The transcription factor Gli3 promotes B cell development in fetal liver through repression of Shh

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Before birth, B cells develop in the fetal liver (FL). In this study, we show that Gli3 activity in the FL stroma is required for B cell development. In the Gli3-deficient FL, B cell development was reduced at multiple stages, whereas the Sonic hedgehog (Hh [Shh])–deficient FL showed increased B cell development, and Gli3 functioned to repress Shh transcription. Use of a transgenic Hh-reporter mouse showed that Shh signals directly to developing B cells and that Hh pathway activation was increased in developing B cells from Gli3-deficient FLs. RNA sequencing confirmed that Hh–mediated transcription is increased in B-lineage cells from Gli3–deficient FL and showed that these cells expressed reduced levels of B–lineage transcription factors and B cell receptor (BCR)/pre-BCR–signaling genes. Expression of the master regulators of B cell development Ebf1 and Pax5 was reduced in developing B cells from Gli3–deficient FL but increased in Shh-deficient FL, and in vitro Shh treatment or neutralization reduced or increased their expression, respectively.

INTRODUCTION

During B cell development in the fetal liver (FL), hematopoietic stem cells, defined as lineage-negative Sca-1+ c-Kit+ cells, mature to gain expression of IL-7Rα (CD127) and are known as common lymphoid progenitor (CLP) cells (Egawa et al., 2001; Mebius et al., 2001). However, this population is multipotent and still contains cells with potential for both lymphoid and myeloid lineages (Mebius et al., 2001). Commitment to the B cell lineage first occurs on embryonic day 12.5 (E12.5), as cells mature to initially express CD19 or B220 and are defined as either B–1 (CD19+B220lo-neg) or B–2 (CD19+B220hi) lineage cells (Egawa et al., 2001; Dorshkind and Montecinos-Rodriguez, 2007; Montecino-Rodriguez and Dorshkind, 2012). B–1 cell development is more prominent in the FL and fetal BM, whereas B–2 cells are mainly produced in the adult BM (Montecino-Rodriguez and Dorshkind, 2012).

Both B–1 and B–2 progenitors mature into B220+CD19+ double-positive cells, which undergo immunoglobulin heavy chain gene rearrangement to give rise to the first cells that express cell surface μH (pre-BCR; Dorshkind and Montecino-Rodriguez, 2007; Montecino-Rodriguez and Dorshkind, 2012). This pre–B cell population can also be identified by cell surface expression of BP-1, before rearrangement of the light chain locus and cell surface expression of IgM (Hardy and Hayakawa, 2001; Dorshkind and Montecino-Rodriguez, 2007; Montecino-Rodriguez and Dorshkind, 2012).

Here, we investigate the role of Sonic hedgehog (Hh [Shh]) and the transcription factor Gli3 in the regulation of B cell development in the FL. Shh is one of three mammalian Hh proteins (Shh, Indian Hh [Ihh], and Desert Hh [Dhh]) that share a common signaling pathway (Ingham et al., 2011; Ramsbottom and Pownall, 2016). Hh proteins signal by binding to their cell surface receptor Patched1 (Ptc1), thereby releasing Ptc1’s repression of Smoothened (Smo), allowing Smo to transduce the Hh signal. At the end of the signaling pathway are the Hh-responsive transcription factors Gli1, Gli2, and Gli3 (Ingham et al., 2011). Gli1 is itself an Hh-target gene and encodes an activator of transcription (Park et al., 2000), whereas Gli2 and Gli3 can be processed to function as transcriptional activators (Gli2A/Gli3A, in the presence of Hh pathway activation) or transcriptional repressors (Gli2R/Gli3R, in the absence of Hh pathway activation; Sasaki et al., 1999). Gli2 is required to initiate the Hh signal and functions largely as a transcriptional activator in vivo (Park et al., 2000; Bai et al., 2002). In contrast, Gli3 functions predominantly as a transcriptional repressor in vivo (Wang et al., 2000). The pathway has multiple positive and negative feedback mechanisms, and Ptc1 is itself an Hh-target gene, functioning to sequester Hh proteins and limit activation of the pathway (Ingham et al., 2011).

Gli3 can have both Hh-independent and Hh-dependent functions (te Welscher et al., 2002; Hager-Theodorides et al., 2009). Gli3R functions to limit Hh pathway activation in many tissues (Wang et al., 2000; Ahn and Joyner, 2004; Hager-Theodorides et al., 2009). There are at least two distinct mechanisms by which Gli3R can limit Hh signaling: it may...
A significant decrease in the proportion of CD19−viding the CD93+ population by expression of ckit, CD127, staining against the B-lineage marker CD93 and then subdi-

lations (fraction E; Fig. 1 H).

of CD19+ cells that expressed the cell surface heavy chain µH

progenitor cells (Fig. 1, C and E). Additionally, the proportion

Gli3 activity is not required for B cell development in the hematopoietic compartment of the FL

To investigate whether the reduction in B cell development in the Gli3-mutant FL is caused by cell-intrinsic Gli3 activity in the hematopoietic compartment or caused by Gli3 activity in the nonhematopoietic compartment (stroma), we used the Cre-loxP system to conditionally delete Gli3 from the hematopoietic lineage in Gli3fl/flVavCre+ (Gli3coKO) embryos. We found no significant difference in B cell differentiation between the control (Cre negative) and Gli3coKO FL, and the proportion of cells that expressed CD19, B220, and BP-1 was not different between control and Gli3coKO (Fig. 1, J–L). Therefore, Gli3 activity in the FL stroma, rather than hematopoietic cell–intrinsic activity, regulates B cell differentiation.

