

Genome-wide analysis of Smad and Schnurri transcription factors in *C. elegans* demonstrates widespread interaction and a function in collagen secretion

Reviewed Preprint

v2 • January 2, 2025

Revised by authors

Reviewed Preprint

v1 • August 19, 2024

Mehul Vora, Jonathan Dietz, Zachary Wing, Jun Liu, Christopher Rongo, Cathy Savage-Dunn 

Waksman Institute, Dept. of Genetics, Rutgers University, USA • ModOmic Ltd, Southampton, UK • Department of Biology, Queens College, CUNY, USA • Department of Molecular Biology and Genetics, Cornell University, USA • PhD Program in Biology, the Graduate Center, CUNY, USA

 https://en.wikipedia.org/wiki/Open_access
 Copyright information

eLife Assessment

Modulation of BMP signalling affects body size in the nematode *Caenorhabditis elegans*, and this paper examines the effects on *C. elegans* body size brought about by the modulation of BMP signalling. The study provides **valuable** analyses of ChIP-seq and RNA-seq data to understand the function of SMA-3 (Smad) and SMA-9 (Schnurri) in this model. The authors provide **compelling** evidence that the BMP-dependent body size effect could be due to defects in cuticle collagen secretion, a finding of interest to those studying organismal growth and epidermal function.

<https://doi.org/10.7554/eLife.99394.2.sa2>

Abstract

Smads and their transcription factor partners mediate the transcriptional responses of target cells to secreted ligands of the Transforming Growth Factor- β (TGF- β) family, including those of the conserved bone morphogenetic protein (BMP) family, yet only a small number of direct target genes have been well characterized. In *C. elegans*, the BMP2/4 ortholog DBL-1 regulates multiple biological functions, including body size, via a canonical receptor-Smad signaling cascade. Here, we identify functional binding sites for SMA-3/Smad and its transcriptional partner SMA-9/Schnurri based on ChIP-seq peaks (identified by modEncode) and expression differences of nearby genes identified from RNA-seq analysis of corresponding mutants. We found that SMA-3 and SMA-9 have both overlapping and unique target genes. At a genome-wide scale, SMA-3/Smad acts as a transcriptional activator, whereas SMA-9/Schnurri direct targets include both activated and repressed genes. Mutations in *sma-9* partially suppress the small body size phenotype of *sma-3*, suggesting some level of antagonism between these factors and challenging the prevailing model for Schnurri function. Functional analysis of target genes revealed a novel role in body size for genes involved in one-carbon metabolism and in the endoplasmic reticulum (ER) secretory pathway, including the disulfide reductase

dpy-11. Our findings indicate that Smads and SMA-9/Schnurri have previously unappreciated complex genetic and genomic regulatory interactions that in turn regulate the secretion of extracellular components like collagen into the cuticle to mediate body size regulation.

Introduction

Members of the TGF- β family of secreted ligands play numerous roles in development and disease. In humans, there are 33 ligand genes that can be broadly separated into two subfamilies: the TGF- β /Activin subfamily and the BMP subfamily [1]. Due to the conservation of these ligands and their signaling pathways across metazoans, genetic studies in invertebrate systems have been instrumental in identifying signaling mechanisms [2, 3]. Canonical signaling occurs when ligand dimers bind to transmembrane receptors generating a heterotetrameric complex consisting of two type I and two type II serine/threonine kinase receptors. Following ligand binding and complex assembly, the constitutively active type II receptor phosphorylates the type I receptor on the GS domain and thereby activates its kinase domain [4]. The activated type I receptor phosphorylates the C-terminus of intracellular receptor-regulated Smads (R-Smads), promoting their heterotrimeric complex formation with co-Smads. The heterotrimeric Smad complex accumulates in the nucleus and binds DNA directly to elicit changes in gene expression [5–15]. Co-Smads for all ligands and R-Smads for TGF- β /Activin ligands bind a 4 bp GTCT Smad Binding Element (SBE); furthermore, R-Smads for BMP ligands associate with GC-rich sequences (GC-SBE) [16–18]. The SBE is considered too degenerate and low affinity to account fully for binding specificity, so transcription factor partners likely contribute to target gene selection [19]. To date, only a few direct target genes of Smads have been extensively studied, including *Drosophila brinker* [20]; *Xenopus mixer* [21] and *Xvent2* [22]; and the mammalian *ATF3* and *Id* genes [23]. Genome-wide studies have the potential to expand these examples and elucidate general principles of target gene selection [24–26]. More of these studies are needed to understand how Smad transcriptional partners influence target gene selection and contribute to the execution of specific biological functions.

In the nematode *Caenorhabditis elegans*, a BMP signaling cascade initiated by the ligand DBL-1 plays a major role in body size regulation [27]. In nematodes, body size is constrained by a collagen-rich cuticle, which is secreted by an epidermal layer (the hypodermis) and remodeled over four successive molts during larval growth and then continuously during adulthood [28, 29]. DBL-1 signals through type I receptor SMA-6, type II receptor DAF-4, and Smads SMA-2, SMA-3, and SMA-4 (founding members of the Smad family), which act together in the hypodermis to promote body size growth during the earliest larval growth stages [30–32]. The exact mechanism by which the DBL-1 pathway regulates body size is not fully understood, but is known to involve the regulated synthesis of cuticular collagen, of which there are over 170 genes [33–35]. A complete understanding of how DBL-1 regulates body size will require the identification of all direct transcriptional targets of the pathway during larval growth.

In addition to body size, the DBL-1 pathway also regulates male tail patterning, mesodermal lineage specification, innate immunity, and lipid metabolism. A transcription factor partner for this pathway, SMA-9, has been identified that plays a role in each of these biological functions [36, 37]. Unlike for the core components of the signaling pathway, however, loss of SMA-9 function can result in a different effect depending on the phenotype, suggesting that this factor can either be an equivalent co-factor, a factor with a more limited role, or an antagonistic factor depending on the specific function [36–38]. SMA-9 is the homolog of *Drosophila* Schnurri, which was identified for its roles in Dpp/BMP signaling [39–41]. Three vertebrate Schnurri homologs regulate immunity, adipogenesis, and skeletogenesis, acting through both BMP-dependent and BMP-independent mechanisms [42–45]. Schnurri proteins are very large transcription factors with multiple Zn-finger domains. At the *brinker* locus in *Drosophila* and the *Xvent2* locus in *Xenopus*, binding of an R-Smad and a Co-Smad with a precise 5 bp spacing

between binding sites has been shown to recruit Schnurri, which controls the direction of transcriptional regulation [22]. This model for Smad-Schnurri interaction has not been tested at a genomic scale.

In this study, we use BETA software to combine RNA-seq and ChIP-seq datasets for SMA-3/Smad and SMA-9/Schnurri to identify direct versus indirect target genes of these factors, as well as to identify common versus unique targets [46, 47]. Analysis of *sma-3*; *sma-9* double mutants further extends our understanding of how these factors interact to produce locus-specific effects on target genes. We use GO term analysis and loss-of-function studies that shed light on the downstream effectors for body size regulation, lipid metabolism, and innate immunity. Finally, we use a ROL-6::wormScarlet reporter for collagen synthesis and secretion to show that SMA-3, SMA-9, and the transcriptional target gene DPY-11 regulate body size growth by promoting the secretion and delivery of collagen into the cuticle.

Methods

C. elegans strains

C. elegans strains were grown at 20°C using standard methods unless otherwise indicated. N2 is the wild-type strain; some strains were provided by the *Caenorhabditis* Genetics Center (CGC), which is funded by NIH Office of Research Infrastructure Programs (P40 OD010440) or generated in previous work. Strong loss-of-function or null alleles were used. The following genotypes were used: *sma-3(wk30)*, *sma-9(ok1628)*, *qclIs6[sma-3p::gfp::sma-3, rol-6(d)]*, *jjIs1253[sma-9p::sma-9C2::gfp+unc-119(+)]* (generated via bombardment), [48], *rrf-3(pk1426)*, *fat-6(tm331)*, *fat-7(wa36)*, *nhr-114(gk849)*, *acs-22(gk373989)*, *lbp-8(gk5151)*, *clec-60(tm2319)*, *sysm-1(ok3236)*, *ins-7(ok1573)*, *sma-2(e502)*, *rol-6(syb2235[rol-6::wormScarlet])* [49], and *pwsI82[hyp-7p::VIT2ss::oxGFP::KDEL, HygR]*. The double mutants *sma-3(wk30)*; *sma-9(ok1628)*, and *rrf-3(pk1426)*; *lon-2(e678)* were generated in this study.

RNA-seq

Developmentally synchronized animals were obtained by hypochlorite treatment of gravid adults to isolate embryos. Animals were grown on NGM plates at 20°C until the late L2 stage. Total RNA was isolated from animals using Trizol (Invitrogen) combined with Bead Beater lysis in three biological replicates for each genotype [46]. Libraries were generated using polyA selection in a paired-end fashion and sequenced on an Illumina HiSeq (2x150 bp configuration, single index, per lane) by Azenta (formerly Genewiz). Reads were mapped to the *C. elegans* genome (WS245) and gene counts generated with STAR 2.5.1a. Normalization and statistical analysis on gene counts were performed with EdgeR using generalized linear model functionality and tagwise dispersion estimates. Principal Component Analysis showed tight clustering within four biological replicates, with a clear separation between SMA-3 and SMA-9 active versus inactive genotypes. Likelihood ratio tests were conducted in a pairwise fashion between genotypes with a Benjamini and Hochberg correction. All RNA-seq raw sequence files as well as normalized counts after EdgeR can be accessed at GEO (Accession Number: GSE266398).

Chromatin Immunoprecipitation Sequencing

Chromatin immunoprecipitation sequencing (ChIP-seq) using a poly-clonal goat IgG anti-GFP antibody (a gift from Tony Hyman and Kevin White) was performed on L2 stage nematodes by Michelle Kudron (Valerie Reinke Model Organism Encyclopedia Of DNA Elements and model organism Encyclopedia of Regulatory Networks group) on the *sma-3(wk30)*; *qclIs6[GFP::SMA-3]* and *LW1253:jjIs1253[sma-9p::sma-9C2::gfp+unc-119(+)]* strains at the late L2 stage [50]. Data are available at encodeproject.org. To calculate distances between SMA-3 and SMA-9 ChIP-seq peaks, each peak was reduced to a centroid position (midpoint between the two border coordinates along

the chromosome). For each chromosome, a matrix of SMA-3 and SMA-9 peak centroids was created, allowing the measurement of distance (in bps) between every SMA-3 and SMA-9 centroid along that chromosome. The shortest distance in the matrix was chosen to define each SMA-3/SMA-9 nearest neighboring pair. The resulting inter-centroid distances were analyzed from all 6 chromosomes. To mimic a random distribution of SMA-3 and SMA-9 peaks, each peak on a given chromosome was reassigned to a location on that chromosome using randomized values (generated by the Microsoft Excel randomization function) within the size range for that chromosome. A matrix of SMA-3 and SMA-9 peak centroids was then analyzed from this randomized dataset as described above for the actual dataset.

Identification of Direct Targets Using BETA and LOA

To identify SMA-3 direct targets, differentially expressed genes (DEGs) from the RNA-seq comparison of wild type vs. *sma-3(wk30)* using an FDR $\leq$ 0.05 were compared against the genomic coordinates of SMA-3 peaks from the ChIP-seq analysis using BETA basic and the WS245 annotation of the *C. elegans* genome [47]. The following parameters were used: 3 kb from TSS, FDR cutoff of 0.05 and one-tail KS test cutoff of 0.05. The input files consisted of .bed files of IDR thresholded peaks and differential expression Log₂FC and FDR values from the RNA-seq. An identical approach was used to identify SMA-9 direct targets using DEGs from the RNA-seq comparison of wild type vs. *sma-9(ok1628)*.

To identify direct targets co-regulated by both SMA-3 and SMA-9, the two pairwise RNA-seq comparisons (wild type vs. *sma-3* and wild type vs. *sma-9*) were analyzed, measuring DEGs for the same genes in both comparisons. Taking a conditional approach, the information from the first comparison (wild type vs. *sma-3*) was examined to see if it affected interpretation in the second (wild type vs. *sma-9*). Using the approach of Luperchio et al. [51], the genes in the second comparison were split into two groups, conditional on the results in the first comparison, with one group comprising genes found to show differential expression in the first comparison, and the second group comprising genes found not to show differential expression. To estimate which genes were differentially regulated, an FDR of 0.01 was used to generate an overlapping list between the two comparisons. BETA basic was then used to identify potential direct targets of the SMA-3/SMA-9 combination using just the ChIP-seq peaks that overlapped between the two transcription factors. The following parameters were used: 3 kb from TSS, FDR cutoff of 0.05 and one-tail KS test cutoff of 0.05. Analysis tools can be obtained at GitHub: <https://github.com/shahlab/hypoxia-multiomics> as per [46]. The WormBase database was used to obtain information about candidate target genes, including sequence, genetic map position, expression pattern, and available mutant alleles [52].

Quantitative RT-PCR analysis

Worms were synchronized using overnight egg lay followed by 4-h synchronization. When animals reached L2 stage, they were collected and washed, and then RNA was extracted using previously published protocol [53] followed by Qiagen RNeasy miniprep kit (Catalogue. No. 74104). Invitrogen SuperScript IV VILO Master Mix (Catalogue. No.11756050) was used to generate cDNA, and qRT-PCR analysis was done using Applied Biosystems Power SYBR Green PCR Master Mix (Catalogue. No. 4367659). Delta delta Ct analysis was done using Applied Biosystems and StepOne software. All qRT-PCR analysis was repeated on separate biological replicates. The following primer pairs were used: 5'-ATGTGTGACGACGAGGTTGCC-3' and 5'-GTCTCCGACGTACGAGTCCTT-3' to detect *act-1*, 5'-GTGGATTCTTCTCGCTCAT-3' and 5'-CACAAGATGACAAGTGGGAA-3' to detect *fat-6*, 5'-CATTTCGATGTTTTGAGGCG-3' and 5'-GATCGAAGTAGGCACCATCT-3' to detect *nhr-114*, 5'-GGCAGGTCTAATCCACGACTTG-3' and 5'-CTAATGTCCGGGTTCCCATCG-3' to detect *C54E4.5*, 5'-CGGAGGTTACGAGACCAGTACG-3' and 5'-TGGAGTCACAGACGGAAGACG-3' to detect *aard-19*, 5'-CTCCAAACCTTCTTTCTCCTTCG-3' and 5'-GGACCGCCAGCCATATTGTC-3' to detect *nspe-7*, 5'-TGTCTCCATGGTTGAGTTATGCT-3' and 5'-GTTTCTTTGCGGGAATGTTGC-3' to detect *nspc-16*, 5'-TTCGGTTGGAGGTGTCGTTG-3' and 5'-

GTTGCTCGGCATTAGTACG-3' to detect *catp-3*, and 5'-TGCTCGTGGAGATTGCCTCATC-3' and 5'-GCATCTTGTTGGCTTCCTCGTC-3' to detect *gdh-1*. All graphs were made using GraphPad Prism software and statistical analysis was performed using One-way ANOVA with Multiple Comparison Test, as calculated using the GraphPad software. There were two biologically independent collections from which three cDNA syntheses were analyzed using two technical replicates per data point.

RNAi Analysis of Body Size

RNAi knockdown of individual target genes was performed in the RNAi-sensitive *C. elegans* mutants *rrf-3(pk1426)* and *rrf-3(pk1426); lon-2(e678)*, which were fed HT115 bacteria containing dsRNA expression plasmid L4440, with or without gene targeting sequences between flanking T7 promoters. NGM growth plates were used containing ampicillin for L4440 RNAi plasmid selection and IPTG (isopropyl β -D-1-thiogalactopyranoside) to induce dsRNA expression. Both *rrf-3(pk1426)* and *rrf-3(pk1426); lon-2(e678)* were exposed to the RNAi food during the L4 stage and allowed to lay eggs for 3 hours and then removed. Following hatching and development to adulthood while exposed to the RNAi food, 2 adult hermaphrodites were transferred to fresh RNAi plates, allowed to lay eggs, and removed from the plate. Upon hatching and development to the L4 stage, hermaphrodites were imaged using an AxioImager M1m (Carl Zeiss, Thornwood, NY) with a 5X (NA 0.15) objective. The RNAi feeding constructs were obtained from the Open Biosystems library (Invitrogen), except for *C54E4.5* RNAi, which was constructed in this study. To analyze the body length of the RNAi exposed animals, 3 independent measurements were made per worm using the segmented line tool on Fiji/ImageJ [54]. 3-5 biological replicates were completed for each RNAi construct. The data were analyzed using ANOVA with Dunnett's post hoc test correction for multiple comparisons.

Hypodermal Imaging of ROL-6::wrmScarlet

Animals expressing ROL-6::wrmScarlet in different genetic backgrounds were imaged using a Chroma/89 North CrestOptics X-Light V2 spinning disk, a Chroma/89North Laser Diode Illuminator, and a Photometrics PRIME95BRM16C CMOS camera via MetaMorph software. Day 1 adults (unless otherwise noted) were used to ensure molting was completed. A 63X oil objective (NA 1.4) was used to detect fluorescence. In order to visualize the cuticle and hypodermis layers of each animal, a z-series was completed using a 0.5 micron step size across 6.5 microns. Each image was analyzed using Fiji/ImageJ for fluorescence quantification in the hypodermis of the animals. Background was subtracted using a rolling ball filter. An outline was drawn around each nematode and the mean fluorescence intensity was calculated within the outline. At least 10 animals were analyzed and pooled across 3-4 biological replicates. Using GraphPad Prism, the individual mean fluorescence intensity values were normalized to the mean for control animals in each experiment and analyzed using ANOVA with Dunnett's post hoc test correction for multiple comparisons. Images were then deconvolved using DeconvolutionLab2 [55].

Animals expressing ROL-6::wrmScarlet together with the ER marker VIT2ss::oxGFP::KDEL were imaged using a Zeiss Elyra 7 Lattice SIM. A 60X water objective (NA 1.2) was used to detect fluorescence, and a z-series was completed as described above.

RNAi treatment of ROL-6::wrmScarlet animals was performed similarly to the RNAi treatment in the body length analysis with these exceptions: nematodes exposed to *dpy-11* RNAi grew for one generation until day 1 adulthood before imaging, nematodes exposed to *C54H2.5* and *F41C3.4*-containing RNAi plasmids were introduced to the animals at the L1 development stage and allowed to develop until day 1 adulthood, and nematodes exposed to *Y25C1A.5* and *Y113G7A.3*-containing RNAi plasmids were introduced to animals at the L4 development stage and grown for 24 hours before imaging. Tunicamycin treatment of ROL-6::wrmScarlet-expressing animals was completed by allowing animals to develop from eggs to L4 stage in the presence of 5 μ g/mL in

NGM plates. Experiments were conducted over 3-4 biological replicates. The data were analyzed using an unpaired two-tailed t test ANOVA with Dunnett's post hoc test correction for multiple comparisons, where appropriate.

Results

Transcription factors SMA-3 and SMA-9 bind overlapping and distinct genomic sites

Smads and Schnurri are known to bind DNA as a physical complex [56, 57], but a limitation of the previous work is that only a small number of specific target genes was analyzed. We sought to determine the extent to which these factors act together or independently by identifying the binding sites of SMA-3 and SMA-9 on a genome-wide scale. We generated GFP-tagged transgenes for SMA-3 and SMA-9, and then demonstrated that they are functional, as evidenced by their ability to rescue the mutant phenotypes of respective loss-of-function *sma-3* and *sma-9* mutants [36, 38]. We provided these constructs to the modENCODE/modERN consortium, which then analyzed genome binding via ChIP-seq at the second larval (L2) stage, a developmental stage at which a Smad reporter is highly active, and both SMA-3 and SMA-9 are first observed to affect body size [58, 59]. ChIP sequencing reads identified 4205 peaks for GFP::SMA-3 and 7065 peaks for SMA-9::GFP (Supplementary File 1). Although these data were previously released publicly as part of the modENCODE/modERN consortium [50, 58], our examination here provides the first comprehensive analysis of these datasets.

