Title
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Permalink
https://escholarship.org/uc/item/4660z9x8

Journal
Proceedings of the National Academy of Sciences of the United States of America, 114(44)

ISSN
0027-8424

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Publication Date
2017-10-17

DOI
10.1073/pnas.1712511114

Peer reviewed
Control of growth and gut maturation by HoxD genes and the associated lncRNA Haglr

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During embryonic development, Hox genes participate in the building of a functional digestive system in metazoans, and genetic conditions involving these genes lead to important, sometimes lethal, growth retardation. Recently, this phenotype was obtained after deletion of Haglr, the HoxD antisense growth-associated long noncoding RNA (lncRNA) located between Hoxd1 and Hoxd3. In this study, we have analyzed the function of Hoxd genes in delayed growth trajectories by looking at several nested targeted deficiencies of the mouse HoxD cluster. Mutant pups were severely stunted during the suckling period, but many recovered after weaning. After comparing seven distinct HoxD alleles, including CRISPR/Cas9 deletions involving Haglr, we identified Hoxd3 as the critical component for the gut to maintain milk-digestive competence. This essential function could be abrogated by the dominant-negative effect of HOXD10 as shown by a genetic rescue approach, thus further illustrating the importance of posterior prevalence in Hox gene function. A role for the lncRNA Haglr in the control of postnatal growth could not be corroborated.

Significance

During development, transcription factors are necessary not only to pattern the body plan but also to control growth. However, the link between these two developmental components has been difficult to establish. Hox genes are involved in the emergence of a functional digestive system in metazoans, thus providing a potential impact on growth through nutrition. Also, genetic conditions involving these genes lead to important growth retardation. We analyzed several targeted mutant lines at the HoxD locus and found that stunted phenotypes can all be explained by the lack of function of Hoxd3, whose role seems to be critical in the developing gut of sucking mice, perhaps as an adaptation to the milk-dependent early postnatal period in mammals.

Author contributions: J.Z. and D.D. designed research; J.Z., F.D., and B.M. performed research; J.Z., F.D., B.M., A.N., and D.D. analyzed data; and J.Z. and D.D. wrote the paper.

Reviewers: N.B., University of Manchester; and N.K., Cornell University.

The authors declare no conflict of interest.

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Data deposition: The data reported in this paper have been deposited in the Gene Expression Omnibus (GEO) database, https://www.ncbi.nlm.nih.gov/geo (accession no. GSE103086).

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This article contains supporting information online at www.pnas.org/lookup/suppl/doi:10.1073/pnas.1712511114/-/DCSupplemental.

In this study, we tried to find a common explanatory framework for the various cases described above. We decided to complete the allelic series with a few more mutant chromosomes necessary to unambiguously interpret the previous observations relating phenotypes to particular genes. By using CRISPR/Cas9 mutagenesis in embryo, we demonstrate that the growth-retardation phenotype observed in HoxD9 (9) mice is caused by the dominant-negative effect of the HOXD10 protein. We also report comparable growth deficits in mice lacking the entire region from Hoxd1 to Hoxd4 [HoxDdel(1-4)] (10) and that a mutation in the HOXD3 DNA-binding domain produces mice with similar growth deficits, in contrast to mice mutant for either HOXD1 or HOXD4. We document pathological signs of intestinal failure in three independent nested deletions. Together, these results converge toward a central role for Hoxd3 in the growth-retardation phenotypes previously recorded and further explain the strong functional hierarchy at work among HOX proteins.

To address the potential function of Haglr in this context, we further engineered a pair of alleles carrying either a deficiency or an inversion of the CpG island containing the bidirectional promoter for both Hoxd1 and the antisense lncRNA. Neither of these two alleles affected postnatal growth, even in the resulting absence of the reported Haglr RNA, suggesting that the Haglr-associated phenotype may result from an interference with Hoxd3.

Slow postnatal weight gain phenotypes can be induced by mutations in a range of genes important for developmental patterning. However, the molecular and physiological bases of such growth retardations are often difficult to pinpoint due to the high pleiotropy associated with these genes. While none of the 39 gene members of the Hox family has been included in this broad phenotypic class thus far, we noticed two cases of postnatal growth retardation during the several-years-long studies of our allelic series at the mouse HoxD locus. First, animals homozygous for a complete HoxD cluster deficiency showed about 30% body mass deficit by the time of weaning. However, given that they suffered severe limb and innervation defects, growth retardation seemed compatible with reduced feeding (1). Secondly, a shorter deficiency removing Hoxd1–Hoxd9 [HoxDdel(1-9)] was associated with postnatal growth retardation in heterozygous mice in the absence of mobility defects. However, some specimens also displayed facial defects, again suggesting the existence of a physical problem potentially affecting the feeding behavior (2).

Highly severe postnatal growth retardation in the absence of any obvious malformations was recently reported following a targeted deletion of the HoxD antisense growth-associated long noncoding RNA (lncRNA) Haglr in mice. This midget (Mdgt) phenotype, which was recorded in homozygous-mutant specimens (3), displayed a reduced viability attributed to a function of the lncRNA distinct from those associated with either Hoxd1 (4, 5) or Hoxd3 (6, 7), the two genes flanking Haglr in the HoxD cluster. Therefore, in these cases, both recessive and dominant phenotypes were recorded, and they were always associated with loci located in the anterior (telomeric) part of the HoxD gene cluster. In addition, other HoxD alleles showed midgut patterning defects, but their detailed analyses were made difficult by lethality at birth (8). Finally, distant cis-acting regulatory regions necessary for the transcriptional control of these genes in midgut were reported within the large regulatory landscape flanking this gene cluster on its telomeric side (9), emphasizing a potential link between growth retardation and alterations in gut development.

