Developmental Programming Mediated by Complementary Roles of Imprinted Grb10 in Mother and Pup

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Abstract

Developmental programming links growth in early life with health status in adulthood. Although environmental factors such as maternal diet can influence the growth and adult health status of offspring, the genetic influences on this process are poorly understood. Using the mouse as a model, we identify the imprinted gene Grb10 as a mediator of nutrient supply and demand in the postnatal period. The combined actions of Grb10 expressed in the mother, controlling supply, and Grb10 expressed in the offspring, controlling demand, jointly regulate offspring growth. Furthermore, Grb10 determines the proportions of lean and fat tissue during development, thereby influencing energy homeostasis in the adult. Most strikingly, we show that the development of normal lean/fat proportions depends on the combined effects of Grb10 expressed in the mother, which has the greater effect on offspring adiposity, and Grb10 expressed in the offspring, which influences lean mass. These distinct functions of Grb10 in mother and pup act complementarily, which is consistent with a coadaptation model of imprinting evolution, a model predicted but for which there is limited experimental evidence. In addition, our findings identify Grb10 as a key genetic component of developmental programming, and highlight the need for a better understanding of mother-offspring interactions at the genetic level in predicting adult disease risk.

Introduction

Growth during prenatal and postnatal development influences adult health status. In humans, low birth weight is associated with an increased risk of metabolic diseases, including obesity and diabetes [1]. In addition to overall size, disproportionate growth during development is also a risk factor for common adult diseases, including coronary heart disease and high blood pressure [2]. It is well-established that environmental stresses, such as poor maternal diet [3], can influence offspring growth, but the genetic control of developmental programming is not fully understood. Additionally, most studies have focused on prenatal development, but development in the postnatal period is also critical in influencing adult health status (reviewed in [4]).

The genetic control of growth and nutrient acquisition in utero is mediated in part by imprinted genes, defined by their expression from a single parental allele [5]. In the placenta, paternally expressed genes generally promote growth and maternally expressed genes suppress growth. For many genes, this pattern is thought to reflect conflict between the parental genomes, played out within the offspring, over maternal resource allocation [6]. Females maximise lifetime reproductive success by evenly distributing their resources to offspring (since a mother is equally related to all of her offspring). However, when there is multiple paternity within or among litters, males are only related to some offspring produced by a female, and so it is in his genetic interest for his offspring to extract as much of his mate’s resources as possible. The functions of a number of imprinted genes are consistent with the predictions of this “parental conflict hypothesis.” For example,
deletion of the paternally expressed Igf2 P0 transcript in the mouse placenta causes a failure in the supply of nutrients to the developing fetus, resulting in growth restriction [7]. Conversely, deficiency of the maternally expressed gene Grb10 causes placental overgrowth and increases placental efficiency [8]. Conflict between the parental genomes appears to be conserved in humans [9].

Postnatally, the majority of imprinted genes influence aspects of metabolism or behaviour. Grb10 is an intriguing example of an imprinted gene with diverse postnatal functions. We have previously described two mouse models of Grb10 ablation, generated by the integration of a LacZ reporter gene-trap cassette [10,11]. Here we more precisely map the gene trap loci (Figures 1A and S1), and also confirm and directly compare the patterns of fetal LacZ expression (Figure 1B). Both the Grb10KO−/− and Grb10KO alleles ablate Grb10 protein with essentially identical phenotypic consequences, yet expression from their LacZ reporter genes is not always equivalent. Maternal transmission of each allele produces similar LacZ expression patterns at embryonic day 14.5 (e14.5; Figure 1B). Contrastingly, LacZ expression in the CNS is apparent after paternal transmission of the Grb10KO allele (Grb10KO+/- embryos) but is not detected in the CNS of Grb10A2-4-v embryos. Expression in adult Grb10A2-4-v brain is detectable but weak relative to Grb10KO+/- (Figure S2).

Gene-trap cassette integration in the Grb10A2-4 allele is coincident with the deletion of 36 kb of endogenous sequence, while only 12 bp are deleted in Grb10KO (Figures 1A and S1) [11]. We considered that the differences in LacZ expression between Grb10KO+/- and Grb10A2-4-v brains might be attributed to a tissue-specific enhancer perturbed by cassette integration in the Grb10A2-4 allele. A screen of the Grb10 genomic sequence for similarity to regulatory elements in Transfac, using PReMod [19], identified a single element of 70 bp, called CRM1, that is highly conserved among vertebrates (Figure 2A), and represents a candidate enhancer element.

CRM1 proved hypersensitive to DNase I digestion in mouse adult brain, but not liver where Grb10 is not transcribed (Figure 2B), consistent with CRM1 being an enhancer. PReMod identified potential recognition sequences within CRM1 for Signal transducer and activator of transcription (STAT) family members (STAT5a/STAT5b, Tst-1, TCF11, and Pax family members (Figure S3A). We reasoned that only factors spatially overlapping with Grb10 expression could potentially regulate Grb10 in vivo, and using public expression data [20], we ruled out all but STAT5b. Using mRNA in situ hybridisation, we confirmed that Stat5b brain expression overlaps extensively with Grb10 (Figure 2C). In a cell transfection assay, CRM1 demonstrated enhancer capability in the presence of constitutively active STAT5b (Figure 2D). The STAT5 recognition sequences [21], but not those of Tst-1, TCF11, or Pax, are 100% conserved between mouse, human,
Grb10KO through each of the parental lines. CNS expression observed in bisected embryos at e14.5 inheriting the

Structure of gene-trap cassettes include splice acceptor (SA) and polyadenylation exons (boxes) and translated regions (filled boxes). The integrated

12.5 of gestation (G7.5, G12.5) and day 6 of lactation (L6), showing

Figure 1. Comparison of Grb10KO and Grb10Δ2-4 mice. (A) Structure of Grb10, according to UCSC annotation, showing numbered exons (boxes) and translated regions (filled boxes). The integrated gene-trap cassettes include splice acceptor (SA) and polyadenylation (pA) signals, and a LacZ reporter. (B) Comparative LacZ staining of bisected embryos at e14.5 inheriting the Grb10KO and Grb10Δ2-4 alleles through each of the parental lines. CNS expression observed in Grb10KO/+ embryos is not detected in Grb10Δ2-4/+ embryos. (C) Comparative LacZ staining of adult mammary glands at days 7.5 and 12.5 of gestation (G7.5, G12.5) and day 6 of lactation (L6), showing pregnancy-dependent reporter expression in Grb10KO+/− but not Grb10Δ2-4/+ females. WT (+/+ glands were stained with carmine alum to illustrate morphological changes.