Because Smads and Schnurri are known to form a complex on DNA, we sought to determine the frequency with which SMA-3 and SMA-9 bind together at a genome-wide scale by analyzing the distances between the centroids of SMA-3 and SMA-9 ChIP-seq peaks. If SMA-3 and SMA-9 bind independently, then we would expect a Gaussian distribution of inter-centroid distances, whereas if they frequently bind in a complex, we should see a non-Gaussian distribution with increased representation of distances less than or equal to the average peak size. This analysis demonstrated an increased representation (approaching 45%) of inter-centroid distances of 100 bp or less (Figure 1a,b), smaller than the average peak size for SMA-3 (400 bp) or SMA-9 (250 bp) (Figure 1c), consistent with the interpretation that SMA-3 and SMA-9 frequently bind as either subunits in a complex or in close vicinity to each other along the DNA. The midpoint of the cumulative probability distribution of inter-centroid distances was 788 bp; by contrast, a randomization of the positions of SMA-3 and SMA-9 ChIP peaks expanded the midpoint of the cumulative probability distribution of inter-centroid distances to 8,211 bp (Figure 1a,b). From this analysis, a substantial subset (3101 peaks) of the SMA-3 (73.7%) and SMA-9 (43.9%) peaks overlap (Figure 1d). We therefore considered these instances of overlapping peaks to be evidence of SMA-3/SMA-9 association (possibly physical complexes, although this would require a formal biochemical demonstration), whereas adjacent but non-overlapping peaks likely represent independent binding, leading us to conclude that (1) SMA-3 typically binds together with SMA-9 to DNA sites, and that (2) over half of all SMA-9 sites do not overlap with these SMA-3 occupied sites.

Identification of direct transcriptional targets of SMA-3 and SMA-9

To determine how these binding sites correlate with changes in gene expression of neighboring genes, we performed RNA-seq on L2 stage samples of *sma-3* and *sma-9* mutants compared with wild-type controls. Principal component analysis (PCA) demonstrated that all three biologically independent replicates of each genotype clustered together (Figure 2a) and that each genotype is transcriptionally distinct from the others. Using a false discovery rate (FDR) ≤ 0.05 , we identified 1093 differentially expressed genes (DEGs) downregulated and 774 upregulated DEGs in *sma-3* mutants (Figure 2b, Supplementary File 2). In *sma-9* mutants, we identified 412 downregulated

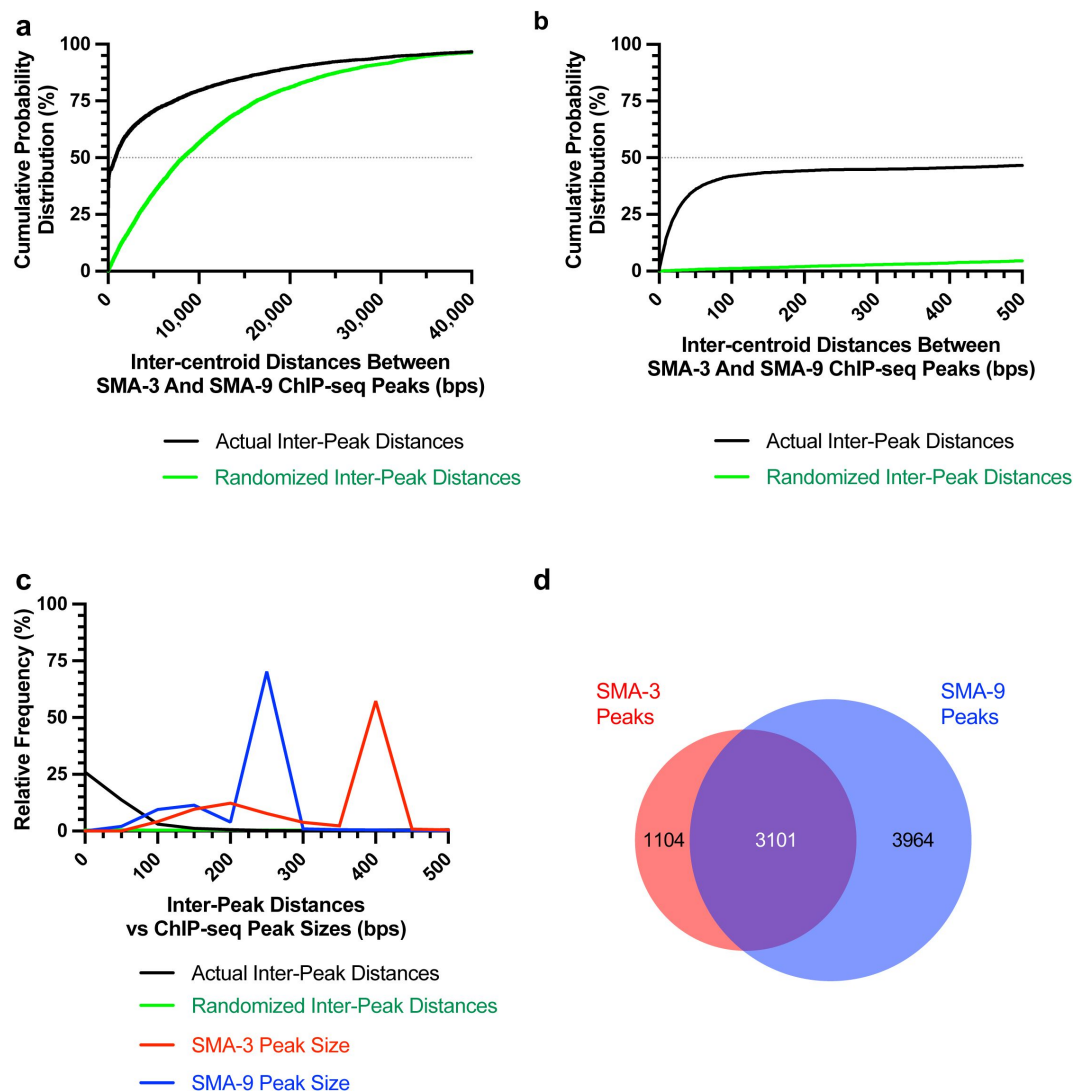


Figure 1.

Transcription factors SMA-3 and SMA-9 bind both overlapping and distinct genomic sites

(a) Cumulative probability distribution graph of the distances between the centroids (base pair position located centrally within each peak) of nearest neighbor SMA-3 and SMA-9 ChIP-seq peaks. The black line represents actual inter-peak distances, whereas the green line represents a hypothetical randomized dataset. The horizontal dotted line indicates the point in the curve at which half of the peak pairs fall. (b) Same cumulative probability distribution as in (a), but focused on distances less than 500 bps. The centroids of nearly half of all SMA-3/SMA-9 neighboring pairs fall within 500 bps of each other. (c) Histogram of the interpeak distances (actual data in black, randomized data in green), as well as the ChIP-seq peak widths (SMA-3 in red, SMA-9 in blue). Most peaks are larger in size than most interpeak centroid distances, indicating substantial peak overlap. (d) Size proportional Venn diagram showing the number of SMA-3 and SMA-9 peaks that either overlap with one another or remain independent. Although most SMA-3 peaks overlap with SMA-9 peaks, more than half of SMA-9 peaks are located independently of SMA-3 peaks.

DEGs and 371 upregulated DEGs (**Figure 2d** [↗](#), Supplementary File 2). Previously identified target genes, such as *fat-6* and *zip-10* [34 [↗](#)], were also found in these datasets, confirming the effectiveness of the RNA-seq experiments.

RNA-seq identifies both direct and indirect transcriptional targets. To identify direct functional targets of each of these transcription factors, we employed BETA software (**Figure 2c,e** [↗](#)), which infers direct target genes by integrating ChIP-seq and RNA-seq data [47 [↗](#)]. BETA analysis identified 367 direct targets for SMA-3 and 332 direct targets for SMA-9 (Supplementary File 3). Every identified direct target of SMA-3 was downregulated in the *sma-3* mutant (**Figure 2b** [↗](#)), indicating that SMA-3/Smad functions primarily as a transcriptional activator. In contrast, 46% of direct targets of SMA-9 were upregulated and 53% were downregulated in the *sma-9* mutant (**Figure 2d** [↗](#), Supplementary File 3). Thus, SMA-9 likely acts as either a transcriptional activator or repressor depending on the genomic context. This conclusion is consistent with our previous analyses of SMA-9 function *in vivo* and in a heterologous system [34 [↗](#)].

Significant overlap in directly regulated DEGs of SMA-3 and SMA-9

Because SMA-3 and SMA-9 ChIP-seq peaks often overlapped along the DNA, we sought to identify a core subset of DEGs co-regulated by these transcription factors. Rather than relying on individual RNA-seq analyses, in which arbitrary cut-offs for significance may lead to an underestimation of the overlap, we performed Luperchio Overlap Analysis (LOA) on *sma-3* and *sma-9* RNA-seq datasets to identify 882 shared DEGs (Supplementary File 4) [46 [↗](#), 51 [↗](#)]. From ChIP-seq data, we identified 3101 peaks that are overlapping between SMA-3 and SMA-9. We used LOA to identify DEGs shared between the pairwise comparison of *sma-3* vs wild type, and between the pairwise comparison of *sma-9* vs wild type, using evidence of potential DEGs in one comparison to inform the state of those potential DEGs in the other comparison. Processing common occupancy sites with the common DEGs through BETA software (**Figure 3a** [↗](#)), we identified 129 co-regulated direct target genes (i.e., target genes showing differential expression in both *sma-3* and *sma-9* mutants versus wild type, and with overlapping SMA-3 and SMA-9 binding peaks nearby (Supplementary File 5)). These results are consistent with SMA-3 and SMA-9 acting either in a protein complex or working together in close association along the DNA. Most (114) of these 129 co-regulated direct targets are activated by both SMA-3 and SMA-9 (**Figure 3b** [↗](#)), but 15 of them have reversed regulation in *sma-9* mutants compared with *sma-3* (**Figure 3c** [↗](#)), suggesting an antagonistic function that we analyze further below. For shared activated targets, loss of SMA-3 caused a greater fold change than loss of SMA-9 (Supplementary File 2).

Our BETA/LOA analysis next allowed us to deduce SMA-3-exclusive and SMA-9-exclusive direct targets (i.e., target genes directly regulated exclusively by one factor or the other, but not both), revealing 238 SMA-3-exclusive direct targets (**Figure 3d** [↗](#)) and 279 SMA-9-exclusive direct targets (**Figure 3e,f** [↗](#)). About half (129) of the 279 SMA-9-exclusive direct targets are activated by SMA-9 (**Figure 3e** [↗](#)), whereas the other half (150) appear to be inhibited by SMA-9 (**Figure 3f** [↗](#)). Surprisingly, many of these target genes contained overlapping SMA-3 and SMA-9 binding peaks (**Figure 3b,e** [↗](#),f), although loss of one of the two factors did not result in changes in gene expression, perhaps suggesting that the presence of the other factor at these targets was sufficient to regulate gene expression to physiological levels. Interpretation is further complicated for target genes surrounded by a mixture of distinct and overlapping SMA-3 and SMA-9 peaks. Nevertheless, our results suggest that (1) SMA-3 and SMA-9 can act independently of one another, (2) they usually (although not always) act as transcriptional activators of shared target genes when they co-occupy the same sites along the DNA, and (3) SMA-9 without SMA-3 can act as either a transcriptional activator or repressor of its own SMA-3-independent targets.

The large number of total SMA-3 and SMA-9 ChIP-seq peaks yet small number of functional peaks identified by BETA was surprising. The ModENCODE/ModERN consortium previously demonstrated the existence of High Occupancy Target (HOT) sites where ChIP-seq association with 15 or more transcription factors occurs, perhaps due to “sticky” regions of the genome leading to

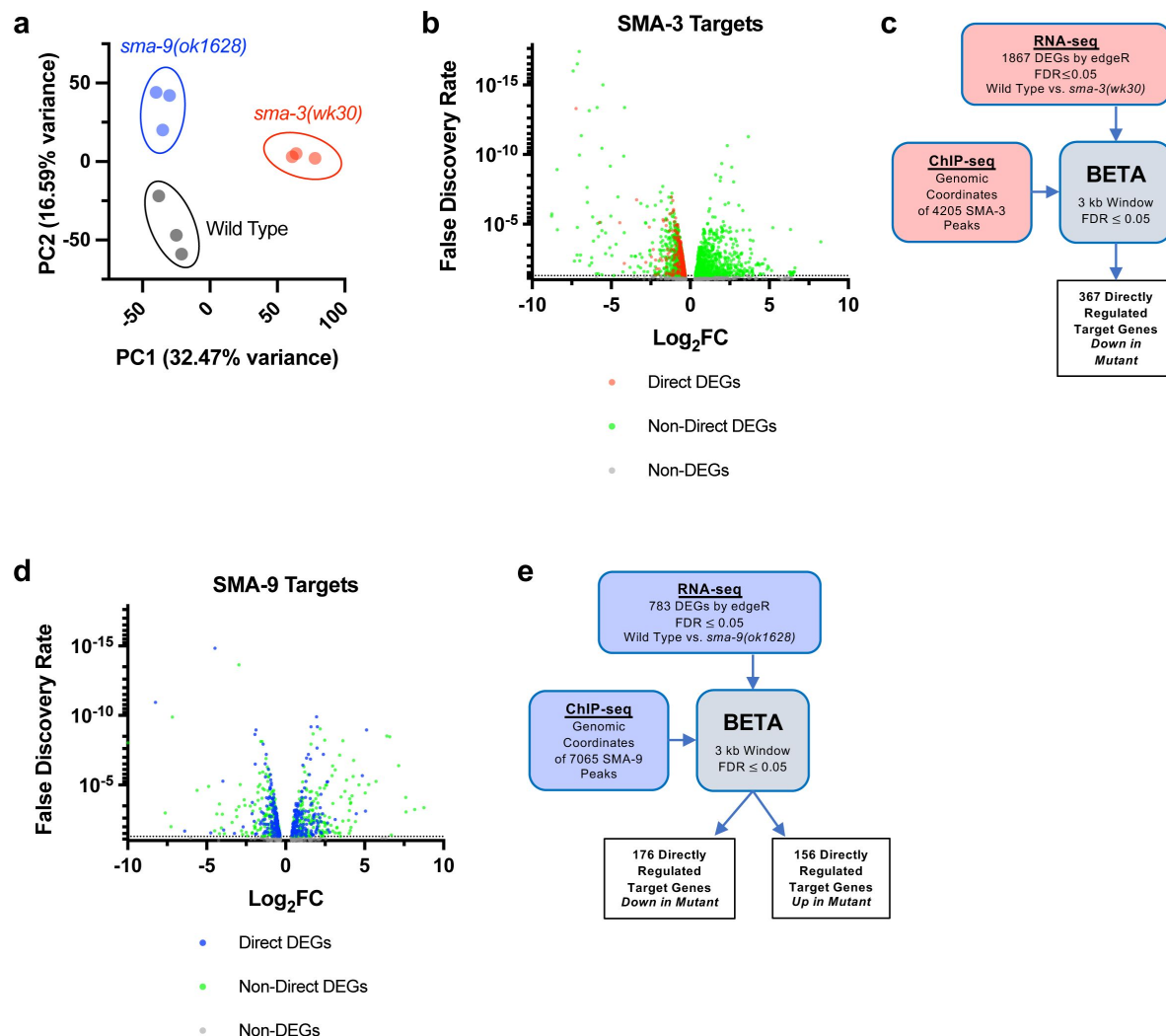
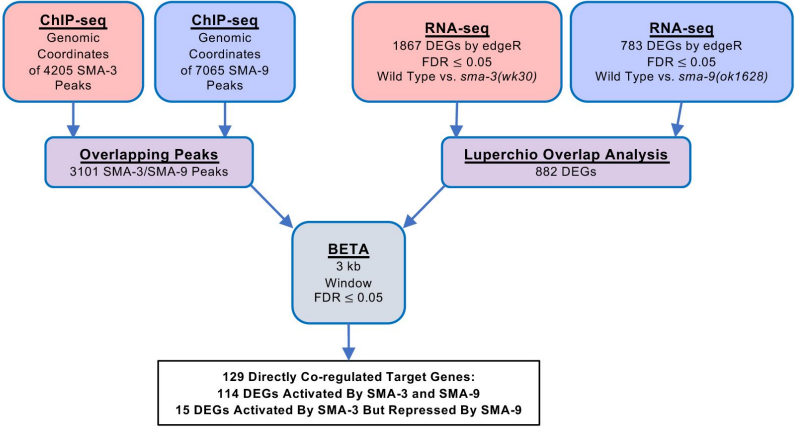


Figure 2.

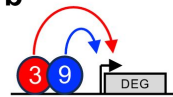
Identification of direct transcriptional targets of SMA-3 and SMA-9

(a) Principal Component Analysis (PCA) over two dimensions (PC1 and PC2) for RNA-seq datasets for wild type (in black), *sma-3(ok1628)* (in red), and *sma-9(ok1628)* (in blue). The percent of variance for each component is indicated. The three biological replicates for each genotype are well clustered. (b) Volcano plot of RNA-seq FDR values versus log₂ fold change (FC) expression for individual genes (squares) in *sma-3* mutants relative to wild type. The direct targets identified by BETA are indicated with red squares; the negative log₂ FC values demonstrate that SMA-3 promotes the expression of these genes. Non-direct target genes nevertheless showing differential expression are indicated with green squares. (c) Strategy for integrating SMA-3 ChIP-seq and mutant RNA-seq data to identify directly regulated targets. (d) Volcano plot of RNA-seq FDR values versus log₂ fold change expression for individual genes (squares) in *sma-9* mutants relative to wild type. The direct targets identified by BETA are indicated with blue squares; the combination of positive and negative log₂FC values demonstrates that SMA-9 promotes the expression of some of these genes and inhibits the expression of others. Non-direct target genes nevertheless showing differential expression are indicated with green squares. (e) Strategy for integrating SMA-9 ChIP-seq and mutant RNA-seq data to identify directly regulated targets.

a



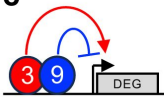
b



114 DEGs
lbp-8, col-94, col-153, ins-37, fat-6, hsp-60, sams-1, cysl-2, nhr-114

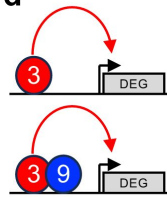
Annotation Cluster	EASE Score
Ribosome Biogenesis	3.46
Flavoproteins	3.01
One-carbon Metabolism	2.63
AAA-type ATPases	1.94
Mitochondria	1.92
Glutathione S-Transferase	1.38

c



15 DEGs
mpc-1, gdh-1 C54E4.5

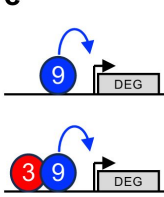
d



238 DEGs
dpy-17, dpy-10, nhr-114, dpy-9, dpy-2, sma-6, sma-2, acdh-1, hsp-3, dpy-11

Annotation Cluster	EASE Score
Nucleus	12.08
Ribosome Biogenesis	3.97
Zinc-finger	3.76
mRNA Splicing	3.38
RNA Helicases	3.08
Chromosome Organization	2.84
ER Chaperones	2.61
DNAJ Domain	1.88

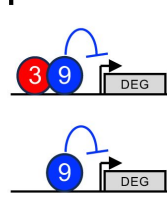
e



129 DEGs
cyp-13A9, lys-4, clec-186

Annotation Cluster	EASE Score
Lipid Metabolism	3.80
Fatty Acid Oxidation	2.99
Peptidases	2.85
Crononases	2.52
Long FA Metabolism	2.42
Oxido-reductases	2.34
Cytochrome P450s	2.19

f



150 DEGs
zip-10, ins-7, lon-1, sma-3

Annotation Cluster	EASE Score
Innate Immunity	5.23

Figure 3.