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transcription or mRNA stabilization rather than from a direct effect of the lncRNA as previously reported (11). As many of the severely stunted mutant mice largely recovered after weaning, we hypothesize that the suckling period and its particular physiological requirements may vitally depend on the function of the Hoxd3 gene in the gut.

Results

Gain of Function-Dependent Growth Retardation. Hoxd deficiencies have been used extensively to study the complex regulation of this gene cluster (12). One of them involving the DNA interval from Hoxd1 to Hoxd9 [HoxD Del(1–9) or Del(1–9), discussed further below] (Fig. S1) resulted in a semilethal slow postnatal weight gain. Heterozygous males crossed with wild-type females produced the predicted 50% proportion of wild-type normal and 50% heterozygous offspring. Soon after birth, growth of half of the progeny lagged. Many growth-retarded individuals dropped below half their normal siblings’ body mass and thus were killed following legal recommendation. However, the majority of growth-retarded specimens survived, and they were genotyped along with their killed littermates. All growth-retarded individuals carried a Del(1–9) chromosome (Fig. L4; red labels), whereas all normally growing siblings were wild type (Fig. L4; green labels). Wild-type individuals showed a peak of body growth between postnatal days (P)2 and P14, followed by a few days of slower growth. The growth curve then resumed and continued until the end of the seventh week.

After birth, however, growth of heterozygous Del(1–9) mutants was continuously retarded until the end of the fifth week. For survivors, growth did return, even though it remained depressed in some individuals as late as the end of the tenth week. The analysis of average body mass at 4 wk revealed that heterozygous Del(1–9) individuals had about half the body mass of their wild-type siblings. The comparison between a group of seven wild-type controls and 10 Del(1–9)-heterozygous siblings gave a statistically valid difference (Table 1). It is noteworthy that, once growth of mutant animals resumed, it reached slopes similar to those of their wild-type siblings weeks before. Therefore, while strong growth retardation occurred during milk feeding, growth could catch up after weaning in the surviving specimens.

Previously, we had observed in various alleles carrying partial deletions in the HoxD cluster (13) that the remaining gene located next to the breakpoint after the deletion had occurred was likely to adopt some of the expression specificities of the deleted genes. This observation, along with the dominant inheritance pattern of this Del(1–9) stock, strongly suggested a gain-of-function mechanism, because even a full deficiency of the HoxD cluster did not induce such severe growth retardation in heterozygous-mutant animals (1). Therefore, we suspected Hoxd10 expression was gained in space and time and thus interfered with more anterior Hox gene function following the property of posterior prevalence.

Posterior prevalence was defined as the capacity of some posterior HOX proteins to override the function of more anterior ones when coexpressed in some contexts (14). As this property may rely upon the binding of these proteins on their DNA target sites, we induced a small deletion within the Hoxd10 homeobox sequence in cis with the Del(1–9) deficiency by using the CRISPR/Cas9 technology in fertilized mouse zygotes. In this HoxD Del(1–9)d10hd allele, while the same Del(1–9) deficiency was present, the adjacent Hoxd10 gene produced a protein that lacks its DNA-binding domain. The Del(1–9)d10hd founder animal had growth comparable to its wild-type littermates and was used to establish a stable mutant line.

Early postnatal growth of the Del(1–9)d10hd-heterozygous animals appeared normal, and females no longer showed atypical courtship, as previously reported for the Del(1–9) allele (2). Likewise, facial malformations were no longer recorded. Transheterozygous crosses generated wild-type, heterozygous, and homozygous offspring, as genotyped at 2 wk of age. By the end of the fourth week,
The mass of all homozygous animals dropped below the 40% limit in comparison with wild-type siblings, and hence animals were killed before the end of the experiment (Table 1). The comparisons of body mass averages between wild-type and heterozygous mice from two combined litters showed that the mass of heterozygous animals was only about 20% below the average mass of the wild-type controls. This was closer to normal than the nearly 50% deficit seen in presence of the intact Hoxd10 locus in cis with the deficiency. This result demonstrated that a major factor in the dominant effects of the Del(1–9) allele was indeed due to a gain of function of Hoxd10 after its relocation near the deletion breakpoint. The nearly 20% difference recorded between wild-type and Del(1–9)d10hd-heterozygous mice was statistically significant, suggesting that beyond the gain of function of Hoxd10, a combined loss of function of several genes in cis also had an impact upon the growth rate.

**Loss of Function-Dependent Growth Retardation.** Next we investigated a smaller deficiency including Hoxd1 to Hoxd4 [HoxD(9)-del(4)] or Del(1–4)], as homozygous specimens were severely retarded, and many did not survive to adulthood, thus further supporting a loss-of-function mechanism being causative of growth retardation. This was unexpected, since previous targeted loss of function of Hoxd1 (4, 5), Hoxd3 (6, 7), or Hoxd4 (15) did not reveal such growth retardation. This phenotype was highly reproducible and was stable over generations, and homozygous escapers were visibly smaller than normal (Fig. 1B). The growth curves of homozygous, heterozygous, and wild-type controls from the same litter and fed by the same dam showed that homozygous specimens lagged in much the same way as Del(1–9)-heterozygous escapers (Fig. 1C). In both conditions, the retardation was similarly recorded by the end of the first week, and animals continued to grow at a reduced rate compared with heterozygous or wild-type littermates until the end of the seventh week. One homozygous animal continued to grow at a relatively steady rate until it caught up with the wild type by the end of the 11th week, whereas the other reached about 80% of wild-type body weight.

