Matrix metalloproteinases promote motor axon fasciculation in the *Drosophila* embryo

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Matrix metalloproteinases (MMPs) are a large conserved family of extracellular proteases, a number of which are expressed during neuronal development and upregulated in nervous system diseases. Primarily on the basis of studies using pharmaceutical inhibitors, MMPs have been proposed to degrade the extracellular matrix to allow growth cone advance during development and hence play largely permissive roles in axon extension. Here we show that MMPs are not required for axon extension in the *Drosophila* embryo, but rather are specifically required for the execution of several stereotyped motor axon pathfinding decisions. The *Drosophila* genome contains only two MMP homologs, *Mmp1* and *Mmp2*. We isolated *Mmp1* in a misexpression screen to identify molecules required for motoneuron development. Misexpression of either MMP inhibits the regulated separation/defasciculation of motor axons at defined choice points. Conversely, motor nerves in *Mmp1* and *Mmp2* single mutants and *Mmp1* *Mmp2* double mutant embryos are loosely bundled/fasciculated, with ectopic axonal projections. Quantification of these phenotypes reveals that the genetic requirement for *Mmp1* and *Mmp2* is distinct in different nerve branches, although generally *Mmp2* plays the predominant role in pathfinding. Using both an endogenous MMP inhibitor and MMP dominant-negative constructs, we demonstrate that MMP catalytic activity is required for motor axon fasciculation. In support of the model that MMPs promote fasciculation, we find that the defasciculation observed when MMP activity is compromised is suppressed by otherwise elevating interaxonal adhesion – either by overexpressing *Fas2* or by reducing *Sema-1a* dosage. These data demonstrate that MMP activity is essential for embryonic motor axon fasciculation.

KEY WORDS: *Drosophila melanogaster*, Motoneuron, Motor axon pathfinding, *Mmp1*, *Mmp2*, *Sema-1a*, Fasciclin II, Timp

INTRODUCTION

Motor axons navigate an extracellular environment rich with potentially competing attractive and repulsive cues. Remarkably, motor axon growth cones are able to both interpret and integrate the signals present in this complex environment en route to their individual muscle targets. The particular axonal trajectory taken by any given motoneuron depends on the nature of the extracellular cues encountered by the extending axon as well as the complement of receptor or adhesion molecules expressed on its growth cone. In addition, several molecules required for either the activation or distribution of extracellular guidance molecules have recently been implicated in axon guidance (Johnson et al., 2004; Meyer and Aberle, 2006; Parker et al., 2006; Serpe and O’Connor, 2006; Steigemann et al., 2004).

The number and diversity of molecules implicated in motor axon pathfinding suggest that work in genetic model systems will continue to be essential to identify and tease apart the relative contributions of proteins involved in this process. In particular, the *Drosophila* embryo provides an important model for the study of motor axon pathfinding as a result of the small number of motoneurons, their defined trajectories and invariant muscle targets (Landgraf et al., 1997; Schmid et al., 1999; Sink and Whittington, 1991). Work by a number of groups has led to the identification and characterization of molecules critical for pathfinding and target recognition by *Drosophila* motor axons (Fox and Zinn, 2005; Terman et al., 2002; Van Vactor et al., 1993). An underlying principle to emerge from these studies is that in order for axons to reach their muscle targets, the activity of adhesion molecules that promote the fasciculation and/or bundling of motor axons must be precisely balanced with repulsive signals that trigger the defasciculation and/or separation of the extending axons (Winberg et al., 1998a; Yu et al., 2000).

Although the mechanisms responsible for limiting defasciculation to defined choice points in the periphery are not clear, a number of molecules necessary for proper defasciculation have been identified. In particular, repulsive signaling mediated by the Semaphorin-Plexin (*Sema-Plex*) pathway is essential for motor axon defasciculation (Ayoob et al., 2006; Terman et al., 2002; Winberg et al., 1998a; Yu et al., 2000). In wild-type embryos, axons of the intersegmental nerve branch b (ISNb) defasciculate from the primary ISN pathway and innervate the ventrolateral muscle (VLM) field. In embryos with reduced *Sema-Plex* pathway activity, however, ISNb axons fail to reach their targets and often remain bundled with the primary ISN branch – a phenotype consistent with diminished interaxonal repulsion. Furthermore, embryos with loss-of-function (LOF) mutations in *nerve* and *protein kinase A RII*, two genes that have been proposed to antagonize *Sema-Plex* signaling, exhibit premature and excessive motor axon defasciculation (Terman and Kolodkin, 2004). By contrast, LOF mutations in the genes for cell adhesion molecules Fasciclin II (*FasII*) or Connectin (*Con*) suppress LOF mutations in *Sema-1a* and *plexA*, arguing that *Sema-1a* and *PlexA* stimulate defasciculation by overcoming axon-axon adhesion maintained by *FasII* and *Con* (Winberg et al., 1998a; Yu et al., 2000). These genetic interaction studies demonstrate the importance of balancing attractive and repulsive forces to enable correct fasciculation and pathfinding.

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To understand how the precise balance of attraction and repulsion is achieved, the roles of additional molecules capable of modulating fasciculation of extending motor axons must be characterized. A number of studies have investigated the roles of metalloproteinases in axon extension and guidance. The metzincin metalloproteinases are zinc-dependent extracellular proteases that are subdivided into four subfamilies based on structure: astacins, serralysins, matrix metalloproteinases (MMPs) and adalysins – a subfamily that includes the ADAMs (a disintegrin and a metalloproteinase) (Sternlicht and Werb, 2001). Classic models of metalloproteinase function in neuronal development proposed that they acted to degrade extracellular matrix (ECM) in order to clear a path for advancing axons (Muir, 1994; Zuo et al., 1998). Recently, the roles of metalloproteinases in axonogenesis have been revisited in a number of experimental systems (McFarlane, 2003). These studies indicate that relevant neuronal metalloproteinase substrates include molecules directly involved in mediating axon pathfinding, including guidance receptors and their ligands. Among the metalloproteinases, the ADAM family is most strongly implicated in the regulation of axon guidance. For instance, ADAM10 terminates the interaction between ephrin A2 and EphA by cleaving ephrin A2, thereby facilitating axon retraction in vitro (Hattori et al., 2000). Analyses of Drosophila embryos mutant for the ADAM family homolog kuzbanian (kuc) further support the idea that ADAMs regulate particular guidance events, as kuc mutations display genetic interactions with mutations in the repulsive midline factor slit (Schimmelpfeng et al., 2001). Interestingly, independent work from several groups has recently provided evidence that tolloid-related 1 (trl; also known as tolkin – FlyBase), a Drosophila astacin-family metalloproteinase, acts through its TGFβ ligand Dawdle to regulate motor axon guidance in the embryo (Meyer and Aberle, 2006; Parker et al., 2006; Serpe and O’Connor, 2006).

As a family, MMPs are able to cleave nearly every component of the ECM, as well as numerous signaling molecules and cell surface receptors (Sternlicht and Werb, 2001). In the CNS, investigations of MMP function have largely centered on the roles of these proteases in nervous system disease, as MMPs are known to be dramatically upregulated in a host of CNS diseases, as well as following nervous system injury (Yong, 2005; Yong et al., 2001). However, in large part due to issues of redundancy and compensation among the twenty-four vertebrate MMP family members, the normal physiological roles of MMPs in the nervous system have remained largely elusive. Notably, a number of vertebrate MMPs display neuronal expression patterns in the embryo, suggesting that they may be involved in normal nervous system development (Gonthier et al., 2007; Hayashita-Kinoh et al., 2001; Hehr et al., 2005). In support of this model, studies of Xenopus retinal ganglion cell axon guidance using MMP pharmacological inhibitors suggest that MMPs are required for specific pathfinding decisions (Hehr et al., 2005). Drosophila affords an attractive genetic model system in which to study MMP function since there are only two MMP family members in the fly, Mmp1 and Mmp2 (Llano et al., 2002; Llano et al., 2000; Page-McCaw et al., 2003). Whereas Mmp1 is a secreted protein, Mmp2 contains a GPI-anchor sequence and has been shown to be membrane-bound in tissue culture cells.

