GPN-1/glypican and UNC-52/perlecan do not appear to function in BMP signaling to pattern the C. elegans postembryonic mesoderm

Melisa S DeGroot¹, Robert Greer¹ and Jun Liu¹§

¹Department of Molecular Biology and Genetics, Cornell University, Ithaca, NY. USA
§To whom correspondence should be addressed: kelly.jun.liu@cornell.edu

Abstract

Heparan sulfate proteoglycans (HSPGs) are diverse macromolecules consisting of a protein core modified with glycosaminoglycan (GAG) chains. HSPGs, including glypicans and perlecans, have been implicated in shaping the extracellular matrix (ECM) to affect growth factor signaling. Here, we tested if GPN-1/glypican or UNC-52/perlecan plays a role in the bone morphogenetic protein (BMP) signaling pathway in patterning the C. elegans postembryonic mesoderm. Using the suppression of sma-9(0) (Susm) assay, we found that animals carrying mutant alleles of gpn-1 or unc-52 do not exhibit any Susm phenotype. We also tested and found that the two glypicans GPN-1 and LON-2 do not share functional redundancy in the BMP pathway. Our results suggest that GPN-1/glypican and UNC-52/perlecan do not play a major role in the C. elegans BMP pathway, at least in patterning of the postembryonic mesoderm.

Figure 1. The Susm phenotypes of lon-2, gpn-1 and unc-52 mutants: A) Diagram depicting the coelomocyte (CC) phenotype of wildtype (WT), sma-9(cc604), or sma-9(cc604); susm worms. sma-9(cc604) mutants lack the two M-derived CCs located in the posterior of WT or sma-9(cc604); susm worms (purple arrows). Created using BioRender.com (version 2021). B) Table showing the penetrance of the Susm phenotype of double mutant strains between sma-9(cc604) and mutant alleles of the specified genes (thanks to CGC). The Susm penetrance refers to the percent of animals with one or two M-derived CCs as scored using the CC::GFP reporter. For each genotype, two independent isolates were generated (as shown in the strain list), three to seven plates of worms from each isolate were scored for the Susm phenotype at 20°C, and the Susm data from the two isolates were combined and presented in the table. a The lack of M-derived CCs phenotype is not fully penetrant in sma-9(cc604) mutants. Statistical analysis was conducted by comparing the double or triple mutants with the sma-9(cc604) single mutants. **** P<0.0001 (unpaired two-tailed Student’s t-test). No significant difference was detected between lon-2(e678) sma-9(cc604) double mutants and lon-2(e678) sma-9(cc604) gpn-1(tm595) triple mutants.

Description

Heparan sulfate proteoglycans (HSPGs) are macromolecules composed of a protein core decorated with glycosaminoglycan (GAG) chains. These highly diverse molecules are classified based on their localization at the membrane or being secreted as part of the extracellular matrix (ECM), such as glypicans or perlecans, respectively (Sarrazin et al. 2011). HSPGs have been shown to play a structural role in the ECM as well as in the distribution of growth factors, such as transforming growth factor-β (TGF-β), fibroblast growth factor (FGF), Wnt, and Hedgehog (Hh), within tissues through highly specific binding interactions (Lin and Perrimon 2000). In vitro studies have demonstrated that human perlecan can bind to the BMP2 ligand (Decarlo et al. 2012). Understanding the biological roles of HSPGs in cell signaling has implications in disease diagnosis and potential treatment.
Bone morphogenetic protein (BMP) belongs to the TGF-β superfamily of signaling molecules. In *C. elegans*, the BMP signaling pathway is known to regulate multiple processes, including body size and postembryonic mesoderm patterning (Savage-Dunn and Padgett 2017). We have shown that mutations in the BMP pathway exhibit the Susm phenotype, namely, they can specifically suppress the mesoderm defects of *sma-9(0)* mutants (Figure 1A, Foehr et al. 2006). We further showed that the Susm assay is a highly specific and sensitive assay for BMP signaling defects (Liu et al. 2015).

