Fibulin-1 Binds to Fibroblast Growth Factor 8 with High Affinity

EFFECTS ON EMBRYO SURVIVAL*

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Fibulin-1 (FBLN1) is a member of a growing family of extracellular matrix glycoproteins that includes eight members and is involved in cellular functions such as adhesion, migration, and differentiation. FBLN1 has also been implicated in embryonic heart and valve development and in the formation of neural crest-derived structures, including aortic arch, thymus, and cranial nerves. Fibroblast growth factor 8 (FGF8) is a member of a large family of growth factors, and its functions include neural crest cell (NCC) maintenance, specifically NCC migration as well as patterning of structures formed from NCC such as outflow tract and cranial nerves. In this report, we sought to investigate whether FBLN1 and FGF8 have cooperative roles in vivo given their influence on the development of the same NCC-derived structures. Surface plasmon resonance binding data showed that FBLN1 binds tightly to FGF8 and prevents its enzymatic degradation by ADAM17. Moreover, overexpression of FBLN1 up-regulates FGF8 gene expression, and down-regulation of FBLN1 by siRNA inhibits FGF8 expression. The generation of a double mutant Fbln1 and Fgf8 mice (Fbn1+/−/− and Fgf8−/−) showed haplo-insufficiency (Fbn1+/− and Fgf8−/−) resulted in increased embryonic mortality compared with single heterozygote crosses. The mortality of the FGF8/Fbln1 double heterozygote embryos occurred between 14.5 and 16.5 days post-coitus. In conclusion, FBLN1/FGF8 interaction plays a role in survival of vertebrate embryos, and reduced levels of both proteins resulted in added mortality in utero. The FBLN1/FGF8 interaction may also be involved in the survival of neural crest cell population during development.

Fibulin-1 (FBLN1)5 is a member of a growing family of proteins that includes eight members (1, 2). FBLN1 binds to itself and many extracellular matrix molecules such as fibronectin (FN), nidogen, laminin, and versican (2, 3). FBLN1 has also been reported to regulate adhesion and migration of cells (4). During vertebrate development, FBLN1 is expressed along the paths of migrating neural crest cells (NCC) and by migrating endocardial cushion mesenchymal cells, suggesting that it might be a regulator of cell migrations essential to heart and pharyngeal arch morphogenesis (5–7). FBLN1 has also been shown to suppress the migratory behavior of embryonic mesenchymal cells as well as the motility and directional movement of cancer cells (4, 8, 9). Morphological analysis of FBLN1-deficient embryos showed cardiac abnormalities, which includes a high incidence of double outlet right ventricle and over-riding aorta (7). The spectrum of malformations seen in FBLN1 null mice is consistent with FBLN1 influencing NCC-dependent development of these tissues (7).

Androgen-induced growth factor was identified as the eighth member of the fibroblast growth factor (FGF8) family and is detected only in the testis of adult tissues (10). During development, expression of FGF8 is restricted to embryonic days 9–13 suggesting that the growth factor plays a role during a specific stage of mouse embryogenesis (10, 11). FGF8a and FGF8b, two variants of FGF8 transcript, are expressed in the mid-hindbrain region during development (12). Although the only difference between FGF8a and FGF8b isoforms is the presence of an additional 11 amino acids at the N terminus of FGF8b, these isoforms possess remarkably different abilities to pattern the midbrain and anterior hindbrain (12). To reveal the structural basis by which alternative splicing modulates the organizing activity of FGF8, the crystal structure of FGF8b in complex with the “c” splice isoform of FGF receptor 2 (FGFR2c) was resolved (12).

Neural crest cells are a transient, multipotent, and migratory cell population unique to vertebrates that gives rise to diverse cell lineages, including craniofacial cartilage and bone, smooth muscle, and peripheral and enteric neurons (13). Abnormalities in neural crest development cause conditions such as frontonasal dysplasia, Waardenburg-Shah syndrome, and DiGeorge syndrome (13). FGF8 signaling has been shown to be required for neural crest delamination and migration (14). In the hindbrain, FGF8 deficiency negatively impacts patterning of cranial nerves derived from NCCs (15). FGF8 has also been shown to regulate migration of NCCs as they travel to the caudal pharyngeal arches (14, 16, 17). Neural crest ablation results in overproliferation of secondary heart field cells due to excessive FGF8