Several such caught-up individuals otherwise proved healthy and fertile. However, more than half of them dropped below 40% of control sibling body mass before the end of the seventh week. Growth trajectories diverged during the period of milk feeding. From these results, a genetically determined period of sensitivity seems to occur between birth and the end of the fourth week. This period was characterized by a reduced capacity to thrive despite the ability to feed. While wild-type and heterozygous body mass values were not appreciably different (Table 1), the average body mass of homozygous individuals was well below the average of the wild-type individuals. This was comparable to the body mass deficit we observed with Del(1–9)-heterozygous mice, and the recovery of the homozygous Del(1–4) individuals was also similarly shifted (Fig. 1, compare A and C). We also observed that Del(1–9)d10hd-heterozygous displayed twice as great a body mass deficit as Del(1–4)-heterozygous (Discussion).

**Coprometric Investigation of Slow Postnatal Weight Gain.** In our daily observations of litters including either Del(1–9)-heterozygous or Del(1–4)-homozygous individuals, we noticed that growth-retarded animals were weak and lethargic. In addition, they dropped few or no fecal pellets. We used the latter observation as a noninvasive measure to characterize and follow the phase of recovery. Analysis of droppings reveals species-specific features of excretory activity (16) and thus reflects the morphology and function of the intestinal tract. Such analysis can start after the end of the third week, once observations of litters including either Del(1–9)-heterozygous escapers (Fig. 1, compare A and C). We also observed that Del(1–9)d10hd-heterozygous displayed twice as great a body mass deficit as Del(1–4)-heterozygous (Discussion).
When we collected the droppings in fractions, we found the majority was released in the first 10 min. Subsequently, their number dropped, indicating that this prolific early release was a defecation reflex (Fig. 1D).

In nearly all cases, the reflex gave comparable numbers of solid pellets per individual released by a similar dynamic. In addition, although the sizes of individual pellets varied, quite a few fell into a rather narrow range. Finally, animals that suffered growth retardation produced smaller but not necessarily fewer pellets of similar consistency (Fig. 1D). The comparable solidity of up to 16 pellets per single collection suggested that this fairly regular size-setting mechanism that presumably operated at a more proximal segment. Because growth-retarded mutants released smaller pellets, we concluded that the gut was of a different anatomical and/or motile character compared with normal controls, while the mechanism of pellet segmentation and reflexive release were intact. As a consequence, we could evaluate gut performance individually in extended time series and in a reproducible non-invasive manner by measuring both the dried pellet mass collected in 30-min defecation-reflex periods and the body mass (Figs. 2-4 and S2).

Hoxd3-Dependent Growth Retardation. Prior analysis of the combined deletion of Hox1, Hoxd3, and Hoxd4 [Del(1–4)] revealed a drastic growth retardation in homozygous specimens (see above), which was not observed in either Hox1 (4, 5) or Hoxd4 (15) single-mutant mice. This could derive either from a combined effect of several gene products and the consequent compensatory mechanisms or from a prominent effect of Hoxd3. To discriminate between these possibilities, we produced a deficiency including the entire Hoxd4 gene, Hoxd4<sup>Δ<sup>500</sup></sup> [Del (4)], as well as a Hoxd3-mutant allele. In the latter case, we used CRISPR-Cas9 to induce an out-of-frame deletion within the Hoxd3 protein homeodomain, which presumably prevented HOXD3 from binding to DNA target sites.

Extensive analyses of Del (4) mice revealed no significant growth defect in homozygous mice (Table 1). In contrast, F0 animals derived from the CRISPR/Cas9 mutation in Hoxd3 (SI Materials and Methods) showed slow postnatal weight gain. Five apparently homozygous F0 animals indeed displayed this growth-retardation problem, even though this was not reported in previous evaluations of mutant Hoxd3-null alleles (6, 7). We crossed these F0 animals and analyzed progeny to confirm the link to Hoxd3. We first mated a Hoxd3<sup>Δ<sup>500</sup></sup>-mutant F0 female with a Del(1–4)-heterozygous male to obtain transheterozygous individuals and heterozygous controls, as well as to eliminate potential recessive off-target mutations since the Del(1–4) stock was generated without CRISPR/Cas9 exposure. However, Del(1–4)+/+ animals were not recovered in the F1 progeny, showing that the F0 Hoxd3<sup>Δ<sup>500</sup></sup>-female was homozygous in the germ line. All Hoxd3<sup>Δ<sup>500</sup></sup>/Del(1–4) compound-mutant individuals were severely stunted (Table 1), and by P28, they reached only two-thirds of the body mass of their Hoxd3<sup>Δ<sup>500</sup></sup>/+ heterozygous siblings. This difference matched that observed between heterozygous and homozygous Del(1–4) specimens and was statistically significant (Figs. S1 and S2C).