Increased Hh signaling in the Gli3-mutant FL

As Gli3 can have Hh-independent and Hh-dependent functions and can act to limit Hh pathway activation, we tested whether the Gli3-mutant FL had increased levels of Hh pathway activation by measuring the transcription of Hh pathway components and target genes by Q-RT-PCR from the tissue (Fig. 2, A–D). The Hh-target genes, the transcription factor Gli1, and the Hh receptor Ptc1 were increased in the Gli3−/− FL compared with WT, as was the Hh–responsive transcription factor Gli2 (Fig. 2, A–C). Transcription of Shh was also increased, consistent with Gli3 functioning to repress Shh expression (Fig. 2 D). Then, we FACSorted CD45+CD19+ (B lineage) and nonhematopoietic CD45+ (stroma) cells from Gli3−/− and littermate WT FL and compared expression of Hh pathway components and target genes (Fig. 2, E–H). Expression of Gli1 was higher in nonhematopoietic WT cells than in the CD19− population, and its expression was increased in the Gli3-deficient populations, with greater increase in the nonhematopoietic (stromal) Gli3-deficient compartment (Fig. 2 E). Gli2 expression was approximately fivefold higher in the stromal cells of the Gli3-deficient FL compared with WT and was relatively very low in the CD19− fraction (Fig. 2 F). In contrast, expression of Ptc1 was increased in both populations sorted from Gli3−/− compared with WT FL (Fig. 2 G). Expression of Shh was greatly up-regulated in the nonhematopoietic (stromal) component of the Gli3−/− FL compared with WT, consistent with Gli3 functioning to repress Shh expression in the FL stroma (Fig. 2 H) and with a previous study on expression of Shh by Dlk+ hepatoblasts (Hirose et al., 2009). Although Gli3 and Gli2 can have overlapping or redundant functions in some tissues, we found no evidence for redundancy between Gli3 and Gli2 in repression of Shh expression in the stroma; in the absence of Gli3, Shh was up-regulated.
Figure 1. B lineage development in E18.5 and E17.5 Gli3<sup>+/+</sup>, Gli3<sup>+/−</sup>, and Gli3<sup>−/−</sup> and E17.5 Gli3<sup>fl/fl</sup>Vav<sup>c</sup>re<sup>+</sup> FL. (A–F) Flow cytometry profile of E18.5 FL from Gli3<sup>+/+</sup> (WT), Gli3<sup>+/−</sup>, and Gli3<sup>−/−</sup> littermates after red blood cell lysis from a representative experiment. (A–D) Dot plots: SSC against CD19 (A), SSC against B220 (B), CD19 versus B220 (C), and SSC against μHI gated on CD19<sup>+</sup> cells (D). (E and F) Bar charts: mean percentage of FL populations, relative
Given that transcription of Hh-target genes and Shh were up-regulated in the absence of Gli3, whereas the B cell progenitor populations were reduced, we tested whether developing B cells and stromal cells are undergoing active Hh signaling in the FL. We used Gli binding site (GBS)–GFP-transgenic reporter mice, in which GFP is expressed when activator forms of Gli proteins bind to the GBS in the transgene, to measure active Hh-dependent transcription (Balaskas et al., 2012). Approximately 4% of CD19+ cells expressed GFP in the WT FL (Fig. 2 I), and a higher level of GFP expression of ∼8% and ∼9% was observed in the CD19+B220+ (B-1 progenitors) and CD19+B220+ (B-2 progenitors), respectively (Fig. 2, J–K), suggesting that Hh signaling is higher in cells transitioning from the immature B1 and B2 progenitor stages toward the CD19+B220+ stage. High proportions of nonhematopoietic (CD45−) stromal FL cells (∼57%) and of the epithelial cell adhesion molecule subset of CD45+ FL cells (∼53%) expressed GFP (Fig. 2 L), confirming the Q-RT-PCR data, which indicated that Hh signaling is also active in the nonhematopoietic stromal compartment (Fig. 2, E and G). The proportion of GFP-expressing CD19+, CD19+B220+, and CD19+B220+ cells was significantly increased in the Gli3−/− compared with WT (Fig. 2, I–K and M). However, there was no significant difference in the proportion of GFP+ cells between Gli3+/− and WT (Fig. 2 M).

Hh signaling is a negative regulator of fetal B cell development

The Gli3−/− FL had increased Shh transcription, increased expression of Hh-target genes, and increased GFP expression in developing B cells in the GBS-GFP reporter–transgenic embryos (Fig. 2). Thus, we tested whether increased Hh signaling reduces B cell development in vitro. We assessed B cell populations after 4 d in WT E17.5 FL organ cultures (FLOCs) treated with recombinant Shh (rShh) alone, with recombinant Hh-interacting protein (Hhip [rHhip]; to bind opposite phenotype, with significantly decreased CD19+, B220+, CD19+B220+, and CD19+B220+ populations compared with WT, with the heterozygote showing intermediate proportions (Fig. 4, A and B). The proportion of B lineage–committed CD93+ cells and the proportion of CD93+ cells that were CD19+ were significantly increased in the Shh−/− FL compared with WT (Fig. 4 C). The proportion of CD19+BP1+ (Pre-B) cells was also significantly increased in the Shh−/− E14.5 FL compared with WT (Fig. 4 D).