Previous work has demonstrated that LON-2/glypican negatively regulates the BMP pathway, and it has been postulated that LON-2 functions by binding to and sequestering the ligand (Gumienny et al. 2007). We have found that the *lon-2(e678)* null mutants exhibit the Susm phenotype (Figure 1B; Foehr et al. 2006; Liu et al. 2015). Here we aim to determine if GPN-1/glypican or UNC-52/perlecan plays a role in BMP signaling by using the Susm assay.

**gpn-1** encodes a glypican, a membrane localized HSPG. *gpn-1* is expressed in the pharynx and ventral nerve cord (VNC) during embryogenesis (Hudson et al. 2006). Previous studies have shown that *gpn-1* mutants do not have a body size phenotype, and *gpn-1* cannot substitute for *lon-2*, which encodes another glypican, to regulate body size (Gumienny et al. 2007; Taneja-Bageshwar et al. 2013). However, the Drosophila glypicans Dally and Dally-like are known to function in the BMP pathway by regulating the distribution of the BMP ligand within the ECM (Belenkaya et al. 2004; Norman et al. 2016). Furthermore, the *C. elegans* BMP ligand, DBL-1, is secreted from cells of the VNC (Suzuki et al. 1999), the same tissue that expresses *gpn-1*. We sought to test if *gpn-1* plays a role in the BMP pathway by using the more sensitive Susm assay. We assayed for the Susm phenotype of *gpn-1(tm595)*, a deletion allele lacking part of exon 2 and all of exon 3 of the *gpn-1* gene. We found that *gpn-1(tm595)* animals exhibited a 2% penetrance of the Susm phenotype, within the range of background observed in the *sma-9(cc604)* single mutants (Foehr et al. 2006; Liu et al. 2015).

Previous studies have shown that *gpn-1* and *lon-2* act redundantly in hermaphrodite specific neuron migration (Kinnunen 2014). To test if these two glypicans may function redundantly in the BMP pathway, we examined the Susm phenotypes of *lon-2(e678) gpn-1(tm595)* double mutants. We found that *gpn-1(tm595)* does not enhance the penetrance of the Susm phenotype of *lon-2(e678)*. Taken together, these results suggest that *gpn-1* does not play a major role in the BMP pathway.

Perlecans is a secreted HSPG, characterized by its localization to the basement membrane. Human perlecans has been shown to be a key component of basement membranes that can bind and sequester growth factors, such as FGFs and VEGFs (Costell et al. 1999; Mongiat et al. 2000; Ishijima et al. 2012). While a study has demonstrated that TGF-β signaling regulates the expression of perlecans (Dodge et al. 1995), a role for perlecans in the TGF-β signaling pathway has not been shown. *C. elegans* has one homolog of the human perlecans: *unc-52* (Rogalski et al. 1993). Localized to the basement membrane of body wall muscles (BWM), UNC-52 has been shown to play a critical role in the assembly and maintenance of the BWM myofilaments (Mullen et al. 1999). Interestingly, previous studies have shown that *unc-52* genetically interacts with *dbl-1/BMP* during distal tip cell (DTC) migration (Merz et al. 2003). We tested if *unc-52* plays a role in the BMP pathway by using the *sma-9* suppression assay. We used two nonsense alleles of *unc-52*, e669 and e998, which introduce an early stop in exon 17 and 18, respectively. Both e669 and e998 are among the multiple *unc-52* alleles used in the study by Merz et al. (2003). Neither *unc-52(e669)* nor *unc-52(e998)* exhibited any Susm phenotype (Figure 1B). Although not all *UNC-52* isoforms are abolished in these two mutants, our results suggest that *UNC-52/perlecans is unlikely to play a major role in the BMP pathway in *C. elegans*.

In summary, using the highly specific and sensitive Susm assay, we have found that unlike LON-2/glypican, GPN-1/glypican and UNC-52/perlecans do not appear to play a major role in the *C. elegans* BMP pathway. The *C. elegans* genome contains three other HSPGs, SDN-1/syndecan, AGR-1/agrin, and CLE-1/collagen XVIII (cle-1). It remains to be determined whether any of them play a role in BMP signaling.