Litters of F2 pups including all three possible Hoxd3<sup>Δ<sup>500</sup></sup> genotypes were monitored, and wild-type and heterozygous females showed similar characteristics as we observed with F0 control males. However, their body weight at the end of the fast growth period at P42 was around 16 g, compared with the average of 20 g recorded with males (Fig. 2A and Fig. S2A). The body weight of wild-type and heterozygous individuals at the end of the third week was typically above 8 g (Fig. 2A, Left), whereas most homozygous-mutant animals weighed less than 7 g (Fig. 2A, Right), and the most severely affected weighed less than 4 g (a more than 60% deficit compared with siblings of that age) (Fig. 2A). The body weight of the least-affected surviving homozygous individual (‘‘escaper’’ rarely exceeded 12 g at the end of the seventh week (a deficit of ca. 25%) (Fig. 2A, Upper). To uncover a potential association with a gut defect, we recorded pellet masses from the beginning of the fourth week.

Like their wild-type siblings, heterozygous-mutant female mice regularly released more than 32 mg of total pellet weight on most days of the fourth week. During the fifth week and later, the total ejected weight was often in excess of 64 mg. In contrast, homozygous surviving females consistently released less than 32 mg of pellets during both the fourth and the fifth week and rarely reached 64 mg output by the end of the seventh week (Fig. 2A, Upper). Similarly, the average pellet weight of heterozygous and wild-type animals was about 4 mg by the end of the seventh week, while pellets of homozygous animals hardly ever reached this value even after the ninth week of age. It is noteworthy that most affected homozygous individuals released far fewer and smaller pellets and, during the terminal periods, released none at all (Fig. 2A, Lower Right).

Examination of the growth deficit including all F2 individuals at P28 also revealed a slight body mass deficit (7%) in the subpopulation of Hoxd3<sup>Δ<sup>500</sup></sup>-heterozygous individuals compared with
wild-type mice, even though this was of poor statistical significance ($P$ value = 1.17$^{-15}$). In the homozygous subpopulation, however, the average body mass deficit was one-third of the average control body mass, a difference that was statistically significant. These observations supported the conclusion that $Hoxd3$ is required for postnatal growth during the suckling period. Again, the distinctly reduced total ejected pellet mass during the fourth week suggested a decrease in the volume of the terminal segments of the gut. While the total ejected pellet mass slowly increased to reach nearly normal levels, the average size of pellets remained significantly smaller even at late stages (Fig. 3). This suggested a permanent loss of isometry in the initial formation of droppings and indicated that postnatal large bowel growth was likely delayed.

**Morphological Alterations.** The anatomical analysis of specimens from various genotypes revealed that droppings were already distinct in the more anterior part of the large bowel in the proximal colon. Consequently, we suspected that the proximal colon was morphologically or functionally insufficient in $Hoxd3^{hd}$-homozygous mutants. Also, in one particularly stunted mutant animal, while all abdominal organs were expectedly reduced in size (the total body mass was decreased by 60%), a clear retention of gut content in the terminal small intestine and in the cecum was recorded (Fig. 2B, Right). This distended region continued in a narrow empty proximal colon segment. Such a severe narrowing was also observed in Del(1–4)-homozygous stunted specimens (Fig. 2B, Middle). In agreement with the coprometric analyses, we concluded that this limitation in proximal colon diameter impeded the passage of luminal content and led to both reduced dropping size and reduced dropping deposition during an induced defecation reflex, leading over time to chronic constipation, malnutrition, and pronounced stunting.

Such a severe condition was further studied, in particular regarding the relative contribution of proximal and terminal colon defects to this slow postnatal weight gain. To this aim, we performed a correlation analysis of $Hoxd3^{hd}$-homozygous and wild-type control siblings. We plotted the body mass against average pellet mass, body mass against total ejected pellet mass, and the total ejected pellet mass against the average pellet mass. The $R^2$ values of wild-type controls were higher in the body mass versus average pellet mass comparison in all three phases than in the body mass versus total pellet mass comparisons (Fig. 4A and B, blue). In the average pellet mass versus total pellet mass comparison, the $R^2$ value reached 0.56 during the growth period ($P < 1.17332^{-15}$) but remained nonsignificant at later stages (Fig. 4C, E9294 | www.pnas.org/cgi/doi/10.1073/pnas.1712511114 Zakany et al. Right).

![Table A and B](https://www.pnas.org/content/114/23/10853/Fig3.large.jpg)

**Fig. 3.** Frequency distributions of dropping weights pooled from three wild-type controls (A) and four homozygous mutants (B). Age in weeks at the time of collection is indicated above, and the total counts of pellets collected during the last two consecutive days are shown below. The size bins set to 0.5-mg increments are indicated on the left. The heat maps reflect the relative frequency of pellet counts in a given lot; the most frequent values are boxed for better visibility.
blue). Average pellet mass was a better predictor of body mass than total ejected pellet mass.

Of note, the same comparisons applied to the Hoxd3<sup>hd-homozygous</sup> samples diverged from this overall picture. The $R^2$ values were as high or indeed slightly higher in the body mass versus total pellet mass comparison than in the body mass versus average pellet mass comparison (Fig. 4A and B, red). This was also confirmed in the average pellet mass versus total pellet mass analysis, and a positive correlation with delayed growth was established during all three periods. Average pellet mass and total pellet mass were positively correlated, and the correlation was of a higher degree at all stages compared with wild-type control (Fig. 4C, red). Average pellet mass as well as total ejected pellet mass were similarly good predictors of body mass in Hoxd3<sup>hd-homozygous</sup> individuals. This correlation analysis therefore supported the inference that Hoxd3<sup>hd-homozygous</sup> guts performed differently from those of wild-type control animals. Absolute values were nevertheless lower compared with controls, which was consistent with the idea that the reduced dimension of both proximal colon, as reflected in average pellet mass, and of the terminal colon, as reflected in total ejected pellet mass, contributed simultaneously to a strong constraint on organismal growth.