As expected, the E14.5 Gli3-mutant FL showed the opposite phenotype, with significantly decreased CD19+, B220+, CD19+B220+, CD19+B220+, and CD19+BP1+ populations compared with WT littermates (Fig. 4, E–G). Treatment with E14.5 Shh−/− FLOCs with rShh for 4 d reduced
Figure 2. Expression of Hh pathway components and active Hh signaling in E14.5 and E17.5 WT and Gli3-mutant FL. (A–H) Bar charts: Representative experiments show mean ± SEM (n = 3) of Q-RT-PCR analysis from WT, Gli3+/−, and Gli3−/− littermates for whole FL Gli1 (A), Gli2 (B), and Ptch1 (C) on E17.5 and Shh on E14.5 (D) and for FACS-sorted CD19+ and CD45− (stromal) cells for Gli1 (E), Gli2 (F), Ptch1 (G), and Shh (H). au, arbitrary units. (I–M)
the proportion of CD19+ cells compared with the untreated control FLOCs (Fig. 4 H), confirming that Shh negatively regulates B cell development.

As Shh inhibited B cell development in B-committed populations, we investigated the impact of Shh deletion and Gli3 deletion on the development of CLPs. We analyzed the proportion of CLPs, defined by the surface markers Lin−CD117−CD127−, and found a significant increase in the CLP population in the Shh-deficient FL and decrease in the Gli3-deficient FL, relative to their WT littermates (Fig. 4 I). Collectively, our experiments indicate that Gli3 and Shh influence B cell development from the CLP populations through to the CD19+B220+ pre-BCR+ stage of development.

**Conditional deletion of Shh from the hematopoietic compartment of the FL does not increase B cell development**

To investigate whether the increase in B cell development in the E14.5 Shh−/− FL is caused by cell-intrinsic loss of Shh expression in the hematopoietic compartment or caused by loss of Shh secretion by the nonhematopoietic compartment (stroma), we used the Cre-loxP system to conditionally delete Shh from the hematopoietic lineage in Shhfl/flVavCre+ (ShhcoKO) embryos. We found no significant differences in B cell differentiation between the control (Cre negative) and ShhcoKO E14.5 FL and no significant differences in the proportions of cells that expressed CD19, B220, and BP-1 and in the proportion of CLPs between control and ShhcoKO (Fig. 5, A–C). We likewise found no significant differences in B cell populations defined by cell surface expression of CD19, B220, and μH on E16.5 and E18.5 and no significant difference in the proportion of CLPs on E18.5 between ShhcoKO and WT (Fig. 5, D–H). Therefore, it is Shh expression by the FL stroma, rather than hematopoietic cell–intrinsic Shh expression, that regulates B cell differentiation. This is consistent with the increase in Shh expression observed in the Gli3−/− FL stroma compared with WT (Fig. 2 H) and with the fact that conditional deletion of Gli3 from the hematopoietic compartment has no influence on B cell differentiation (Fig. 1, J–L). Collectively, these experiments indicate that Gli3 activity in the FL stroma promotes B cell development by repression of Shh expression in the stroma.

**Gli3 mutation inhibits transcription of B cell–lineage commitment, signaling, and maturation genes**

To investigate the mechanisms of action of Gli3 on B cell development, we measured transcription in developing B cells in the Gli3-mutant FL. We used RNA sequencing to analyze whole-genome expression in FACS-sorted CD19+B220+ FL B cells in the WT and Gli3 mutants. First, we analyzed the dataset in an unbiased manner using principal component analysis (PCA). The dataset segregated by genotype on both principal component axis 1 (PC1) and PC3 (Fig. 6 A). PC1, the axis attributing to the largest differences in the dataset (60% variability), separated the WT from the Gli3 mutants (Gli3+/- and Gli3−/−), whereas PC3 showed differences between Gli3+/- and Gli3−/− (Fig. 6 A).

Further analysis of the genes with high positive and negative scores on PC1 showed that PC1 reflected differences in genes associated with Hh signaling and genes associated with B cell signaling and differentiation. Key Hh signaling and target genes, including Gli1, Hdac3, and Smo, had positive PC1 scores, indicating that the expression of these is higher in the Gli3 mutant. In contrast, genes that were lower in the Gli3 mutants had high negative PC1 scores and were mainly B cell–signaling and –lineage commitment genes. Thus, not only did Gli3 mutation reduce the proportion of CD19+B220+ B-committed cells in the FL, but also, within that sorted population, expression of genes required for B cell differentiation was reduced.

To understand better the genome-wide differences in the dataset, we intersected the differentially expressed genes identified by Ebayes statistics with the genes identified by PCA. We selected the 3,000 genes (highest and lowest scorers) that contributed most to the PC1 axis and intersected these with the 3,000 most significantly differentially expressed genes by Ebayes statistics (Table S1). The resulting 1,122 genes were clustered, and a heat map showing their gene expression was drawn (Fig. 6, B and C). This intersection highlighted genes that have been previously shown to be Shh–target genes in other tissues, such as Stmn1, Hngb1, Hngb2, Hoxa4, Cul4a, and Bmi1, which were all up-regulated in the Gli3 mutant (Fig. 6 C; Itou et al., 2011; Wang et al., 2012; Lu et al., 2015; Yang et al., 2015). In contrast, master regulators of early B cell development Ebf1 and Foxo1 were down-regulated in the Gli3 mutants compared with WT, and several other B lineage differentiation and maturation genes, including Klf13, Egr1, Irf1, Irf4, and Cdx69, were also lower in the Gli3 mutant (Gururajan et al., 2008; Lu, 2008; Outram et al., 2008). B cell activation and signaling genes including genes involved in modulating MAPK signaling such as Dusp1, Dusp2, Map3k3, MapKapk2 (Lang et al., 2006), and canonical NF-κB signaling genes (Nkbid, Nkbiz, and Tafap3) were all down-regulated in the Gli3 mutant. In addition, the AP1
components *Fosb, Jun*, and *Junb*, required for pre-BCR signal transduction (de Gorter et al., 2007), and *Klf2*, an essential late target gene of the pre-BCR, were also lower in the *Gli3* mutant (Winkelmann et al., 2014).