In this work, we present an analysis of MMP function during Drosophila embryonic neuronal development. Both LOF and gain-of-function (GOF) analyses support the model that MMP activity promotes motor axon fasciculation in the embryo. Misexpression of either Mmp1 or Mmp2 drives excessive motor axon fasciculation. By contrast, we find aberrant defasciculation in MMP LOF mutants. Although Mmp1 mutants display relatively mild pathfinding defects, many motor axons separate prematurely and aberrantly in Mmp2 single mutants and Mmp1 Mmp2 double mutants, indicating that Mmp2 plays a primary role in motor axon fasciculation. We have analyzed the embryonic expression of both MMPs and find that whereas Mmp1 exhibits a limited embryonic expression profile, Mmp2 is expressed in neurons and glia – supporting a primary role for Mmp2 in embryonic neuronal development. Importantly, we find aberrant motor axon defasciculation in embryos misexpressing the endogenous MMP inhibitor Temp and in embryos misexpressing MMP dominant-negative constructs, indicating that MMP catalytic activity is essential for pathfinding. Finally, we show that the defasciculation phenotype exhibited by MMP LOF mutants are dominantly suppressed by LOF mutations in Sema-1a, arguing that MMP activity normally acts to promote fasciculation by antagonizing Sema-1a function. Together, our results indicate that MMPs are not required for motor axon extension per se, but instead may modulate the responses of the axons of defined neuronal populations to specific guidance cues.

MATERIALS AND METHODS
Gene misexpression screen

To identify novel factors required for embryonic CNS development, we conducted a GOF screen for genes whose misexpression disrupted motoneuron fate or pathfinding. We screened a collection of 2800 Drosophila lines harboring P elements containing the yeast GAL4 binding site UAS (Rorth et al., 1998; Toba et al., 1999; Viquez et al., 2006). Males from these P-element insertion lines were crossed to elavGAL4 virgin females to drive misexpression of the gene adjacent to the P-element insertion in all post-mitotic neurons (DiAntonio et al., 2001; Yao and White, 1994). We first selected those lines in which elavGAL4-dependent misexpression was lethal, as we reasoned this would enrich for genes with neuronal misexpression phenotypes. As a secondary screen, we crossed males from the 114 elavGAL4-dependent lethal lines to elavGAL4 virgins and collected embryos to screen for neuronal phenotypes. We analyzed CNS cell fate by staining with antibodies labeling specific neuronal populations, including anti-Even-skipped, anti-Hb9 [also known as Extra-extra (Exex) – FlyBase], and anti-Nk6 [also known as HGTX – FlyBase] (Broihier et al., 2002; Broihier and Skeath, 2004; Landgraf et al., 1999). For lines in which neuronal fate appeared normal, we screened for axon guidance phenotypes using anti-Fasciclin II (anti-FasII) (Van Vactor et al., 1993) to label motor axon projections.

Fly stocks

Stocks used in this work include: Mmp2W307*, Mmp2E258Ae1-1-Mmp2, Mmp1Q112*, Mmp1F1, Mmp2W307* Mmp1Q112*, Mmp2W307* (2R/aie1-Mmp2 Mmp1Q112*, UAS-TIMP, UAS-Mmp2, UAS-Mmp1 (Page-McCaw et al., 2003), UAS-Mmp2W307* (below), UAS-Mmp1Q112* (Zhang et al., 2006), UAS-Fas2 from A. DiAntonio (Washington University, St Louis, MO), gcm/P element from M. Freeman (University of Massachusetts, Worcester, MA), repoGAL4 from J. Simpson (HHMI Janelia Farm Research Campus, Ashburn, VA), Hb9GAL4 (Broihier and Skeath, 2002). The Sema-1aP1 Mmp2W307*, Sema-1aP1 Mmp1Q112* recombinant chromosomes were generated by standard genetic techniques. All other stocks were obtained from Bloomington Stock Center.

Transgenic MMP constructs

US-6-Mmp1E225A contains a missense mutation in the conserved catalytic core that renders the enzyme catalytically inactive; in cell culture Mmp1E225A acts dominantly to inhibit Mmp1 function (Zhang et al., 2006). Similarly, US-Mmp2E225A disrupts the conserved catalytic core of Mmp2 and is expected to function as a dominant negative; the PCR-generated mutant cDNA was cloned into pUAST and injected into flies by standard methods. For the misexpression analysis with elavGAL4 and repoGAL4, similar results were observed with each of two independent transgenic lines for both
**UAS-Mmp1** and **UAS-Mmp2** (Page-McCaw et al., 2003). This similarity argues that the observed phenotypic differences are unlikely to be the result of expression level differences between the UAS responder lines.

**Antibodies**

*Drosophila* embryos were fixed by gentle rocking for 4 minutes in 2 ml heptane and 2 ml 37% formaldehyde followed by 30 seconds of shaking in 6 ml methanol to devitellinize. The following primary antibodies were used: mouse anti-FasII/1D4 at 1:10 (generated by C. Goodman and obtained from the Developmental Studies Hybridoma Bank (DSHB)), rabbit anti-GFP at 1:100 (Invitrogen), mouse anti-Wrapper at 1:10 (generated by C. Goodman and obtained from the DSHB), mouse anti-Repo at 1:10 (generated by C. Goodman and obtained from the DSHB), mouse anti-β-gal at 1:1000 (Promega), rat anti-Islet at 1:100 and rabbit anti-Hb9 at 1:500 (Broshier and Skeath, 2002), and an anti-Mmp1 monoclonal cocktail (a 1:1:1 mixture of 3B8, 5H7 and 23G1) at 1:50 (generated by A. Page-McCaw and obtained from the DSHB). Species-specific biotinylated secondary antibodies were used at 1:300 in concert with the ABC Elite kit for immunohistochemistry (Vector Labs). Species-specific Alexa Fluor 488 and Alexa Fluor 568 (Molecular Probes) were used for immunofluorescence. Embryos stained with anti-GFP were fixed for 40 minutes in 3 ml heptane and 3 ml 4% paraformaldehyde. For these embryos, incubation with ABC was followed by treatment with the TSA Biotin System kit (PerkinElmer), followed by another incubation with ABC before developing.

**In situ hybridization**

An antisense digoxigenin-labeled Mmp2 RNA probe was generated with T7 polymerase from a full-length cDNA. Sense probes generated with T3 polymerase did not result in specific hybridization. Embryos were incubated with riboprobe at 57°C overnight. RNA probe hybridization was visualized with an alkaline phosphatase-conjugated anti-DIG antibody (Roche) with riboprobe at 57°C overnight. RNA probe hybridization was visualized with anti-DIG-POD antibody (Roche) followed by storage in 70% ethanol overnight and standard antibody staining. For fluorescent labeling, an anti-DIG-POD antibody (Roche) was used to recognize the probe and was amplified using the TSA Plus Fluorescence system (PerkinElmer).

**Microscopy and data analysis**

Embryos were filleted in 70% glycerol under a Leica MZ125 dissecting microscope. Specimens were analyzed on a Zeiss Axioplan 2 microscope with a 63× or 100× oil-immersion objective using Nomarski optics, and images were captured with an AxioCam MRc camera. Brightness and contrast were adjusted using Adobe Photoshop. Fluorescence images were obtained on a Zeiss Axio Imager.Z1 confocal microscope and edited with LSM 5 Image Browser. Statistical analyses were performed using Fisher’s exact test.

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**Table 1. Mmp/Timp misexpression phenotypes**