Significant overlap in directly regulated DEGs of SMA-3 and SMA-9

(a) Strategy for integrating SMA-3 and SMA-9 ChIP-seq and mutant RNA-seq data to identify common versus unique directly regulated targets. (b-f) Cartoon representations of the different types of direct target genes, their neighboring SMA-3 and/or SMA-9 binding sites, and the effect of those sites on that gene's expression. The red circle labeled "3" represents SMA-3 binding sites, whereas the blue circle labeled "9" represents SMA-9 binding sites. Arrows represent that the wild type transcription factor promotes the expression of the neighboring DEG (gray), whereas T-bars indicate that it inhibits the expression of the DEG. Types of regulation include (b) SMA-3 alone promoting DEG expression, (c) SMA-3 and SMA-9 combined promoting expression, (d) SMA-3 and SMA-9 showing antagonistic regulation of expression, (e) SMA-9 alone promoting DEG expression, and (f) SMA-9 alone inhibiting DEG expression. Example DEGs and tables of annotation clusters for gene ontology terms for those DEGs (via DAVID, with accompanying statistical EASE score) are shown under the cartoon demonstrating each type of regulation.

false signals [58]. We surveyed the binding sites of transcription factors within the ModERN database for overlap with either SMA-3 or SMA-9 sites (**Figure 3 – figure supplement 2**). Less than 25% of all the numerous SMA-3 or SMA-9 sites were associated with HOT sites.

Restricting our analysis to just functional SMA-9 sites identified by BETA reduced HOT site association down to 15%, although a similar effect was not observed for functional SMA-3 sites identified by BETA. SMA-9-exclusive sites showed even lower HOT site association, whereas 40% of SMA-9 sites overlapping with SMA-3 sites (i.e., co-regulated) were associated with HOT sites. These results suggest that the large number of total SMA-3 and SMA-9 sites is not explained by binding to HOT sites, although there might be some affinity for SMA-3/SMA-9 co-regulated genes to be near HOT sites.

Integration of SMA-3 and SMA-9 function

SMA-3 and SMA-9 both regulate body size, and a loss of function mutation in either gene results in a small body size phenotype [2, 36, 37]. We used double mutant analysis to determine whether SMA-3 and SMA-9 regulate body size independently or together. For two gene products that act together in the same pathway, we expect the double mutants to resemble one of the single mutants. If they function independently, then we expect the double mutant to be more severe than the single mutants (i.e., additive phenotypes). We constructed a *sma-3; sma-9* double mutant and measured its body length at the L4 stage in comparison with a wild-type control, *sma-3* mutants, and *sma-9* mutants. Contrary to expectations, the double mutant was neither the same as nor more severe than the single mutants; instead, it showed an intermediate phenotype (**Figure 4a**). This result suggests that SMA-9 may act as both a positive and negative regulator of body size, indicating some antagonistic activity towards SMA-3. One mechanism for this antagonism could be the repression of SMA-3 target genes by SMA-9. Alternatively, SMA-9-exclusive target genes could negatively regulate body size. There is precedent for a BMP pathway component to have dual, opposite roles in body size regulation [60].

We hypothesized that the interaction between SMA-3 and SMA-9 may be context dependent, with different target genes showing independent, coordinated, or antagonistic interactions between the transcription factors. We tested this hypothesis by performing qRT-PCR on select target genes in wild type, *sma-3* mutants, *sma-9* mutants, and *sma-3; sma-9* double mutants at the L2 stage. We first considered three target genes: *fat-6*, which has overlapping SMA-3 and SMA-9 peaks and is downregulated in both *sma-3* and *sma-9* mutants; *nhr-114*, which has both overlapping and distinct non-overlapping SMA-3 and SMA-9 peaks and is downregulated in both *sma-3* and *sma-9* mutants; and *C54E4.5*, which has overlapping SMA-3 and SMA-9 peaks yet shows opposite direction of regulation in *sma-3* versus *sma-9* mutants. For two of the tested target genes, *fat-6* and *nhr-114*, there was no significant difference in expression levels between the single and double mutants (**Figure 4b**), consistent with the transcription factors acting together. The third target gene, *C54E4.5*, was selected because it is a co-regulated direct target yet the RNA-seq data shows changes in its expression in opposite directions in *sma-3* versus *sma-9* mutants, downregulated in *sma-3* yet upregulated in *sma-9* relative to wild type. In the double mutant, *C54E4.5* is upregulated and indistinguishable from the expression in *sma-9* single mutants (**Figure 4b**). Thus, for this target gene, the *sma-9* loss-of-function phenotype is epistatic to that of *sma-3*, indicating that SMA-9 is required for SMA-3 to regulate its expression.

We wanted to know whether this interaction occurred more generally, so we analyzed an additional five target genes that are regulated in opposite directions by SMA-3 and SMA-9: *arrd-19*, *nspe-7*, *nspc-16*, *catp-3*, and *gdh-1* (Figure 4 – figure supplement 2). For each of these five genes the direction of regulation was confirmed by RT-PCR, although only two of them reached statistical significance. Furthermore, for all five genes, as for *C54E4.5*, expression in the *sma-3; sma-9* double mutant was not significantly different from that in the *sma-9* single mutant. Thus, for multiple

target genes in which SMA-9 represses expression, the *sma-9* loss-of-function phenotype is epistatic to that of *sma-3*, indicating that SMA-3 fails to regulate expression of these genes in the absence of SMA-9.

Biological functions of SMA-3 and SMA-9 target genes

Gene Ontology analysis showed that direct target genes of SMA-3 and SMA-9 shared some annotation clusters, including for fatty acid metabolism, collagens, and one-carbon metabolism (Figure 3b, Figure 3 – figure supplement 1), but also showed that each regulated its own annotation clusters. SMA-3-exclusive direct targets were enriched for ribosome biogenesis factors, mitochondrial proteins, and ER chaperones (Figure 3d). Direct targets that were positively yet exclusively regulated by SMA-9 were enriched for genes involved in oxidation-reduction reactions and cytochrome P450s (Figure 3e), whereas direct targets that were negatively yet exclusively regulated by SMA-9 were enriched for innate immunity factors (Figure 3f).

Using a candidate gene approach, we previously identified several cuticle collagen genes that mediate regulation of body size downstream of BMP signaling [35]. Here, we sought to validate and extend this analysis in an unbiased manner by screening target genes for a function in body size regulation. We selected 45 genes to analyze for a role in body size, selecting candidate genes so as to ensure broad representation of the different types of regulation (e.g., co-regulated direct targets versus SMA-3 and SMA-9 exclusive direct targets), gene ontology (e.g., collagens, ER chaperones, lipid metabolism), and RNAi clone or mutant availability. For nine genes for which mutants were available, we measured body length at the L4 stage (Figure 5, Figure 5 – figure supplement 1). We also measured *sma-3* and *sma-9* mutants as controls, finding them to be smaller, as expected. As we previously showed, *fat-6* and *fat-7* mutants were not significantly different from wild type in body size [61]. Of the remaining six genes for which mutants were available, only *ins-7* showed significantly reduced body size with a statistical effect size (Glass' effect size: the difference between the mean of the mutant and the mean for wild type, divided by the standard deviation of wild type) greater than one. To test the functions of genes for which mutants were not available, we used RNAi depletion in the *rrf-3* mutant (Figure 5 – figure supplement 1). RRF-3 encodes an RNA-dependent RNA polymerase, and *rrf-3* mutants are often used in screens and phenotypic analyses because of their RNAi hypersensitivity [62]. RNAi depletion of controls *sma-3* and *sma-9* reduced the body length as expected. We chose 37 target genes to analyze, representing a variety of molecular functions and including SMA-3-exclusive and SMA-9-exclusive in addition to co-regulated genes (Figure 5).

Is there any correlation between whether a gene shows a large Glass' effect size on body length and whether it is regulated by SMA-3 exclusively, SMA-9 exclusively, or co-regulated? We compared the reduction in body length caused by RNAi or mutation of each tested target (normalized as Glass' effect size in which larger values indicate smaller body lengths compared to control) against the adjusted p-value for body length compared to control for target genes in each of these three categories (Figure 5a). The genes that showed the largest and most statistically significant effect size were either SMA-3-exclusive or co-regulated. For each gene, we also compared body length effect size, gene ontology/classification, and the BETA rank scores for SMA-3 and SMA-9 ChIP-seq/RNA-seq data, which gives an indication of whether a gene is a direct target of one or both factors (Figure 5b). For each gene, we plotted the $-\log_{10}$ for each BETA rank score (for SMA-3 on the X-axis and SMA-9 on the Y-axis) such that the greater the $-\log_{10}$ BETA rank value, the greater probability that gene is a direct target of that transcription factor. Circles represent individual genes tested such that the coordinate of the circle reflects the coordinate SMA-3 and SMA-9 BETA ranks, and the size of the circle represents the reduction in body size, normalized as Glass' effect size, relative to control. Circle color represents key associated GO terms for each gene. We found that the genes that promoted body length and belonged to the SMA-3-exclusive category encoded chaperones and collagen secretion factors. SMA-9-exclusive genes that promoted body

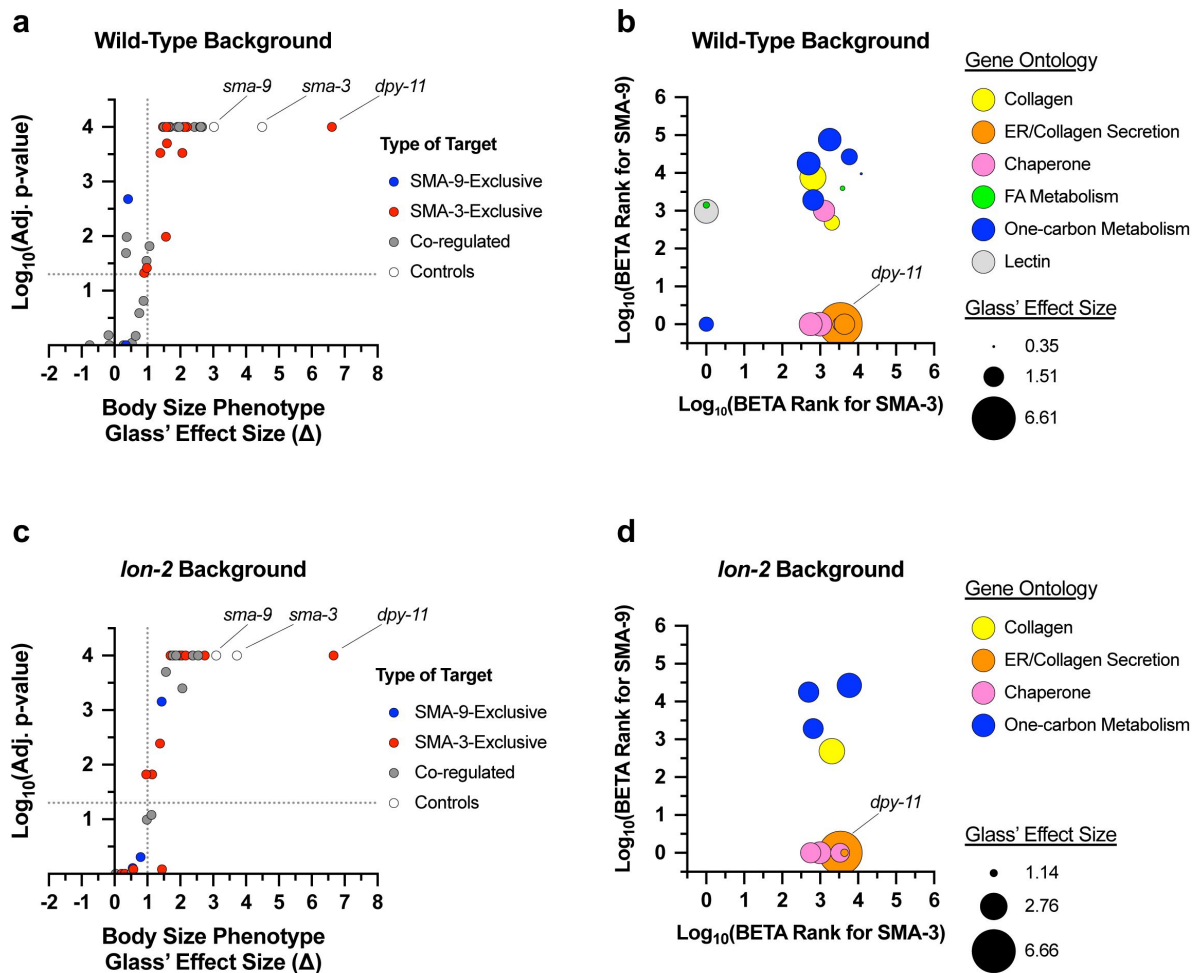


Figure 5.

Multiple SMA-3 and SMA-9 target genes regulate body size

(a,c) The adjusted p-value (plotted as $-\log_{10}$) for mean body size for genes either knocked down by RNAi or mutation compared to control (empty vector and wild type, respectively) is shown for individual genes giving the indicated Glass' effect size D for body size when knocked down. Larger Glass' effect values indicate smaller bodies compared to control. Genes regulated by SMA-9 exclusively, SMA-3 exclusively, or by both factors are indicated by blue, red, and gray circles, respectively. The horizontal dotted line indicates a p-value cutoff of 0.05. The vertical dotted line indicates an effect size cutoff of 1. The *sma-3* and *sma-9* controls are indicated by empty circles. (b,d) The BETA rank values for SMA-3 or SMA-9 (plotted as $-\log_{10}$ and acting as measures of ChIP-seq/RNA-seq correlation demonstrating the direct target nature of those factors) are shown as circles for individual genes. Each circle gives the Glass' effect size for body size (indicated by the area of each circle – larger circles indicate greater decreases in body size when the indicated gene is knocked down or mutated) and gene ontology group (indicated by circle color). Two genetic backgrounds are shown: (a,b) wild type and (c,d) *lon-2*. The circle for *dpy-11* is highlighted.

length encoded a lectin and a gene involved in one-carbon metabolism. Co-regulated genes showing a role in body length also encoded one-carbon metabolism factors, as well as collagens and chaperones.

We reasoned that if target genes truly act downstream of the DBL-1 signaling pathway to regulate body size, then we would also expect them to act downstream of the negative regulator LON-2, a glypican which antagonizes the DBL-1 pathway with respect to body size at the level of ligand-receptor interactions [63]. Thus, we also performed RNAi depletion in a *lon-2*; *rrf-3* double mutant, which demonstrates exaggerated DBL-1 signaling and elongated body size; we expected that candidate transcriptional effectors of the DBL-1 pathway might have a more prominent requirement in mediating the exaggerated growth defect of a *lon-2* mutant and hence show a suppression phenotype in this genetic background. RNAi of one of the target genes, *mttr-1*, prevented the development of *rrf-3*; *lon-2* animals to the L4 stage, so body length could not be quantified at this stage. Nearly two thirds of the remaining 36 genes tested caused a statistically significant reduction in body length (with a statistical effect size greater than one) upon RNAi treatment in at least one of the two genetic backgrounds. Half of the genes tested caused a significant reduction in body length in both genetic backgrounds (Figure 5c, Figure 5 – figure supplement 2), making them strong candidates for direct transcriptional effectors of body size regulation. Consistent with our results in the wild-type background, we found that SMA-3-exclusive regulators of body size were enriched for chaperones and factors involved in ER secretion, whereas co-regulated genes mediating body size growth were enriched for one-carbon metabolism factors and collagens (Figure 5d), suggesting that the upregulation of these activities is a key aspect of how DBL-1 signaling promotes growth.

DBL-1 signaling promotes body size through collagen secretion

We observed that *dpy-11* depletion via RNAi resulted in the most severe reduction in body length among the tested target genes (Figure 5a,c). The *dpy-11* gene encodes a protein-disulfide reductase involved in cuticle development [64], and the expression of this gene is regulated by SMA-3 but not by SMA-9 (Figure 5b,d). We hypothesized that *dpy-11* may represent a function for BMP signaling in cuticle collagen secretion, in addition to the previously established role in cuticle collagen gene expression. Furthermore, this role may be SMA-9-independent. We tested this hypothesis by monitoring the expression and localization of a cuticle collagen, ROL-6, a cuticle collagen gene with a demonstrated role in body size [35]. We previously showed that *rol-6* mRNA levels are reduced in *dbl-1* mutants at L2 [35], although RNA-seq analysis did not find enough of a statistically significant change in *rol-6* to qualify it as a transcriptional target and total levels of protein are also not significantly reduced in mutants (Figure 6f,g).

The hypodermis synthesizes and secretes collagen into the cuticle in a pattern of circular annuli that surround the animal along its length (Figure 6a). These collagen-rich annuli and the newly synthesized collagen inside the hypodermal cells underneath the cuticle can be distinguished using confocal microscopy (Figure 6b). We generated a functional endogenously tagged allele of *rol-6* that expresses a ROL-6::wormScarlet fusion protein, taking care to preserve the proteolytic processing sites such that wormScarlet remains attached to the final protein product. As previously shown [49], this fusion protein localizes to the cuticle (Figure 6c). In L4 animals at high magnification, the total cuticular fluorescence was reduced in both *sma-3* and *sma-9* mutants, with clear patches of decreased ROL-6::wormScarlet (Figure 6d,e). Interestingly, the hypodermal subcellular distribution of ROL-6::wormScarlet was altered in *sma-3* and *sma-9* mutants, with ROL-6::wormScarlet protein accumulating intracellularly in these mutants (quantified in Figure 6f) compared to wild type, often underneath the clear patches observed in the cuticular layer, which showed depressed levels of ROL-6::wormScarlet protein in *sma-3* mutants (quantified in Figure 6g). This phenomenon is consistent with changes in collagen secretion upon impaired BMP signaling, and it suggests that this role is not SMA-9-independent. We used structured illumination super-resolution microscopy to compare an endoplasmic reticulum (ER) marker, VIT2ss::oxGFP::KDEL [65], with subcellular ROL-6::wormScarlet, and we found that ROL-6

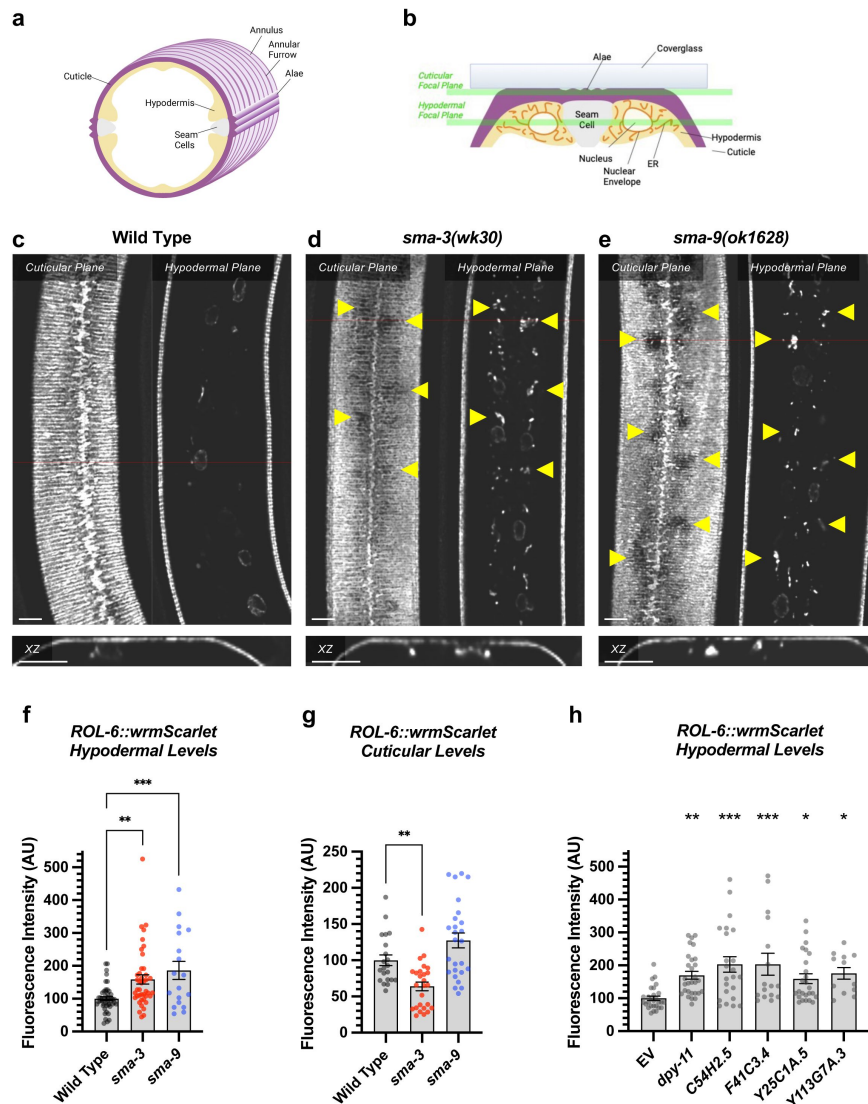


Figure 6.