**Epithelial Defects in Hoxd3<sup>hd</sup>- and Hoxd3<sup>D<sub>Del(1–9)id10hd</sub></sup>-Mutant Small Intestines.** Following the abrogation of Hoxd3 function, only about half of the variance in body mass could be accounted for by noninvasive coprometry. As body mass deficit first occurred before excrement could be collected, we investigated juvenile gut histology of stunted animals and normal littermates on P14 and P7. The duodenum of Hoxd3<sup>hd-homozygous</sup> mutants and wild-type control siblings showed a reduction in diameter and in epithelium thickness (Fig. 5A and B). When the body mass was plotted as a function of the average length of villi, it showed a positive correlation with the length of duodenum villi (Fig. 5B). Up to 90% of the variance in body mass could be accounted for by variation in duodenum epithelial structure.
Next we extended this analysis to Del(1–9)d10hd specimens and investigated wild-type control, heterozygous, and homozygous siblings 1 wk after birth. Examination of villus length also revealed a positive correlation between body mass and villus length (Fig. 5B). Body mass values were lower than at P14, consistent with the animals’ younger age. Although a positive correlation was obtained between body mass and villus length, the slope of the fit line was clearly less steep than in the case of Hoxd3hd mice at P14, and the $R^2$ value was only 0.28. Since body mass reduction and lethality was more severe in Del(1–9)d10hd animals, we surmised that changes beyond villus length contributed to the severity of this allele. More detailed observations using high-power images revealed reduced maximal villus length in both cases (Fig. 5C and D). Del(1–9)d10hd-homozygous individuals also showed an extended region of villus disintegration (Fig. 5D, Bottom). The tips of villi were ill-formed, and more basal surfaces were devoid of the enterocyte layer, indicative of epithelial necrosis. From these histological observations, we concluded that early during milk feeding, epithelial dysgenesis occurred in Hoxd3hd-homozygous mutants, which hindered proper alimination of pups. This condition was further aggravated in the absence of an extended genomic locus, which in addition to Hoxd3 removed Hoxd10, Hoxd9, Hoxd8, Hoxd4, and Hoxd1 functions.

These results further supported the hypothesis that gut defects were a cause rather than a consequence of small body size.

**Contribution of the LncRNA Haglr to Growth Retardation.** In a recent report, a similar semilethal recessive slow postnatal weight gain was observed upon disruption of the Haglr lncRNA, leading to the midget (Mdgt) phenotype (3). The HoxD antisense Haglr RNA starts from the Hoxd1 bidirectional promoter and extends to the Hoxd3 transcription unit. To further evaluate a potential function of this lncRNA on the growth-retardation phenotype, we produced two mutant alleles in which Haglr was presumably affected without removing the entire Hoxd1–Hoxd3 intergenic region, which includes two other noncoding Gm14426 and Gm14424 RNAs (Fig. 6A).

Transcriptome analysis of E8.5 embryos revealed that Hoxd1 and Haglr share the same bidirectional start site located within the CpG island 114. On the reverse Hox strand, two Haglr start sites were mapped, as well as alternatively spliced transcripts including a short Haglr exon (Fig. 6B). We used CRISPR/Cas9 to produce two lines of mice, the first carrying a deletion of the CpG island 114 [HoxD Del(CpG114) or Del(CpG114)] and the second carrying an inversion of the same DNA fragment [HoxD Inv(CpG114) or Inv(CpG114)]. Nine Del(CpG114) F0 founders were obtained.

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**Fig. 5.** Reduced small intestine diameter and epithelial dysgenesis in Hoxd3hd and HoxD Del(1–9)d10hd milk-fed pups. (A) Two wild-type controls (Upper) and two Hoxd3hd-homozygous siblings (Lower) are shown. (B) The longest villi from at least six available sections from each individual were selected and photographed, and their longest axis was measured. In the diagram the body weight was plotted as a function of the average longest villus length. The Hoxd3hd stock at P14 is shown as red diamonds and a red line. The two diamonds on the right represent wild-type (wt) mice, and the two on the left represent homozygous (hom) siblings. A similar analysis was carried out with Del(1–9)d10hd at 7 d after birth and is depicted as blue diamonds and a blue line. The two values at the left represent homozygous animals (hom), the two in the middle represent heterozygous animals (het), and the one on the right is a wild-type control (wt). (C) H&E-stained paraffin sections of gut villi from wild-type control and two pairs of sections from two HoxD Del(1–9)d10hd-homozygous specimens showing representative morphologies. (D) High-power photomicrographs of H&E sections of wild-type and heterozygous specimens and from two Del(1–9)d10hd-homozygous animals showing representative morphologies. (Scale bar, 1 mm in A and 100 μm in C and D.)

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http://www.pnas.org/cgi/doi/10.1073/pnas.1712511114
that were homozygous for the deficiency, and none of them suffered from growth retardation.