As both pre-BCR/BCR signaling and IL-7 signaling are important regulators of B cell development, we compared expression levels of genes that encode downstream components of these signaling pathways or are their immediate tran-

Figure 3. Modulation of B cell development by rShh and rHhip treatment of WT and *Gli3*−/− FLOCs. (A–E) WT E17.5 FLOCs were treated with recombinant proteins, as stated, for 4 d and analyzed by flow cytometry. n = 4. (A) Dot plots: SSC versus CD19 staining in control (untreated) and treated with rShh, rHhip, and rShh + rHhip. (B) Bar charts: mean ± SEM, relative to the mean of control untreated FLOCs from littersmates, showing statistical significance by Student’s t test compared with untreated for CD19+ cells (rShh treatment, P = 0.002; rHhip treatment, P = 0.04; left), and CD19+B220+ cells (rShh treatment, P = 0.002; rHhip treatment, P = 0.04; right). The dotted line indicates mean of untreated control WT. (C) Dot plots: µH+ gated on the CD19+ population in control (untreated) and treated with rShh, rHhip, and with rShh and rHhip together. (D) Bar chart: mean ± SEM, relative to the mean of control untreated FLOCs showing statistical significance by Student’s t test compared with untreated for µH+ gated on the CD19+ population (rShh treatment, P = 0.03). The dotted line indicates mean of untreated control WT. (E) *Gli3*−/− FLOCs treated with rHhip and control untreated *Gli3*−/− FLOCs were cultured for 4 d. Dot plots: SSC versus CD19 staining. Differences in the mean percentages were statistically significant between rHhip treatment and control untreated. P = 0.02 for CD19+ cells, and P = 0.03 for CD19+B220+ cells. *, P ≤ 0.05; **, P ≤ 0.01.
Figure 4. **B cell development in the E14.5 Shh-deficient and Gli3-deficient FL and Shh+/− FLOC.** (A–D) Flow cytometry of E14.5 FLs from Shh+/+ (WT), Shh+/−, and Shh−/− littermates. (A) Dot plots: SSC against CD19 staining (top) and CD19 staining against B220 staining (bottom). (B) Bar charts: relative mean percentage ± SEM, relative to the mean of WT littermates for Shh−/− (n = 7), Shh+/− (n = 10), and WT (n = 4) of populations stated, showing...
consistent with the Q-RT-PCR showing Shh up-regulation in the transcriptional targets of IL-7 signaling in B-lineage cells; Fig. 6E). We did not detect Shh expression in any dataset (Fig. 6E), consistent with the Q-RT-PCR, showing Shh up-regulation in Gli3+/− FLs being restricted to stromal cells and not B-lineage cells (Fig. 2H) and with the fact that conditional deletion of Shh from B-lineage cells had no impact on their development (Fig. 5).

Together these analyses indicate that the Gli3-mutant B220+CD19+ population has increased Hh-dependent transcription, consistent with our previous results showing increased Shh transcription in the Gli3-mutant FL stroma (Fig. 2H) and increased Hh signaling in Gli3+/− B-lineage cells (Fig. 2, G, I–K, and M). Gli3 deficiency also decreased transcription of genes required for B cell differentiation, maturation, and signaling within the sorted B220+CD19+ population. Thus, increased Shh signaling reduced transcription of regulators of B lineage commitment and differentiation. Therefore, we investigated whether Shh treatment can directly down-regulate transcription of the key B-lineage transcription factors Ebf1 and Pax5 in vitro.

Shh signaling leads to reduced Ebf1 and Pax5 expression during B lineage development

Ebf1 and Pax5 are master regulators of B-lineage commitment and B cell development. B cell-lineage commitment from the CLP stage is regulated by Ebf1 (Zhang et al., 2003), which promotes its own transcription as well as Pax5 transcription. Pax5 further increases Ebf1 transcription (Roessler et al., 2007) creating a positive feedback loop between itself and Ebf1. This mechanism allows Ebf1 and Pax5 to regulate B cell development and maturation. Therefore, we tested whether the increase in Shh in the Gli3 mutant influences Ebf1 and Pax5 expression during B cell development.

First, we measured overall Ebf1 and Pax5 transcription in the Gli3-mutant E17.5 FL and found a reduction in both Gli3+/− and Gli3−/− relative to WT (Fig. 7A), consistent with the RNA sequencing data and the reduction in B cell development. In contrast, we found an increase in the expression of both transcription factors in the Shh+/− and Shh−/− E14.5 FL, consistent with increased commitment to the B lineage in the absence of Shh (Fig. 7A).