DBL-1 signaling promotes body size through collagen secretion

(a) Cartoon illustrating a cross section through the nematode body (dorsal oriented up). Rings of cuticular collagen annuli (magenta), secreted by the underlying hypodermal cell layer (tan) surround the body. Lateral alae containing collagen, secreted by the underlying seam cells (gray), run orthogonal along the length of the body. (b) Cartoon illustrating a cross section through a portion of the nematode body (lateral oriented up) underneath a microscope cover glass. Horizontal green bars indicate the cuticular versus hypodermal plates captured by confocal microscopy in panels c-e. (c) ROL-6::wrmScarlet fluorescence detected in annuli and alae in the cuticular layer, as well as in nuclear envelopes in the underlying hypodermal layer in wild-type animals. The horizontal red line indicates the specific xz cross section shown below the cuticular and hypodermal plane panels. The bar indicates 5 microns. (d) ROL-6::wrmScarlet in *sma-3* mutants, visualized as per wild type. Patches of cuticular surface show diminished levels of ROL-6::wrmScarlet, whereas the protein is detected in the hypodermal layer just under these patches (yellow arrowheads), suggesting a failure to deliver collagen to the surface cuticle (easily visualized in the xz panel). (e) Mutants for *sma-9* show the same phenotype as *sma-3*. (f,g) Quantification of ROL-6::wrmScarlet fluorescence in the (f) hypodermal layer or (g) cuticular layer of indicated mutants. Dots indicate the fluorescence of individual animals. Asterisks over pairwise comparison bars indicate one way ANOVA with (f) Sidák's multiple comparison test or (g) the Kruskal-Wallis comparison test (*** $P < 0.001$, ** $P < 0.01$). (h) A similar analysis for RNAi knockdowns of the SMA-3 target gene *dpy-11*, as well as four known ER secretion factors as comparative controls. Asterisks above each column indicate one way ANOVA with Dunnett's multiple comparison test against wild type (*** $P < 0.001$, ** $P < 0.01$, * $P < 0.05$). The bar indicates 5 microns.

becomes trapped in and accumulates at the hypodermal ER in *sma-3* mutants (**Figure 7a-l**). We also noted that ER structures in *sma-3* mutants were thinner, with less complex and branched tubules, relative to wild type (**Figure 7j,l**), consistent with a defect in secretion.

To assess the loss of the BMP signaling target *dpy-11* on collagen release, we depleted *dpy-11* via RNAi in nematodes expressing ROL-6::wrmScarlet. Consistent with a role for DPY-11 in the secretion of collagens, including ROL-6, we observed a severe disruption in both intracellular and cuticular deposition of ROL-6::wrmScarlet (**Figure 6h**; **Figure 6 – figure supplement 1**). To validate that the perturbed ROL-6::wrmScarlet distribution and localization exhibited in *sma-3* and *sma-9* mutants (as well as *dpy-11* RNAi) was caused by disturbances in ER-specific processes, we targeted the ER chemically and genetically. We observed similar ROL-6::wrmScarlet subcellular distribution in tunicamycin treated ROL-6::wrmScarlet expressing animals as seen in *sma-3* and *sma-9* mutants (**Figure 7m**; **Figure 7 – figure supplement 1**). Tunicamycin inhibits the glycan biosynthesis pathway, disrupts ER-mediated secretion, and induces ER stress. Moreover, RNAi-mediated depletion of genes involved in various steps of ER-derived vesicle production and transport, including *C54H2.5* (SURF4 ortholog/ER cargo release), *F41C3.4* (GOLT1A/b ortholog/ER to Golgi apparatus transport), *Y25C1A.5* (COPB-1/COPI coat complex subunit), and *Y113G7A.3* (COPII coat complex subunit) increased ROL-6::wrmScarlet hypodermal intracellular accumulation and left empty patches in the cuticle, similar to BMP signaling mutants (**Figure 6g**; **Figure 6 – figure supplement 1**). To test whether impaired secretion through the ER alone could compromise body size, we examined nematodes treated with tunicamycin and found that they showed a strong decrease in body size (**Figure 7n**). Taken together, our results suggest that signaling by DBL-1/BMP signaling promotes body size growth by promoting ER-specific processes involved in collagen maturation, transport, and secretion into the cuticular ECM.

Discussion

SMA-9/Schnurri is a Smad transcriptional partner with both joint and unique targets

TGF- β signaling pathways regulate sets of target genes to execute biological functions in a context-dependent manner. Canonical signaling is mediated by the Smad transcription factor complex, but Smad binding sites are too degenerate and low affinity to account for the specific context-dependent effects, so transcription factor partners must also be involved. Some of the characterized partners are cell type-specific transcription factors. In contrast, Schnurri proteins are transcriptional partners that co-regulate target genes across multiple cell types. Here we used genome-wide RNA-seq and ChIP-seq integrated through a novel software analysis pipeline to untangle the roles of Smad and Schnurri transcription factors in the developing *C. elegans* larva. We chose the second larval (L2) stage because Smad activity is elevated at this stage as determined by the RAD-SMAD activity reporter [59], and because this stage is the earliest point at which one can observe a clear difference for one of the best studied Smad mutant phenotypes: body size growth.

Using ChIP-seq, we detected numerous SMA-3 and SMA-9 binding sites. The large number of sites could reflect the low affinity and degenerate DNA sequence recognition of known targets for their respective families of transcription factors. By using an analysis pipeline that combines BETA, which integrates ChIP-seq and RNA-seq data to identify targets, with LOA, which integrates two separate RNA-seq pairwise comparisons to identify shared DEGs, we identified nearby direct transcriptional targets based on their functional impact on transcript levels in corresponding mutants. Only a fraction of the total SMA-3 and SMA-9 sites were classified as functional based on BETA analysis of the ChIP-seq and RNA-seq datasets. Most SMA-3 and SMA-9 site were not found at HOT sites, which are often considered to be non-specific binding sites typically found in open regions of chromatin. The high number of additional sites classified as non-functional could

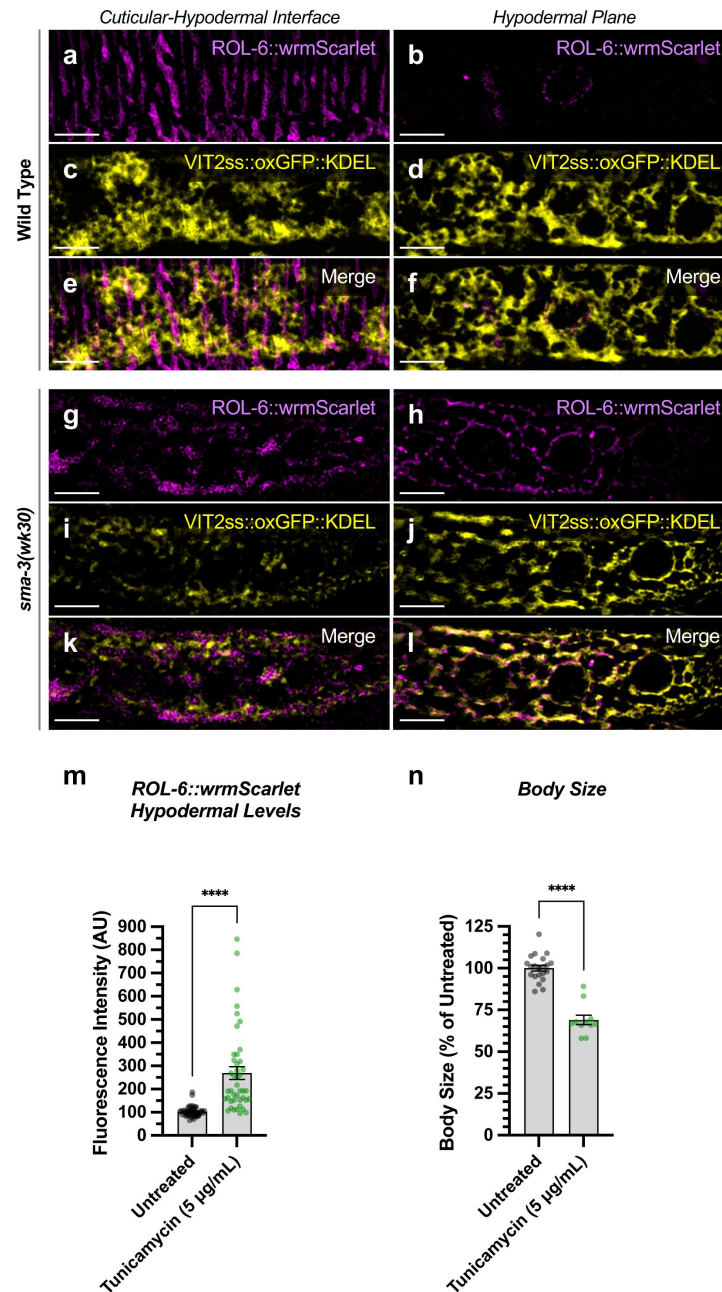


Figure 7.

ROL-6::wormScarlet accumulates in the ER of *sma-3* mutants

ROL-6::wormScarlet (magenta) and VIT2ss::oxGFP::KDEL (an ER marker, shown here in yellow) shown separately (a-d, g-j) or merged (e-f, k-l) in either (a-f) wild type or (g-l) a *sma-3* mutant. (a,c,e,g,i,k) shows the interface between the cuticle and the hypodermis, as visualized by SIM super resolution microscopy. (b,d,f,h,j,l) shows the hypodermal layer at a focal plane centered around the nuclear envelope. In wild type, most ROL-6::wormScarlet is delivered into the cuticle. In *sma-3* mutants, lower levels of ROL-6::wormScarlet are present in the cuticle and rapidly bleached under the SIM laser even under low power, whereas abundant ROL-6::wormScarlet colocalized with the ER VIT2ss::oxGFP::KDEL marker (yellow). We noted that ER reticulation in *sma-3* was thinner and skeletonized compared to wild type, perhaps suggesting reduced secretory throughput. (m) Quantification of ROL-6::wormScarlet fluorescence in the hypodermal layer of tunicamycin treated versus untreated nematodes. (n) Mean body length of L4 animals (normalized to untreated) for tunicamycin treated versus untreated nematodes. (m,n) Dots indicate the values for individual animals. Asterisks over pairwise comparison bars indicate a student t test (**** $P < 0.0001$). The bar indicates 5 microns.

represent the detection of weak affinity targets that do not have an actual biological purpose. Alternatively, these sites could have an additional role in DBL-1 signaling besides transcriptional regulation of nearby genes, or they could be regulating the expression of target genes at a far enough distance to not be detected by our BETA analysis. The difference between total binding sites and those associated with changes in gene expression underscores the importance of combining RNA-seq with ChIP-seq to identify the most biologically relevant targets.

Functional interactions between SMA-3/Smad and SMA-9/Schnurri

Our analysis revealed that SMA-3/Smad and SMA-9/Schnurri have target genes that are co-regulated by both factors, as well as separate target genes that they independently and exclusively regulate (**Figure 8**). ChIP-seq data demonstrated that 73.7% of SMA-3 binding peaks overlap with SMA-9 binding sites, while approximately half of all SMA-9 binding sites did not overlap with SMA-3 sites. The significant number of shared (co-regulated) target genes with overlapping binding peaks is consistent with a model in which SMA-3 and SMA-9 bind as a complex (or at least adjacent along DNA), as has been demonstrated at a few loci in *Drosophila* and *Xenopus*. Our results extend this model to a genome-wide level. Further investigation will be needed to determine if SMA-3 and SMA-9 form a direct complex at these sites, and whether the presence of one factor affects the binding of the other.

Our combined BETA and LOA analysis further demonstrated that SMA-3/Smad acts primarily as a transcriptional activator, whereas SMA-9/Schnurri can function as either an activator or a repressor depending on the locus. These dual functions for SMA-9/Schnurri are consistent with previous studies that demonstrated that different domains of SMA-9 can act as activators or repressors in a heterologous system [34]. Furthermore, SMA-9 DNA-binding domain fusions with known transcriptional activation or repression domains could each rescue a subset of mutant defects in *sma-9* mutants [34]. Most co-regulated genes were activated by both SMA-3 and SMA-9, with a small subset activated by SMA-3 and repressed by SMA-9. We used double mutant analysis of *sma-3*; *sma-9* animals to determine how these factors interact to produce normal body size. While both single mutants were phenotypically small, the *sma-9* mutation partially suppressed the small body size of *sma-3* mutants so that double mutants were intermediate in size, suggesting that these factors may have antagonistic interactions in addition to the expected cooperative effects. Antagonism would be consistent with the observed interaction between SMA-9 and the BMP pathway in mesodermal lineage specification [36, 66], and with the observation of factors that have both positive and negative effects on body size [60].

We used RT-PCR to determine how SMA-3 and SMA-9 function together at a locus-specific level. For co-activated target genes, genetic analysis was consistent with the proteins acting together rather than additively. In the *sma-3*; *sma-9* double mutant, genes regulated in opposite directions by SMA-3 and SMA-9 showed upregulation as in *sma-9* single mutants. Thus, SMA-3 activation of these genes is dependent on the presence of SMA-9. This dependence could occur if SMA-9 is needed to recruit SMA-3 to the DNA. This possibility would be a novel mode of interaction, because for the previously analyzed *brinker* and *Xvent2* target genes, Schnurri was shown to be recruited by the Smad complex rather than vice versa. A second possibility is that SMA-3 can bind in the absence of SMA-9 but cannot engage with the transcriptional machinery; that is, both proteins are required to form a transcriptional activation complex. With either possibility, SMA-9 represses expression of these genes in the absence of SMA-3.

Biological functions of target genes

DBL-1 signaling regulates multiple developmental and physiological processes in *C. elegans*, including body size, lipid metabolism, innate immunity, and male tail development. Our samples were not enriched for males, precluding an analysis of targets involved in male tail development. Binding sites and their nearby regulated targets fell into three classes: SMA-3-exclusive, SMA-9-exclusive, and co-regulated. Interestingly, the GO terms for both shared and independent target

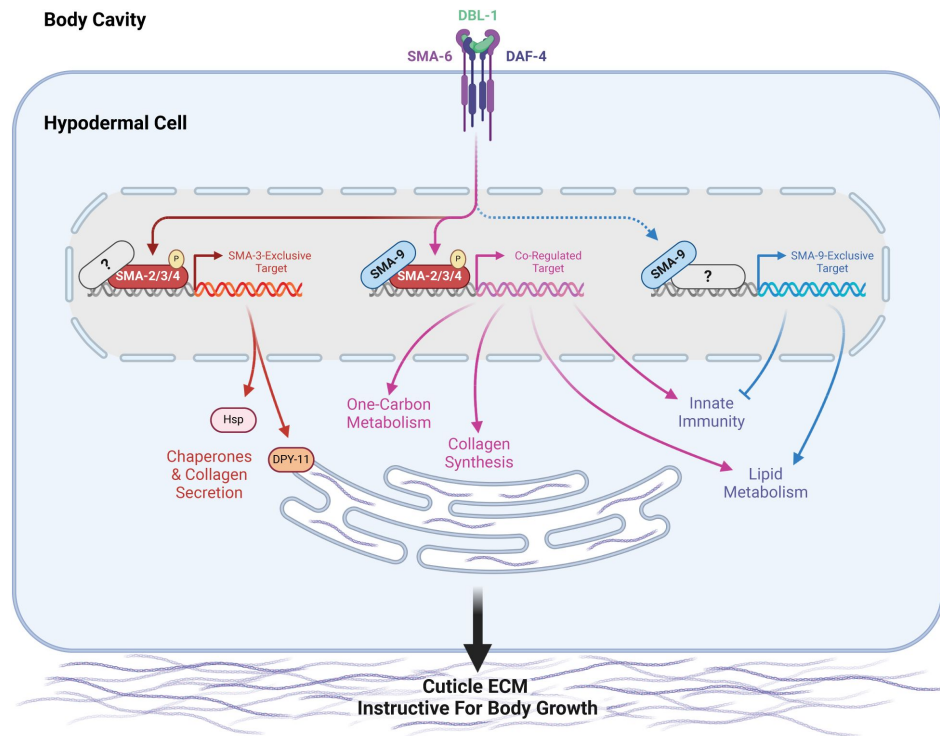


Figure 8.

A model for the regulation of growth by DBL-1/BMP Signaling

During early larval development, DBL-1 ligand binds to the BMP receptors SMA-6 and DAF-4, which activate the Smads SMA-2, SMA-3, and SMA-4. The resulting Smad complex binds to one category of sites along the genome either alongside or in complex with SMA-9, co-regulating neighboring genes (in purple). These co-regulated genes include several collagen genes, factors involved in one-carbon metabolism, innate immunity genes, and genes involved in lipid metabolism. The Smad complex also binds to another category of sites (in orange/red) which lack SMA-9, perhaps associating instead with other transcription factors or co-factors (gray question mark). These SMA-3-exclusive genes include chaperones and the disulfide reductase DPY-11, which in turn promote the secretion of collagen into the cuticular extracellular matrix, thereby remodeling the cuticle to allow for growth. In addition to binding either with or near Smad complex components, SMA-9 also binds to sites along the genome lacking Smad (or at least SMA-3, in blue), perhaps associating instead with other transcription factors or co-factors (gray question mark). These SMA-9-exclusive genes, which can be either positively or negatively regulated by SMA-9, play a minimal role in body size growth, but rather are associated with innate immunity and lipid metabolism.

genes partially overlap, suggesting broad similarity in biological functions. Within the subset of SMA-3-exclusive target genes, we noticed GO term enrichment for chaperones and factors involved in collagen secretion. Given the low affinity and degenerate nature of Smad binding sites, we speculate that additional binding factors associate with SMA-3 at these SMA-3-exclusive targets to facilitate regulation. Future studies will be needed to identify these novel partners.