Clean stocks for both the deficiency and the inversion were further established, and RNAs were isolated from pairs of homozygous and wild-type control siblings at E9 for RNA-sequencing (RNA-seq). Browser Extensible Data (BED) graphs of mapped reads on both the forward and the reverse strands of the *HoxD* cluster indicated that in wild-type mice *Hoxd1*, *Hoxd3*, and *Hoxd4* were all transcribed as expected from the *Hox* forward strand (Fig. 6C). On the reverse strand, reads mapping to the *Haglr* locus were clearly recovered, even though the fragments per kilobase of transcript per million mapped reads (FPKM) value was five- to 10-fold reduced compared with *Hox* genes transcripts. In Del(CpG114)-homozygous animals, *Hoxd1* transcripts were missing, as were the long isoforms of *Haglr* on the opposite strand. Nonetheless, a signal was present over the third and fourth exons of the *Haglr* locus. In terms of FPKM values, this was around one order of magnitude below that of the wild-type *Haglr* signal. This observation showed that, besides the *Hox* promoters in the CpG island 114, at least one other start site contributed to the expression of the last two exons of *Haglr*. When interrogating the transcriptome genome-wide, only two loci were found with a statistically significant difference after adjusting the P values for multiple testing. One was *Hoxd1* and the other *Haglr*, as predicted by the genomic deficiency. Both Del and Inv(CpG114) alleles were bred to homozygosity, but these animals failed to show any slow postnatal weight gain, lethality, or loss of fertility (Table 1). We concluded that neither the deficiency nor the inversion alleles of the CpG1 island 114 had any effect on organismal growth.

**Discussion**

**HoxD Cluster-Dependent Gut Maturation and Organisinal Growth.**

Even though mammalian *Hox* gene functions have been scrutinized in great detail, a potential involvement in postnatal growth has remained undocumented. Here we report that four distinct mutant alleles associated with the *HoxD* cluster induced an early postnatal growth deficit. Growth retardation set in early, and a proportion of animals became fatally wasted. It is therefore likely that an important function for this gene cluster, probably linked to the proper morphogenesis of the gut, was impaired in these various alleles. We followed surviving individuals and determined that growth was systematically resumed once milk feeding was terminated. During this recovery period, the initially reduced excrement size and mass grew, showing an improvement of gut function along with an increase in body mass. Escapers formed small pellets reflecting a retarded expansion of their proximal colon. In addition, the initially meager total dropping mass improved progressively, indicating a delayed expansion of their distal colon.

Likewise, we also noticed that fatally stunted individuals suffered from partial atresia of the proximal colon. In addition, epithelial dysgenesis in the small bowel was noticed in both homozygous *Hoxd3*−/− and *HoxD*<sup>Del(1–9)d10hd</sup>-mutant specimens, in the latter case with severe enterocyte necrosis at the end of the first week of age. This extensive epithelial cell erosion in *HoxD*<sup>Del(1–9)d10hd</sup>-homozygous mice is somewhat reminiscent of necrotizing enterocolitis mouse models, which present similar pathological features (17). The repeated occurrence of such pathological deviations in small and large intestine in *HoxD* mutants provides evidence for a broad dysfunction along the intestine at the time the animals fed on milk. Interestingly, previous work involving *Hox* genes reported problems either in producing milk or in the proper regulation of these genes’ expression during mammary gland development (18, 19), showing the diverse panel of functions that these genes likely acquired to accompany the emergence of lactation (20).

Notably, this *Hox*-dependent inability to thrive on a milk diet followed by a more-or-less efficient recovery after weaning adds a further piece to the genetic study of milk-adapted gut function.
Previous work has shown that a distinct genetic program was in place in mice to ensure that milk digestion remained active for the necessary period of time. In the absence of Blimp1, for example, early enterocytes are lost prematurely, precluding growth of the organism due to the incompetence of the adult-type enterocytes to digest milk (21, 22). Our observations suggest that, similar to Blimp1, Haglr may promote the maintenance of milk-digesting enterocytes, raising the possibility that the two genes belong to the same genetic pathway, even if Blimp1 function is required in the epithelium whereas Hoxd3 gene expression is restricted to mesenchymal cells (22–24). The importance of Hoxd genes for the patterning of gut mesenchyme derivatives, such as sphincters (25, 26), has been well documented. However, with exception of the ano-rectal transitory epithelium (27), direct function of the HoxD cluster in gut epithelium seems unlikely, and hence any functional mechanism linking mesenchymal Hoxd3 expression to enterocyte survival may imply epithelial–mesenchymal interactions.

**Essential Function of Hoxd3 in Gut Development.** Clearly, Hoxd3 is the major Hox gene involved in this particular aspect of gut development, as determined by our genetic approaches. Indeed, the loss of function of this gene alone was sufficient to elicit severe growth retardation in homozygous animals. While this phenotype was not described in previously reported studies in which Hoxd3 was inactivated (6, 7), it was likely observed but not characterized in detail. Hoxd3 is nevertheless not the only Hox gene to contribute to proper gut formation, since, although the single loss of function of Hoxd1, Hoxd4, Hoxd8, or Hoxd9 did not generate any discernable phenotype, combined loss of function in cis in addition to Hoxd3 strengthened the severity of the alterations. For instance, homozygous Hoxd9\Delt(1–9) animals in which Hoxd1, Hoxd3, and Hoxd4 were all missing displayed a phenotype stronger than that in the simple Hoxd3-mutant specimens. However, growth retardation in the latter condition was not as strong as in homozygous HoxD\Delt(1–9)\hd-hd animals in which Hoxd8 and Hoxd9 had also been removed. It is possible that Hoxd genes other than Hoxd3 can compensate for the lack of function of the latter, even though they may not functionally contribute in the wild-type context. Alternatively, they may have a genuine function that is perhaps too subtle to be revealed in the presence of the HoxD3 protein.