<table>
<thead>
<tr>
<th>Genotype</th>
<th>Total aberrant ISNb % (n)</th>
<th>Stall</th>
<th>Fusion bypass</th>
<th>Total</th>
<th>Hyposfasculation ISNb %</th>
<th>Total aberrant SNa % (n)</th>
<th>Hyperfasculation SNa %</th>
<th>Hypofasculation SNa %</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Wild type</strong></td>
<td>13 (140)</td>
<td>7</td>
<td>0</td>
<td>7</td>
<td>6</td>
<td>11 (160)</td>
<td>5</td>
<td>7</td>
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<tr>
<td>elav&gt;Mmp1</td>
<td>74 (138)</td>
<td>33</td>
<td>14</td>
<td>47</td>
<td>11</td>
<td>50 (129)</td>
<td>39</td>
<td>11</td>
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<tr>
<td>repo&gt;Mmp1</td>
<td>46 (121)</td>
<td>17</td>
<td>9</td>
<td>26</td>
<td>16</td>
<td>68 (131)</td>
<td>44</td>
<td>24</td>
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<tr>
<td>elav&gt;Mmp2</td>
<td>72 (147)</td>
<td>39</td>
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<td>50</td>
<td>1</td>
<td>80 (145)</td>
<td>68</td>
<td>12</td>
</tr>
<tr>
<td>repo&gt;Mmp2</td>
<td>82 (120)</td>
<td>33</td>
<td>30</td>
<td>63</td>
<td>3</td>
<td>70 (109)</td>
<td>61</td>
<td>9</td>
</tr>
<tr>
<td>elav&gt;Timp</td>
<td>54 (425)</td>
<td>7</td>
<td>1</td>
<td>8</td>
<td>41</td>
<td>58 (439)</td>
<td>17</td>
<td>44</td>
</tr>
<tr>
<td>repo&gt;Timp</td>
<td>65 (362)</td>
<td>4</td>
<td>0</td>
<td>4</td>
<td>54</td>
<td>75 (357)</td>
<td>24</td>
<td>54</td>
</tr>
<tr>
<td>elav&gt;Mmp2F225A</td>
<td>66 (167)</td>
<td>13</td>
<td>1</td>
<td>14</td>
<td>37</td>
<td>64 (125)</td>
<td>49</td>
<td>23</td>
</tr>
<tr>
<td>repo&gt;Mmp2F225A</td>
<td>72 (141)</td>
<td>4</td>
<td>2</td>
<td>6</td>
<td>50</td>
<td>54 (163)</td>
<td>26</td>
<td>36</td>
</tr>
<tr>
<td>elav&gt;Mmp1F225A</td>
<td>58 (147)</td>
<td>1</td>
<td>0</td>
<td>1</td>
<td>34</td>
<td>42 (147)</td>
<td>9</td>
<td>33</td>
</tr>
<tr>
<td>repo&gt;Mmp1F225A</td>
<td>61 (150)</td>
<td>3</td>
<td>0</td>
<td>3</td>
<td>39</td>
<td>34 (149)</td>
<td>9</td>
<td>24</td>
</tr>
</tbody>
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n: The number of hemisegments scored for each genotype.

*Includes hyperfasciulated, hypofasciulated and loss/reduction of the synapse in the 6/7 muscle cleft, which could be attributed to either hypo- or hyperfascication.

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**RESULTS**

**Pan-neuronal misexpression of either Mmp1 or Mmp2 inhibits motor axon defasciculation**

We conducted a misexpression screen to identify genes required for embryonic neuronal fate and axon pathfinding (see Materials and methods). In this manner, we identified several P-element lines in which the wild-type pattern of motor axon projections was disrupted. In wild type, ISNb axons defasciculate or separate from the primary ISN nerve at their first choice point proximal to the ventrolateral muscle (VLM) field. Within the VLM field, ISNb axons continue to extend dorsally, with axonal subsets defasciculating from the ISNb at secondary choice points when they contact their muscle targets (Fig. 1A,D). Embryos from one of the lines isolated in the screen, GS2402, exhibited strongly stalled ISNb motor axons (termed a ‘stall’ phenotype; data not shown). Inverse PCR analysis indicated that this line contained a P element inserted directly upstream of Mmp1.

To confirm that Mmp1 misexpression was responsible for the motor axon phenotypes observed in GS2402, we used a UAS-Mmp1 transgene (Page-McCaw et al., 2003) to drive Mmp1 throughout the embryonic CNS via elavGAL4. Consistent with the identification of Mmp1 in our screen, neuronal misexpression of Mmp1 interferes with embryonic motor axon guidance (Table 1; Fig. 1A,B). ISNb morphology was disrupted in elavGAL4/UASMmp1 mutant embryos in 74% of hemisegments scored (n=138). The majority of affected hemisegments displayed phenotypes indicative of increased motor axon fasciculation, ranging from relatively mild defects to a complete block of proper ISNb defasciculation. Specifically, aberrant hemisegments often exhibited ISNb stall phenotypes, in which ISNb axons separated from the ISN at their first choice point, but subsequently failed to defasciculate from each other at their individual muscle targets, instead stalling in the ventral longitudinal muscle field (33%; Table 1; Fig. 1B,E). In 14% of hemisegments we observed a stronger ‘fusion bypass’ phenotype, in which ISNb axons failed to defasciculate from the ISN at the first ISNb choice point and remained bundled with ISN axons (e.g. Fig. 1C).

To investigate whether the effects of Mmp1 misexpression were restricted to the ISNb branch, we evaluated segmental nerve branch (SNa) guidance in embryos with Mmp1 expressed pan-neuronally. In wild type, axons within SNa exit the CNS and extend dorsally past the ventral longitudinal muscles to innervate the lateral muscle...
field. Just dorsal to the ventral longitudinal muscles, SNa axons reach their first choice point and separate into dorsal and posterior branches. Axons in the posterior branch innervate muscle 8, whereas axons in the dorsal branch extend dorsally between muscles 22 and 23 before subdividing again at their second choice point with a posterior sub-branch turning to innervate muscle 24 (Fig. 1G,J; Table 1). We found that neuronal misexpression of Mmp1 disrupted SNa pathfinding in 50% of hemisegments, with most hemisegments (39%) containing SNa nerves that failed to branch appropriately or stalled in the lateral muscle field. Typically, axons in the dorsal SNa branch failed to separate at the second choice point resulting in a failure to innervate muscle 24 (Fig. 1H,K; Table 1). These data demonstrate that neuronal Mmp1 misexpression drives axon hyperfasciculation in multiple embryonic motor nerve pathways.

Fig. 1. Pan-neuronal misexpression of either Mmp1 or Mmp2 inhibits motor axon defasciculation. In each micrograph, two abdominal hemisegments of stage 17 dissected embryos stained with α-FasII to label the motor projections are shown with anterior left and dorsal up. Below each image are schematics diagramming the observed phenotypes with motor axons in brown and muscles represented by gray boxes. In all ISNb schematics, the muscles are drawn as if transparent in order to depict both the ISN and ISNb pathways. However, note that the ISN extends in an external plane whereas the ISNb extends in an internal plane. (A,D) In wild type, ISNb axons defasciculate from the ISN at a choice point proximal to the VLM field (arrowheads), then continue to extend dorsally to innervate muscles 7, 6, 13, 12. (B,C,E,F) In elav>Mmp1 and elav>Mmp2 embryos, ISNb axons appear to defasciculate correctly from the ISN at their first choice point, but fail to defasciculate at their appropriate muscle targets, a phenotype referred to as ‘stall’. (G,J) In wild type, the SNa branch innervates the lateral musculature and comprises dorsal and posterior branches. The posterior branch extends posteriorly to innervate muscle 8, whereas the dorsal branch makes two stereotyped turns en route to muscles 23 and 24. (H,K) In elav>Mmp1 embryos, the dorsal branch of the SNa stalls (arrowhead) before reaching its final target. (I,L) In elav>Mmp2 embryos, the dorsal (arrowheads) and lateral branches of the SNa stall before reaching their synaptic targets. Scale bar: 15 μm.

Since vertebrate MMPs often display overlapping substrate specificities (Page-McCaw et al., 2007), we wanted to determine whether neuronal misexpression of Mmp2 would have similar phenotypic consequences to Mmp1 misexpression. We found that elavGAL4/UASMmp2 embryos also exhibit aberrant axonal phenotypes consistent with increased motor axon fasciculation (Fig. 1; Table 1). In these embryos, ISNb pathfinding is aberrant in 72% of hemisegments, with 50% of all hemisegments displaying either ISNb stall or fusion bypass phenotypes (n=147; Fig. 1C,F). Furthermore, neuronal misexpression of Mmp2 interfered with SNa pathfinding in 80% of hemisegments, with axons in 68% of hemisegments either stalling or failing to branch appropriately (Fig. 1I,L). Although Mmp1 and Mmp2 misexpression have comparable effects on ISNb pathfinding, SNa appears particularly sensitive to Mmp2 levels since the penetrance of SNa phenotypes is significantly higher with Mmp2 misexpression (P<0.0001; Table 1). Together, these data indicate that pan-neuronal misexpression of either MMP inhibits the ability of motor axons in both ISNb and SNa to appropriately defasciculate en route to their muscle targets and raises the possibility that matrix metalloproteinases contribute to proper motor axon guidance in the embryo.
MMPs exhibit distinct and spatially restricted expression profiles in embryogenesis

To further investigate the possibility that MMP activity plays a role in neuronal development, we characterized the embryonic expression patterns of \( \text{Mmp1} \) and \( \text{Mmp2} \). Previous studies have established that both genes are embryonically expressed (Llano et al., 2002; Llano et al., 2000; Page-McCaw et al., 2003). Using anti-Mmp1 antibodies, we found Mmp1 protein to be expressed in essentially the same spatiotemporal expression profile as has been described for \( \text{Mmp1} \) RNA. The most prominent embryonic expression of Mmp1 is in the proventriculus and hindgut (data not shown). Consistent with previous studies (Llano et al., 2000; Page-McCaw et al., 2003), we found Mmp1 CNS expression to be restricted to small clusters of segmentally repeating cells at the CNS midline (data not shown). We also detected Mmp1 expression in the chordotonal organs of the peripheral nervous system (Fig. 2A) and in two cells situated in the ventral mesodermal region (Fig. 2B). This expression is undetectable in \( \text{Mmp1} \)-null mutant embryos, \( \text{Mmp1}^{\text{null}} \), confirming antibody specificity (data not shown).