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chimpanzee, cow, and chicken (Figure S3B). Together, these data suggest STAT5 promotes Grb10 expression in mouse brain. Although CRM1 is not within the deleted sequence of Grb10Δ2-4, its 5’ end is within 366 bp of the deletion. STAT5 binding, or its affect on Grb10 transcription, might therefore be perturbed by the deletion in the Grb10Δ2-4 allele, which could account for the observed expression differences in the CNS. One explanation is that the deletion alters the local chromatin conformation, reducing the interactions between CRM1 and the Grb10 promoter. Consistent with this, the deletion includes at least one binding site in brain for CTCF [22], a regulator of chromatin architecture.

Grb10 was previously identified as a STAT5-responsive gene in mammary epithelial cells [24]. More recently, genome-wide ChIP-seq mapping of STAT5 binding sites in mammary tissue identified three binding sites within the Grb10 locus, including one coincident with CRM1, confirming that CRM1 can bind STAT5 in vivo [23]. We examined Grb10 expression in the mammary epithelia of our mouse models utilising LacZ reporter activity as a readout, predicting that reporter expression from the Grb10Δ2-4 allele would be weaker than from the Grb10KO allele because of a perturbation of CRM1 activity, similar to the differences observed in the CNS. We first demonstrated pregnancy-dependent expression of Grb10 in mammary epithelium using Grb10KO+/− females. No reporter activity was detected at day 7.5 of gestation (G7.5), a subset of epithelial cells were LacZ-positive at G12.5, and widespread epithelial expression was observed at day 6 of lactation (Figure 1C), an expression profile comparable with other transcriptional targets of STAT5 signalling [24]. Mammary epithelial expression is restricted to the maternally inherited copy (no LacZ staining was detected in Grb10KO/+ females), consistent with Grb10 imprinting in other peripheral tissues; expression of the Grb10 maternal allele is widespread during fetal development [8,10,11] and in neonatal tissues (Figure S4), but more restricted in the adult [10,12]. Comparable with expression differences in the CNS, no LacZ expression was detected in Grb10Δ2-4/+ epithelium.

The functional significance of imprinting in the mammary gland, which regulates nutrient allocation in the postnatal period, has not been widely considered. We were therefore intrigued by the pregnancy-dependent, imprinted expression of Grb10 observed in the mammary gland and its potential functional importance.

Pup growth is the ultimate correlate of gland function [25], and we thus compared growth of WT (+/+ pups born to WT and Grb10KO+/− dams. At e17.5, WT embryos of Grb10KO+/− females are 10% smaller than those of WT females, due to an increased litter size [8]. Despite this embryonic growth disadvantage, WT pups born to Grb10KO+/− dams gained more weight postnatally than those born to WT dams, after standardising litter size (Figure 3A). We initially interpreted this as an enhanced provisioning capacity of Grb10KO+/− dams, suggesting that Grb10 functions in mothers to suppress nutrient supply postnatally. However, WT pups born to Grb10KO+/− dams also had Grb10KO+/− siblings, which were 16%±5.4% larger than their WT littermates at birth (Figures 3B, 3C, and S5A). It was therefore necessary to consider whether these larger siblings might be impacting on WT growth, and to separate as far as possible these effects from the genotype of the dam.

We used a cross-fostering strategy to differentiate the postnatal growth effects of Grb10 ablation in pup from those in dam and sibling (Figure 3C). Similar approaches have been used previously to differentiate between parental and offspring effects on traits,
including in the context of genomic imprinting (e.g., [26–29]). Pup weights at days 1, 8, and 15 were modelled as described in Materials and Methods. Data were analysed using a generalised linear mixed model (GLMM). Cross-fostering had no main effect on any trait ($p > 0.2$ for all traits; Table S1), consistent with other studies, and therefore was not included in the final models (see also Figure S5B). The effect of $\text{Grb10}^{\text{ablation}}$ in the dam alone was assessed by comparing the growth of pure WT litters raised by WT or $\text{Grb10}^{\text{KO}+/+}$ nurses. Reduced weight gain was observed in pups raised by $\text{Grb10}^{\text{KO}+/+}$ nurses (Figure 3D, purple line) compared to those raised by WT nurses (black), demonstrating that $\text{Grb10}^{\text{KO}+/+}$ nurses exhibit compromised nutrient supply, and therefore the function of $\text{Grb10}$ in the mother is to promote nutrient provisioning postnatally. Compromised supply from $\text{Grb10}^{\text{KO}+/+}$ nurses was confirmed by our modelling, which showed a significant effect of nurse genotype at day 8 ($F_{1,21} = 15.08; p < 0.001$) and day 15 ($F_{1,21.6} = 25.60; p < 0.0001$), but not day 1 ($F_{1,19.9} = 0.53; p = 0.4744$) (Table 1, which presents hypotheses tested and key findings from the data; Tables S1, S2, S3, which present the results of the models in full). The observations in our initial experiment that WT pups born to $\text{Grb10}^{\text{KO}+/+}$ dams gained more weight postnatally than those born to WT dams could therefore not be attributed to dam genotype alone, but were likely to be influenced by sibling genotype. In support of this, WT pups with $\text{Grb10}^{\text{KO}+/+}$ siblings gained more weight than WT pups with only WT siblings, when raised by WT nurses (Figure 3D, red and
black, respectively). This is consistent with the idea that $\text{Grb10KO}^{m/+}$ pups exhibit increased demand for nutrients, to which WT nurses respond with improved provisioning, enabling increased postnatal weight gain in WT littermates. However, because all litters born to $\text{Grb10KO}^{m/+}$ dams contained at least one $\text{Grb10KO}^{m/+}$ pup, this result is also consistent with a maternal effect in which exposure to the $\text{Grb10KO}^{m/+}$ uterine environment promotes increased postnatal weight gain in both WT and $\text{Grb10KO}^{m/+}$ pups. Although the effects of siblings and the dam are correlated, we examined whether the postnatal growth of an individual is influenced by the frequency of $\text{Grb10KO}^{m/+}$ siblings, with this relationship being significant for growth from day 1 to day 8 ($\beta = 0.97$, 21 degrees of freedom [df], $p = 0.022$) and from day 1 to day 15 ($\beta = 1.34$, 21.5 df, $p = 0.018$). Thus, $\text{Grb10}$ has pleiotropic and complementary roles in dam and pup, enhancing nutrient supply in dams and suppressing demand in pups.