By contrast, the subset of SMA-9-exclusive target genes were enriched in GO terms associated with lipid metabolism and innate immunity. Although SMA-3 functions in both fat storage and pathogen resistance, respectively [38, 67–72], these SMA-9-exclusive target genes imply Smad-independent roles for SMA-9 in these functions. A Smad-independent role for SMA-9 in immunity is consistent with the pronounced role of vertebrate Schnurri homologs in immunity [43], which have not been reported to overlap with TGF- β -regulated functions. In vertebrates, Schnurri homologs are shown to be direct DNA binding proteins with diverse biological functions that include TGF- β -responsive and TGF- β -independent roles. In TGF- β -independent roles they bind NF κ B-like sequences [73], and can interact with other transcription factors including TRAF2 and c-Jun [74, 75]. It will be interesting to determine whether the SMA-9/Schnurri-exclusive target genes are responsive to TGF- β signals and/or to other signaling ligands.

Identification of target genes that mediate body size regulation

GO term analysis readily identified target genes involved in lipid metabolism and pathogen response, but target genes required for body size regulation remain more difficult to predict based on sequence alone. Furthermore, we have previously shown that the body size and lipid metabolism functions are separable [38]. We therefore conducted a functional analysis of these target genes by performing body size measurements on their corresponding mutants. We also performed body size measurements on RNAi knockdowns for identified target genes in an RNAi sensitive strain, examining their effect in both a wild-type background and a *lon-2* background in which DBL-1 signaling is exaggerated, resulting in an elongated body size. Normalizing these data using Glass' effect size allowed us to make broad comparisons between mutants and RNAi knockdowns. These analyses confirmed previous work focusing on the role of the cuticle in mediating body size regulation by DBL-1/BMP [35]. Although RNAi knockdowns of *clec-1*, *fah-1*, *C52D10.3*, *dre-1*, *hsp-12.3*, *wrt-1* reduced body size in the *rrf-3* mutant background, they failed to reduce the body size in *lon-2*; *rrf-3* mutants, suggesting that they regulate body size upstream or independently of the DBL-1 pathway. By contrast, RNAi knockdowns of *haf-9*, *his-32*, *zip-10*, *emb-8*, *F25B5.6*, *nath-10*, and *hsp-3* reduced body size in *lon-2*; *rrf-3* double mutants but not in *rrf-3* single mutants, suggesting that they might be factors whose effects are only detectable in the context of an overactive pathway; these warrant future study. Seventeen genes showed a body reduction with a statistically significant effect size equal to or greater than one in both genetic backgrounds, making them of particular interest. These genes had GO terms associated with either one-carbon metabolism or chaperone/ER secretion, suggesting that the upregulation of these activities is a key aspect of how DBL-1 signaling promotes growth (Figure 8).

How could one-carbon metabolism play a role in body size growth? This complex set of interlinked metabolic cycles is critical for methionine and folate homeostasis. It also provides the methyl groups needed to synthesize nucleotides, amino acids, the antioxidant glutathione, creatine, and phospholipids like phosphatidylcholine, a fundamental component of membranes [76]. One-carbon metabolism also provides the methyl groups needed to make epigenetic marks on DNA and chromatin. The specific role of this metabolic pathway in body size growth will be an important topic of future study.

As in previous datasets, this RNA-seq analysis identified collagen genes (*col-94* and *col-153*) as direct co-regulated targets of SMA-3 and SMA-9. An enrichment of ER secretion and chaperone factors in the list of direct targets involved in body size growth was unexpected, but reasonable given that one of the key functions of the hypodermis is to secrete cuticular collagen. The role of collagens in body size and morphology is well documented [29, 77], and the secreted

ADAMTS metalloprotease ADT-2 modifies cuticle collagen organization and regulates body size [78]. The thioredoxin-like DPY-11 was a particularly compelling target given its established role in cuticle formation and the dramatic effect of its loss on body size growth, as well as the known role for these enzymes in processing secreted proteins moving through the ER/Golgi network [64]. To test whether DBL-1 regulates ER secretion of collagen, we turned to endogenously tagged cuticle collagen ROL-6::wrmScarlet to analyze subcellular localization. Using this reporter for collagen synthesis and secretion, we demonstrated that the DBL-1 pathway influences the secretion of this cuticle collagen. In particular, ROL-6::wrmScarlet accumulates in a perinuclear ER compartment in both *sma-3* and *sma-9* mutants. Consistent with a secretion defect, we found a corresponding decrease in the amount of ROL-6::wrmScarlet in the cuticle of *sma-3* mutants, although not in *sma-9* mutants, which could reflect the differential enrichment of *dpy-11* and chaperones in the list of SMA-3-exclusive target genes. Interestingly, treatment with tunicamycin, which impairs ER secretion, was sufficient to reduce body size, which is consistent with a model in which BMP signaling promotes collagen secretion to foster growth (Figure 8). We remain cautious in our interpretation of this result, as blocking ER secretion with tunicamycin could affect the secretion of the BMP receptors or other proteins that function together with the receptors, which could also lead to a body size defect.

The collagenous cuticle is a major target of DBL-1/BMP signaling in body size regulation. For example, others have also demonstrated that DBL-1 signaling regulates cuticle collagen LON-3 post-transcriptionally [79]. In addition to direct transcriptional regulation of cuticle components, here we highlight the importance of regulating other target genes such as *dpy-11* that are needed for collagen post-transcriptional processing. One powerful element of our approach was that our ChIP-seq/RNA-seq BETA analysis identified direct target genes and combined those findings with a functional analysis of a subset of those targets, thereby demonstrating that a combination of SMA-3-exclusive targets (including chaperones and collagen secretion factors) work together with SMA-3/SMA-9 co-regulated targets (including collagen genes and factors involved in one-carbon metabolism) to affect the process of body growth through their regulation of the extracellular matrix of the surrounding cuticle. TGF- β family members are well known regulators of collagen deposition and extracellular matrix composition, suggesting that this class of transcriptional targets is conserved over evolutionary time [80, 81]. Thus, it is likely that the multi-level interactions identified in *C. elegans* are also relevant to the functions of these factors in vertebrates.

Acknowledgements

We thank Michelle Kudron with the Model Organism ENCyclopedia of DNA Elements and model organism Encyclopedia of Regulatory Networks projects for performing chromatin immunoprecipitation sequencing. Some strains were provided by the *Caenorhabditis* Genetics Center, which is funded by the National Institutes of Health (NIH) Office of Research Infrastructure Programs (P40 OD-101440). We thank Barth Grant for the *pwSi82* strain, and Nanci Kane for her assistance with the Zeiss Elyra 7 Lattice SIM within the Waksman Institute Shared Imaging Facility (Rutgers, The State University of New Jersey). We thank Derek Gordon for guidance and assistance with the analysis of the ChIP-seq distance matrix. This work was supported by NIH grants R15GM112147 to CSD, R21AG075315 to CSD and CR, R35GM130351 to JL, and R01GM101972 to CR.

a		b	
SMA-3 Direct Targets Annotation Clusters		SMA-9 Direct Targets Annotation Clusters	
Annotation Cluster	EASE Score	Annotation Cluster	EASE Score
Ribosome Biogenesis	6.18	Innate Immunity	7.44
Oxido-reductases	3.31	Fatty Acid Metabolism	4.03
Mitochondria	3.10	One-carbon Metabolism	3.23
One-carbon Metabolism	3.03	Amino Acid Metabolism	2.73
RNA Helicases	2.95	Anti-Bacterial	2.67
ER Chaperones	2.89	Fatty Acid Transporters	2.62
Chromosome Organization	2.66	Cytochrome P450	2.58
mRNA Splicing	2.64	Lysosomes & Proteolysis	2.56
Fatty Acid Metabolism	2.58	Cofactor Biosynthesis	2.33
Amino Acid Biosynthesis	2.25	Crononases	2.14
RNA Binding	2.08	Long FA Metabolism	2.05
Methionine Biosynthesis	2.00	Glutathione Metabolism	1.61
Apple Domain	1.86	C-type Lectins	1.60
Acyl-CoA Dehydrogen	1.74		
Isomerases	1.67		
DNAJ Domain	1.46		

Figure 3 – figure supplement 1.

DAVID annotation clusters of gene ontology terms for identified SMA-3 and SMA-9 targets.

Tables of annotation clusters for gene ontology terms for direct target DEGs (via DAVID, with accompanying statistical EASE score) are shown for (a) SMA-3 and (b) SMA-9.

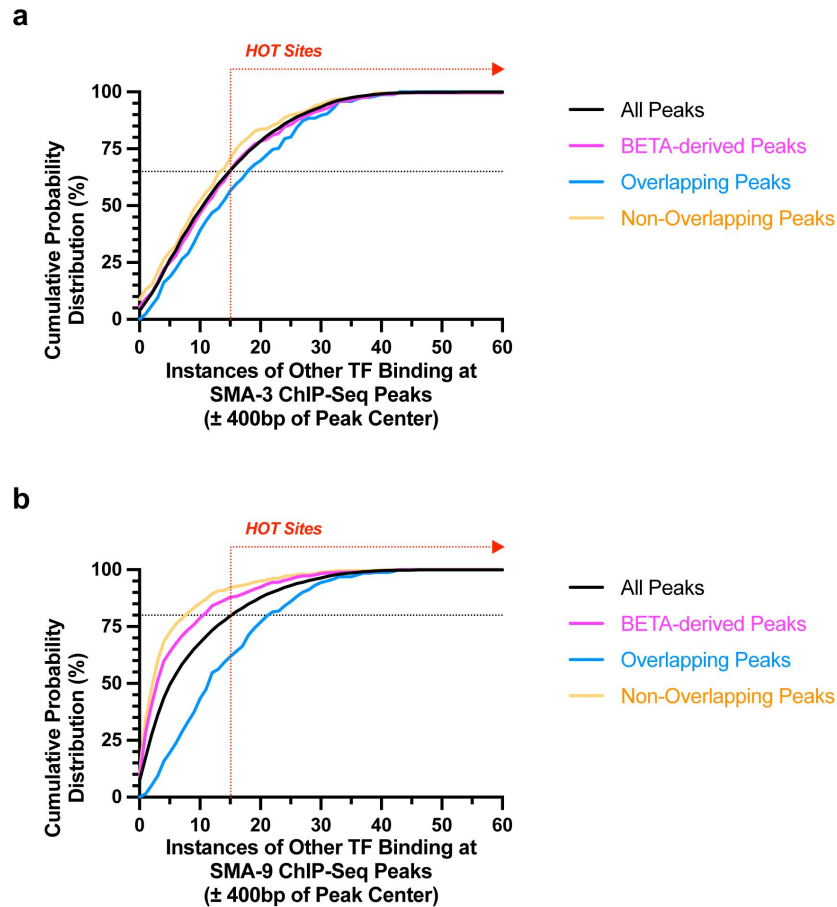
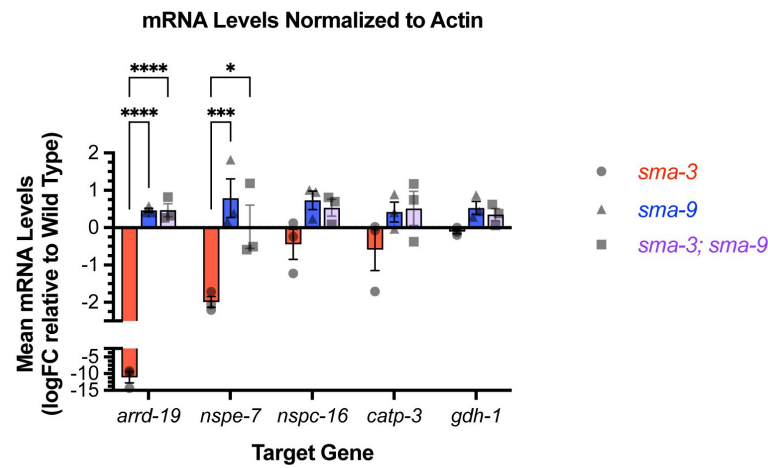


Figure 3 - figure supplement 2.

SMA-3 and SMA-9 sites tend not to be at HOT sites.

(a,b) Cumulative probability distributions measuring the number of (a) SMA-3 or (b) SMA-9 ChIP-seq peaks against the number of other transcription factors known from ModENCODE/ModERN analysis to bind to each site's region of the genome (within 400 bps of each ChIP-seq peak center). The black line indicates all SMA-3 or SMA-9 ChIP-seq peaks, whereas the magenta line indicates functional SMA-3 or SMA-9 ChIP-seq peaks identified by BETA analysis. The cyan line indicates SMA-3 and SMA-9 sites that overlap near co-regulated genes. The orange line indicates SMA-3-exclusive or SMA-9-exclusive sites. The red dotted vertical line with the rightward arrow indicates the minimum cutoff for high occupancy target (HOT) sites, which bind to 15 or more different transcription factors as determined by modENCODE/modERN. The black dotted horizontal line indicates the cumulative probability distribution percentage at which the curve for all ChIP-seq peaks intersects the cutoff for HOT sites (i.e., 15 or more TFs binding within 400 bps).

a



b

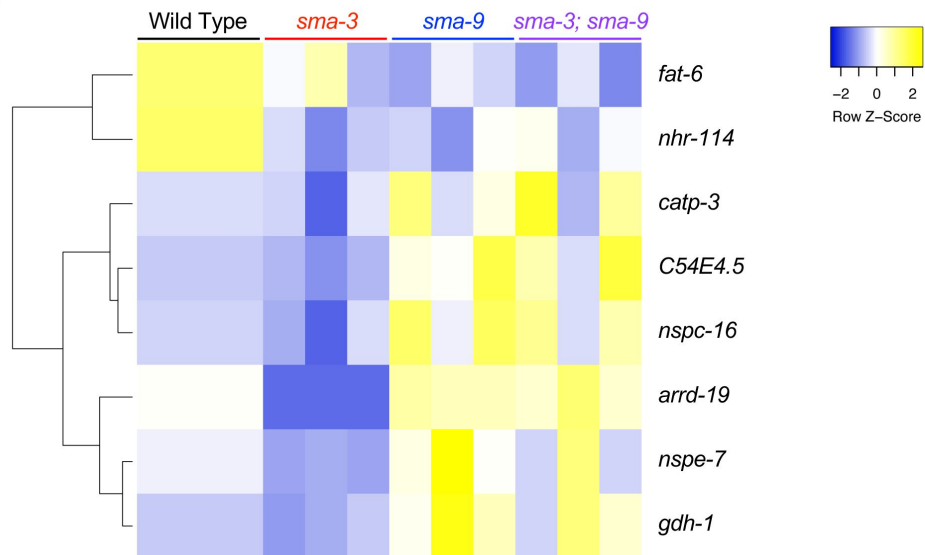


Figure 4 – figure supplement 1.

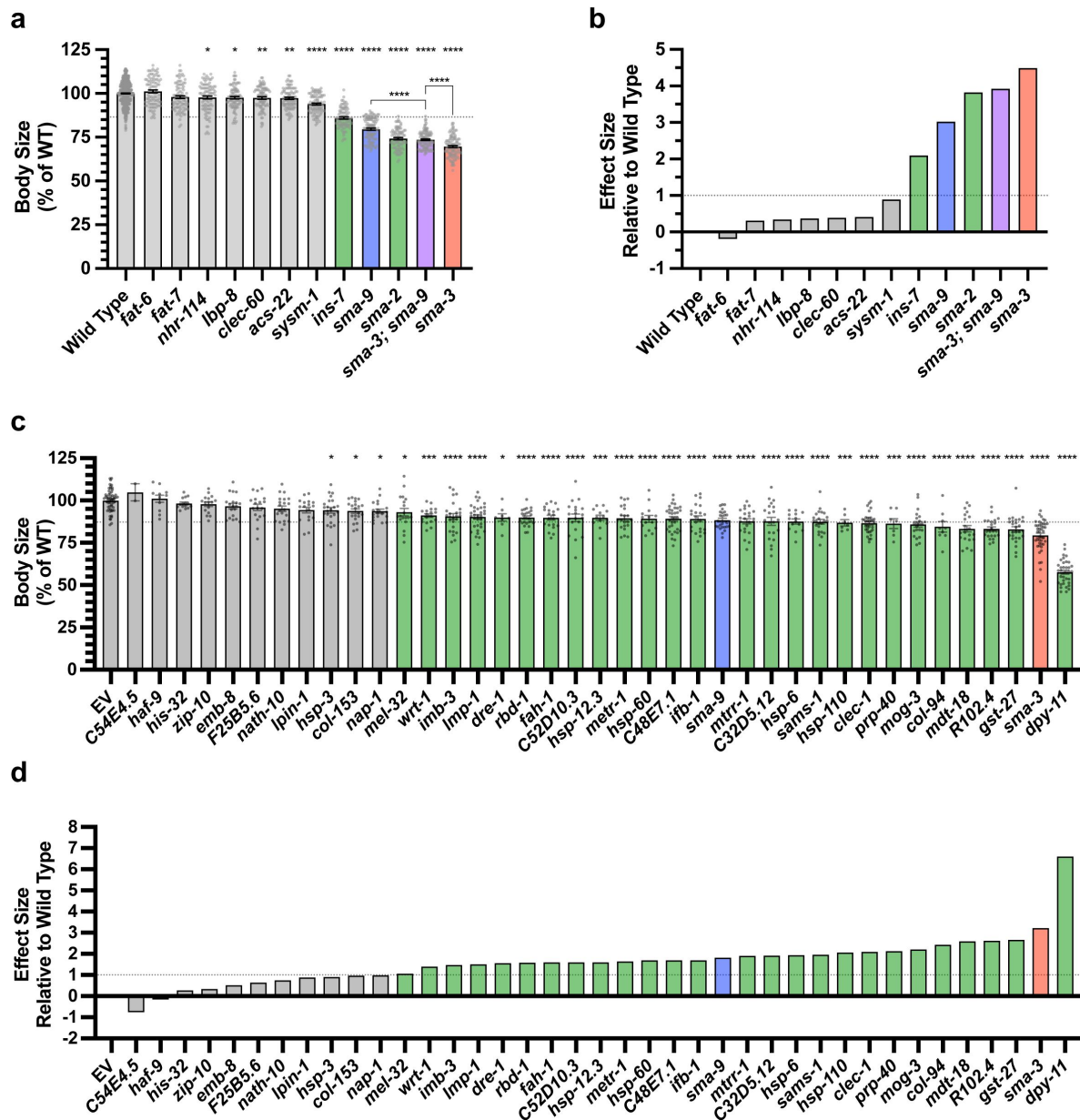


Figure 5 – figure supplement 1.