We next characterized the expression pattern of \( \text{Mmp2} \) via whole-mount RNA in situ hybridization. In contrast to \( \text{Mmp1} \), \( \text{Mmp2} \) is widely expressed in the embryonic CNS (Fig. 2C). To identify the neuronal cells, we double labeled wild-type embryos with \( \text{Mmp2} \) RNA and markers for specific neural and glial populations. We found that \( \text{Mmp2} \) is expressed in midline glia as \( \text{Mmp2} \) RNA is co-expressed with \( \text{Wrapper} \) in these cells (Fig. 2D) (Noordermeer et al., 1998). We next tested whether \( \text{Mmp2} \) is expressed in additional glial populations by co-labeling embryos with \( \text{Mmp2} \) RNA and the glial marker anti-Repo (Xiong et al., 1994). At stage 15, \( \text{Mmp2} \) and Repo are co-expressed in approximately three glial cells per hemisegment (arrows). The position and morphology of these cells suggest they correspond to exit glia, a group of peripheral glia originating within the CNS before migrating into the periphery during embryogenesis along extending motor axons (Klambt and Goodman, 1991; Sepp et al., 2000). To confirm that these \( \text{Mmp2} \)-expressing cells are glia, we asked whether they are absent in embryos mutant for \( \text{glial cells missing} \) (\( \text{gcm} \)), in which the number of glial cells is greatly reduced (Jones et al., 1995). In support of this conclusion, \( \text{gcm} \) mutant embryos specifically lack the \( \text{Mmp2} \)-expressing cells situated at the boundary between the CNS and periphery (arrows in Fig. 2F).

The observation that \( \text{Mmp2} \)-positive cells within the CNS do not co-express Repo suggested that they are probably neurons. To determine whether they correspond to well-characterized subsets of motoneurons or interneurons, we double labeled embryos with \( \text{Mmp2} \) RNA and antibodies specific for particular neuronal populations. We detected co-expression between \( \text{Mmp2} \) and \( \text{Islet} \), a marker for distinct motoneuron and interneuron populations (Thor...

**Fig. 2.** Embryonic expression profiles of \( \text{Mmp1} \) and \( \text{Mmp2} \). (A-E,G,H) Stage 15 wild-type embryos stained for indicated markers. (F) Stage 15 \( \text{gcm}^{\text{sh2}} \) homozygous mutant embryo stained for \( \text{Mmp2} \) RNA and labeled with anti-Repo. (A) Mmp1 is expressed in PNS neurons in the chordotonal organs and (B) in two cells in the ventral longitudinal muscle field (arrows). (C) Expression of \( \text{Mmp2} \) RNA indicates that \( \text{Mmp2} \) is expressed in a subset of CNS neurons and glia (circled in red). (D) \( \text{Mmp2} \) RNA (green) colocalizes with anti-\( \text{Wrapper} \) (red) in midline glia. (E) Nuclear anti-Repo (brown) and cytoplasmic \( \text{Mmp2} \) RNA (purple) in a subset of exit glia (arrows). (F) In \( \text{gcm}^{\text{sh2}} \) embryos, which lack most glia, \( \text{Mmp2} \) RNA is no longer expressed at the lateral edge of the CNS where the exit glia are located (arrows). (G) Anti-\( \text{Islet} \) (brown) colocalizes with \( \text{Mmp2} \) RNA (purple) in approximately three neurons per hemisegment (arrows). The location of these neurons is consistent with an interneuron identity. (H) Anti-\( \text{Hb9} \) (brown) does not colocalize with \( \text{Mmp2} \) RNA (purple). Insets in G and H show high-magnification views of \( \text{Mmp2} \) expression. Dotted white line marks the CNS boundary. Anterior is up in all panels. Dorsal is right in A,B,E,F. Scale bars: 10 \( \mu \text{m} \) in A,B,E,F; 20 \( \mu \text{m} \) in C,D,G,H.
and Thomas, 1997), in three neurons per hemisegment in the lateral CNS (arrows in Fig. 2G). We next asked whether these Mmp2-expressing neurons are Hb9-positive motoneurons. We did not detect co-expression between Hb9 and Mmp2 RNA (Fig. 2H), suggesting that the Mmp2-positive neurons in the lateral CNS are Islet-positive interneurons. In sum, whereas Mmp1 exhibits a limited neuronal expression pattern, Mmp2 is expressed in stereotyped populations of neurons and glia, consistent with a role for Mmp2 in neuronal development.

**MMP misexpression in glia blocks motor axon defasciculation.**
Mmp1 is a secreted protein, whereas Mmp2 contains a GPI-anchor and is membrane-associated (Llano et al., 2002; Llano et al., 2000; Page-McCaw et al., 2003) – suggesting that the distribution of Mmp2 may be critical for Mmp2 to have access to its substrate. Although we did not detect endogenous Mmp2 RNA expression in the mesoderm or in motoneurons, Mmp2 is expressed in a subset of peripheral glia that are closely associated with extending motor axons. To test if glial expression of Mmp2 might play a role in motor axon pathfinding, we analyzed the phenotypic consequences of Mmp2 misexpression in glia using a repoGAL4 driver. For comparison, we also quantified motor axon pathfinding in repoGAL4>Mmp1 embryos. We first visualized glia in repo>Mmp1 and repo>Mmp2 embryos with anti-Repo since MMP misexpression might interfere with the migration of peripheral glia along the motor nerves (Sepp et al., 2000) and thereby indirectly influence motor axon pathfinding. We found that the number and position of Repo-positive glia are unaltered with glial misexpression of either Mmp1 or Mmp2 (data not shown).

We then analyzed motor axon pathfinding in repo>MMP embryos. Glial misexpression of either MMP leads to phenotypes that are qualitatively similar to those observed with neural misexpression. In these embryos, axons in both ISNb and SNa stall prematurely and fail to branch appropriately (Table 1; Fig. 3). For Mmp1, the frequency of ISNb hyperfasciculation decreases from 47% in elav>Mmp1 embryos to 26% in repo>Mmp1 embryos, suggesting that the level of secreted Mmp1 may be higher with glial misexpression. By contrast, glial misexpression of Mmp2 significantly increases the frequency of motor axon fasciculation defects compared to neural misexpression of Mmp2 in the ISNb (63% vs 50%; P<0.05; Table 1; Fig. 3C,F). This is particularly striking for the ISNb fusion bypass phenotype – the strongest class of ISNb hyperfasciculation. We observed a fusion bypass phenotype in 11% of hemisegments in elav>Mmp2 embryos, compared to 30% in repo>Mmp2 embryos (Table 1). Hence, glial misexpression of Mmp1 does not enhance the phenotypes above those observed with elavGAL4; by contrast, Mmp2 misexpression in glia yields phenotypes significantly stronger than those induced by neuronal misexpression.

Since MMP misexpression in neurons or glia increases motor axon fasciculation, we next wanted to determine whether MMP misexpression in other embryonic tissues is also sufficient to interfere with motor axon pathfinding. Hence, we analyzed motor axon guidance in embryos misexpressing either Mmp1 or Mmp2 in mesoderm (using 24B-Gal4 and dme>2GAL4 drivers) or hemocytes (using HeGAL4 and CrGAL4 drivers). We did not detect motor axon phenotypes in embryos with MMP misexpression using any of these GAL4 drivers (data not shown), indicating that motor axon pathfinding is not affected by MMP misexpression in mesoderm or...
hemocytes, but is sensitive to elevated MMP levels in neurons and glia. For Mmp2 in particular, the penetrance and expressivity of motor axon phenotypes observed with glial Mmp2 misexpression as well as the endogenous expression of Mmp2 in a subset of peripheral glia suggest that Mmp2 expression levels in peripheral glia are critical for proper motor axon guidance.