We next considered the compound effects of $\text{Grb10}$ ablation in nurse and pup, hypothesising that more demanding $\text{Grb10KO}^{m/+}$ pups might not reach their full size potential when suckling from $\text{Grb10KO}^{m/+}$ nurses with reduced supply. Supporting this, $\text{Grb10KO}^{m/+}$ pups raised by WT nurses gained more weight than those raised by $\text{Grb10KO}^{m/+}$ nurses at day 8 ($t = 4.78$, 43.6 df, $p < 0.0001$) and day 15 ($t = 5.47$, 52.3 df, $p < 0.0001$), but not at day 1 ($t = 1.76$, 43.7 df, $p = 0.086$) (Tables 1 and S2). $\text{Grb10KO}^{m/+}$ pups suckling from

Figure 3. $\text{Grb10}$ controls postnatal supply and demand. (A) WT (+/+ ) pups born to $\text{Grb10KO}^{m/+}$ (m/+ ) dams gained more weight to postnatal day 15 than WT pups born to WT dams. (B) $\text{Grb10KO}^{m/+}$ and WT male siblings on the day of birth. (C) Schematic of dam/pup relationships studied. All crosses used WT sires (white squares). WT dams (white circles) gave birth only to WT pups (i), while $\text{Grb10KO}^{m/+}$ dams (half-filled circles) gave birth to mixed litters of WT and $\text{Grb10KO}^{m/+}$ pups (ii). Cross-fostering (dashed line) enabled switching of dam/pup genotypes (iii and iv). Pure WT litters were cross-fostered to non-biological WT nurses as a control (v). (D) Effects of nurse or sibling genotype on WT pup growth. (E) Effects of $\text{Grb10}$ genotype interactions between nurse and offspring on pup growth. Values represent means ± standard error.

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Table 1. Summary of hypotheses tested by the datasets obtained in the cross-fostering study.

<table>
<thead>
<tr>
<th>Hypothesis</th>
<th>Supporting Evidence</th>
<th>Interpretation</th>
</tr>
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<tbody>
<tr>
<td>The process of cross-fostering does not influence pup growth</td>
<td></td>
<td>No significant effect from cross-fostering, therefore this effect was excluded from the final models</td>
</tr>
<tr>
<td>m/+ nurses have reduced nutrient supply</td>
<td></td>
<td>Pups gain more weight if suckling from +/- nurses than if suckling from m/+ nurses</td>
</tr>
<tr>
<td>m/+ pups have increased nutrient demand</td>
<td></td>
<td>m/+ pups are larger than +/- siblings at days 1, 8, and 15</td>
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<tr>
<td>+/- pups are more responsive to high m/+ pup demand than m/+ pups</td>
<td></td>
<td>m/+ pups gain more weight if suckling from +/- nurses than if suckling from m/+ nurses</td>
</tr>
<tr>
<td>Gbr10 ablation in both nurse and pup normalises m/+ pup</td>
<td></td>
<td>m/+ pups suckling from m/+ nurses are not significantly different from +/- pups suckling from +/- nurses at days 8 and 15, despite being larger at day 1</td>
</tr>
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**Pup weights on day 1, day 8, and day 15 of the study period were compared using GLMM to determine the effects of pup genotype, biological dam genotype, and nurse genotype. Each row states the hypothesis to be tested, the relevant comparisons to be made to test the hypothesis, p-values at the three time points determined from the models, and an interpretation of the results from the GLMM. Comparisons are those shown graphically in Figure 3. Details of the model are presented in the Materials and Methods. The “source” in column 2 refers to one of Tables S1, S2, S3 that contains the full model results.**

*Table S1.*

*Table S2.*

*Table S3.*

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Gbr10KO<sup>+/+</sup> mice were larger than their WT littermates at day 1, but their growth trajectories converged within a few days (Figure 3E, brown and grey, respectively). However, Gbr10KO<sup>+/+</sup> pups remained larger than WT siblings throughout the experimental period when suckling from WT nurses (Figure 3E, blue and red, respectively). Modelling of the pup/nurse interaction confirmed these observations, with the contrast between Gbr10KO<sup>+/+</sup> pups suckling from WT nurses compared to other combinations being significant at day 8 (F<sub>1,52.3</sub> = 39.33, p < 0.0001) and day 15 (F<sub>1,70.4</sub> = 38.83, p < 0.0001), while the difference between Gbr10KO<sup>+/+</sup> pups with Gbr10KO<sup>−/−</sup> nurses was significantly different to that of WT pups with Gbr10KO<sup>−/−</sup> nurses at day 1 (t = 6.28, 113 df, p < 0.0001), but not day 8 (t = 1.48, 115 df, p = 0.14) or day 15 (t = 0.25, 119 df, p = 0.80) (Table S3). Thus, oversized Gbr10KO<sup>+/+</sup> neonates rapidly adjust to WT size after birth, but only when the nurse genotype is also Gbr10KO<sup>−/−</sup>, implying a role for Gbr10 in influencing mother-offspring coadaptation. Our cross-fostering experiments show that WT body size is achieved through the complementary actions of Gbr10 in mother and offspring.