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5 The abbreviations used are: FBLN1, fibulin 1; r, recombinant; NCC, neural crest cells; qPCR, quantitative real time PCR; FN, fibronectin; dpc, days post-coitus.
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signaling in the caudal pharynx (18) and elevated expression of FGF8 target genes Erm and Pea3 (19, 20). Inhibition of FGF8 signaling following NCC ablation reversed this phenotype. Studies show that inhibition of FGF8 signaling in the absence of NCC ablation causes under-proliferation of secondary heart field cells, resulting in a shortened outflow tract (18). Additionally, it has been shown that FGF8 acts as a chemotactic and chemokinetic signal for cardiac neural crest cells both in vitro and in vivo (21). Thus, precise levels of FGF8 signaling seem critical for normal outflow tract development and morphogenesis.

Given the similarity of effects of both FBLN1 and FGF8 on NCC migration, this study investigated whether there is a collaborative role during the development of vertebrate embryos. Herein, we report the finding that FBLN1 binds to FGF8 with high affinity and protects it from enzymatic degradation. We also show that FBLN1 and FGF8 double mutant heterozygote embryos show a synergistic effect on mortality compared with either FGF8 or FBLN1 null heterozygote embryos alone.

Results

Binding of FBLN1 to FGF8—We employed an ELISA procedure to test whether FBLN1 binds to FGF8. When plates were coated with FGF8b, and FBLN1 was added in solution phase, the apparent affinity constant ($K_D$) of the interaction was about 20 nM (Fig. 1A). When FBLN1 was coated on the surface and FGF8b was in solution phase, the apparent $K_D$ was about 100 nM but was not saturable due to the propensity of FBLN1 to bind to itself (Fig. 1B). When the surface plasmon resonance technique was used, the association constant ($K_a$) was $3.47 \times 10^4$ M$^{-1}$ s$^{-1}$; the dissociation constant ($K_d$) was $1.71 \times 10^{-3}$ S$^{-1}$, and the affinity constant ($K_D$) was about 50 nM (Fig. 1C).

FBLN1 Protects FGF8b from Enzymatic Degradation—We tested whether preparations of FBLN1 have a detectable activity of FGF8. As shown in Fig. 4A (left panel), detection of FBLN1 preparations with anti-FGF8 monoclonal antibody revealed the presence of two high molecular mass bands at about 120 and 175 kDa (Fig. 4A, arrows). When preparations were re-probed with monoclonal and polyclonal antibodies against FBLN1 (Fig. 4A, middle and right panel), both monomeric and dimeric FBLN1 forms were detected. The high molecular weight complexes detected in Fig. 4A (left panel) were also detected in rFBLN1C or rFBLN1D preparations, purified from HT1080 FBLN1C or FBLN1D-transfected cells.
as shown in Fig. 4B (left panel, arrows). It is possible that FGF8 binds to monomer as well as to the dimer forms of FBLN1. Detection of FGF8 binding to rFBLN1C is much lower than that of rFBLN1D (Fig. 4B, left panel, arrows), which can be due to the masking of the FGF8 epitope by rFBLN1C binding to FGF8 but is not in the case of rFBLN1D binding to FGF8. Re-probing the blot with polyclonal antibodies against FBLN1 (Fig. 4B, left panel) detected the presence of both FBLN1 isoforms C and D. We also tested whether we were able to immunoprecipitate FGF8b using FBLN1-conjugated Sepharose. FBLN1-bound Sepharose immunoprecipitated FGF8b (Fig. 4C, left lanes), although plain Sepharose did not bind any FGF8b (2 right lanes). The apparent decrease in molecular mass of FGF8 when incubated with plain Sepharose is probably due to enzymatic degradation that occurred in some FGF8 preparations during the 18-h incubation.

siRNA Inhibition of FBLN1 Expression Decreases FGF8 mRNA Levels in P19.C16 Mouse Embryonic Teratocarcinoma Cells—We have chosen the mouse embryonic teratocarcinoma cell line P19.C16 to test whether levels of Fbln1 affect Fgf8 expression, which is transiently elevated during differentiation of the cell line. We used quantitative real time PCR (qPCR, Table 1) to detect Fgf8, Fbln1C, and Fbln1D mRNA expression for 5 days after transfection of the cells with Fbln1 siRNA. Transient inhibition of Fbln1 expression reduced Fgf8 mRNA expression (Fig. 5, upper panel). Results indicate that Fgf8 expression was decreased by about 30%, and Fgf8 peak expression was shifted by about ½ day (2 days versus 2½ days, Fig. 5, upper panel). Expression of both Fbln1C and Fbln1D mRNA returned to the levels of control siRNA-transfected cells at day 5 (Fig. 5, middle and lower panel, respectively).