**MMP LOF mutants display inappropriate motor axon defasciculation**

To determine if MMP function is necessary for neuronal development, we quantified motor axon pathfinding defects in Mmp1 and Mmp2 single mutant embryos as well as Mmp1 Mmp2 double mutants. In contrast to the hyperfasciculation phenotypes observed with MMP misexpression, MMP homozygous LOF mutants exhibit reduced fasciculation of the ISNb nerve (Table 2; Fig. 4). For Mmp1, we scored embryos homozygous mutant for a null allele, Mmp1<sup>Q112+</sup>, as well as embryos heterozygous for Mmp1<sup>Q112+</sup> and Mmp1<sup>2</sup>, a deletion removing almost all coding sequence (Page-McCaw et al., 2003). In embryos carrying either allelic combination of Mmp1, we found similar, if relatively mild, ISNb phenotypes. In affected hemisegments, ISNb pathfinding was roughly wild type, though the nerve was less tightly bundled and had a frayed appearance (compare Fig. 4A and B). Whereas 50% of Mmp1<sup>Q112+</sup>/Mmp1<sup>Q112+</sup> hemisegments displayed a loosely fasciculated ISNb morphology, the penetrance fell to 28% for Mmp1<sup>Q112+</sup>/Mmp1<sup>2</sup> embryos (Table 2), suggesting that a second-site mutation in the Mmp1<sup>Q112+</sup> line contributes to the observed ISNb phenotype.

For Mmp2, we analyzed embryos homozygous for the null allele, Mmp2<sup>W307+</sup>, and embryos heterozygous for Mmp2<sup>W307+</sup> and Mmp2<sup>2</sup> (2R)Uba1-Mmp2 (Mmp2<sup>2</sup>), a deletion removing the first three coding exons of Mmp2 (Page-McCaw et al., 2003). Embryos of both of these genotypes exhibited marked defects in ISNb fasciculation. The Mmp2 LOF phenotypes included not only the loosely bundled morphology observed in Mmp1 homozygotes, but also exuberant branching of the ISNb – with ectopic axonal projections splintering off inappropriately and extending improperly within the ventral longitudinal muscle field (compare Fig. 4A and C). Quantifying these phenotypes, we find that 85% of hemisegments from Mmp2<sup>W307+</sup> homozygotes and 74% of Mmp2<sup>W307+</sup>/Mmp2<sup>2</sup> hemisegments displayed either a frayed appearance or excessive projections (n=187 and 238; Table 2). The ISNb phenotypes apparent in both Mmp1 and Mmp2 homozygotes suggest that both MMPs contribute to proper bundling of the ISNb motor nerve branch, with Mmp2 playing the major role.

![Fig. 4. MMP LOF mutants display inappropriate ISNb defasciculation.](image-url)
Analyses of MMP double mutants have provided evidence for redundancy between MMPs in vertebrates (Oh et al., 2004; Stickens et al., 2004). To determine if the incomplete penetrance observed in Mmp1 and Mmp2 single mutants might be explained by genetic redundancy between Drosophila MMPs, we quantified motor axon pathfinding defects in Mmp1 Mmp2 double mutant embryos. We scored ISNb pathfinding in two different allelic combinations of Mmp1 Mmp2 double mutants – Mmp2W307* Mmp1Q112* homozygotes and Mmp2W307* Mmp12 Mmp2W307* Mmp1Q112/Mmp2Df.Mmp12. The guidance defects in the double mutants mirrored the phenotypes observed in Mmp2 single mutants both qualitatively and quantitatively (Fig. 4D; Table 2). We observed both loosely associated ISNb axons and ISNb axons separating prematurely and ectopically from the main nerve branch. The frequency of the hypofasciculation phenotypes is roughly 75% in both double mutant allelic combinations. This penetrance is nearly identical to that observed for Mmp2 single mutants, arguing that Mmp1 activity does not substantially compensate for the loss of Mmp2 function in promoting ISNb fasciculation.

To assess the LOF phenotypes in a second independent manner, we used Hb9GAL4 to drive expression of membrane-bound GFP in MMP mutant embryos, thereby limiting visualization to axonal projections of ventrally and laterally projecting Hb9-positive motoneurons (Fig. 4I-P) (Broihier and Skeath, 2002). By focusing on the projections of Hb9-expressing neurons, we can exclude the possibility that the ectopic ISNb projections observed in MMP mutants are the result of misrouting of motor axons that normally extend in different pathways, such as Eve-positive dorsally projecting motor axons (Landgraf et al., 1999). Hb9GAL4>GFP Mmp1 single mutant embryos stained with anti-GFP displayed comparable fraying of the ISNb to those stained with FasII antibody (compare Fig. 4B and J). Similarly, Hb9GAL4>GFP Mmp2 single mutants and Hb9GAL4>GFP Mmp1 Mmp2 double mutant embryos continued to exhibit loosely bundled axons and ectopic branching of the ISNb when stained with anti-GFP displayed comparable fraying of the ISNb to those stained with FasII antibody (compare Fig. 4B and J). Similarly, Hb9GAL4>GFP Mmp1Mmp2 double mutant embryos continued to exhibit loosely bundled axons and ectopic branching of the ISNb when stained with anti-GFP (Fig. 4D.C.D.K.L.). As ectopic ISNb projections are still frequently observed in these embryos, they likely correspond to misguided ISNb axons rather than motor axons misrouted from other pathways. These data support our quantitative FasII analysis and indicate that MMP activity is necessary for ISNb fasciculation.

### Table 2. Mmp1 and Mmp2 loss of function mutant phenotypes

<table>
<thead>
<tr>
<th>Genotype</th>
<th>Total aberrant ISNb</th>
<th>Hypofasciculation ISNb</th>
<th>Total aberrant SNa</th>
<th>Hypofasciculation SNa</th>
</tr>
</thead>
<tbody>
<tr>
<td>Wild type</td>
<td>13 (140)</td>
<td>7</td>
<td>12 (138)</td>
<td>7</td>
</tr>
<tr>
<td>Mmp1Q112*/Mmp1Q112*</td>
<td>70 (175)</td>
<td>1</td>
<td>50 (132)</td>
<td>2</td>
</tr>
<tr>
<td>Mmp1Q112*/Mmp12</td>
<td>74 (160)</td>
<td>1</td>
<td>28 (143)</td>
<td>3</td>
</tr>
<tr>
<td>Mmp2W307*/<em>Mmp2W307</em></td>
<td>90 (187)</td>
<td>1</td>
<td>85 (183)</td>
<td>3</td>
</tr>
<tr>
<td>Mmp2W307*/*Mmp2Df</td>
<td>77 (238)</td>
<td>3</td>
<td>74 (248)</td>
<td>6</td>
</tr>
<tr>
<td>Mmp2W307*/*Mmp12</td>
<td>86 (196)</td>
<td>0</td>
<td>79 (180)</td>
<td>3</td>
</tr>
<tr>
<td>Mmp2W307*/<em>Mmp1Q112</em>/</td>
<td>86 (175)</td>
<td>0</td>
<td>75 (186)</td>
<td>3</td>
</tr>
</tbody>
</table>

n, The number of hemisegments scored for each genotype.
†Includes hyperfasciculated, hypofasciculated and loss/reduction of the synapse in the 6/7 muscle cleft, which could be attributed to either hypo- or hyperfasciculation.

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**Fig. 5. MMP LOF mutants exhibit excessive SNa defasciculation.** In each micrograph, two abdominal hemisegments of stage 17 dissected embryos stained with α-FasII to label the motor projections, are shown with anterior left and dorsal up. Below each image are schematics of the observed phenotypes with motor axons in brown and muscles represented by gray boxes. (A,E) In wild type, the two branches of the SNa stay tightly bundled after dividing into dorsal and posterior branches and go on to correctly innervate their lateral muscle targets. (B,F) In Mmp1Q112*/Mmp12 embryos, axons within the dorsal and posterior SNa branches project ectopically (arrowheads). (C,G) Mmp2W307*/Mmp2Df mutants display aberrant SNa defasciculation (arrowheads) phenotypes similar to those observed in Mmp1 mutants. (D,H) SNa-projecting axons in Mmp2W307* Mmp1Q112*/Mmp2Df Mmp12 double mutant embryos branch aberrantly and are less tightly bundled (arrowheads). The penetrance of SNa defasciculation observed in MMP double mutants is increased relative to either MMP single mutant. Scale bar: 15 μm.
To determine if MMP LOF phenotypes are limited to the ISNb branch, we quantified SNa morphology in single and double mutant MMP embryos. Similar to the phenotypes observed for ISNb, we find evidence of decreased SNa fasciculation in MMP mutant embryos. Embryos of all six single and double mutant allelic combinations displayed SNa phenotypes consistent with decreased axonal fasciculation (Table 2; Fig. 5). In most cases, axons branched prematurely or inappropriately from either the dorsal or posterior SNa secondary branches (arrowheads in Fig. 5B,C,D). Whereas Mmp2 is primarily responsible for promoting ISNb fasciculation, we do not observe a statistically significant difference in the frequency of SNa defasciculation in Mmp1 (36%) compared to Mmp2 (44%) single mutants (P=0.1). These data indicate that Mmp1 plays a relatively more significant role in SNa pathfinding than in ISNb pathfinding. Consistent with an increased genetic requirement for Mmp1 activity in SNa fasciculation, mutant analysis indicates that Mmp1 activity alone can promote substantial SNa fasciculation. In double mutant embryos, the penetrance of SNa defasciculation is significantly increased relative to that of either single mutant (Table 2). Specifically, 57% of double mutant hemisegments displayed ectopic SNa branches, relative to 36% for Mmp1 mutants and 44% for Mmp2 (P<0.05 for both). These data indicate that in contrast to ISNb, Mmp1 and Mmp2 serve partially redundant functions in SNa fasciculation. Together, our analyses indicate that MMP activity promotes motor axon fasciculation of multiple motor nerves in the embryo. Whereas Mmp2 contributes significantly to fasciculation of both ISNb and SNa, we find that the role of Mmp1 in pathfinding is largely specific to SNa.