In addition to overall size, disproportionate growth can also be a risk factor for adult disease. In adulthood, Gbr10KO<sup>+/+</sup> and Gbr10KO<sup>−/−</sup> mice have an altered body composition, exhibiting increased lean mass and reduced adiposity relative to WT animals, which results in enhanced glucose metabolism [12, 13]. The finding in the present study that growth is influenced by Gbr10 in both mother and pup prompted us to examine the lean/fat ratios of animals used in the cross-fostering study. More specifically, we set out to ask whether the increased lean/fat ratio of a Gbr10KO<sup>−/−</sup> mouse is a result of Gbr10 depletion within that mouse, or if the genotype of the nurse also contributes to this phenotype. To address this question, we analysed the body composition of cross-fostered pups at the end of the growth study period using dual-emission X-ray absorptiometry (DXA). Ablating Gbr10 in either nurse or pup increased the lean/fat ratio compared to WT pups raised by WT nurses (Figure 4A). When Gbr10 was ablated in offspring alone, the increased lean/fat ratio was caused by a gain in lean mass, with fat mass unchanged (Figure 4B and 4C; compare red with blue). Conversely, Gbr10 ablation in nurse alone caused a reduction in adipose tissue, while lean mass remained unchanged (Figure 4B and 4C; compare black with purple). Therefore, Gbr10 expressed in the mother has the major influence on adipose deposition, while offspring Gbr10 largely influences lean mass. A WT lean/fat ratio requires functional Gbr10 in both mother and pup.

Since Gbr10KO<sup>+/+</sup> neonates adjust to WT size when suckling from a Gbr10KO<sup>+/+</sup> nurse, we asked whether this normalisation effect was also reflected in the lean/fat ratios. Consistent with the adjustment in body size, the lean/fat ratio of Gbr10KO<sup>+/+</sup> animals raised by Gbr10KO<sup>−/−</sup> nurses was comparable to that of their WT littermates, and also to that of WT pups raised by WT nurses (Figure 4D; compare brown with grey and black). This provides further evidence that the pleiotropic functions of Gbr10 in mother and pup are complementary.

To inform on the mechanism through which Gbr10 regulates postnatal nutrient supply, we examined Gbr10KO<sup>+/+</sup> mammary gland gross morphology at different stages, but did not detect any obvious differences from WT glands (Figure S6A). We also measured various parameters in histological sections of glands harvested at day 5 of lactation. Since we had shown that Gbr10KO<sup>+/+</sup> pups demonstrate increased nutrient demand, we compared glands from Gbr10KO<sup>+/+</sup> dams to glands from Gbr10KO<sup>+/−</sup> dams. Unlike WT dams, both Gbr10KO<sup>+/+</sup> and Gbr10KO<sup>+/−</sup> dams raise comparable mixed genotype litters, but the absence of Gbr10 expression from the paternally-expressed allele in mammary glands (Figure 1C) means that Gbr10KO<sup>+/−</sup> females are effectively WT for Gbr10 in this tissue. No differences were observed in total abdominal gland weight or surface area (Figure S6B and S6C). To gain more detailed insight into gland structure, we quantified the total number, total area, mean area, mean...
perimeter, mean Feret diameter and mean minimum Feret diameter for lumina and adipocytes, but found no differences (Figures S6D and S6E). These analyses were repeated on a separate cohort of glands isolated 48 hours after a forced wean at day 15 of lactation, and we made similar observations (unpublished data). In support of these morphometric analyses, no significant differences were found between WT and Grb10KOm/+ dams observed in our earlier experiments was due to compromised milk letdown since, if anything, they were able to transfer more milk to pups than Grb10KOv/+ dams (Figure S8A). Although Grb10 is almost exclusively expressed from the paternally inherited allele in adult brain, and therefore Grb10KOv/+ females are unlikely to demonstrate perturbed maternal behaviour, we confirmed that pup retrieval and nest building behaviours are comparable between Grb10KOm/+ and Grb10KOv/+ dams (Figure S8B–S8E). The protein and fat content of milk was also comparable between nurses used in the cross-fostering study (Figure S9A and S9B). Together these data suggest that milk letdown, maternal behaviour or the proportions of fat and protein in milk are not the basis for reduced provisioning in Grb10KOv/+ dams. However, prolactin expression in the pituitary glands of Grb10KOv/+ nurses was significantly elevated relative to WT nurses, when raising WT litters, whereas pituitary growth hormone levels were unchanged (Figure S9C). Reduced provisioning causes pups to suckle more vigorously, promoting maternal pituitary prolactin expression that normally stimulates increased milk production [30]. Our data suggest that mammary glands of Grb10KOv/+ females are resistant to elevated prolactin.

**Discussion**

In mice, most imprinted genes are expressed in the placenta and many have been shown experimentally to influence placental development and function. The parental conflict hypothesis, which, at a gross level, predicts that paternally expressed genes promote growth while maternally expressed genes suppress growth, is consistent with the functions of several genes imprinted in the placenta, including Grb10 [8,11]. While the conflict hypothesis can potentially explain the occurrence of imprinting at many loci, the functions of a considerable number of imprinted genes cannot be easily reconciled with the predictions of the model, such as those involved in maternal care behaviours. Recent extensions to the model have considered cases in which asymmetries between genes inherited from mothers and fathers can arise from various patterns of interactions with kin, but they do not provide strong predictions about the nature of imprinting in adult tissues [13,31]. There are also alternative models that do not consider conflict, such as the maternal-offspring coadaptation model, which describes how the combination of alleles expressed in mothers and their offspring jointly determines offspring fitness [18]. Whether each of these models could potentially account for the complex patterns of Grb10 expression and imprinting is unclear, but we present here some of the strongest empirical evidence that coadaptation could play a role, without necessarily ruling out alternative hypotheses.