Because the Gli3 mutant has increased Shh signaling and rShh treatment decreased the CD19+ population in FLOCs, we tested whether we could influence both Pax5 and Ebf1 transcription and protein expression in vitro by modulating Hh signaling in FLOCs by treatment with rShh or rHhip over a 4-d culture period. We measured the expression of intracellular Pax5 and Ebf1 by FACS analysis to investigate protein expression in single cells. On day 1 after treatment, there were no significant differences in the proportions of Ebf1+Pax5+ and Ebf1+Pax5− cells (not depicted). However, a significant reduction in the proportion of Ebf1+Pax5+ cells was seen on days 2 and 4 of rShh treatment (Fig. 7B). This Ebf1+Pax5+ population significantly increased and was sustained in the rHhip-treated cultures, whereas the cultures in which both rShh and rHhip were added together were not different from the control cultures (Fig. 7B). Comparison of the ratio of Ebf1+Pax5+ cells to Ebf1−Pax5− cells showed that rHhip treatment increased the ratio by twofold by day 4 in culture, indicating that inhibition of Hh signaling accelerated the transition from Ebf1+Pax5− cell to Ebf1+Pax5+ cell. In contrast, rShh treatment reduced this ratio on both days 2 and 4 of culture, suggesting that Shh signaling repressed the induction of Pax5 and the transition to Ebf1+Pax5+ cell. The changes in the Ebf1 and Pax5 proteins were consistent with the changes in transcription of Ebf1 and Pax5 on day 4 (Fig. 7C). In the Gli3−/− FL, the proportion of Ebf1+Pax5+ cells was reduced compared with WT, consistent with the Q-RT-PCR data (Fig. 7D).

Then, we FACS sorted CD19+ cells from Gli3−/− and WT littermates and analyzed the expression of Ebf1 and Pax5. We observed a decrease in both Ebf1 and Pax5 transcription in purified CD19+ cells from the Gli3-mutant FL compared with WT (Fig. 7E). Interestingly, the decrease in expression...
Figure 5. B cell development in the Shh<sup>fl/fl</sup>VavCre FL. (A–H) Flow cytometry of the E14.5 FL (A–C), E16.5 FL (D and E), and E18.5 FL (F–H) from Shh<sup>fl/fl</sup>VavCre<sup>−</sup> (E14.5, n = 5; E16.5, n = 3; E18.5, n = 5) and Shh<sup>fl/fl</sup>VavCre<sup>+</sup> (E14.5, n = 3; E16.5, n = 5; and E18.5, n = 3) littermates. (A, D, and F) Dot plots: SSC against CD19 staining (left), CD19 staining against B220 staining (middle), and µH staining for D and F (right). (B, E, and G) Bar charts: mean percentage,
of both Ebf1 and Pax5 in the sorted Gli3\(^{-/-}\) CD19\(^+\) cells was more pronounced than the reduction in transcript expression in the unsorted FL and was also greater than the proportional change in the CD19\(^+\) population in the Gli3\(^{-/-}\) FL compared with WT. This was consistent with the action of Shh to reduce B cell development in FLOCs, in which the magnitude of the reduction in Pax5 and Ebf1 transcription was greater than the change in the Ebf1 \(^{\prime}\)Pax5\(^{\prime}\) population (Fig. 7, B and C) and also greater than the magnitude of the change in the overall proportion of B-lineage cells caused by Shh treatment (Fig. 3 A). Thus, Shh treatment in vitro or Gli3 deficiency in vivo not only reduced the proportion of CD19 cells that were present, but also led to a reduction in transcription of the key B-lineage master regulators Ebf1 and Pax5 within the B lineage–committed population, most likely by signaling to up-regulate the transcription of an intermediate transcriptional repressor of Ebf1 and/or Pax5.

To investigate the relationship between Hh-mediated transcription and the reduction in transcription of Ebf1 and Pax5, we measured intracellular Ebf1 and Pax5 expression in rShh-treated and control untreated GBS-GFP–transgenic FLOCs. We found that \(>62\%\) of Ebf1 \(^{\prime}\)Pax5\(^{\prime}\) cells expressed high levels of GFP, indicating that this population actively mediates Hh-dependent transcription, which is therefore compatible with Ebf1 protein expression (Fig. 7 F). These cells are the earliest B cell population that differentiates from the CLP stage (Egawa et al., 2001; Mebius et al., 2001). Interestingly, GFP expression was reduced to \(<0.3\%\) in the later Ebf1 \(^{\prime}\)Pax5\(^{\prime}\) population (Fig. 7 F), indicating that Hh signaling decreases as cells become more mature and that, once Pax5 is expressed, very few cells are undergoing Hh-mediated transcription. This is consistent with Shh signaling acting directly or indirectly to inhibit Pax5 transcription. The Ebf1\(^{-/-}\)Pax5\(^{-/-}\) population was Hh responsive, as expression of GFP in the Ebf1 \(^{\prime}\)Pax5\(^{\prime}\) population was increased on rShh treatment, with the proportion of GFP-negative cells decreasing from \(~38\%) to \(~28\%). In contrast, GFP was not induced by rShh treatment in the Pax5\(^{-/-}\)Ebf1\(^{-/-}\) population during the 2-d culture, and the proportion of GFP-negative cells remained \(>99.7\%\) under both conditions.

Collectively, our experiments indicate that the Gli3-mutant FL had increased Hh signaling resulting in decreased B cell development. Furthermore, loss of Shh in vitro and in vivo led to increased B-lineage commitment and development. We propose that Shh signaling either directly or indirectly represses Pax5 expression (most likely by transcriptional activation of a transcriptional repressor of Pax5) and that this leads to loss of Pax5’s induction of Ebf1, reduction in both Pax5 and Ebf1 expression, and therefore to the negative regulation of the B lineage development observed.