Although our data suggest that MMPs are directly involved in pathfinding, in vertebrates MMPs have been shown to regulate processes as diverse as cell proliferation, survival, and differentiation (Page-McCaw et al., 2007). To address the possibility that MMPs might indirectly influence axon pathfinding by affecting earlier aspects of neurogenesis, we analyzed neuronal fate in MMP LOF and GOF mutants using a battery of molecular markers for distinct neuronal populations including anti-Eve, anti-Hb9, and anti-Nx6 (Broihier et al., 2004; Broihier and Skeath, 2002). We do not detect any aberrations in neuronal fate specification in any MMP mutant background (C.M.M. and H.T.B., unpublished). The finding that MMPs do not appear to play a role in neural development prior to axon outgrowth is consistent with our expression analysis (see above) indicating that the MMP expression in the CNS initiates at stage 14 in post-mitotic neurons and glia.

**Inhibition of MMP catalytic activity disrupts motor axon guidance**

Our studies indicate that the level of MMP expression is a critical determinant of the degree of motor axon bundling. To test whether MMP catalytic activity regulates axon pathfinding, we specifically interfered with MMP catalytic activity by several different means. We first used a UAS-Timp construct to misexpress Timp (Tissue inhibitor of metalloproteinases) in embryonic neurons and glia via elavGAL4 and repoGAL4, respectively. TIMPs are secreted protein inhibitors that interfere with MMP catalytic activity by binding to the active site of the enzyme (Gomis-Ruth et al., 1997). The Drosophila genome contains a single Timp gene that inhibits both Mmp1 and Mmp2 function in vivo (Page-McCaw et al., 2003). We

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**Fig. 6. MMP catalytic activity is required for motor axon pathfinding.** In each micrograph, two abdominal hemisegments of Stage 17 dissected embryos stained with α-FasII to label the motor projections are shown with anterior left and dorsal up. Below each image are schematics of the observed phenotypes with motor axons in brown and muscles represented by gray boxes. (A,D) In wild type, the ISNb exhibits a highly stereotyped morphology as its axons innervate their muscle targets. (B,E) In elav>Timp embryos, ISNb axons appear loosely bundled. (C,F) In repo>Timp embryos, ISNb axons are loosely bundled and project ectopically. (G,I) elav>Mmp2E258A embryos exhibit aberrant ISNb projections with axons failing to innervate their appropriate targets. (H,J) In repo>Mmp2E258A embryos, ISNb axons are loosely bundled and often branch ectopically. Scale bar: 15 μm.
find that ISNb morphology is aberrant in Temp misexpression embryos (Table 1; Fig. 6B,C,E,F). Whereas ISNb axons are tightly bundled in wild type, they appeared disorganized with Temp misexpression. Individual axons were often apparent, suggesting the nerves are more loosely associated than in wild type. Additionally, axons separated inappropriately from the ISNb and extended over the VLM field, similar to the phenotype observed in Mmp2 single and Mmp1 Mmp2 double mutant embryos. To test the extent of the Temp misexpression phenotypes, we assayed SNa motor axon guidance. We find that SNa pathfinding is sensitive to Temp expression levels as SNa morphology is aberrant with Temp misexpression. Most commonly, we observed ectopic branches extending from either the dorsal or posterior SNa branches (Table 1). Thus, Temp misexpression gives phenotypes roughly comparable to those observed in MMP LOF mutants in two distinct motor pathways, suggesting that MMP enzymatic activity is required for proper motor axon fasciculation.

Although TIMPs are best characterized as MMP inhibitors, Drosophila Temp has been shown to interfere with the activity of other metalloproteinases (Wei et al., 2003), raising the possibility that Temp misexpression inhibits metalloproteinases other than MMPs in embryonic neuronal development. Additionally, vertebrate MMP-MT1 regulates cell migration independent of its catalytic domain (Cao et al., 2004), suggesting that Drosophila MMPs could have proteolysis-independent functions. Therefore, we evaluated whether the neuronal overexpression of catalytically inactive MMPs impaired axon pathfinding. Overexpression of a catalytically inactive form of Mmp1, Mmp1E225A, in cell culture acts as a dominant negative (Zhang et al., 2006), presumably by competing with wild-type Mmp1 for substrate binding. To determine whether overexpression of catalytically inactive forms of Mmp1 and Mmp2 interfered with MMP function in vivo, we tested whether misexpression of Mmp1E225A and an Mmp2 mutant predicted to be catalytically inactive, Mmp2E258A, disrupted motor axon pathfinding. We found that misexpression of either Mmp1E225A or Mmp2E258A had comparable effects on ISNb morphology to that of Temp misexpression (Table 1; Fig. 6G,H,J). Namely, the ISNb in these embryos exhibited defasciculation with loose bundling and ectopic branches. Interestingly, for Mmp2E258A, we found that glial misexpression results in a significantly higher frequency of ISNb defects than does neural misexpression (50% vs 37%, respectively; \( P < 0.5 \)). This increased penetrance may be explained by the fact that Mmp2 is thought to be both membrane-tethered and normally expressed in glia, raising the possibility that a glial-derived catalytically inactive form of Mmp2 is better positioned to compete with the endogenous enzyme. It is also noteworthy that the defasciculation phenotypes observed with Mmp1E225A are stronger than those observed in Mmp1 single LOF mutants (Tables 1 and 2), raising the possibility that the MMPs have overlapping substrate specificities (see Discussion). Together, the analyses of MMP LOF mutants and the MMP enzymatic inhibitor studies demonstrate that MMP catalytic activity is necessary for motor axon fasciculation.

### Table 3. MMP/Temp genetic interactions

<table>
<thead>
<tr>
<th>Genotype</th>
<th>Total aberrant ISNb % (n)</th>
<th>Hyperfasciculation ISNb %</th>
<th>Hypofasciculation ISNb %</th>
<th>Total aberrant SNa % (n)</th>
<th>Hypofasculation SNa %</th>
<th>Total aberrant SNa % (n)</th>
<th>Hypofasculation SNa %</th>
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</thead>
<tbody>
<tr>
<td>Wild type</td>
<td>13 (140)</td>
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<td>0</td>
<td>6</td>
<td>12 (138)</td>
<td>5</td>
<td>7</td>
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<tr>
<td>elav&gt;Fas2</td>
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<td>28</td>
<td>26</td>
<td>0</td>
<td>NS</td>
<td>NS</td>
</tr>
<tr>
<td>elav&gt;Fas2, Temp</td>
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<td>11</td>
<td>15</td>
<td>42</td>
<td>0</td>
<td>NS</td>
<td>NS</td>
</tr>
<tr>
<td>Mmp1\textsuperscript{E225A}/Mmp1\textsuperscript{E225A}</td>
<td>74 (160)</td>
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<td>1</td>
<td>28</td>
<td>39 (143)</td>
<td>3</td>
</tr>
<tr>
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<td>25</td>
<td>35 (113)</td>
<td>16</td>
</tr>
<tr>
<td>Mmp2\textsuperscript{E225A}/Mmp2\textsuperscript{E258A}</td>
<td>77 (238)</td>
<td>0</td>
<td>0</td>
<td>3</td>
<td>74</td>
<td>50 (248)</td>
<td>6</td>
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<tr>
<td>Sema-1a\textsuperscript{P1}/Mmp1\textsuperscript{Q112P}+Mmp2\textsuperscript{E258A}</td>
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<td>0</td>
<td>0</td>
<td>5</td>
<td>39</td>
<td>39 (169)</td>
<td>8</td>
</tr>
</tbody>
</table>

\( \text{n} \) The number of hemisegments scored for each genotype. NS, not scored.