Earlier studies involving reciprocal crosses, and cross-fostering, between two distinct mouse strains established that parent-of-origin effects such as genomic imprinting could contribute to coadaptation between genotypes (e.g., [26,29]). These studies provide evidence that maternal provisioning is influenced by maternal and offspring genotypes [27] and that provisioning is optimal when mother and offspring are of the same genotype [29]. A study mapping quantitative trait loci on adult mouse body weight and organ weights indicated that a number of imprinted

Figure 4. Functional Grb10 is required in mother and pup for WT offspring body proportions. (A) Lean/fat mass ratio in a subset of cross-fostered pups indicating that Grb10 ablation in either nurse or pup increases the lean/fat mass ratio relative to WT pups raised by WT nurses. (B) Total lean mass. (C) Total fat mass. (D) Lean/fat mass ratio in a subset of cross-fostered pups, indicating that the body composition of Grb10KOm/+ pups raised by Grb10KOv/+ nurses is similar to that of WT pups raised by WT or Grb10KOm/+ nurses. Data points represent individual animals; mean values are represented by horizontal lines. Datasets in (B) and (C) were analysed using one-way ANOVA with Tukey’s post hoc test. **p<0.01. ns, not significant. doi:10.1371/journal.pbio.1001799.g004
loci had small but detectable effects on these traits [28]. This genome-wide mapping is complementary to our approach, the manipulation of a single imprinted gene, which shows that Grb10 can contribute functionally to body weight and proportions through actions in both mother and offspring.

Grb10 is an intriguing model with which to study imprinted gene function and evolution, because its two parental alleles are expressed in different tissues where they influence distinct physiological and behavioural processes [10]. Our earlier work characterising the same knockout mice used in this study established that maternally expressed Grb10 regulates fetal and placental growth [8,11], consistent with the conflict hypothesis, as well as glucose homeostasis in adulthood [12]. In the present study, we demonstrate that Grb10 also controls postnatal growth through imprinted expression in mammary epithelium. The two archetypal mammalian tissues differ fundamentally in that the placenta contains both maternal and paternal genetic contributions, as in the offspring, but the mammary gland shares only maternal genes with offspring. Thus, while they are functionally analogous in supporting offspring growth, the placenta can be a site of direct conflict between the maternal and paternal genomes, whereas the mammary gland is not [14]. Consequently, our findings do not appear to fit with the simple predictions of the conflict hypothesis. The finding that WT body size and proportions require the combined and complementary actions of Grb10 in mother and pup (Figure 5), provides support for the coadaptation model of imprinting evolution, although further work would be needed to confirm that the effects of Grb10 lead to increased fitness. However, even if coadaptation explains the imprinting of Grb10 in pups, the coadaptation process would not favour imprinted expression in the mammary gland. Either a different hypothesis is needed to explain why the gene is imprinted in this tissue, or the pattern of expression in the mammary gland could simply reflect the selection that led to imprinting earlier in life. It should also be noted that our study compares WT Grb10 with a single knockout allele. Strong support for the coadaptation theory would come from an analysis of different allelic variants. Pups from combinations where mothers and offspring are expressing the same allelic variant would be expected to have higher fitness than those from combinations expressing different alleles.

Conflict between the parental genomes, coadaptation of processes regulating postnatal nutrient acquisition, or indeed some other driving force, could have provided the initial selective pressure for the evolution of imprinting. However, a mechanism other driving force, could have provided the initial selective pressures regulating postnatal nutrient acquisition, or indeed some of Grb10 expression of both the maternally and paternally inherited alleles. This need not be mutually exclusive [32]. Indeed, expression of both the maternally and paternally inherited alleles of Grb10 in different tissues, influencing different phenotypes, strongly supports this notion, since the same selective forces presumably could not have led to both patterns of expression. Evidence for the later evolutionary acquisition of novel functions or imprinted expression of a gene in adult tissues could be viewed as consistent with this idea. In this context it is interesting that in at least one marsupial species, the tammar wallaby, Grb10 is expressed in a range of fetal and adult tissues, including lactating mammary gland, but its expression appears not to be imprinted [33]. Future work on the expression and functions of Grb10 in non-mammalian species will help to unravel the likely evolutionary course of this pleiotropic gene.

The mechanism through which Grb10 regulates postnatal nutrient supply is not clear, but its pregnancy-dependent expression in the mammary epithelium is consistent with Grb10 controlling supply through this tissue. Our data suggest that Grb10 might mediate the response of the epithelium to pituitary prolactin, but further work will be needed to define its mode of action. We could not detect any phenotype associated with Grb10KO in analyses of mammary glands at the cellular level or in analyses of milk fat and protein content. One intriguing possibility is that Grb10 in mammary epithelium could regulate the release of signalling molecules that influence growth or metabolism of suckling offspring. Evidence exists for such lactocrine signalling playing a role in offspring development [34].

Environmental influences on the programming of adult health status during development have been widely investigated. In humans, maternal and child undernutrition are risk factors for high glucose concentration and blood pressure in adulthood [3]. Chemical insults can also adversely affect development with implications for adult health. Bisphenol A (BPA), which mimics oestrogen, has garnered much attention recently because of its widespread use in the manufacture of baby bottles, coatings for food cans and other commonly used items. Effects of exposure during development to environmentally relevant levels of BPA, using rodent models, include increased body weight, advanced puberty, and altered reproductive function, as well as a possible predisposition to mammary and prostate cancers [35]. This is effected, at least in part, through alterations to the fetal genome, including reduced levels of DNA methylation, which is associated with changes in gene transcription [36,37].

The genetic control of developmental programming of adult health status is relatively poorly understood. We have previously
shown that Grb10 determines the proportions of lean and fat tissue during development, and that altering the lean/fat ratio by ablating Grb10 affects glucose homeostasis in adulthood [12]. In the present study, we find that this programming of adult metabolic state during postnatal development is not the result of Grb10 acting in the pup alone, but is achieved through the combined actions of Grb10 in mother and offspring. Interestingly, two recent mouse studies of nutrient restriction during gestation have demonstrated up-regulation of Grb10 expression in offspring, consistent with our findings that Grb10 plays a key role in responding to nutrient supply [38,39]. Our work highlights the need for a much better understanding of genetic interactions between mother and offspring in predicting adult health status.

**Materials and Methods**

**Ethics Statement**

Experiments involving mice were conducted under a UK Home Office licence granted following local ethical review.