Target genes required for exaggerated growth

(a) Mean body length of L4 animals (normalized to wild type) for the indicated mutants. Dots indicate the size of individual animals. Asterisks above each column indicate one way ANOVA with Dunnett's multiple comparison test against wild type (**** $P < 0.0001$, *** $P < 0.001$, ** $P < 0.01$, * $P < 0.05$). Asterisks over pairwise comparison bars indicate one-way ANOVA with Sidák's multiple comparison test. The dotted line indicates the size value falling two standard deviations below the mean of wild type. (b) Glass' effect size (the difference between the mean of the mutant and the mean for wild type, divided by the standard deviation of wild type) for the indicated mutants. The dotted line indicates an effect size of one. (c,d) Mean body size and Glass' effect size for RNAi knockdowns of the indicated gene in the *rrf-3* RNAi sensitive strain. "EV" indicates the empty RNAi vector as a negative control. Asterisks above each column indicate one way ANOVA with Dunnett's multiple comparison test against EV (**** $P < 0.0001$, *** $P < 0.001$, ** $P < 0.01$, * $P < 0.05$). For all graphs, red, blue, and purple columns indicate values for *sma-3* (mutant or RNAi knockdown), *sma-9* (mutant or RNAi knockdown), and their double mutant combination, respectively. Green bars indicate genotypes for which the mutant or RNAi knockdown resulted in a statistically significant reduction ($P < 0.05$) with a Glass' effect size of one or greater.

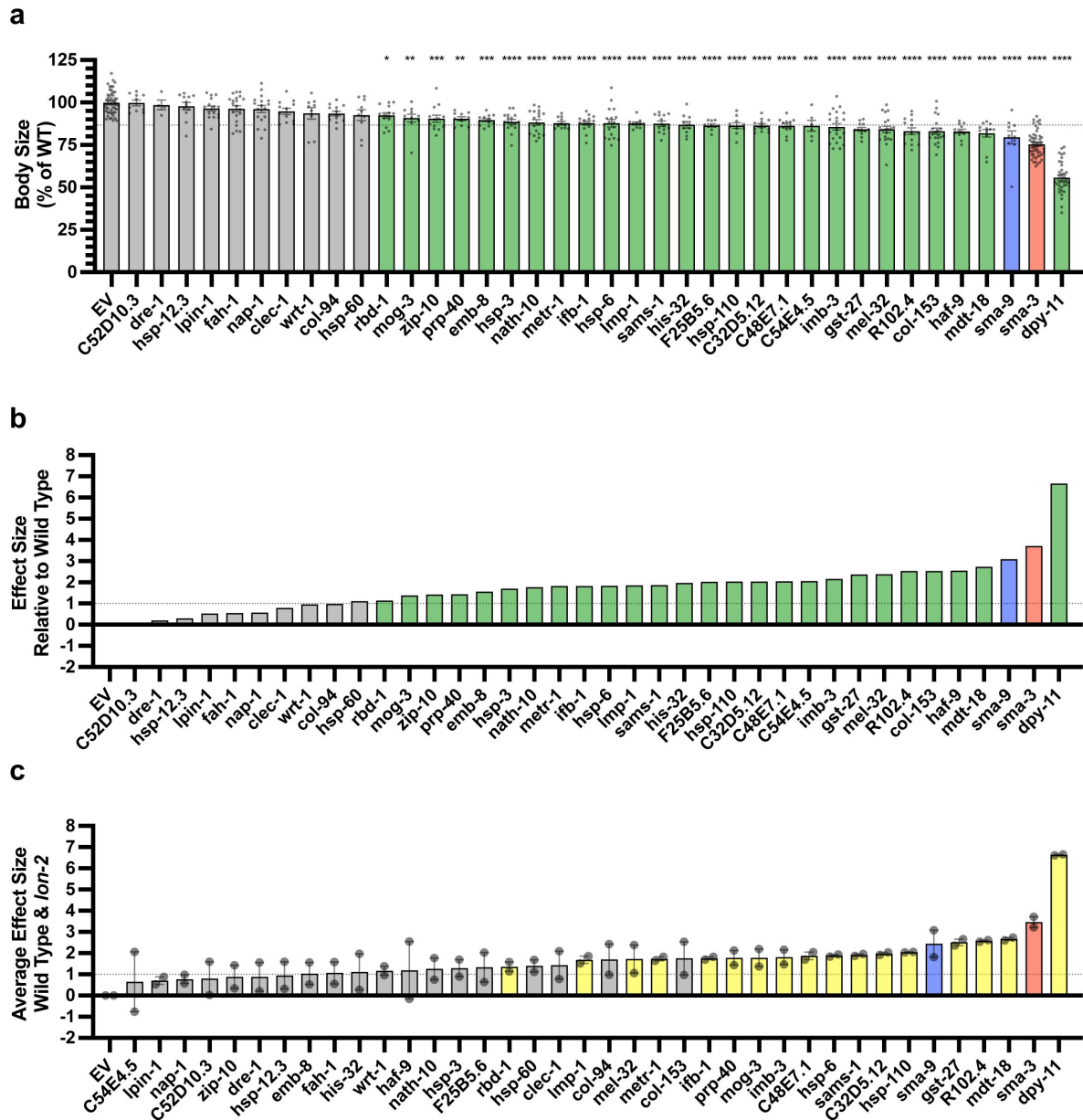


Figure 5 – figure supplement 2.

Target genes required for exaggerated growth in *lon-2* mutants

(a) Mean body length of L4 animals (normalized to EV) for the indicated RNAi knockdowns in the *rrf-3; lon-2* double mutant. “EV” indicates the empty RNAi vector as a negative control. Dots indicate the size of individual animals. Asterisks above each column indicate one way ANOVA with Dunnett’s multiple comparison test against EV (**** $P < 0.0001$, *** $P < 0.001$, ** $P < 0.01$, * $P < 0.05$). The dotted line indicates the size value falling two standard deviations below the mean of EV (b) Glass’ effect size (the difference between the mean of the RNAi knockdown and the mean for EV, divided by the standard deviation for EV) for the indicated gene undergoing knockdown. The dotted line indicates an effect size of one. Green bars indicate genotypes for which the RNAi knockdown resulted in a statistically significant reduction ($P < 0.05$) with a Glass’ effect size of one or greater. (c) The average of the Glass’ effect size between the *rrf-3* wild-type background and the *rrf-3 lon-2* mutant background (individual dots for each are shown). For (c), yellow bars indicate genotypes for which the RNAi knockdown resulted in a statistically significant reduction ($P < 0.05$) with a Glass’ effect size of one or greater in both the wild-type and the *lon-2* mutant background. For all graphs, red and blue columns indicate values for *sma-3* and *sma-9* RNAi knockdown, respectively.

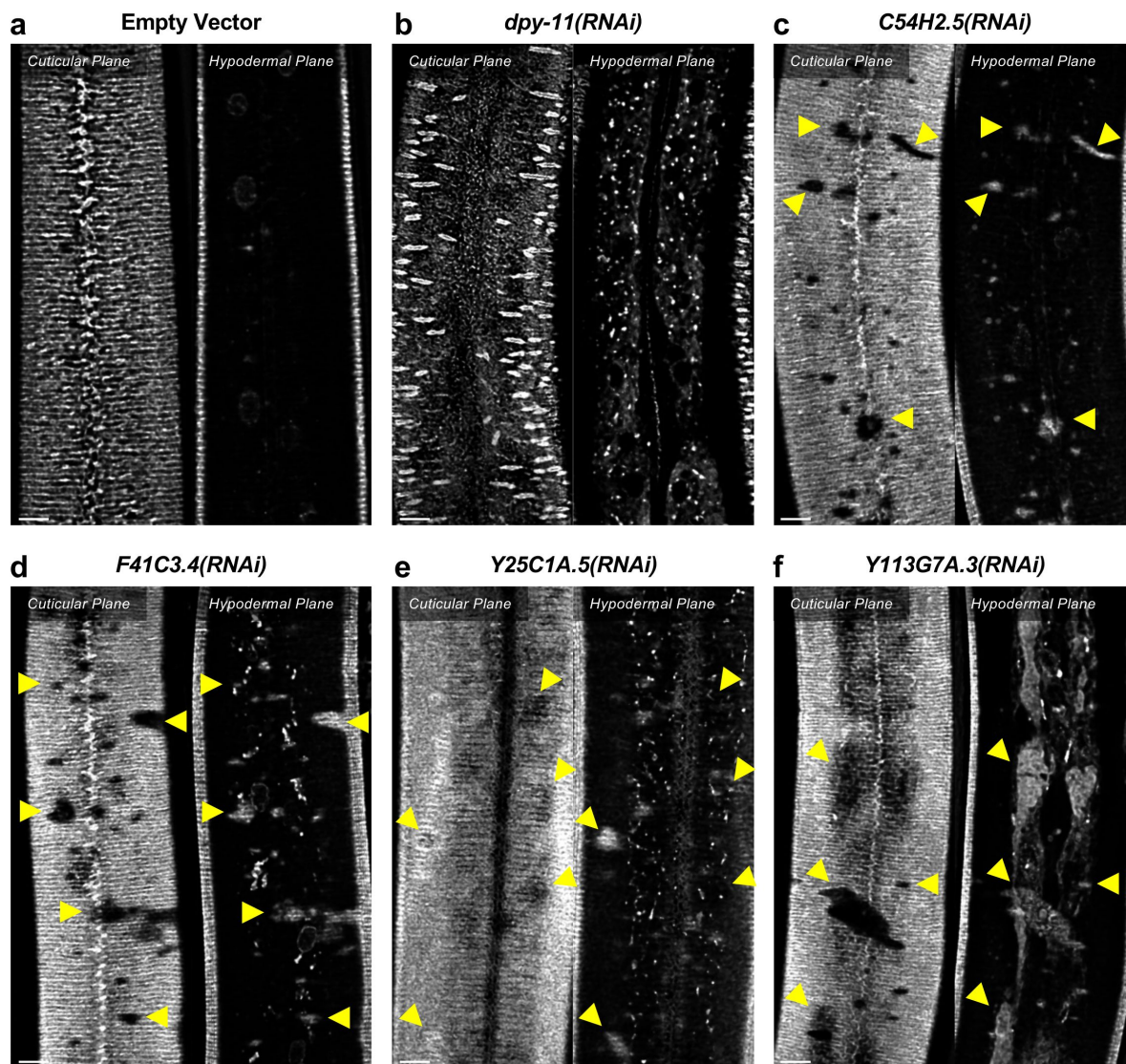


Figure 6 – figure supplement 1.

DPY-11 promotes body size through collagen secretion

(a) ROL-6::wrmScarlet fluorescence detected in annuli and alae in the cuticular layer, as well as in nuclear envelopes in the underlying hypodermal layer in wild-type animals exposed to an empty vector for RNAi knockdown. (b-f) ROL-6::wrmScarlet in animals exposed to RNAi knockdown for the indicated gene. (b) In animals knocked down for *dpy-11*, little ROL-6::wrmScarlet makes it to the cuticle, instead accumulating intracellularly in the hypodermis. (c-f) In animals knocked down for known ER secretory factors, patches of cuticular surface show diminished levels of ROL-6::wrmScarlet, whereas the protein is detected in the hypodermal layer just under these patches (yellow arrowheads), similar to what is observed in *sma-3* and *sma-9* mutants, and consistent with a failure to deliver collagen to the surface cuticle. The bar indicates 5 microns.

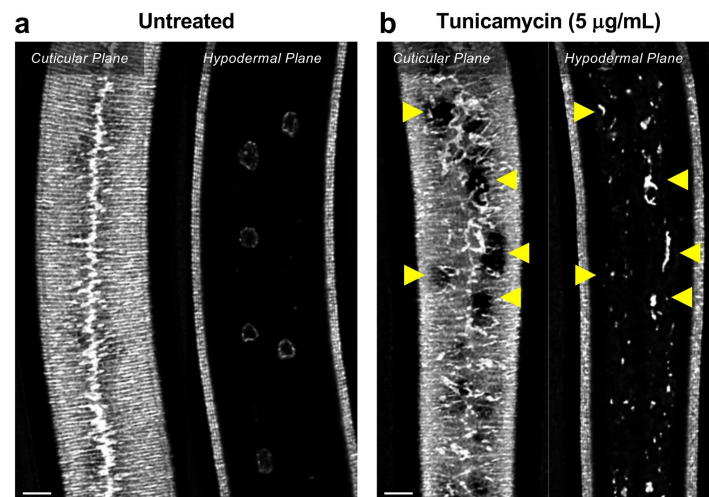


Figure 7 – figure supplement 1.

Tunicamycin treatment mimics the effect of *sma-3* and *sma-9* mutations on collagen secretion

(a) ROL-6::wrmScarlet fluorescence detected in annuli and alae in the cuticular layer, as well as in nuclear envelopes in the underlying hypodermal layer in untreated wild-type animals. (b) ROL-6::wrmScarlet in animals exposed to tunicamycin. Patches of cuticular surface show diminished levels of ROL-6::wrmScarlet, whereas the protein is detected in the hypodermal layer just under these patches (yellow arrowheads), similar to what is observed in *sma-3* and *sma-9* mutants, and consistent with a failure to deliver collagen to the surface cuticle. In addition, collagen in the lateral alae is disorganized, suggesting secretion is impaired in the seam cells. The bar indicates 5 microns.

References

1. Massague J. (1998) **TGF-beta signal transduction** *Annu Rev Biochem* **67**:753–91 <https://doi.org/10.1146/annurev.biochem.67.1.753>
2. Savage C, Das P, Finelli AL, Townsend SR, Sun CY, Baird SE, et al. (1996) **Caenorhabditis elegans genes sma-2, sma-3, and sma-4 define a conserved family of transforming growth factor beta pathway components** *Proc Natl Acad Sci U S A* **93**:790–4 <https://doi.org/10.1073/pnas.93.2.790>
3. Sekelsky JJ, Newfeld SJ, Raftery LA, Chartoff EH, Gelbart WM (1995) **Genetic characterization and cloning of mothers against dpp, a gene required for decapentaplegic function in Drosophila melanogaster** *Genetics* **139**:1347–58
4. Wrana JL, Attisano L, Wieser R, Ventura F, Massague J (1994) **Mechanism of activation of the TGF-beta receptor** *Nature* **370**:341–347 <https://doi.org/10.1038/370341a0>
5. Liu F, Ventura F, Doody J, Massague J (1995) **Human type II receptor for bone morphogenic proteins (BMPs): extension of the two-kinase receptor model to the BMPs** *Mol Cell Biol* **15**:3479–86
6. Wrana J, Attisano L, Carcamo J, Zentella A, Doody J, Laiho M, et al. (1992) **TGF-β signals through a heteromeric protein kinase receptor complex** *Cell* **71**:1003–14 [https://doi.org/10.1016/0092-8674\(92\)90395-S](https://doi.org/10.1016/0092-8674(92)90395-S)
7. Estevez M, Attisano L, Wrana JL, Albert PS, Massague J, Riddle DL (1993) **The daf-4 gene encodes a bone morphogenetic protein receptor controlling C. elegans dauer larva development** *Nature* **365**:644–9 <https://doi.org/10.1038/365644a0>
8. Wu JW, Hu M, Chai J, Seoane J, Huse M, Li C, et al. (2001) **Crystal structure of a phosphorylated Smad2. Recognition of phosphoserine by the MH2 domain and insights on Smad function in TGF-beta signaling** *Mol Cell* **8**:1277–89
9. Chacko BM, Qin BY, Tiwari A, Shi G, Lam S, Hayward LJ, et al. (2004) **Structural basis of heteromeric smad protein assembly in TGF-beta signaling** *Molecular cell* **15**:813–23 <https://doi.org/10.1016/j.molcel.2004.07.016>
10. Souchelnytskyi S, Tamaki K, Engstrom U, Wernstedt C, ten Dijke P, Heldin CH. (1997) **Phosphorylation of Ser465 and Ser467 in the C terminus of Smad2 mediates interaction with Smad4 and is required for TGF-β signaling** *J Biol Chem* **272**:28107–15
11. Qin BY, Chacko BM, Lam SS, de Caestecker MP, Correia JJ, Lin K (2001) **Structural basis of Smad1 activation by receptor kinase phosphorylation** *Mol Cell* **8**:1303–12
12. Zhang Y, Feng X, We R, Derynck R (1996) **Receptor-associated Mad homologues synergize as effectors of the TGF-beta response** *Nature* **383**:168–72 <https://doi.org/10.1038/383168a0>
13. Abdollah S, Macias-Silva M, Tsukazaki T, Hayashi H, Attisano L, Wrana JL (1997) **TGF-β RI phosphorylation of Smad2 on Ser465 and Ser467 is required for Smad2-Smad4 complex formation and signaling** *J Biol Chem* **272**:27678–85

14. Lagna G, Hata A, Hemmati-Brivanlou A, Massague J (1996) **Partnership between DPC4 and SMAD proteins in TGF-beta signalling pathways** *Nature* **383**:832–6 <https://doi.org/10.1038/383832a0>
15. Nicolas FJ, De Bosscher K, Schmierer B, Hill CS (2004) **Analysis of Smad nucleocytoplasmic shuttling in living cells** *Journal of Cell Science* **117**:4113–25 <https://doi.org/10.1242/jcs.01289>
16. Kim J, Johnson K, Chen HJ, Carroll S, Laughon A (1997) **Drosophila Mad binds to DNA and directly mediates activation of vestigial by Decapentaplegic** *Nature* **388**:304–308 <https://doi.org/10.1038/40906>
17. Gao S, Steffen J, Laughon A (2005) **Dpp-responsive silencers are bound by a trimeric Mad-Medea complex** *The Journal of biological chemistry* **280**:36158–64 <https://doi.org/10.1074/jbc.M506882200>
18. Rushlow C, Colosimo PF, Lin M-c, Xu M, Kirov N. (2001) **Transcriptional regulation of the Drosophila gene zen by competing Smad and Brinker inputs** *Genes & Development* **15**:340–51 <https://doi.org/10.1101/gad.861401>
19. Hill CS (2016) **Transcriptional Control by the SMADs** *Cold Spring Harb Perspect Biol* **8** <https://doi.org/10.1101/cshperspect.a022079>
20. Pyrowolakis G, Hartmann B, Muller B, Basler K, Affolter M (2004) **A simple molecular complex mediates widespread BMP-induced repression during Drosophila development** *Dev Cell* **7**:229–40 <https://doi.org/10.1016/j.devcel.2004.07.008>
21. Germain S, Howell M, Esslemont GM, Hill CS (2000) **Homeodomain and winged-helix transcription factors recruit activated Smads to distinct promoter elements via a common Smad interaction motif** *Genes Dev* **14**:435–51
22. Yao LC, Blitz IL, Peiffer DA, Phin S, Wang Y, Ogata S, et al. (2006) **Schnurri transcription factors from Drosophila and vertebrates can mediate Bmp signaling through a phylogenetically conserved mechanism** *Development* **133**:4025–34 <https://doi.org/10.1242/dev.02561>
23. Kang Y, Chen CR, Massague J (2003) **A self-enabling TGFbeta response coupled to stress signaling: Smad engages stress response factor ATF3 for Id1 repression in epithelial cells** *Mol Cell* **11**:915–26 [https://doi.org/10.1016/s1097-2765\(03\)00109-6](https://doi.org/10.1016/s1097-2765(03)00109-6)
24. Deignan L, Pinheiro MT, Sutcliffe C, Saunders A, Wilcockson SG, Zeef LA, et al. (2016) **Regulation of the BMP Signaling-Responsive Transcriptional Network in the Drosophila Embryo** *PLoS Genet* **12** <https://doi.org/10.1371/journal.pgen.1006164>
25. Chiu WT, Charney Le R, Blitz IL, Fish MB, Li Y, Biesinger J, et al. (2014) **Genome-wide view of TGFbeta/Foxh1 regulation of the early mesendoderm program** *Development* **141**:4537–47 <https://doi.org/10.1242/dev.107227>
26. Morikawa M, Koinuma D, Tsutsumi S, Vasilaki E, Kanki Y, Heldin CH, et al. (2011) **ChIP-seq reveals cell type-specific binding patterns of BMP-specific Smads and a novel binding motif** *Nucleic Acids Res* **39**:8712–27 <https://doi.org/10.1093/nar/gkr572>
27. Suzuki Y, Yandell MD, Roy PJ, Krishna S, Savage-Dunn C, Ross RM, et al. (1999) **A BMP homolog acts as a dose-dependent regulator of body size and male tail patterning in Caenorhabditis elegans** *Development* **126**:241–50