\( ^{1} \)Includes hyperfasciculated, hypofasciculated and loss/reduction of the synapse in the 6/7 muscle cleft, which could be attributed to either hypo- or hyperfasciculation.
Timp (Table 3; compare Fig. 7B and C). The frequency of bypass phenotypes decreases from 27% in elav>Fas2 embryos to 11% in elav>Fas2, Timp embryos. Similarly, the frequency of detour phenotypes is reduced from 28% in elav>Fas2 embryos to 15% in elav>Fas2, Timp embryos (P<0.05 for both phenotypic classes). The Timp-mediated suppression of ISNb hyperfasciculation observed with Fas2 overexpression indicates that MMP activity normally promotes Fas2-dependent motor axon adhesion.

To provide additional evidence that MMPs are required for motor axon fasciculation, we asked whether they normally act in opposition to the Sema-1a-plexA pathway by testing whether MMP LOF mutant phenotypes are dominantly suppressed by a null allele of Sema-1a. In fact, we find that the penetrance of ISNb defasciculation in Mmp2 mutants is significantly reduced in a Sema-1a heterozygous background (Table 3; Fig. 7G-L). In particular, the frequency of loose bundling/ectopic branches for ISNb is decreased roughly twofold: from 74% in Mmp2<sup>W3077/Mmp2<sup>2Df</sup> heterozygotes to 39% in Sema-1a<sup>+/1</sup> Mmp2<sup>W3077/+/Mmp2<sup>2Df</sup></sup> embryos. The Sema-1a suppression of Mmp2 LOF mutations demonstrates that Mmp2 activity normally counteracts Sema-1a-mediated repulsive signaling to regulate defasciculation of the ISNb motor projection. By contrast, the mild ISNb defects observed in Mmp1 single mutants are not dominantly suppressed by Sema-1a (Table 3), in agreement with our phenotypic analysis indicating that Mmp1 does not contribute significantly to ISNb fasciculation. Since the aberrant motor axon defasciculation observed in MMP mutants is not limited to the ISNb, we wanted to determine whether the pathfinding defects apparent in the SNa pathway were also suppressed by reducing Sema-1a dosage. Therefore, we compared the penetrance of SNa defects in Mmp1 and Mmp2 single mutants to those observed in MMP mutants in a heterozygous Sema-1a background. The excessive defasciculation apparent in SNa in Mmp1 and Mmp2 mutants is also suppressed by reducing Sema-1a dosage (Table 3), though the suppression is not as strong as was observed for Mmp2 mutants in ISNb. The modest suppression observed is consistent with published data demonstrating that the relatively large number of adhesion molecules promoting fasciculation of SNa decreases the strength of genetic interactions between any two factors (Yu et al., 2000). Combined with the strong dominant suppression observed for ISNb, these data demonstrate a critical and widespread role for MMPs in achieving the required balance between attractive and repulsive factors underlying proper axon pathfinding.

**DISCUSSION**

This work demonstrates that the level of MMP catalytic activity dictates the degree of motor axon fasciculation in the Drosophila embryo. MMP misexpression is sufficient to inhibit separation of motor axons during outgrowth, but both of the primary embryonic motor nerve branches display striking defasciculation in MMP LOF mutants. The opposing axonal phenotypes observed in MMP LOF and GOF embryos indicates that the level of MMP activity is critical for pathfinding and further suggests that the relevant MMP substrate(s) plays an instructive role in motor axon guidance. In support of the hypothesis that MMPs influence axon outgrowth by modulating the activity of established guidance cues, we show that Mmp2 LOF mutants are dominantly suppressed by a null mutation in Sema-1a, arguing that MMP function is tightly coupled to guidance decisions. Here we discuss possible substrates for Mmp2.
in motor axon pathfinding and put our findings in the context of proposed neural functions for metalloproteinases in vertebrates and invertebrates.

**Mmp1 and Mmp2 are required for Drosophila embryonic CNS development**

Both fly MMPs were previously shown to be expressed in the embryonic CNS (Llano et al., 2002; Llano et al., 2000; Page-McCaw et al., 2003), suggesting that they regulate aspects of neuronal development. However, the finding that both MMP single mutants and the Mmp1 Mmp2 double mutant survived embryogenesis called into question the extent of any possible roles for the MMPs in embryogenesis (Page-McCaw et al., 2003). In this work we present genetic evidence that MMP catalytic activity is essential for motor axon fasciculation. Whereas Mmp1 mutants display subtle fasciculation errors, we find that motor axons in Mmp2 mutants are markedly defasciculated, with many embryonic nerves appearing frayed and poorly organized. Consistent with this phenotypic analysis, the CNS expression profile of Mmp2 is considerably broader than that of Mmp1: Mmp2 is expressed in midline glia, in clusters of interneurons and in peripheral/exit glia but CNS expression of Mmp1 is limited to the midline. The prominent expression of Mmp1 and Mmp2 at the CNS midline prompted us to examine whether either MMP might be required for proper guidance there. However, we do not find any alterations in the behavior of axons at the midline in either MMP LOF or GOF mutant backgrounds or any genetic interactions between Mmp1 and Slit or Mmp1 and Robo (C.M.M. and H.T.B., unpublished). These data indicate that MMPs do not contribute significantly to embryonic midline guidance in the fly.

Although the Mmp1 and Mmp2 LOF phenotypes are distinct, several pieces of evidence suggest that they have overlapping substrate specificities and can cleave the same guidance cue(s). First, misexpression of either Mmp1 or Mmp2 yields qualitatively indistinguishable guidance phenotypes with many motor axons remaining inappropriately bundled together. Second, misexpression of an Mmp1 dominant-negative transgene gives phenotypes nearly identical to those observed with a dominant negative Mmp2. Furthermore, the phenotypes observed with these constructs are stronger and more penetrant than the phenotypes of Mmp1 LOF mutants (Tables 1 and 2), suggesting that the Mmp1 dominant-negative transgene affects motor axon pathfinding by interfering with Mmp2 function by binding to the relevant Mmp2 substrate(s). Lastly, if Mmp1 and Mmp2 cleave the same substrate(s), they might be expected to be genetically redundant, as removal of one would be compensated for by the presence of the other. In fact, we have shown that Mmp1 and Mmp2 play partially redundant roles in SNa pathfinding, as the double mutant phenotype is significantly stronger than the phenotype observed in either single mutant. These results are in agreement with analyses of enzymatic activity of vertebrate MMPs that suggest that there is overlap between the substrates cleaved by individual MMPs (Page-McCaw et al., 2007).

Mmp2 contains a predicted GPI anchor and is membrane associated in Drosophila tissue culture cells (Llano et al., 2002). Thus, the expression pattern of Mmp2 in the embryo would be expected to reflect the locations of Mmp2-dependent proteolysis. We find Mmp2 RNA to be expressed in restricted populations of interneurons and peripheral glia, but not in motoneurons (Fig. 2). Peripheral glia originate at the lateral edge of the CNS and migrate into the periphery along elongating motor axons. By the end of embryogenesis, they extend cytoplasmic processes and wrap axon bundles in a manner similar to vertebrate non-myelinating Schwann cells (Jacobs and Goodman, 1989; Sepp et al., 2000; Sepp et al., 2001). We propose that peripheral glial-derived Mmp2 modulates the activity of factors required for pathfinding. This model implies that peripheral glia play a significant role in regulating motor axon fasciculation. This finding contrasts slightly with the results of Sepp et al. (Sepp et al., 2001) who found more subtle errors in the motor axon projection pattern when peripheral glia were genetically ablated. One possible explanation for the weaker phenotypes in the peripheral glia-ablated embryos relative to Mmp2 LOF mutants is that peripheral glia express several factors that influence axon pathfinding in opposing directions—for example, proteins that both inhibit and stimulate fasciculation. In this way, peripheral glia would somewhat resemble midline glia which express both an axonal attractant (Netrin) and repellent (Slit) (Dickson, 2002). Therefore, ablation of the entire cellular population would be expected to yield different phenotypes than mutating individual molecules. Another possibility is that although Mmp2 is likely to act locally, its substrate might be secreted and could regulate motor axon guidance at a distance. In this case, Mmp2 need not be expressed at the site of fasciculation decisions, and either midline or interneuron-derived Mmp2 might provide the relevant proteolytic activity.