Remarkably, the strongest allele in the series was the Hoxd9\Delt(1–9) chromosome, as even heterozygous animals displayed a strong growth deficit. This heterozygous condition was largely rescued when the Hox10 gene was inactivated on the same chromosome, demonstrating that most of the dominant phenotype was induced by a gain of function of this gene, likely following its relocation as the now-leading Hoxd gene on the telomeric side of the gene cluster. While such gain of expression of Hoxd genes flanking the breakpoints of internal cluster deletions have been documented in the past in a variety of developmental contexts (28–30), the mechanism underlying this dominant-negative effect remains to be fully clarified. The HOXD10 protein ectopically expressed with the Hoxd3 tissue specificity may trigger an inappropriate genetic program leading to the misexpression of gut morphology.

Nevertheless, we favor an alternative explanation whereby HOXD10 exerts its dominant-negative effect upon other, more anterior Hox genes such as Hoxd3. This dominant-negative effect of some posterior HOX proteins over more anterior members of the same family (“posterior prevalence” [31–33]) has been documented in a variety of situations (8, 30, 34, 35). In this view, the gain of Hoxd10 expression following its new genomic position within the gene cluster would affect the function of all anterior HOX proteins, somewhat equivalent to a global homoyzous loss of function of Hox genes. The fact that many heterozygous HoxD\Delt(1–9) animals were as strongly affected as homozygous HoxD\Delt(1–9)\hd-hd animals and displayed a very related phenotype involving gut morphology supports this explanation. As a consequence, the HoxD\Delt(1–9)-heterozygous condition would be merely yet another loss-of-function HoxD allele, one produced by the dominant-negative interference of the HOXD10 protein. Since rescuing the mutation of Hoxd10 in the HoxD\Delt(1–9) chromosome involves a microdeletion into its DNA-binding domain, it is possible that this dominant effect requires the binding of HOXD10 to DNA target sites normally occupied by other HOX proteins. In this particular case, we consider other proposed mechanisms to trigger this negative effect, such as disturbed interactions with cofactors of the TALE homeodomain protein family (36, 37) or the involvement of microRNAs (35), as less plausible.

**Is the LncRNA Haglr Involved in Postnatal Growth?** According to the description of Mdgt mice, i.e., animals lacking the lncRNA Haglr (3), Hoxd9\Delt(1–9)-heterozygous animals and Hoxd9\Delt-homozygous specimens suffered from a comparable slow postnatal weight gain. In the HoxD\Delt(1–9) animals, however, a full wild-type haplotype of the HoxD cluster was present, including an intact copy of Haglr, whereas in Hoxd9\Delt-hd mice both Haglr loci were intact. The Hoxd3\Delt phenotype was particularly intriguing, since the Haglr RNA extends up to the 3′ end of the Hoxd3 UTR, thus raising the possibility that the deletion of Haglr would, in fact, affect the function of Hoxd3 (11). To verify this hypothesis, a transcriptome analysis of Mdigt mice would be necessary. On our side, we investigated this alternative by trying to knock down Haglr transcription while preserving the activity of Hoxd3. The targeted deletion of Cpg114 indeed abrogated all long isoforms of the Haglr transcript in E9.5 embryos, corresponding to the extent of the deletion reported in ref. 3. In these embryos, the Hoxd3 transcripts were normal in all respects. Despite the absence of Haglr transcripts, growth deficit was not observed in homoyzous mice, indicating that variation of Haglr RNA level had no appreciable consequence in organosomal growth.

Shorter transcripts were nevertheless still initiated from the anti-Hox strand in the Del(Cpg114) chromosome (although at a much lower level) and terminated exactly at the position of the termination site of the Hoxd3 UTR (Fig. 6). These transcripts, which were also named “Haglr” in the Ensembl database even though they have an independent start site, initiated within the last exon of Haglr. It is not known whether such transcripts are still present in Mdigt mice after the large targeted deletion and lacZ reporter replacement (3). If these additional RNAs were not maintained in Mdgt embryos, it is possible that their absence would perturb the transcription of Hoxd3, thus leading to growth retardation. In such a scenario, however, the function of these RNAs would be exerted in cis rather than in trans (38), as a result of transcriptional interference. Taking these results together, we conclude that the effect of the Mdgt deletion is more likely due to the extent of the genomic deficiency or the insertion of foreign DNA such as the LacZ transcription unit over the Hoxd3 gene rather than to the absence of the specific Haglr transcript. This lncRNA may result from a bidirectional transcription at the Hoxd1 start site (39) and may not have any particular function in controlling postnatal growth.

**Materials and Methods**

**Mouse Strains.** Mice were handled according to the Swiss law on animal protection (LPA) with the authorizations GE/81/14 (to D.D.) and GE/29/26 (to B.M.). Animal experiments were agreed upon by the ethical committee of the Canton of Geneva. Genetically modified mice were maintained and bred in the Department of Medical and Molecular Genetics, University of Geneva (GE/29/26). The appropriate plasmids were injected in equimolar solution.

Zygotes were derived from (B6CBA)F1 females crossed to (B6CBA)F1 males. Founder animals were crossed with males or females of the (B6CBA)F1 wild-type genotype, and routine strain maintenance was continued by crossing heterozygous males of the allele in question to (B6CBA)F1 wild-type females.
Target sequences were identified using the web tool at crispr.mit.edu during the year 2013. Nucleotide positions are based on GRCh38mm10.

The production of the various mutant alleles used in this study is described in the SI Materials and Methods section.