**Reagents**

**Strains:**

<table>
<thead>
<tr>
<th>Strain No.</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>LW0040</td>
<td><em>arIs37[secreted CC::gfp] I; cup-5(ar465) III; smo-9(cc604) X</em></td>
</tr>
<tr>
<td>LW5711</td>
<td><em>arIs37[secreted CC::gfp] I; unc-52(e669) II; cup-5(ar465) III; smo-9(cc604) X isolate 1</em></td>
</tr>
<tr>
<td>LW5712</td>
<td><em>arIs37[secreted CC::gfp] I; unc-52(e669) II; cup-5(ar465) III; smo-9(cc604) X isolate 2</em></td>
</tr>
<tr>
<td>LW5734</td>
<td><em>arIs37[secreted CC::gfp] I; unc-52(e998) II; cup-5(ar465) III; smo-9(cc604) X isolate 1</em></td>
</tr>
<tr>
<td>LW5735</td>
<td><em>arIs37[secreted CC::gfp] I; unc-52(e998) II; cup-5(ar465) III; smo-9(cc604) X isolate 2</em></td>
</tr>
<tr>
<td>LW5778</td>
<td><em>arIs37[secreted CC::gfp] I; cup-5(ar465) III; lon-2(e678) smo-9(cc604) X isolate 1</em></td>
</tr>
<tr>
<td>LW5779</td>
<td><em>arIs37[secreted CC::gfp] I; cup-5(ar465) III; lon-2(e678) smo-9(cc604) X isolate 2</em></td>
</tr>
<tr>
<td>LW5709</td>
<td><em>arIs37[secreted CC::gfp] I; cup-5(ar465) III; smo-9(cc604) gpn-1(tm595) X isolate 1</em></td>
</tr>
<tr>
<td>LW5710</td>
<td><em>arIs37[secreted CC::gfp] I; cup-5(ar465) III; smo-9(cc604) gpn-1(tm595) X isolate 2</em></td>
</tr>
</tbody>
</table>
Primers used for genotyping:

**cc604**: MLF-69: CGCAACAAAGTTCATTCTCCA. MLF-70: CTTGGCTAAGATCCCATGCT. Sequence using LW-40: TCCGACTTGACACTTCATCAG.

**e678**: JKL-1053: TTGTATTGCTCTACCGGTCC. JKL-1054: TTGCCCGGAATTTCAACTGC. JKL-1055: TCAACTTACGGAAGCGATCG.


**e998**: JKL-1873: CAAAATCGTTAGTGGCCGAG. JKL-1874: CCTGTTCACTCCCACTTCTC. Sequence using JKL-1873.

**tm595**: MSD-72: TGGCTTCATGATTAGTGCCCGAG. JKL-1868: ACCGTTCACATGGATCTTGAC. JKL-1870: CCATGCATACTCGCTGATCG.

References


Funding: This work was supported by the National Institutes of Health R35 GM130351 grant to J.L.. M.S.D. was partially supported by a National Science Foundation (NSF) Graduate Research Fellowship (DGE-1650441). R.G. was partially supported by a NYSTEM-RET Grant for Pre-College teachers.

Author Contributions: Melisa S DeGroot: Conceptualization, Investigation, Writing - original draft, Writing - review and editing. Robert Greer: Investigation. Jun Liu: Conceptualization, Investigation, Project administration, Funding acquisition, Writing - review and editing.

Reviewed By: Cathy Savage-Dunn

History: Received July 27, 2021 Revision received August 5, 2021 Accepted August 10, 2021 Published August 13, 2021

Copyright: © 2021 by the authors. This is an open-access article distributed under the terms of the Creative Commons Attribution 4.0 International (CC BY 4.0) License, which permits unrestricted use, distribution, and reproduction in any medium, provided the original author and source are credited.

Citation: DeGroot, MS; Greer, R; Liu, J (2021). GPN-1/glypican and UNC-52/perlecan do not appear to function in BMP signaling to pattern the C. elegans postembryonic mesoderm. microPublication Biology. https://doi.org/10.17912/micropub.biology.000437