28. Lazetic V, Fay DS (2017) **Molting in *C. elegans*** *Worm* **6** <https://doi.org/10.1080/21624054.2017.1330246>
29. Page AP, Johnstone IL. (2007) **The cuticle** *WormBook* :1–15 <https://doi.org/10.1895/wormbook.1.138.1>
30. Gumienny TL, Savage-Dunn C (2013) **TGF-beta signaling in *C. elegans*** *WormBook* :1–34 <https://doi.org/10.1895/wormbook.1.22.2>
31. Yoshida S, Morita K, Mochii M, Ueno N (2001) **Hypodermal expression of *Caenorhabditis elegans* TGF-beta type I receptor SMA-6 is essential for the growth and maintenance of body length** *Dev Biol* **240**:32–45 <https://doi.org/10.1006/dbio.2001.0443>
32. Wang J, Tokarz R, Savage-Dunn C (2002) **The expression of TGFbeta signal transducers in the hypodermis regulates body size in *C. elegans*** *Development* **129**:4989–98
33. Roberts AF, Gumienny TL, Gleason RJ, Wang H, Padgett RW (2010) **Regulation of genes affecting body size and innate immunity by the DBL-1/BMP-like pathway in *Caenorhabditis elegans*** *BMC Dev Biol* **10** <https://doi.org/10.1186/1471-213X-10-61>
34. Liang J, Yu L, Yin J, Savage-Dunn C (2007) **Transcriptional repressor and activator activities of SMA-9 contribute differentially to BMP-related signaling outputs** *Dev Biol* **305**:714–25 <https://doi.org/10.1016/j.ydbio.2007.02.038>
35. Madaan U, Yzeiraj E, Meade M, Clark JF, Rushlow CA, Savage-Dunn C (2018) **BMP Signaling Determines Body Size via Transcriptional Regulation of Collagen Genes in *Caenorhabditis elegans*** *Genetics* **210**:1355–67 <https://doi.org/10.1534/genetics.118.301631>
36. Foehr ML, Lindy AS, Fairbank RC, Amin NM, Xu M, Yanowitz J, et al. (2006) **An antagonistic role for the *C. elegans* Schnurri homolog SMA-9 in modulating TGFbeta signaling during mesodermal patterning** *Development* **133**:2887–96 <https://doi.org/10.1242/dev.02476>
37. Liang J, Lints R, Foehr ML, Tokarz R, Yu L, Emmons SW, et al. (2003) **The *Caenorhabditis elegans* schnurri homolog sma-9 mediates stage- and cell type-specific responses to DBL-1 BMP-related signaling** *Development* **130**:6453–64 <https://doi.org/10.1242/dev.00863>
38. Clark JF, Meade M, Ranepura G, Hall DH, Savage-Dunn C (2018) ***Caenorhabditis elegans* DBL-1/BMP Regulates Lipid Accumulation via Interaction with Insulin Signaling** *G3 (Bethesda)* **8**:343–51 <https://doi.org/10.1534/g3.117.300416>
39. Staehling-Hampton K, Laughon AS, Hoffmann FM (1995) **A *Drosophila* protein related to the human zinc finger transcription factor PRDII/MBPI/HIV-EP1 is required for dpp signaling** *Development* **121**:3393–403 <https://doi.org/10.1242/dev.121.10.3393>
40. Grieder NC, Nellen D, Burke R, Basler K, Affolter M (1995) **Schnurri is required for *Drosophila* Dpp signaling and encodes a zinc finger protein similar to the mammalian transcription factor PRDII-BF1** *Cell* **81**:791–800 [https://doi.org/10.1016/0092-8674\(95\)90540-5](https://doi.org/10.1016/0092-8674(95)90540-5)
41. Arora K, Dai H, Kazuko SG, Jamal J, O'Connor MB, Letsou A, et al. (1995) **The *Drosophila* schnurri gene acts in the Dpp/TGF beta signaling pathway and encodes a transcription factor homologous to the human MBP family** *Cell* **81**:781–90 [https://doi.org/10.1016/0092-8674\(95\)90539-1](https://doi.org/10.1016/0092-8674(95)90539-1)

42. Jin W, Takagi T, Kanesashi SN, Kurahashi T, Nomura T, Harada J, et al. (2006) **Schnurri-2 controls BMP-dependent adipogenesis via interaction with Smad proteins** *Dev Cell* **10**:461–71 <https://doi.org/10.1016/j.devcel.2006.02.016>
43. Jones DC, Glimcher LH (2010) **Regulation of bone formation and immune cell development by Schnurri proteins** *Adv Exp Med Biol* **658**:117–22 https://doi.org/10.1007/978-1-4419-1050-9_13
44. Jones DC, Wein MN, Oukka M, Hofstaetter JG, Glimcher MJ, Glimcher LH (2006) **Regulation of adult bone mass by the zinc finger adapter protein Schnurri-3** *Science* **312**:1223–1227 <https://doi.org/10.1126/science.1126313>
45. Steinfeld H, Cho MT, Retterer K, Person R, Schaefer GB, Danylchuk N, et al. (2016) **Mutations in HIVEP2 are associated with developmental delay, intellectual disability, and dysmorphic features** *Neurogenetics* **17**:159–64 <https://doi.org/10.1007/s10048-016-0479-z>
46. Vora M, Pyontek SM, Popovitchenko T, Matlack TL, Prashar A, Kane NS, et al. (2022) **The hypoxia response pathway promotes PEP carboxykinase and gluconeogenesis in C. elegans** *Nat Commun* **13** <https://doi.org/10.1038/s41467-022-33849-x>
47. Wang S, Sun H, Ma J, Zang C, Wang C, Wang J, et al. (2013) **Target analysis by integration of transcriptome and ChIP-seq data with BETA** *Nat Protoc* **8**:2502–15 <https://doi.org/10.1038/nprot.2013.150>
48. Praitis V, Casey E, Collar D, Austin J (2001) **Creation of low-copy integrated transgenic lines in Caenorhabditis elegans** *Genetics* **157**:1217–26 <https://doi.org/10.1093/genetics/157.3.1217>
49. Aggad D, Brouilly N, Omi S, Essmann CL, Dehapiot B, Savage-Dunn C, et al. (2023) **Meisosomes, folded membrane microdomains between the apical extracellular matrix and epidermis** *Elife* **12** <https://doi.org/10.7554/eLife.75906>
50. Gerstein MB, Lu ZJ, Van Nostrand EL, Cheng C, Arshinoff BI, Liu T, et al. (2010) **Integrative analysis of the Caenorhabditis elegans genome by the modENCODE project** *Science* **330**:1775–1787 <https://doi.org/10.1126/science.1196914>
51. Luperchio TR, Boukas L, Zhang L, Pilarowski G, Jiang J, Kalinousky A, et al. (2021) **Leveraging the Mendelian disorders of the epigenetic machinery to systematically map functional epigenetic variation** *Elife* **10** <https://doi.org/10.7554/eLife.65884>
52. Davis P, Zarowiecki M, Arnaboldi V, Becerra A, Cain S, Chan J, et al. **WormBase in 2022-data, processes, and tools for analyzing Caenorhabditis elegans** *Genetics* **220** <https://doi.org/10.1093/genetics/iyac003>
53. Yin J, Madaan U, Park A, Aftab N, Savage-Dunn C (2015) **Multiple cis elements and GATA factors regulate a cuticle collagen gene in Caenorhabditis elegans** *Genesis* **53**:278–84 <https://doi.org/10.1002/dvg.22847>
54. Schindelin J, Arganda-Carreras I, Frise E, Kaynig V, Longair M, Pietzsch T, et al. (2012) **Fiji: an open-source platform for biological-image analysis** *Nat Methods* **9**:676–82 <https://doi.org/10.1038/nmeth.2019>
55. Sage D, Donati L, Soulez F, Fortun D, Schmit G, Seitz A, et al. (2017) **DeconvolutionLab2: An open-source software for deconvolution microscopy** *Methods* **115**:28–41 <https://doi.org/10.1016/j.ymeth.2016.12.015>

56. Dai H, Hogan C, Gopalakrishnan B, Torres-Vazquez J, Nguyen M, Park S, et al. (2000) **The zinc finger protein schnurri acts as a Smad partner in mediating the transcriptional response to decapentaplegic** *Dev Biol* **227**:373–87 <https://doi.org/10.1006/dbio.2000.9901>
57. Muller B, Hartmann B, Pyrowolakis G, Affolter M, Basler K (2003) **Conversion of an extracellular Dpp/BMP morphogen gradient into an inverse transcriptional gradient** *Cell* **113**:221–33 [https://doi.org/10.1016/s0092-8674\(03\)00241-1](https://doi.org/10.1016/s0092-8674(03)00241-1)
58. Kudron MM, Victorsen A, Gevirtzman L, Hillier LW, Fisher WW, Vafeados D, et al. (2018) **The ModERN Resource: Genome-Wide Binding Profiles for Hundreds of Drosophila and Caenorhabditis elegans Transcription Factors** *Genetics* **208**:937–49 <https://doi.org/10.1534/genetics.117.300657>
59. Tian C, Sen D, Shi H, Foehr ML, Plavskin Y, Vatamaniuk OK, et al. (2010) **The RGM protein DRAG-1 positively regulates a BMP-like signaling pathway in Caenorhabditis elegans** *Development* **137**:2375–84 <https://doi.org/10.1242/dev.051615>
60. DeGroot MS, Williams B, Chang TY, Maas Gamboa ML, Larus IM, Hong G, et al. (2023) **SMOC-1 interacts with both BMP and glypican to regulate BMP signaling in C. elegans** *PLoS Biol* **21** <https://doi.org/10.1371/journal.pbio.3002272>
61. Clark JF, Savage-Dunn C (2018) **Delta-9 fatty acid desaturase mutants display increased body size** *MicroPubl Biol* <https://doi.org/10.17912/SS8E-6587>
62. Simmer F, Tijsterman M, Parrish S, Koushika SP, Nonet ML, Fire A, et al. (2002) **Loss of the putative RNA-directed RNA polymerase RRF-3 makes C. elegans hypersensitive to RNAi** *Curr Biol* **12**:1317–9 [https://doi.org/10.1016/s0960-9822\(02\)01041-2](https://doi.org/10.1016/s0960-9822(02)01041-2)
63. Gumienny TL, MacNeil LT, Wang H, de Bono M, Wrana JL, Padgett RW (2007) **Glypican LON-2 is a conserved negative regulator of BMP-like signaling in Caenorhabditis elegans** *Curr Biol* **17**:159–64 <https://doi.org/10.1016/j.cub.2006.11.065>
64. Ko FC, Chow KL (2003) **A mutation at the start codon defines the differential requirement of dpy-11 in Caenorhabditis elegans body hypodermis and male tail** *Biochem Biophys Res Commun* **309**:201–8 [https://doi.org/10.1016/s0006-291x\(03\)01545-6](https://doi.org/10.1016/s0006-291x(03)01545-6)
65. Tang LTH, Trivedi M, Freund J, Salazar CJ, Rahman M, Ramirez-Suarez NJ, et al. (2021) **The CATP-8/P5A-type ATPase functions in multiple pathways during neuronal patterning** *PLoS Genet* **17** <https://doi.org/10.1371/journal.pgen.1009475>
66. Liu Z, Shi H, Szymczak LC, Aydin T, Yun S, Consta K, et al. (2015) **Promotion of bone morphogenetic protein signaling by tetraspanins and glycosphingolipids** *PLoS Genet* **11** <https://doi.org/10.1371/journal.pgen.1005221>
67. Mallo GV, Kurz CL, Couillault C, Pujol N, Granjeaud S, Kohara Y, et al. (2002) **Inducible antibacterial defense system in C. elegans** *Curr Biol* **12**:1209–14 [https://doi.org/10.1016/s0960-9822\(02\)00928-4](https://doi.org/10.1016/s0960-9822(02)00928-4)
68. Yu Y, Mutlu AS, Liu H, Wang MC (2017) **High-throughput screens using photo-highlighting discover BMP signaling in mitochondrial lipid oxidation** *Nat Commun* **8** <https://doi.org/10.1038/s41467-017-00944-3>

69. Clark JF, Ciccarelli EJ, Kayastha P, Ranepura G, Yamamoto KK, Hasan MS, et al. (2021) **BMP pathway regulation of insulin signaling components promotes lipid storage in *Caenorhabditis elegans*** *PLoS Genet* **17** <https://doi.org/10.1371/journal.pgen.1009836>
70. Zugasti O, Ewbank JJ (2009) **Neuroimmune regulation of antimicrobial peptide expression by a noncanonical TGF-beta signaling pathway in *Caenorhabditis elegans* epidermis** *Nat Immunol* **10**:249–56 <https://doi.org/10.1038/ni.1700>
71. Ciccarelli EJ, Bendelstein M, Yamamoto KK, Reich H, Savage-Dunn C (2024) **BMP signaling to pharyngeal muscle in the *C. elegans* response to a bacterial pathogen regulates anti-microbial peptide expression and pharyngeal pumping** *Mol Biol Cell* **35** <https://doi.org/10.1091/mbc.E23-05-0185>
72. Ciccarelli EJ, Wing Z, Bendelstein M, Johal RK, Singh G, Monas A, et al. (2024) **TGF-beta ligand cross-subfamily interactions in the response of *Caenorhabditis elegans* to a bacterial pathogen** *PLoS Genet* **20** <https://doi.org/10.1371/journal.pgen.1011324>
73. Gaynor RB, Muchardt C, Diep A, Mohandas TK, Sparkes RS, Lusis AJ (1991) **Localization of the zinc finger DNA-binding protein HIV-EP1/MBP-1/PRDII-BF1 to human chromosome 6p22.3-p24** *Genomics* **9**:758–61 [https://doi.org/10.1016/0888-7543\(91\)90371-k](https://doi.org/10.1016/0888-7543(91)90371-k)
74. Oukka M, Kim ST, Lugo G, Sun J, Wu LC, Glimcher LH (2002) **A mammalian homolog of *Drosophila schnurri*, KRC, regulates TNF receptor-driven responses and interacts with TRAF2** *Mol Cell* **9**:121–31 [https://doi.org/10.1016/s1097-2765\(01\)00434-8](https://doi.org/10.1016/s1097-2765(01)00434-8)
75. Oukka M, Wein MN, Glimcher LH (2004) **Schnurri-3 (KRC) interacts with c-Jun to regulate the IL-2 gene in T cells** *J Exp Med* **199**:15–24 <https://doi.org/10.1084/jem.20030421>
76. Clare CE, Brassington AH, Kwong WY, Sinclair KD (2019) **One-Carbon Metabolism: Linking Nutritional Biochemistry to Epigenetic Programming of Long-Term Development** *Annu Rev Anim Biosci* **7**:263–87 <https://doi.org/10.1146/annurev-animal-020518-115206>
77. McMahon L, Muriel JM, Roberts B, Quinn M, Johnstone IL (2003) **Two sets of interacting collagens form functionally distinct substructures within a *Caenorhabditis elegans* extracellular matrix** *Mol Biol Cell* **14**:1366–78 <https://doi.org/10.1091/mbc.e02-08-0479>
78. Fernando T, Flibotte S, Xiong S, Yin J, Yzeiraj E, Moerman DG, et al. (2011) ***C. elegans* ADAMTS ADT-2 regulates body size by modulating TGFbeta signaling and cuticle collagen organization** *Dev Biol* **352**:92–103 <https://doi.org/10.1016/j.ydbio.2011.01.016>
79. Suzuki Y, Morris GA, Han M, Wood WB (2002) **A cuticle collagen encoded by the lon-3 gene may be a target of TGF-beta signaling in determining *Caenorhabditis elegans* body shape** *Genetics* **162**:1631–9
80. Kim KK, Sheppard D, Chapman HA (2018) **TGF-beta1 Signaling and Tissue Fibrosis** *Cold Spring Harb Perspect Biol* **10** <https://doi.org/10.1101/cshperspect.a022293>
81. MacFarlane EG, Haupt J, Dietz HC, Shore EM (2017) **TGF-beta Family Signaling in Connective Tissue and Skeletal Diseases** *Cold Spring Harb Perspect Biol* **9** <https://doi.org/10.1101/cshperspect.a022269>

Author information

Mehul Vora*

Waksman Institute, Dept. of Genetics, Rutgers University, USA, ModOmics Ltd, Southampton, UK

ORCID iD: [0000-0002-1239-6458](https://orcid.org/0000-0002-1239-6458)

*These two authors contributed equally

Jonathan Dietz*

Waksman Institute, Dept. of Genetics, Rutgers University, USA

*These two authors contributed equally

Zachary Wing

Department of Biology, Queens College, CUNY, USA

Jun Liu

Department of Molecular Biology and Genetics, Cornell University, USA

Christopher Rongo

Waksman Institute, Dept. of Genetics, Rutgers University, USA

Cathy Savage-Dunn

Department of Biology, Queens College, CUNY, USA, PhD Program in Biology, the Graduate Center, CUNY, USA

ORCID iD: [0000-0002-3457-0509](https://orcid.org/0000-0002-3457-0509)

For correspondence: cathy.savagedunn@qc.cuny.edu

Editors

Reviewing Editor

Kavita Babu

Indian Institute of Science Bangalore, Bangalore, India

Senior Editor

Sofia Araújo

University of Barcelona, Barcelona, Spain

Reviewer #1 (Public review):

Summary:

BMP signaling is, arguably, best known for its role in the dorsoventral patterning, but not in nematodes, where it regulates body size. In their paper, Vora et al. analyze ChIP-Seq and RNA-Seq data to identify direct transcriptional targets of SMA-3 (Smad) and SMA-9 (Schnurri) and understand the respective roles of SMA-3 and SMA-9 in the nematode model *Caenorhabditis elegans*. The Authors use SMA-3 and SMA-9 ChIP-Seq data and RNA-Seq data from SMA-3 and

SMA-9 mutants, and bioinformatic analyses to identify the genes directly controlled by these two transcription factors (TFs) and find approximately 350 such targets for each. They show that all SMA-3-controlled targets are positively controlled by SMA-3 binding, while SMA-9-controlled targets can be either up- or downregulated by SMA-9. 129 direct targets were shared by SMA-3 and SMA-9, and, curiously, the expression of 15 of them was activated by SMA-3 but repressed by SMA-9. In case of such opposing effects, the SMA-9 appears to act epistatically to SMA-3. Since genes responsible for cuticle collagen production were eminent among the SMA-3 targets, the Authors focused on trying to understand the body size defect known to be elicited by the modulation of BMP signaling. Vora et al. provide compelling evidence that this defect is likely to be due to problems with the BMP signaling-dependent collagen secretion necessary for cuticle formation.

Strengths:

Vora et al. provide a valuable analysis of ChIP-Seq and RNA-Seq datasets, which will be very useful for the community. They also shed light on the mechanism of the BMP-dependent body size control by identifying SMA-3 target genes regulating cuticle collagen synthesis and by showing that downregulation of these genes affects body size in *C. elegans*.

Weaknesses:

(1) Although the analysis of the SMA-3 and SMA-9 ChIP-Seq and RNA-Seq data is extremely useful, the goal "to untangle the roles of Smad and Schnurri transcription factors in the developing *C. elegans* larva", has not been reached. While the role of SMA-3 as a transcriptional activator appears to be quite straightforward, the function of SMA-9 in the BMP signaling remains obscure.

