriptional regulators. On the ISNb the CAM *Fasciclin 3 (Fas3)* and *robo2* are regulated in RP MNs by *nrx6* [37,114]. *Isl* and *lim3* interact genetically with *beat 1c* in TN MNs targeting ventral muscles rather than the LBD neuron, suggesting it may be downstream these transcriptional regulators [117]. A recent study has shown that *Isl*, but not *Hb9* or *lim3*, is required for expression of *fra*, in an ISNb MN (RP3) which normally projects to ventral muscles 6 and 7. *fra* mRNA is completely missing or significantly decreased in *Isl* mutant RP3s. Similar to the *fra* phenotype, lack of *Isl* results in innervation defects of muscle 6/7 by RP3 MN and restoring *fra* expression in *Isl* mutant RP3 neurons significantly rescues their innervation defects [21]. A parallel function of *hb9* and *nrx6*, but not *Isl*, regulates the expression of *robo2* receptor in RP3. Muscles 6/7 innervation by RP3 is severely affected in *hb9* mutants and to a lesser extent in *robo2* mutants. Furthermore, *robo2* expression is down regulated in *hb9* mutant RP3 neurons. Consistent with this, restoring *robo2* expression in *hb9* mutant RP3 MNs partially rescues innervation defects of muscles 6/7 [37]. *Isl*, *hb9* double mutants exhibit higher rate of muscle 6/7 innervation defects than either single mutant, similar to embryos lacking both *robo2* and *fra* [37]. *nrx6* also collaborates with *hb9* to regulate *robo2* as removal of one copy of *nrx6* in an *hb9* background leads to a further reduction of *robo2* expression in RP3 neurons and enhances the muscle innervation phenotype seen in *hb9* mutants [37] (Fig. 3).

Ubx mediates the formation of specific neuromuscular connections regulating the expression of Wnt4 repellent cue, a member of the Wnt family of signalling molecules in muscles. In addition to ventral muscles 6,7,12, and 13 *Ubx* is expressed on the ISNb

RPBs [120]. A similar innervation phenotype to *Ubx* is also seen in embryos lacking *Wnt4*, which is highly expressed in MN-13 of wild type embryos [121]. *Wnt4* acts as a repellent in muscle 13 for MNs projecting to muscle 12. Lack of *Ubx* results in loss of *Wnt4* in abdominal M13 muscles, and ectopic expression of *Ubx* in thoracic muscles activates *Wnt4* expression on them [120]. Although *Ubx* target in NMs is not known yet it may be a *Wnt4* receptor such as *frizzled 2* (*fz2*) or the RYK family *derailed-2* (*drl-2*), whose mutants show the same phenotype [121]. In this way *Ubx* may be regulating the guidance receptor and its ligand, a regulation seen by other homeobox transcription factors outside the nervous system [122,123].

Many other guidance genes have been described as putative targets of *isl*, *hb9*, *lim3* and *eve* through high throughput screens using DNA adenine methyltransferase identification (DamID) [124]. Results from these studies suggest a combinatorial regulation as multiple transcription factors interact with putative regulatory regions of individual genes [124,125].

4.3. Dorsoventral determination and transcriptional repression

Interestingly, there are crossrepressive interactions between transcription factors specific for dorsal and ventral projecting MNs. Parallel function of *nkx6* and *hb9* limits *eve* expression to dorsal MNs and panneuronal misexpression of *eve* represses *hb9* and *nkx6* effectively locking a code for dorsal MNs versus ventral MNs within the ISN branch [108,113–116]. In addition *eve* misexpression in RP MN represses *lim3* and *Isl* [114]. This function is consistent with *Nkx6*, *Hb9*, and *Eve* functioning as repressors, as they contain corepressor interacting domains required for their rescue of motor axon guidance in *eve* and *hb9* mutants [37,109] (Fig. 3).

The repressor domain of *Hb9* is also required for promoting *robo2* expression, perhaps through the suppression of a *robo2* direct inhibitor [37]. In a recent study in which microarray gene expression profiling and the genome-wide DamID were applied in parallel, *hb9* and *nkx6* were shown to exert their effect mainly through the repression of a wide range of target genes, most of which are transcription factor coding genes [126]. It is likely that these dorsal and ventral MN determinants work in this particular fashion to lock the fates of the NMs they specify preventing globally expression of any gene that could trigger a different program.

5. Redundancy and cooperation

A common aspect in the motor system is a relatively low penetrance of phenotypes in mutants for guidance molecules contrasting with strong misexpression effects of the same molecule [127]. With relatively few exceptions Mutants show defects in 20–40% of hemisegments, and many times lower with relatively mild defects affecting a reduced number of branches or muscle contacts. Misexpression studies of single or double combinations of ligands in the muscle field not only revealed functions of these molecules unidentified in mutant studies but started to point out that growth cones respond based on “combinatorial” input of multiple cues [53,62]. The robustness of the neuromuscular system seems to be built in functional redundancy. This is perhaps most obvious when families of molecules and effects of single and compound mutants are studied. For example in the RPTP family (Section 3.4) only 3 of them, *lar*, *Ptp69D* and *Ptp52F*, present an obvious phenotype in the neuromuscular system. However, it is clear from compound mutants that *Ptp99A* and *Ptp10D* also play a role [76,79,80]. This functional redundancy likely arises from gene duplication as is seen in Beat family where Beats of the same subgroup have very similar expression pattern in individual neurons and bind the same ligand [91]. Obviously, subfunctionalization and

expression pattern divergence in occur over time and is responsible for nervous system complexity (Table 1).

The robustness in the motor system does not seem to arise through functional redundancy but through cooperative functions that result in a similar response. This is clearly exemplified in compound mutant studies of molecules with diverse function (Section 3) like *Unc-5*, a repulsive receptor, *Beat 1a* (an attractive receptor/CAM) and two CAMs (*Fas2* and *Nrg*) [20]. Mutants on each one of their genes results in mild or no phenotype in the ISN but double or triple mutants of these genes show more severe defects [20] (Table 1). In addition, their combinatorial restoration in aCC and RP2 cells lacking them all (an *eve* mutant background) results in more efficient rescue than single gene re-expression [20]. Strikingly, combined misexpression of these membrane molecules in CNS local interneurons that do not exit the CNS makes them behave as MN and redirects their axons toward the muscle field. Combines misexpression in this case is critical as exit rarely happens when these genes are misexpressed individually [20]. This study shows that concerted function of attractive and repulsive receptors along with cell adhesion molecules is required to achieve the adequate guidance response indicating that different functions cooperate in the process.

Motor guidance of each individual branch seems to be governed by common regulators on each branch and it is interesting that ISN (dorsal branch) is specified by one regulator, *eve*, that seems to control the global expression of the guidance molecules collaborating in its pathfinding [20]. In a similar way ventral determinants collaborate on the ISNb [21]. While *robo2* and *fra* deficient embryos present deficient innervation of muscles 6/7 from the ISNb, double mutants show a stronger effect, highlighting their cooperative response [21]. This response is again coordinated by the concerted action of the ventral determinants *dhhb9* and, likely, *nkx6* (through *Isl*) [21]. Individual MN within the same branch will likely have a slightly different repertory of guidance molecules differentially regulated through transcription as it has been shown for aCC and RP2 [110].

Thus, motor axon guidance is an intricate process where master transcriptional determinants seem to globally regulate a shared battery of downstream guidance effectors, which cooperate with one another for proper motor nerve guidance.

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