**DISCUSSION**

Here, we showed that Gli3, expressed by the stromal compartment, is required for B cell development in the FL. Mutation of Gli3 led to an overall reduction in B lineage–committed cells, reduction in the proportion of pre-B cells, and reductions in CLPs and both the CD19\(^{\prime}\)B220\(^{-/-}\) B1 progenitor population on E14.5 and the CD19\(^{\prime}\)B220\(^{-/-}\) B2 progenitor population on E17.5. Gli3 mutation additionally reduced expression of B lineage–specifying and –signaling genes within the B220\(^{-/-}\) CD19\(^+\) population, indicating that the effect of Gli3 mutation is not entirely caused by its influence on CLPs and the earliest B cell progenitors but that it continues to influence the more mature B lineage–committed population. The changes in B cell differentiation in the Gli3-mutant FL could be caused by Hh–dependent or Hh–independent effects. We found that loss of Gli3 led to increased Shh expression and overall increased Hh signaling in the mouse FL. Thus, Gli3 was acting as a repressor of the Hh pathway in the FL, as observed in the development of other cells and tissues, such as the neural stem cells, vertebrate limb bud, and thymus (te Welscher et al., 2002; Hager-Theodorides et al., 2009; Petrova et al., 2013; Saldaña et al., 2016). Treatment of Gli3-deficient FLOCs with rHhip (to neutralize endogenous Hh proteins) increased B cell development, and therefore, the reduction in B cell development in the Gli3 mutants was Hh dependent and caused by increased Shh expression in the Gli3\(^{-/-}\) FL.

In contrast, the Shh–deficient FL had increased B lineage commitment and B cell differentiation, demonstrating that Shh negatively regulates B cell development in vivo. We showed that both Shh transcription in FL stroma and Hh signaling to B-lineage cells are increased in the Gli3–deficient FL and that Shh negatively regulates B cell development by signaling directly to developing hematopoietic cells, as Hh–target genes were up-regulated in the Gli3\(^{-/-}\) CD19\(^{\prime}\)B220\(^{-/-}\) population, and the Hh-reporter transgenic FL showed increased GFP expression in the Gli3\(^{-/-}\) CD19\(^+\) population.

Expression of the master regulators of B cell development, Ebf1 and Pax5, was reduced in the Gli3–deficient FL but increased in the Shh–deficient FL, and treatment of WT FLOCs with Hhip to neutralize endogenous Hh molecules in the cultures increased the proportion of Ebf1 \(^{\prime}\)Pax5\(^{\prime}\) cells and increased transcription of both Ebf1 and Pax5 within the CD19\(^+\) population, whereas rShh treatment had the opposite effect. The Ebf1 \(^{\prime}\)Pax5\(^{\prime}\) population showed high Hh–mediated transcription in the Hh-reporter transgenic FL, and therefore, we proposed that Shh signaling within the Ebf1 \(^{\prime}\)Pax5\(^{\prime}\) cells reduced expression of Pax5, thereby also reducing the Pax5–dependent induction of Ebf1 expression, leading to an overall reduction in B cell development.

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relative to mean of WT littermates \(\pm\) SEM of the B220\(^+\), CD19\(^+\), CD19\(^{\prime}\)B220\(^{-/-}\), CD19\(^{\prime}\)B220\(^{-/-}\), CD19\(^{\prime}\)BP-1\(^{-/-}\), and CD19\(^{\prime}\)µH\(^{-/-}\) populations. (C and H) Bar charts: mean percentage \(\pm\) SEM of Lin\(^{\prime}\)CD117\(^{-/-}\)CD127\(^{-/-}\) CLPs. There were no significant differences by Student’s t test. Shaded bars are Cre\(^{-/-}\), and unshaded bars are Cre\(^{\prime}\).
**Figure 6.** RNA sequencing detects transcriptional differences in Hh signaling genes and B cell differentiation and signaling genes between the WT and Gli3-mutant CD19^+^B220^+^ cells. (A) PCA showing sample relationships in PC1 and PC3 for WT (n = 2), Gli3^+/−^ (n = 2), and Gli3^−/−^ (n = 2) CD19^+^B220^+^ populations from E17.5 FLs. (B) Venn diagram: 1,122 genes intersect out of the 3,000 genes that contributed most to PC1 (highest and lowest scoring genes) and the 3,000 most significant differentially expressed genes by Ebayes statistics. (C) Gene expression heat map showing Hh signaling genes in blue and B cell differentiation and signaling genes in black. Normalized expression signals are represented as a z score where green is lower expression and red is higher expression levels. (D and E) Transcript expression (reads per million kilobases) of pre-BCR/BCR signaling and target genes (D) and Shh, IL-7, and IL-7/thymic stromal lymphopoietin (TSLP) signaling and target genes (E) in the Gli3^−/−^ (green; n = 2) and WT (blue; n = 2) RNA sequencing datasets.
Figure 7. Expression of Pax5 and Ebf1 in the FL. (A) Representative experiment showing mean ± SEM (n = 3) of Q-RT-PCR for Pax5 and Ebf1 in FLs from Gli3 and Shh mutants compared with WT littermates. au, arbitrary units. (B and C) WT FLOCs (n = 3) were treated with rShh, rHhip, and rShh + rHhip for 2 and 4 d, compared with untreated control cultures, and analyzed by flow cytometry and Q-RT-PCR. (B) Dot plots: anti-Ebf1 and anti-Pax5 staining on day 2 (top) and day 4 (bottom). Charts: ratio of Ebf1+Pax5+ to Ebf1+Pax5− cells in the different culture conditions on day 2 (top) and day 4 (bottom).
Shh signaling from follicular dendritic cells to B cells in the adult spleen has been shown to promote B cell survival and function (Sacedón et al., 2005), and in the adult BM, components of the Hh signaling pathway are expressed in developing B cells (Heng et al., 2008; Cooper et al., 2012). However, conditional deletion of Smo from the B cell lineage did not influence B cell development in the adult BM (Cooper et al., 2012). Our study demonstrates that the Hh signaling pathway is active in developing fetal B cells and regulates B cell development in the FL. Therefore, there may be tissue- or life stage–specific differences in the function of Hh signaling between FL and adult BM. Alternatively, it is possible that Hh pathway activation is noncanonical (Smo independent) in B-lineage cells, which do not have primary cilia, or that a balance between canonical and noncanonical signaling may exist, as described in osteoblast differentiation (Yuan et al., 2016).