**LacZ Expression and In Situ Hybridisation**

Embryos were isolated at e14.5, bisected and assayed for β-galactosidase activity as described previously [10]. Abdominal mammary glands (gland number 4) were isolated from gravid and lactating females, all 10 weeks old and virgins at mating. For lactating females, litters were standardised to seven pups at birth. Glands were mounted on APTS-subbed slides, fixed for 2 hours in 2% (w/v) paraformaldehyde (PFA), 0.01% (v/v) glutaraldehyde, 0.01% (w/v) Igepal CA-630 in 0.1× PBS, and further fixed for 2 hours in 2 mM MgCl2, 0.01% (w/v) sodium deoxycholate, 0.02% (v/v) Igepal CA-630 in 0.1× PBS. Glands were incubated in X-gal as described for embryos for 18 hours at 28°C. Glands were cleared in acetone for 6.5 hours, dehydrated through an ascending ethanol series and stored in xylene. The ascending ethanol series and stored in xylene.

**Enhancer Analyses**

ExactPlus [40] was used to detect sequence conservation among Grb10 homologs, obtained from the UCSC Genome Browser. The minimum length of exact match to seed was 6 bp; the minimum number of species to seed was equivalent to the number for that alignment; and the minimum number of species to extend a hit was 2. Murine Grb10 exons were excluded from the alignment. 15 bp of intronic sequence flanking each exon were also excluded to eliminate conserved splice recognition sequences. Custom tracks were submitted to the UCSC Genome Browser. The genomic sequence of murine Grb10 was submitted to PreMod [19] for analysis.

**DXA**

A subset of animals from the growth studies were analysed by dual-emission X-ray absorptiometry (DXA) (PIXImus scanner, Lunar) [12]. For Figure 4A–4C, animals were analysed at day 17: +/+ born to +/+ raised by +/+ (three litters); +/+ born to +/+ raised by +/+ (three litters); +/+ born to m/+ raised by m/+ (three litters); m/+ born to m/+ raised by m/+ (three litters); m/+ born to m/+ raised by m/+ (three litters); m/+ born to m/+ raised by m/+ (three litters); m/+ born to m/+ raised by m/+ (three litters). Figure 4D: +/+ raised by biological +/+ dam, n = 20 pups (three litters); +/+ raised by nurse +/+ dam, n = 31 pups (five litters). Pups were culled on postnatal days 15 or 17, and genotyped following tissue biopsy [11].
overnight in 4% PFA (w/v) in PBS, dehydrated and sectioned at and surface areas measured using ImageJ. Glands were fixed were spread across APTS-subbed slides, photographed on grids and three fields per sample were used.

**Gene-Trap Cassette Mapping**

Southern blots and PCR were performed using standard protocols. Primer sequences are available upon request.

**Allele-Specific Expression of Grb10**

RNA isolation from day 1 neonatal tissues, cDNA synthesis, PCR, and sequencing were performed as described previously [44]. 30 cycles of amplification were used with forward (5’-GCCTGGACCTCTGGTGAACAGC-3’) and reverse (5’-GGCA-CAGATACAGCTTCTTC-3’) primers.

**Immunofluorescence**

WT and Grb10KO+/+ abdominal glands were isolated from females 48 hours after a forced wean at day 15 of lactation. All females were 7 weeks old and virgins at mating. The litter size of all females was normalised to 7 pups on the day of birth. Glands were sectioned and fixed as described for haematoxylin and eosin staining. Immunofluorescence was performed essentially as described [45], using the following antibodies: CK14 (L1002, Abcam), CK18 (Ks 18.04, Progen Biotechnik), Alexa555-conjugated goat anti-mouse IgG1 cross-adsorbed (Invitrogen), and Alexa488-conjugated goat anti-mouse IgG3 cross-adsorbed (Invitrogen). Sections were counter-stained with DAPI. Images were taken using a Zeiss LSM510META confocal laser scanning microscope. Cells were counted by assigning DAPI-stained nuclei as either luminal epithelial- (CK18+) or myoepithelial-associated (CK14+). Counts from three fields were combined for each sample. WT, n = 3; Grb10KO+/+, n = 3.

**Flow Cytometry**

Single cells were prepared from fourth mammary fat pads of mice aged 17–25 weeks, at day 7–10 of gestation, with pregnancy confirmed during harvest of mammary tissue [46,47]. Cell suspensions at 10^6 cells/ml were stained with anti-CD24-FTTC (clone M/69 at 1.0 µg/ml; BD Biosciences), anti-Scal-1-APC (clone D7 at 1.0 µg/ml; eBioscience), anti-CD45-PE-Cy7 (clone 30-F11 at 1.0 µg/ml; BD Biosciences), and anti-CD49f-PE-Cy5 (clone GoH3 at 3.0 µg/ml; BD Biosciences). Cells were sorted at low pressure (20 psi using a 100 µm nozzle) on a FACSArria (Becton Dickerson) equipped with violet (404 nm), blue (488 nm), green (532 nm), yellow (561 nm), and red (635 nm) lasers and using FACSDiva software. There was no intervening culture period between cell isolation, staining, and flow sorting. Mammary epithelial cell subpopulations were defined as in [47].

**Milk and Pituitary Gland Analyses**

At postnatal day 17, nurses used in the cross-fostering study were anaesthetised with an intraperitoneal injection of 0.1% (w/v) xylazine, 0.5% (w/v) ketaset in 0.9% (w/v) NaCl at 16 µl/g mouse. Milk collection was aided by an intraperitoneal injection of 200 µl 10 IU/ml oxytocin (Sigma Aldrich) in 0.1% PBS. A vacuum pump was used to harvest 100–200 µl milk. Milk fat and protein content were analysed as described [46]. After fat removal, protein was diluted 1/5 in 50 mM Tris HCl (pH 8.0), 150 mM NaCl, 1% (w/v) Igepal CA-630, boiled for 10 minutes, and mixed with an equal volume of reducing sample buffer. Samples were run on a 15% Criterion Tris-HCl gel (Bio-Rad Laboratories) alongside pre-stained molecular weight markers. Fixation and drying were performed using standard methods.

After milk collection, nurses were humanely killed by cervical dislocation and pituitary glands harvested. RNA was extracted from pituitaries using TRI Reagent (Sigma Aldrich). Total RNA (1 µg) was DNase-treated with RQ1 RNase-free DNase I (Promega). cDNA was synthesised using random hexamers with SuperScript III RNase H^- Reverse Transcriptase (Invitrogen). Real-time PCR (qRT-PCR) was used to measure expression of prolactin and growth hormone normalised to β-actin. Reactions were performed in duplicate and analysed as described previously [8].