**What guidance cues could be MMP targets in Drosophila motor axon pathfinding?**

In principle, since MMP cleavage might either activate or inhibit the function of a molecule required for axon guidance, the motor axon phenotypes observed in MMP mutants could be expected to be identical to or opposite that of the phenotypes displayed by substrate mutations. Based solely on phenotypic considerations, several guidance molecules could be considered candidate MMP substrates. For example, LOF mutations in a number of genes give hyperfasciculation and/or stalled motor axon phenotypes. These include beaten path (beat) and sidestep (side), two immunoglobulin superfamily proteins required for proper defasciculation of both ISNb and SNa (Fambrough and Goodman, 1996; Sink et al., 2001). There are also five CNS-expressed receptor protein tyrosine phosphatases (RPTPs) that have combinatorial roles in the regulation of motor axon pathfinding. A number of these RPTPs, in particular LAR, are involved in ISNb defasciculation decisions (Desai et al., 1997; Schindelholz et al., 2001). Additionally, Plexin proteins and their receptors, the semaphorins, are critical regulators of motor axon fasciculation. Sema-Plex pathway activity promotes inter-axonal repulsion so that LOF mutations in Sema-Plex pathway components result in ISNb stall phenotypes (Ayyob et al., 2006; Terman et al., 2002; Winberg et al., 1998a; Yu et al., 1998). Importantly, it has also been shown that for axons to remain tightly bundled during normal axon outgrowth, Sema-Plex signaling must be actively antagonized, as LOF mutations in two downstream inhibitors, nerry and Protein kinase A, give aberrant defasciculation phenotypes similar to that observed in MMP mutations (Terman and Kolodkin, 2004). Hence, levels of Sema-plex activity must be tightly controlled to ensure that defasciculation occurs properly at guidance choice points. And similar to what we describe here for MMPs, reciprocal GOF and LOF mutations in the pathway can result in opposing hyper- and hypo-fasciculation phenotypes.

The MMP family as a whole does not cleave a conserved amino acid sequence in their targets, meaning that Drosophila substrates must be determined empirically, not computationally. One identified Mmp1 substrate, Ninjurin A (NjA), represented an appealing candidate in motor axon guidance as it is a signaling protein that regulates cell adhesion whose vertebrate homologs are upregulated in response to nerve injury (Zhang et al., 2006). However, we do not
detect any aberrations to motor axon pathfinding in either NijA LOF or GOF mutants (C.M.M. and H.T.B., unpublished), indicating that NijA is unlikely to be a relevant substrate in this context. Although few other Drosophila MMP substrates have been identified, the Drosophila homologs of several putative vertebrate MMP substrates make appealing candidates for MMP targets in embryonic CNS development. For instance, vertebrate membrane type MMP1 (MT1-MMP), has been shown to interact with the transmembrane heparan sulfate proteoglycan Syndecan 1 and trigger Syndecan 1 ectodomain shedding (Endo et al., 2003). Syndecan 1 processing stimulated cell migration on collagen, suggesting that this cleavage has functional consequences in vivo. Interestingly, Fox and Zinn (Fox and Zinn, 2005) identified Drosophila Syndecan (Sdc) as a ligand for the LAR RPTP. Accordingly, genetic interaction studies indicate that Sdc and LAR act in concert to regulate ISNnb pathfinding. As it is currently unknown whether LAR binds membrane-bound or soluble Sdc, MMP activity could potentially regulate the LAR/Sdc interaction. In addition, MT1-MMP has also recently been shown to be required for ectodomain shedding of Semaphorin 4D in a model of tumor-induced angiogenesis – a processing event required for the induction of blood vessel growth in vivo (Basilie et al., 2007). As discussed above, Semaphorin signaling plays a well-documented role in regulating motor axon behavior. Furthermore, since we have found that Sema-1a mutations display strong genetic interactions with Mmp2 mutations in this system, it is conceivable that MMPs directly modulate Sema-Plex signaling activity.

**Metalloproteinases serve constructive functions in the CNS**

MMP expression levels are highly elevated in a number of neuronal pathologies and after nervous system injury. MMP upregulation in CNS disease states raises the issue of whether MMP induction has an overall positive or negative effect on disease outcome. There is substantial evidence that the net effect of high MMP expression in some diseases is detrimental (Yong, 2005; Yong et al., 2001). For example, treatment with broad-spectrum metalloproteinase inhibitors is able to alleviate or prevent experimental autoimmune encephalomyelitis (EAE), a mouse multiple sclerosis model (Chandler et al., 1997; Yong et al., 1998). There is also, however, growing recognition of beneficial functions for MMPs following CNS injury. The diverse functions for MMPs in disease states have become increasingly apparent as investigators have moved beyond the use of general metalloproteinase inhibitors to the study of particular MMPs. For example, increased expression of individual MMPs has been shown to correlate with periods of regeneration and repair following nervous system injury (Ahmed et al., 2005; Demestre et al., 2004; Shubayev and Myers, 2004). The functional significance of elevated MMP expression on regenerating axons has not been established, though in some regeneration models treatment with active MMPs promotes axon outgrowth (Heine et al., 2004; Siebert et al., 2001). In regeneration, it is thought that MMPs influence axon growth by degrading chondroitin sulphate proteoglycans (CSPGs), which normally inhibit regrowth beyond the glial scar.

In the context of neuronal development, there is substantial support for the idea that metalloproteinases, and in particular the ADAM subfamily, regulate axon outgrowth and pathfinding (McFarlane, 2003). Early work in the field suggested that metalloproteinases play a largely permissive role in axon outgrowth – by degrading the ECM in order to clear a path for extending axons (Muir, 1994; Nordstrom et al., 1995; Zuo et al., 1998). In support of a role for MMPs in outgrowth, it has been shown that a number of MMPs are expressed on the growth cones of vertebrate neurites extending in vitro (Chambaut-Guerin et al., 2000; Hayashita-Kinoh et al., 2001; Nordstrom et al., 1995; Zuo et al., 1998). More recent work has demonstrated that in vitro, metalloproteinases are capable of modulating the interactions between guidance cues and their receptors (Galko and Tessier-Lavigne, 2000; Hattori et al., 2000). For example, the interaction between ephrin A2 and Eph receptor is terminated by ephrin A2 cleavage via ADAM10 (also known as Kuzbanian-like – FlyBase) and/or Kuz. Functionally, this cleavage allows growth cone withdrawal of hippocampal neurons in culture, as a cleavage-inhibiting mutation delays axon retraction (Hattori et al., 2000). Metalloproteinases have also been implicated in DCC (deleted in colorectal carcinoma) receptor activity as broad-spectrum metalloproteinase inhibitors inhibit ectodomain shedding of DCC and potentiate netrin-mediated axon outgrowth (Galko and Tessier-Lavigne, 2000). In vivo support for the role of ADAM proteases in axon outgrowth and pathfinding comes from work in Drosophila (Fambrough et al., 1996; Schimmelpfeng et al., 2001). kuz mutant embryos display ectopic axon crossing at the midline suggesting that kuz is required for repulsive signaling mediated by Slit-Roundabout (Robo). Supporting this idea, kuz and slit mutations genetically interact, and Kuz appears to be required for the clearance of the Robo receptor from commissural axons (Schimmelpfeng et al., 2001).

Although a number of vertebrate MMPs display neuronal expression patterns in the embryo (Gonthier et al., 2007; Hayashita-Kinoh et al., 2001; Jaworski, 2000; Sekine-Aizawa et al., 2001), until relatively recently there was little direct evidence supporting a role for this metalloproteinase subclass in axon pathfinding. Studies of retinal ganglion cell (RGC) pathfinding in frogs argue that MMP activity is required for axon guidance at several defined choice points. Hehr et al. (Hehr et al., 2005) used an MMP-specific inhibitor to demonstrate that MMPs are required for RGC guidance decisions both at the optic chiasm and tectum. This work suggested that MMPs are normally required for axon guidance during vertebrate development, though the particular MMPs involved in RGC pathfinding remain to be identified. Exploiting the relative simplicity of the Drosophila model system, we have now established that individual MMPs play critical and distinct roles in well-defined axon pathfinding decisions during development. To extend this work to more complex vertebrate systems, it will be critical to analyze axon outgrowth and pathfinding in MMP single and compound mutant mice.

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