Our genome-wide RNA sequencing data from the sorted CD19^{+}B220^{+} population in the Gli3 mutants revealed many differentially expressed genes between Gli3^{+/−} and WT. Many Hh-target genes (e.g., Stmn1, Hdac3, Hoxa4, Hmgb2, Bmi1, and Cull4a) were up-regulated in the Gli3 mutants, consistent with the increased Hh-mediated transcription measured using the GBS-GFP reporter and confirming that Shh signals directly to developing B cells.

In contrast, many B cell signaling pathway genes involved in NF-κB activity (Nkbtid, Nkbtiz, and Tnaiap3), MAPK signaling (MapKapk2 and Map3k3), and components of AP-1 (Junb and Fosb) were decreased in the Gli3 mutant. These pathways are required for pre-BCR and BCR signaling (Feng et al., 2004; de Gorter et al., 2007). In addition, Tnaiap3 regulates marginal zone and B1 cell development in the adult (Chu et al., 2011), and we observed a reduction in B1 progenitor cells in the E14.5 Gli3^{−/−} FL. Interestingly, Hh-mediated transcription in developing and mature T cells also represses expression of genes that regulate activity of NF-κB, MAPK, and AP1, leading to reduced pre-TCR and TCR signaling (Rowbotham et al., 2007, 2009; Furmanski et al., 2012, 2015; Barbarulo et al., 2016).

In addition to the decreased transcription of genes associated with pre-BCR and BCR signaling, the RNA sequencing revealed a significant decrease in key transcriptional regulators of B cell differentiation including Ebf1, Foxo1, Runx1, and Irf4 (Dengler et al., 2008; Niebuhr et al., 2013). Ebf1 is required from the early CLP stage to the late mature stages of B cell development (Roessler et al., 2007; Nechanitzky et al., 2013) and, importantly, activates transcription of another key master regulator of B cell development, Pax5. Then, Pax5 promotes Ebf1 transcription, creating a positive feedback loop, which supports all stages of B cell development (Roessler et al., 2007).

We found high Hh pathway activity (measured by GFP expression in the Hh-reporter embryo) in Ebf1^{+}Pax5^{+} cells, but GFP expression ceased in the next Ebf1^{+}Pax5^{+} population. Both Ebf1 and Pax5 protein and gene expression were reduced by rShh treatment and increased by neutralization of Hh proteins by rHip treatment in FLOCs, and manipulation of Hh signaling influenced the transition from Ebf1^{+}Pax5^{−} to Ebf1^{+}Pax5^{+} cell. Therefore, we propose that Shh signaling to developing B cells functions to reduce Pax5 expression, which then breaks the positive feedback loop, leading to reduction in Ebf1 expression. Interestingly, Shh signaling has been shown to interact with and regulate other Pax family members in the development of other tissues (Chi and Epstein, 2002; Blake and Ziman, 2014).

Dysregulated Hh pathway activation is involved in some B cell malignancies (Dierks et al., 2007; Lin et al., 2010), including B cell acute lymphoblastic leukemia (B-ALL; Ramirez et al., 2012; Qu et al., 2013), a common cancer of early childhood, and microarray expression profiles show that Hh pathway components are expressed in human FL and BM (Fig. S1 A; Su et al., 2004). Understanding the function of Hh signaling in normal fetal B cell development and its effect on Pax5 and Ebf1 expression will be important to our understanding of its role in B-ALL. In the future, it will be important to investigate how dysregulated Hh signaling influences Pax5 and Ebf1 activity in B-ALL.

In summary, we show that Gli3 activity in the FL stroma is required for normal B cell development. We showed that Shh signaling directly to B-lineage cells negatively regulates their development.

**MATERIALS AND METHODS**

**Mice**

C57BL/6 mice were purchased from Envigo. GBS-GFP–transgenic (GBS-GFP-tg) mice were provided by J. Briscoe (Crick Institute, London, England, UK; de Boer et al., 2003), and Shh^{fl/fl} mice by P. Beachy (Stanford University School of Medicine, Palo Alto, California; Chiang et al., 1996) and were backcrossed for >12 generations on C57BL/6 mice. Gli3^{+/−} mice were provided by J. Briscoe (Crick Institute, London, England, UK; de Boer et al., 2003), and Shh^{fl/fl} mice by P. Beachy (Stanford University School of Medicine, Palo Alto, California; Chiang et al., 1996) and were backcrossed for >12 generations on C57BL/6 mice. Gli3^{+/−}, Shh^{fl/fl}, and Gli3^{+/−} mice on C57BL/6 background were purchased from The Jackson Laboratory. Time mates were obtained by mating overnight, and the next day was counted as E0.5. Mice were bred and maintained at University Col-

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(C) Bar charts: representative experiment showing mean ± SEM (n = 3) of Q-RT-PCR for Pax5 and Ebf1 on day 4 of WT FLOCs treated with rShh or rHip and control untreated. (D) Dot plots: anti-Pax5 and anti-Ebf1 staining in Gli3^{−/−} and Gli3^{+/−} littermate FLs. (E) Representative experiment showing mean ± SEM (n = 3) of Q-RT-PCR for Pax5 and Ebf1 in purified CD19^{+} cells from Gli3^{−/−} and Gli3^{+/−} E17.5 FLs. All transcript expression levels were normalized relative to HpRt. (F) Histograms: GFP expression in Ebf1^{+}Pax5^{−} and Ebf1^{+}Pax5^{+} cells in the E17.5 GBS-GFP–transgenic FLOCs, control (continuous lines), and rShh treated (dotted lines) FLs, cultured for 2 d.
le College London under UK Home Office regulations, and experiments were approved by the University College London ethical approval committee.