(2) The Authors clearly show that both TFs can bind independently of each other, however, by using distances between SMA-3 and SMA-9 ChIP peaks, they claim that when the peaks are close these two TFs likely act as complexes. In the absence of proof that SMA-3 and SMA-9 physically interact (e.g. that they co-immunoprecipitate - as they do in *Drosophila*), this is an unfounded claim, which still has to be experimentally substantiated. In the revised version of the manuscript, the authors acknowledge this.

(3) The second part of the results (the collagen story) is loosely connected the first part. dpy-11 encodes an enzyme important for cuticle development, and it is a differentially expressed direct target of SMA-3. dpy-11 can be bound by SMA-9, but it is not affected by this binding according to RNA-Seq. Thus, technically, this part of the paper does not require any information about SMA-9. However, this can likely be improved by addressing the function of the 15 genes, with the opposing mode of regulation by SMA-3 and SMA-9.

Comments on revisions:

In comparison to the first version of the manuscript, the authors have significantly improved the "readability" of the paper, made the Discussion much better, and toned down some of the less supported arguments.

<https://doi.org/10.7554/eLife.99394.2.sa1>

Author response:

The following is the authors' response to the original reviews.

Reviewer #1 (Public Review):

Summary:

*BMP signaling is, arguably, best known for its role in the dorsoventral patterning, but not in nematodes, where it regulates body size. In their paper, Vora et al. analyze ChIP-Seq and RNA-Seq data to identify direct transcriptional targets of SMA-3 (Smad) and SMA-9 (Schnurri) and understand the respective roles of SMA-3 and SMA-9 in the nematode model *Caenorhabditis elegans*. The authors use publicly available SMA-3 and SMA-9 ChIP-Seq data, own RNA-Seq data from SMA-3 and SMA-9 mutants, and bioinformatic analyses to identify the genes directly controlled by these two transcription factors (TFs) and find approximately 350 such targets for each. They show that all SMA-3-controlled targets are positively controlled by SMA-3 binding, while SMA-9-controlled targets can be either up or downregulated by SMA-9. 129 direct targets were shared by SMA-3 and SMA-9, and, curiously, the expression of 15 of them was activated by SMA-3 but repressed by SMA-9. Since genes responsible for cuticle collagen production were eminent among the SMA-3 targets, the authors focused on trying to understand the body size defect known to be elicited by the modulation of BMP signaling. Vora et al. provide compelling evidence that this defect is likely to be due to problems with the BMP signaling-dependent collagen secretion necessary for cuticle formation.*

We thank the reviewer for this supportive summary. We would like to clarify the status of the publicly available ChIP-seq data. We generated the GFP tagged SMA-3 and SMA-9 strains and submitted them to be entered into the queue for ChIP-seq processing by the modENCODE (later modERN) consortium. Thus, the publicly available SMA-3 and SMA-9 ChIP-seq datasets used here were derived from our efforts. Due to the nature of the consortium's funding, the data were required to be released publicly upon completion. Nevertheless, our current manuscript provides the first comprehensive analysis of these datasets. We have updated the text to clarify this point.

Strengths:

*Vora et al. provide a valuable analysis of ChIP-Seq and RNA-Seq datasets, which will be very useful for the community. They also shed light on the mechanism of the BMP-dependent body size control by identifying SMA-3 target genes regulating cuticle collagen synthesis and by showing that downregulation of these genes affects body size in *C. elegans*.*

Weaknesses:

*(1) Although the analysis of the SMA-3 and SMA-9 ChIP-Seq and RNA-Seq data is extremely useful, the goal "to untangle the roles of Smad and Schnurri transcription factors in the developing *C. elegans* larva", has not been reached. While the role of SMA-3 as a transcriptional activator appears to be quite straightforward, the function of SMA-9 in the BMP signaling remains obscure. The authors write that in SMA-9 mutants, body size is affected, but they do not show any data on the mechanism of this effect.*

We thank the reviewer for directing our attention to the lack of clarity about SMA-9's function. We have revised the text to highlight what this study and others demonstrate about SMA-9's role in body size. Simply stated, SMA-9 is needed together with SMA-3 to promote the expression of genes involved in one-carbon metabolism, collagens, and chaperones, all of which are required for body size. SMA-3 has additional, SMA-9-independent transcriptional targets, including chaperones and ER secretion factors, that also contribute to body size. Finally, SMA-9 regulates additional targets independent of SMA-3 that likely have a minimal role in body size. We have adjusted Figure 5 with new graphs of the original data to make these points more clear.

(2) The authors clearly show that both TFs can bind independently of each other, however, by using distances between SMA-3 and SMA-9 ChIP peaks, they claim that when the peaks are close these two TFs act as complexes. In the absence of proof that SMA-3 and SMA-9 physically interact (e.g. that they co-immunoprecipitate - as they do in Drosophila), this is an unfounded claim, which should either be experimentally substantiated or toned down.

We acknowledge that we have not demonstrated a physical interaction between SMA-3 and SMA-9 through a co-immunoprecipitation, and we have indicated in the text that a formal biochemical demonstration would be required to make this point. Moreover, we toned down the text by stating that our results suggest that either SMA-3 and SMA-9 frequently bind as either subunits in a complex or in close vicinity to each other along the DNA. As the reviewer has indicated, a physical interaction between Smads and Schnurris has been amply demonstrated in other systems. A limitation in these previous studies is that only a small number of target genes were analyzed. Our goal in this study was to determine how widespread this interaction is on a genomic scale. Our analyses demonstrate for the first time that a Schnurri transcription factor has significant numbers of both Smad-dependent and Smad-independent target genes. We have revised the text to clarify this point.

(3) The second part of the paper (the collagen story) is very loosely connected to the first part. dpy-11 encodes an enzyme important for cuticle development, and it is a differentially expressed direct target of SMA-3. dpy-11 can be bound by SMA-9, but it is not affected by this binding according to RNA-Seq. Thus, technically, this part of the paper does not require any information about SMA-9. However, this can likely be improved by addressing the function of the 15 genes, with the opposing mode of regulation by SMA-3 and SMA-9.

We appreciate this suggestion and have clarified in the text how SMA-9 contributes to collagen organization and body size regulation.

(4) The Discussion does not add much to the paper - it simply repeats the results in a more streamlined fashion.

We thank the reviewer for this suggestion. We have added more context to the Discussion.

Reviewer #2 (Public Review):

In the present study, Vora et al. elucidated the transcription factors downstream of the BMP pathway components Smad and Schnurri in C. elegans and their effects on body size. Using a combination of a broad range of techniques, they compiled a comprehensive list of genome-wide downstream targets of the Smads SMA-3 and SMA-9. They found that both proteins have an overlapping spectrum of transcriptional target sites they control, but also unique ones. Thereby, they also identified genes involved in one-carbon metabolism or the endoplasmic reticulum (ER) secretory pathway. In an elaborate effort, the authors set out to characterize the effects of numerous of these targets on the regulation of body size in vivo as the BMP pathway is involved in this process. Using the reporter ROL-6::wrmScarlet, they further revealed that not only collagen production, as previously shown, but also collagen secretion into the cuticle is controlled by SMA-3 and SMA-9. The data presented by Vora et al. provide in-depth insight into the means by which the BMP pathway regulates body size, thus offering a whole new set of downstream mechanisms that are potentially interesting to a broad field of researchers.

The paper is mostly well-researched, and the conclusions are comprehensive and supported by the data presented. However, certain aspects need clarification and potentially extended data.

(1) The BMP pathway is active during development and growth. Thus, it is logical that the data shown in the study by Vora et al. is based on L2 worms. However, it raises the question of if and how the pattern of transcriptional targets of SMA-3 and SMA-9 changes with age or in the male tail, where the BMP pathway also has been shown to play a role. Is there any data to shed light on this matter or are there any speculations or hypotheses?

We agree that these are intriguing questions, and we are interested in the roles of transcriptional targets at other developmental stages and in other physiological functions, but these analyses are beyond the scope of the current study.

(2) As it was shown that SMA-3 and SMA-9 potentially act in a complex to regulate the transcription of several genes, it would be interesting to know whether the two interact with each other or if the cooperation is more indirect.

A physical interaction between Smads and Schnurri has been amply demonstrated in other systems. Our goal in this study was not to validate this physical interaction, but to analyze functional interactions on a genome-wide scale.

(3) It would help the understanding of the data even more if the authors could specifically state if there were collagens among the genes regulated by SMA-3 and SMA-9 and which.

We thank the reviewer for this suggestion. col-94 and col-153 were identified as direct targets of both SMA-3 and SMA-9. We noted this in the Discussion.

(4) The data on the role of SMA-3 and SMA-9 in the regulation of the secretion of collagens from the hypodermis is highly intriguing. The authors use ROL-6 as a reporter for the secretion of collagens. Is ROL-6 a target of SMA-9 or SMA-3? Even if this is not the case, the data would gain even more strength if a comparable quantification of the cuticular levels of ROL-6 were shown in Figure 6, and potentially a ratio of cuticular versus hypodermal levels. By that, the levels of secretion versus production can be better appreciated.

We previously showed that rol-6 mRNA levels are reduced in dbl-1 mutants at L2, but RNA-seq analysis did not find enough of a statistically significant change in rol-6 to qualify it as a transcriptional target and total levels of protein are also not significantly reduced in mutants. We added this information in the text.

(5) It is known that the BMP pathway controls several processes besides body size. The discussion would benefit from a broader overview of how the identified genes could contribute to body size. The focus of the study is on collagen production and secretion, but it would be interesting to have some insights into whether and how other identified proteins could play a role or whether they are likely to not be involved here (such as the ones normally associated with lipid metabolism, etc.).

We have added more information to the Discussion.

Reviewer #1 (Recommendations For The Authors):

Figure 1 - Figure 3: The authors might want to think about condensing this into two figures.

To avoid confusion with the different workflows, we prefer to keep these as three separate figures.

Figure 1a-b: Measurement unit missing on X.

We added the unit “bps” to these graphs.

Line 244-246: The authors should stress in the Results that they analyzed publicly available ChIP-Seq data, which was not generated by them, - not just by providing a reference to Kudron et al., 2018. As far as I understood, ChIP was performed with an anti-GFP antibody. Please mention this, and specify the information about the vendor and the catalog number in the Methods.

We would like to clarify the status of the publicly available ChIP-seq data. We generated the GFP tagged SMA-3 and SMA-9 strains and submitted them to be entered into the queue for ChIP-seq processing by the modENCODE (later modERN) consortium. Thus, the publicly available SMA-3 and SMA-9 ChIP-seq datasets used here were derived from our efforts. Due to the nature of the consortium’s funding, the data were required to be released publicly upon completion. Nevertheless, our current manuscript provides the first comprehensive analysis of these datasets. We have clarified these issues in the text. We have also added information regarding the anti-GFP antibody to the Methods.

Line 267-270: The authors should either provide experimental evidence that SMA-3 and SMA-9 form complexes or write something like "significant overlap between SMA-3 and SMA-9 peaks may indicate complex formation between these two transcription factors as shown in Drosophila" - but in the absence of proof, this must be a point for the Discussion, not for the Results. Moreover, similar behavior of fat-6 (overlapping ChIP peaks) and nhr-114 (non-overlapping ChIP peaks) in SMA-3 and SMA-9 mutants may be interpreted as a circumstantial argument against SMA-3/SMA-9 complex formation (see Lines 342-348). Importantly, since ChIP-Seq data are available for a wide array of C. elegans TFs, it would be very useful to have an estimate of whether SMA-3/SMA-9 peak overlap is significantly higher than the peak overlap between SMA-3 and several other TFs expressed at the same L2 stage.

We have clarified our goals regarding SMA-3 and SMA-9 interactions and softened our conclusions by indicating in the text that a formal biochemical demonstration would be required to demonstrate a physical interaction. Moreover, we toned down the text by stating that our results suggest that either SMA-3 and SMA-9 frequently bind as either subunits in a complex or in close vicinity to each other along the DNA. We have added an analysis of HOT sites to address overlap of binding with other transcription factors. We disagree with the interpretation that transcription factors with non-overlapping sites cannot act together to regulate gene expression; however, nhr-114 also has an overlapping SMA-3 and SMA-9 site, so this point becomes less relevant. We have clarified the categorization of nhr-114 in the text.

Lines 272-292: The authors do not comment on the seemingly quite small overlap between the RNA-Seq and the ChIP-Seq dataset, but I think they should. They have 3205 SMA-3 ChIP peaks and 1867 SMA-3 DEGs, but the amount of directly regulated targets is 367. It is important that the authors provide information on the number of genes to which their peaks have been assigned. Clearly, this will not be one gene per peak, but if it

were, this would mean that just 11.5% of bound targets are really affected by the binding. The same number would be 4.7% for the SMA-9 peaks.

We have added a discussion of the discrepancy between binding sites and DEGs. The high number of additional sites classified as non-functional could represent the detection of weak affinity targets that do not have an actual biological purpose. Alternatively, these sites could have an additional role in DBL-1 signaling besides transcriptional regulation of nearby genes, or they could be regulating the expression of target genes at a far enough distance to not be detected by our BETA analysis as per the constraints chosen for the analysis. The difference between total binding sites and those associated with changes in gene expression underscores the importance of combining RNA-seq with ChIP-seq to identify the most biologically relevant targets. And as the reviewer indicated, more than one gene can be assigned to a single neighboring peak.

Lines 294-323: I feel like there is a terminology problem, which makes reading very difficult. The authors use "direct targets" as bound genes with significant expression change, but then run into a problem when the gene is bound by SMA-9 and SMA-3, but significant expression change is only associated with one of the two factors. I am not sure this is consistent with the idea of the SMA3/SMA9 complex. Also, different modalities of the SMA3 and SMA9 effect in 15 cases can be explained by co-factors. Reading would be also simplified if the order of the panels in Figure 3 were different. Currently, the authors start their explanation by referring to the shared SMA-3/SMA-9 targets (Figures 3c-d), and only later come to Figure 3b. In general, the authors should start with a clear explanation of what is on the figure (currently starting on Line 313), otherwise, it is unclear why, if the authors only discuss common targets, it is not just $114+15=129$ targets, but more.

We have re-ordered the columns in Figure 3 to match the order discussed in the text. We also incorporated more precise language about regulation by SMA-3 and/or SMA-9 in the text.

Lines 325-355: The chapter has a rather unfortunate name "Mechanisms of integration of SMA-3 and SMA-9 function", although the authors do not provide any mechanism. Using 3 target genes, they show that if the regulatory modality of SMA-3 and SMA-9 is the same (2 examples), there is no difference in the expression of the targets, but if the modalities are opposing (1 example), SMA-9 repressive action is epistatic to the SMA-3 activating action. Can this be generalized? The authors should test all their 15 targets with opposite regulations. Moreover, it seems obvious to ask whether the intermediate phenotype of the double-mutants can be attributed to the action of these 15 genes activated by SMA-3 and repressed by SMA-9. I would suggest testing this by RNAi. I would also suggest renaming the chapter to something better reflecting its content.

We have removed the word "mechanism" from the title of this section. We also performed additional RT-PCR experiments on another 5 targets with opposing directions of regulation. The results from these genes are consistent with the result from C54E4.5, demonstrating that the epistasis of sma-9 is generalizable.

Figure 4b: Why was a two-way ANOVA performed here? With the small number of measurements, I would consider using a non-parametric test.

These data are parametric and the distribution of the data is normal, so we chose to use a parametric test (ANOVA).

Lines 354-355. The authors offer two suggestions for the mechanism of the epistatic action of SMA-9 on SMA-3 in the case of C54E4.5, but this is something for the Discussion.

If they want to keep it in the Results they should address this experimentally by performing SMA-3 ChIP-seq in the SMA-9 mutants and SMA-9 ChIP-Seq in the SMA-3 mutants.

We moved these models to the discussion as suggested.

Lines 365-367: "We expect that clusters of genes involved in fatty acid metabolism and innate immunity mediate the physiological functions of BMP signaling in fat storage and pathogen resistance, respectively." - This is pretty confusing since the Authors claim in the previous sentence that regulation of immunity by SMA-9 is TGF-beta independent.

Co-regulation of immunity by BMP signaling and SMA-9 is already known. The novel insight is that SMA-9 may have an additional independent role in immunity. We have clarified the language to address this confusion.

Lines 377, and 380: Please explain in non-C. elegans-specific terminology, what rrf-3 and LON-2 are (e.g. write "glypican LON-2" instead of just "LON-2") and add relevant references.

We added information on the proteins encoded by these genes.

Lines 382-384: I am not sure what the Authors mean here by "more limiting".

We substituted the phrase “might have a more prominent requirement in mediating the exaggerated growth defect of a lon-2 mutant”.

Lines 388-392: I found this very confusing. What were these 36 genes? Were these direct targets of SMA-3, SMA-9, or both? Top 36 targets? 36 targets for which mutants are available?

The new Figure 5 clarifies whether target genes are SMA-3-exclusive, SMA-9-exclusive, or co-regulated. The text was also updated for clarity.

Line 397: This is the first time the authors mention dpy-11 but they do not say what it is until later, and they do not say whether it is a target of SMA3/SMA9. Checking Figure 3, I found that it is among the 238 genes bound by both but upregulated only by SMA3. The authors need to explicitly state this - from this point on, they have a section for which SMA-9 appears to be irrelevant.

We added the molecular function of dpy-11 at its first mention. Furthermore, we included the hypothesis that SMA-3 may regulate collagen secretion independently of SMA-9. Our subsequent results with sma-9 mutants disprove this hypothesis.

Line 402: Is ROL-6 a SMA-3/SMA-9 target or just a marker gene?

We previously showed that rol-6 mRNA levels are reduced in dbl-1 mutants at L2, but RNA-seq analysis did not find enough of a statistically significant change in rol-6 to qualify it as a transcriptional target and total levels of protein are also not significantly reduced in mutants. We added this information in the text.

Line 421: I am not sure what "more skeletonized" means.

Replaced with “thinner and skeletonized”

Figure 2b and 2d legends: "Non-target genes nevertheless showing differential expression are indicated with green squares." (l. 581-582 and again l. 588-589) I think should be "Non-direct target genes..."

Changed to "non-direct target genes"

Figure 7 legend: Please indicate the scale bar size in the legend.

Indicated the scale bar size in the legend.

Figure 7: The ER marker is referred to as "ssGFP::KDEL" (in the image and Line 700), however in the text it is called "KDEL::oxGFP" (Line 419). Please use consistent naming.

We fixed the inconsistent naming.

All the experiment suggestions made are optional and can, in principle, be ignored if the authors tone down their claims (for example, the SMA-3/SMA-9 complex formation).

Reviewer #2 (Recommendations For The Authors):

(1) As a control: Have the authors found the known regulated genes among the differentially regulated ones?

Previously known target genes such as fat-6 and zip-10 were identified here. We have added this information in the text.

(2) How many repetitions were performed in Figure 4b? I am wondering as the deviation for C54E4.5 is quite large and that makes me worry that the significant differences stated are not robust.

There were two biologically independent collections from which three cDNA syntheses were analyzed using two technical replicates per point.

(3) Lines 333-336: Can you really make this claim that the antagonistic effects seen in the regulation of body size can be correlated with some targets being regulated in the opposite direction? I would assume that the situation is far more complex as SMADs also regulate other processes.

We agree with the reviewer that multiple models could explain this antagonism, and we have added distinct alternatives in the text.

(4) Lines 367-369: Add the respective reference please.

We have added the relevant references.

<https://doi.org/10.7554/eLife.99394.2.sa0>