**Supporting Information**

Figure S1 Mapping of the gene-trap cassette integration sites in Grb10KO and Grb10KO2-4. (A) Schematic of the Grb10 gene around exons 6–8 (black boxes). 5’ RACE experiments (unpublished) demonstrated splicing of transcripts from Grb10 exon 6 onto the gene-trap cassette in the Grb10KO allele, and so cassette integration was initially assumed to be within intron 6. The positions of relevant restriction enzyme recognition sequences and probe B (thick black line) are shown. The amplicons generated by primer sets A–C are illustrated by grey lines. The gene-trap cassette, consisting of a 5’-splice donor sequence (SD), a 5’-splice acceptor sequence (SA), 9 LacZ reporter, and 3’ polyadenylation sequence (pA), is shown with dashed lines indicating its integration site at the 5’ end of exon 7. A broken line indicates intronic sequence not shown. Diagram not to scale. (B) Upper panel: Southern blots of BamHI- and PstI-digested genomic DNA from tail clips of a WT (+/+ ) animal and animals heterozygous (+/p) and homozygous (m/p) for the Grb10KO allele, challenged with probe B. A 4.5 kb BamHI digestion fragment was detected for all genotypes indicating that cassette integration occurred downstream of the intron 6 BamHI restriction site. A 6.7 kb PstI fragment was detected in WT and Grb10KO+/+ DNA, but was absent from Grb10KO+/+ DNA. A band of ~10 kb was detected in DNA from animals heterozygous...
and homozygous for the Ghr10KO allele. The gene-trap cassette contains a PstI site ~4.3 kb from the 5′ end, suggesting the integration site is ~5.7 kb downstream of the exon 5 PstI site, close to the 3′ end of exon 7. Lower panel: Primer sets A, B, and C were designed to span the approximate site of cassette integration determined by Southern blotting, to enable finer mapping. PCR was performed on WT and Ghr10KO wt DNA. Primer set B failed to amplify from Ghr10KOMtDNA indicating the site of integration was between the two primers. (C) The forward primer from set B was used with a reverse primer complementary to a sequence within the gene-trap cassette to amplify from Ghr10KOp DNA. The amplicon was cloned and sequenced. Cassette integration (dashed lines) is coincident with the deletion of 11 bp from the 3′ end of exon 7 (bold) and 1 bp from the 5′ end of intron 7. Despite integrating at the 3′ end of exon 7, transcripts initiating upstream splice from exon 6 onto the SA sequence of the gene-trap cassette, as determined by 5′ RACE (unpublished). (D) For Ghr10Δ2-4, the approximate site of integration has been mapped previously by Southern blotting and is coincident with the deletion of ~36 kb of endogenous Ghr10 sequence including exons 2–4 [11]. In the present study, the 5′ end of the deleted sequence was mapped with greater resolution using PCR. A schematic of the Ghr10 gene around exon 2 (black box) is shown. Amplicons generated by primer sets D–H are illustrated by grey lines. CRM1 is indicated by a grey box. The gene-trap cassette integration site is illustrated by dashed lines; the 3′ end of the integration site is downstream of exon 4 (unpublished). (E) Primer sets D, E, F, and G were designed to span the approximate site of cassette integration in Ghr10Δ2-4 determined by Southern blotting (not shown). Primer sets D and E readily amplified from WT and Ghr10Δ2-4 mtDNA, indicating that the sequence spanned by these primers is present in both genotypes. Primer sets F and G amplified from WT, but not Ghr10Δ2-4 mtDNA, indicating that the 5′ end of the deletion lies within the sequence spanned by primer set F. (F) Genomic sequence around CRM1 (bold text) showing its proximity to the 5′ end of the deleted sequence in the Ghr10Δ2-4 allele. The positions of primer sets F and H are indicated. Primer set H amplified from WT and Ghr10Δ2-4 mtDNA (not shown) indicating the 5′ end of the deleted sequence lies between the reverse primer of set H (H rev) and the reverse primer of set F (F rev). Genome coordinates are based on mouse build mm9, and were obtained from the UCSC genome browser.

**Figure S2** Comparative LacZ expression in Ghr10KO+Wt and Ghr10Δ2-4 Wt adult brain sections. Adult brain sections were assayed for β-galactosidase activity for the same duration. At all sites, reporter expression was weaker in Ghr10Δ2-4 Wt than Ghr10KO+Wt sections. (A)/(A′) Expression in the dorsal raphé nucleus (DRN), ventrotemporal nucleus (VTg), and raphé magnus nucleus (Mrn). (B)/(B′) Expression in the ventrotegmental area (VTA) and the substantia nigra pars compacta (SNC) but not the substantia nigra pars reticulata (SNR). (C)/(C′) Expression in the rostral and lateral interpeduncular nucleus (IPR and IPLs, respectively) but not the caudal portion (IPC).

**Figure S3** Sequence analysis of CRM1. (A) The mouse Ghr10 sequence was submitted to PreMot for analysis. A single putative regulatory module of 70 bp (CRM1) was detected, consisting of a number of potential transcription factor binding sites, ranked by relative likelihood scores, calculated by an alignment with consensus sequences in the TransFac 7.2 database. TransFac module codes are presented with transcription factor names on the left hand side. (B) Sequence alignment of CRM1 between four mammalian and one avian species. Potential transcription factor binding sites identified by PreMot are illustrated with brackets. The conserved STAT5 recognition sequences are in bold text.

**Figure S4** Maintenance of Ghr10 imprinting in neonatal tissues. Tissues were isolated from day 1 neonates generated from intercrosses of C57Bl6 (B) and Mus musculus castaneus (C) animals. cDNA was synthesised and amplified using primers spanning a single nucleotide polymorphism (SNP) in exon 8 between the two parental strains. Amplicons were sequenced across the SNP to determine the parental origin of the expressed allele. For all tissues examined, neonates generated from a BxC cross (maternal genotype presented first) demonstrated expression exclusively from the maternally inherited allele. This finding was reproduced in tissue samples from the reciprocal cross (CxB), confirming that Ghr10 is maternally expressed in postnatal heart, liver, lung, and tongue.