RNA Extraction and RNA-Seq. RNA extraction and RNA-seq were as described in ref. 18. Haglr transcript isoforms were cloned and sequenced starting from an E8 mouse tail-bud total RNA preparation as a source for first-strand cDNA synthesis using SuperScript II reverse transcriptase from Invitrogen, following the manufacturer’s protocol. cDNA was amplified using Phusion High Fidelity DNA polymerase from Thermo Scientific. Amplicons were cloned into the pGEM-T Easy plasmid vector (1360, Promega) and transformed into JM109 cells; cloned and plasmid DNA samples were isolated by the Qiagen Midi protocol.

RNA-seq-processed and raw datasets were deposited in the Gene Expression Omnibus (GEO) database with accession number GSE103086.

Histology and Coprometric Analyses. For histology and coprometric analyses, see SI Materials and Methods.

ACKNOWLEDGMENTS. We thank members of the D.D. laboratories for sharing material and discussions, the histology platform at Ecole Polytechnique Fédérale (Lausanne) (EPFL), the genomics platform in Geneva, Olivier Schaaf for advice on statistical analyses, and Thomas Alexander McKee for discussions. This work was supported by funds from the EPFL, the University of Geneva, Swiss National Research Fund Grant 310030B_138662, European Research Council Grants SystemHox 232790 and RegulHox 588029, and the Clara Foundation (D.D.).

1. Spitz F, et al. (2001) Large scale transgenic and cluster deletion analysis of the HoxD complex separate an ancestral regulatory module from evolutionary innovations. *Genes Dev* 15:2209–2214.

2. Zakany J, Duboule D (2012) A genetic basis for altered sexual behavior in mutant female mice. *Curr Biol* 22:1676–1680.

3. Sauvageau M, et al. (2013) Multiple knockout mouse models reveal lincRNAs are required for life and brain development. *Elife* 2:e01179.

4. Guo T, et al. (2011) An evolving NGF-Hoxd1 signaling pathway mediates development of divergent neural circuits in vertebrates. *Nat Neurosci* 14:31–38.

5. Zakany J, Kmita M, Alarcon P, de la Pompa JL, Duboule D (2001) Localized and transient expression of Hox genes suggests a link between patterning and the segmentation clock. *Cell* 106:207–217.

6. Condie BG, Capcchi MR (1993) Mice homozygous for a targeted disruption of Hoxd-4 (Hox-4.1) exhibit anterior transformations of the first and second cervical vertebrae, the atlas and the axis-3. *Development* 119:579–595.

7. Greer JM, Puetz J, Thomas KR, Capcchi MR (2000) Maintenance of functional equivalence during paralogous Hox gene evolution. Nature 403:661–665.

8. Zacchetti G, Duboule D, Zakany J (2007) Hox gene function in vertebrate gut morphology: The case of the caecum. *Development* 134:3967–3973.

9. Delpeort S, et al. (2013) Multiple enhancers regulate Hoxd genes and the Hotdog lncRNA during ecumenic cell. *Cell Rep* 3:137–150.

10. Tschopp P, Christen AU, Duboule D (2012) Bidirectional control of Hox gene transcription in the spinal cord defines two regulatory subclusters. *Development* 139:929–939.

11. Bassett AR, et al. (2014) Considerations when investigating lincRNA function in vivo. *Elife* 3:e03058.

12. Tschopp P, Duboule D (2011) A genetic approach to the transcriptional regulation of Hox gene clusters. *Annu Rev Genet* 45:145–166.

13. Tarchini B, Duboule D (2006) Control of Hoxd genes’ colinearity during early limb development. *Dev Cell* 10:93–103.

14. Duboule D, Morata G (1994) Colinearity and functional hierarchy among genes of the homeotic complexes. *Trends Genet* 10:358–364.

15. Horan GS, Kovacs EN, Behringer RR, Featherstone MS (1995) Mutations in paralogous Hox genes result in overlapping homeotic transformations of the axial skeleton: Evidence for unique and redundant function. *Dev Biol* 169:359–372.

16. Gouat P (1992) Facetal pellet size difference as a field criterion to distinguish between two Ctenodactylus species (Mammalia, Rodentia). *Z Saugetierkd* 57:183–185.

17. Neal MD, et al. (2013) A critical role for TLR4 induction of autophagy in the regulation of enterocyte migration and the pathogenesis of necrotizing enterocolitis. *J Immunol* 190:3541–3551.

18. Chen F, Capcchi MR (1999) Paralogous mouse Hox genes, HoxA9, HoxB9, and HoxD9, function together to control development of the mammary gland in response to pregnancy. *Proc Natl Acad Sci USA* 96:541–546.

19. Schep R, et al. (2016) Control of Hoxd gene transcription in the mammary bud: hijacking a preexisting regulatory landscape. *Proc Natl Acad Sci USA* 113: E7720–E7728.

20. Duboule D (1999) No milk today (my Hox have gone away). *Proc Natl Acad Sci USA* 96:322–323.

21. Harper J, Mould A, Andrews RM, Bikoff EK, Robertson EJ (2011) The transcriptional repressor B limp1/Pdm1 regulates postnatal reprogramming of intestinal enterocytes. *Proc Natl Acad Sci USA* 108:10585–10590.

22. Muncam V, et al. (2011) Blimp1 regulates the transition of neonatal to adult intestinal epithelium. *Nat Commun* 2:452.

23. Gurdziel K, Vogt KR, Walton KD, Schneider GK, Gumucio DL (2016) Transcription of the inner circular smooth muscle of the developing mouse intestine: Evidence for