**Flow cytometry, antibodies, and cell purification**

FL cell suspensions were made by crushing each FL between two frosted slides. Where stated, red blood cells were lysed using 1× RBC lysis buffer (eBioscience) according to the manufacturer’s instructions. Cells were stained as described previously (Hager-Theodorides et al., 2005) using directly conjugated antibodies from BD, BioLegend, and eBioscience. Data were acquired on a C6 Accuri flow cytometer (BD) and analyzed using FlowJo software (Tree Star). Live cells were gated by forward scatter and side scatter (SSC) profiles. The data represent at least three experiments. In some experiments, CD19+ cells were purified using the EasySep biotin magnetic bead positive selection kit (STEMCELL Technologies) according to the manufacturer’s instructions, and RNA was extracted for Q-RT-PCR analysis.

**FLOs**

FLs were extracted from embryos at different stages of development. They were cut into ∼1-mm cubes and cultured on 0.8-µm filters (EMD Millipore) in 1 ml of AIM-V serum-free medium (Invitrogen) in 24-well plates for up to 4-d at 37°C and 5% CO2 before analysis. In some experiments, rHhip (Sigma-Aldrich) or rShh (R&D Systems) was added at 1 µg/ml. To allow comparison between litters for statistical analysis, relative numbers or percentages for each genotype or treatment were calculated by dividing by the mean of controls from the same litter (untreated control or WT littermates).

**RNA sequencing and data analysis**

FL from WT, Gli3+/−, and Gli3+/− embryos (n = 2) were dissected on E17.5 and crushed between two frosted slides. The cell suspension was stained using the antibodies CD19-APC and B220-PECy7, and the double-positive B220+CD19+ population was FACS sorted. RNA from this population was extracted using an Arcturus PicoPure RNA Isolation kit (Applied Biosystems), and quantity and quality were determined by a Bioanalyzer 2100 (Agilent Technologies).

RNA sequencing data were sequenced by University College London Genomics on a NextSeq 500 system (Illumina). The sequenced data are publically available in the GEO database under accession no. GSE81467. The RNA sequencing dataset was processed and standardized using the Bioconductor package DESeq2. The Bioconductor package DESeq2 was used to generate normalized estimates of transcript abundance, expressed as RPKM (reads per kilobase of transcript per million mapped reads). Differentially expressed genes were determined using the moderated Ebayes t statistic P < 0.05 from the limma package in Bioconductor. PCA was performed using the CRAN package ade4.

**Q-RT-PCR**

RNA extraction and cDNA synthesis were performed as described previously (Sahni et al., 2015). We used the QuantiTect primers for Gli1, Gli2, Shh, Hhip, Gli3, Smo, Ptc1, Ebf1, and Pux5 from QIAGEN. The cDNA samples were prepared using the qZ SYBR Green Supermix (Bio-Rad Laboratories) according to the manufacturer’s instructions and run on an iCycler system (Bio-Rad Laboratories). Gene transcript levels were normalized relative to HPRT.

For quantification of VH to JH rearrangements, we prepared RNA from FAC-sorted CD19+ cells from Gli3+/− and WT E17.5 FL and followed the protocol described by Braikia et al. (2014), using the primers combinations: VH7183-Fw and JH11R; VHJ558-Fw and JH11R; and HS5-Fw1 and HS5-R1 for normalization.

**PCR analysis for genotyping**

DNA for PCR analysis was extracted from tissues by digesting in lysis buffer containing 50 mM KCl, 1.5 mM MgCl2, 10 mM Tris HCl, pH 8.5, 0.01% gelatin, 0.45% Nonidet P-40, 0.45% Tween 20, and 0.5 µg/ml proteinase K (Sigma-Aldrich) in water. Approximately 1 µg DNA was used as a template in each PCR reaction, using primers for Shh−/−, Shh+/−, and Shh+/+ as described by Shah et al. (2004). Gli3+/−, Gli3+/+, and Gli3−/− were distinguished phenotypically (Johnson, 1967), and genotype was confirmed by PCR as previously described (Hager-Theodorides et al., 2005). Gli3+/−, Shh+/−, and Vav-iCre-tg mice were genotyped as previously described (Saldaña et al., 2016).

**Statistical analysis**

Statistical analysis was performed using unpaired two-tailed Student’s t-tests, and probabilities were considered significant if P ≤ 0.05 (*), P ≤ 0.01 (**), or P ≤ 0.001 (***)

**Online supplemental material**

Fig. S1 represents the transcript expression of Hh pathway members (GLI1, GLI2, GLI3, PTC1H1, SMO, and SHH) in the human BM and FL and shows transcript expression of Hh molecules (Shh, Ihh, and Dhh) and pathway components Gl1, Gl2, Gl3, Ptc1, and Smo from the ImmGen database in mouse FL. Table S1 is available as an Excel file and contains a list of 3,000 differentially expressed genes, significant by Ebayes statistics, 1,500 genes with high positive PC1 scores, and 1,500 genes with high negative PC1 scores.

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The authors declare no competing financial interests.