**Figure S5** Additional postnatal growth data. (A) Growth of WT (+/+ ) and Ghr10KO+Wt pups raised by their biological dams. The graph is reproduced from Figure 3A with the addition of the Ghr10KO+Wt siblings of WT pups born to Ghr10KO+Wt dams (brown line in Figure 3E), illustrating the postnatal catch-up growth of WT siblings in a mixed litter. (B) Growth of WT pups raised by biological WT and nurse WT mothers, as a control for the process of cross-fostering. No weight differences were detected on the day of birth or on the day after cross-fostering (day 2), at which point any effects of pup rejection would be detectable. No differences were detected at the end of the experimental period (day 15). These data confirm that the process of cross-fostering does not influence pup growth. Modelling of the data also confirmed no effect of cross-fostering at days 1, 8, and 15.

**Figure S6** Assessment of mammary gland morphology in Ghr10KO+Wt females. (A) No gross morphological differences were detected between the abdominal mammary glands of WT and Ghr10KO+Wt dams at G7.5, G12.5, and L6 (WT gland images are reproduced from Figure 1C): ad, adipose tissue; teb, terminal end bud; pr, primary branch; se, secondary branch. (B-E) Abdominal mammary glands were isolated at day 5 of lactation from females raising six of their own pups (no cross-fostering). Glands from Ghr10KO+Wt females were compared with those from Ghr10KO+Wt females, which do not show any perturbation of Ghr10 expression in the mammary gland. No significant differences were found for total gland weight (B) or surface area (C), by Student’s t-test. Sectioned glands were assessed for occupancy, size and shape of lumina (D) and adipocytes (E). No significant differences were found using Student’s t-test. Similar experiments were also performed on glands isolated 48 hours after a forced wean, but no statistically significant differences were observed (unpublished).

**Figure S7** Cellular analyses of Ghr10KO+Wt mammary glands. (A) Representative immunofluorescence image of a WT mammary gland section assessed for luminal epithelial and myoepithelial cell occupancy with anti-Ck18 and anti-Ck14, respectively. (B) No significant differences were detected between WT and Ghr10KO+Wt glands for luminal epithelial or myoepithelial cell number, or for the ratio of luminal/myoepithelial cells, assessed by Student’s t-test. (C) Epithelial cell population sizes determined by FACS. Representative scatter plots of unstained control samples and samples from mid-gestation WT and...
Analyses of mid-gestation WT and Grb10KO+/m+ dams stained with antibodies to CD24, Sca-1, and CD49f. Only data from the epithelial cells are shown. Non-epithelial cells were gated out prior to this analysis as described [47]. (D) Percentages of myoepithelial, luminal estrogen receptor negative (ER-) and luminal ER+ cells from two independent analyses of mid-gestation WT and Grb10KO+/m+ mice as gated in (C). Note that the dot plots in (C) correspond to experiment 1. (TIF)

Figure S8 Maternal behaviour and milk letdown in Grb10KO+/m+ females. Behaviour and letdown in Grb10KO+/m+ dams was compared to Grb10KO+/p dams on the day of birth following separation of dam and pups for one hour. (A) Mean pup weight change following separation and reunion, as a measure of milk letdown. Letdown appeared to be greater in Grb10KO+/m+ than Grb10KO+/p dams, and this was significant by Student’s t-test at 1 hour and 3 hours after reunion. (B–E) Upon reunion, pups were placed in a corner of the cage away from the nest. No significant differences were observed in the time taken for the dam to retrieve the first (B) or last (C) pup, or in the time taken to begin nest building (D) or settle on the nest (E). Datasets were compared with Student’s t-test. *p<0.05, **p<0.01. (TIF)

Figure S9 Analyses of nurses used in the cross-fostering study. (A) Milk was isolated from nurses at day 17 of lactation and analysed for protein content by SDS-PAGE. Each lane represents milk protein isolated from a separate dam. No consistent differences were observed between any of the datasets. The molecular weights (MW) of protein standards are indicated, and bands corresponding to some key milk proteins are annotated: WAP, whey acidic protein. (B) Percentage fat content of milk following separation of dam and pups for one hour. (A) Mean pup weight change following separation and reunion, as a measure of milk letdown. Letdown appeared to be greater in Grb10KO+/m+ than Grb10KO+/p dams, and this was significant by Student’s t-test at 1 hour and 3 hours after reunion. (B–E) Upon reunion, pups were placed in a corner of the cage away from the nest. No significant differences were observed in the time taken for the dam to retrieve the first (B) or last (C) pup, or in the time taken to begin nest building (D) or settle on the nest (E). Datasets were compared with Student’s t-test. *p<0.05, **p<0.01. (TIF)

Table S1 Tests of cross-fostering effect. The cross-fostering effect was tested using the same GLMM described in the Materials and Methods. The F tests all have one numerator degree of freedom, so the df column indicates denominator degrees of freedom. (DOC)

Table S2 Pup weight modelled at days 1, 8, and 15. Pup weight was modelled as described in Materials and Methods. Num DF, numerator degrees of freedom. Den DF, denominator degrees of freedom. +/- WT, m+/+, Grb10KO+/m+. Model estimated means were generated using the Least-Squares Means statement in the Mixed Procedure in SAS from the full model. (DOCX)

Table S3 Pairwise tests of differences in pup weights at days 1, 8, and 15 as a function of the genotype of nurse and pup. Rows and columns indicate the pup/nurse genotype combinations being compared. m/+ indicates the Grb10KO+/m+ genotype while +/- indicates the WT genotype, d is the difference in means between the two categories being compared (calculated as the mean of the value indicated by the row combination minus the column combination). The estimated model means being compared are given in Table S2. (DOC)

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Author Contributions

The author(s) have made the following declarations about their contributions: Conceived and designed the experiments: MCo AW. The author(s) have made the following declarations about their contributions: Conceived and designed the experiments: MCo AW. Performed the experiments: MCo ASG MM-S MCh MS JS AB RJF SC KM AW. Analyzed the data: MCo RWC MJS JBW AW. Contributed reagents/materials/analysis tools: LKJ RJO. Wrote the paper: MCo AW.

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