Overexpression of FBLN1C or -1D Induces the Expression of FGF8 in HT1080 Cells—Using qPCR (primers are listed in Table 1), we tested the effect of overexpression of FBLN1C and FBLN1D in stably transfected HT1080 on expression of FGF8. Both FBLN1D and 1C increased the expression of FGF8 by 1.7–2.7-fold, respectively, compared with empty vector-transfected cells when normalized to the amount of FBLN1 expression of each cell line (Fig. 6).

Fgf8 and Fbln1 Co-localized in the Cardiac Outflow Tract of 10.5 dpc Mouse Embryos—Immunohistochemistry was performed to determine the in vivo localization of Fgf8 and Fbln1 (Fig. 7). Previous studies have demonstrated that Fgf8 and Fbln1 are present at developmental time points where cardiac neural crest and anterior heart field cells migrate to and populate the cardiac outflow tract (7, 19). Using histological sections

![FIGURE 2. Placental fibulin-1 protects FGF8b from enzymatic degradation.](image)

![FIGURE 3. Fibulin-1 inhibits activation of FGF8 phosphorylation of ERK1/2.](image)
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from developing mice, hearts were immunostained for Fbln1 (Fig. 7, A and C (green)) and Fgf8 (Fig. 7, A and C (blue)). IgG control sections are depicted in Fig. 7, B and D.

Genotypic Analysis of 4-Week-old Mice from Fgf8/Fbln1 (Fgf8+/− and Fbln1+/−) Heterozygote Cross and Fgf8/Fbln1 Double Heterozygote Cross (Fgf8+/− Fbln1+/− Sibling Cross)—Mice heterozygous for Fgf8 were mated with mice heterozygous for Fbn1 and offspring were genotyped at 4 weeks of age. As shown in Table 2, the number of animals and the expected ratio of double Fgf8/Fbn1 heterozygotes were lower than the predicted Mendelian ratios (16% versus 25%), indicating increased mortality of double heterozygote animals compared with the Fgf8 or Fbn1 heterozygote cross alone. When animals that were heterozygote for Fgf8/Fbn1 were crossed with each other, the expected Mendelian ratio for the double heterozygote was also lower (33% versus 44%, see Table 3). When genotyping was performed on embryos at 10.5, 14.5 (Table 4), 16.5 (Table 5), and 18.5 dpc, the expected Mendelian ratio was lower at 16.5 dpc (Table 5, 20% versus 33%) but not at 14.5 dpc (Table 4, 33% versus 32%), indicating that the mortality in the double heterozygote embryos occurred between 14.5 and 16.5 dpc. All surviving embryos at 16.5 and 18.5 dpc and 4 weeks of age were examined for heart and cranial nerve developmental defects, but none were detected. The absence of any abnormalities in the surviving embryos and adult mice led us to speculate that these abnormalities might be present in the animals that die and were resorbed between 14.5 and 16.5 dpc.

Discussion

In this report, we have investigated whether FBLN1, a known extracellular glycoprotein (7) as well as an intracellular integrin β1-binding protein (22), and FGF8, a known effector of NCC migration (21), associate with each other biochemically and have synergistic effects on embryonic development or survival. Herein, we show for the first time that FBLN1 binds with high affinity to FGF8 and protects it from enzymatic degradation by ADAM17. Additionally, overexpression of FBLN1 stimulates FGF8 mRNA production, although siRNA inhibition of FBLN1 down-regulates FGF8 message. Adult mice at 4 weeks of age that are heterozygote for both Fbn1 and Fgf8 show increased embryonic mortality compared with single heterozygote animals. By examining embryos at different developmental stages (10.5–18.5 dpc), it was determined that loss of double heterozygote animals in utero occurs between 14.5 and 16.5 dpc.

We have previously shown that Fbn1 is expressed along the paths of migrating NCCs (7) and by migrating endocardial...
cushion mesenchymal cells (5, 6, 9), suggesting that it might be a regulator of cell migration essential to heart and pharyngeal arch morphogenesis. Morphological analysis of Fbln1-deficient embryos has also been shown to exhibit cardiac and outflow tract abnormalities, which include a high incidence of double outlet right ventricle and over-riding aorta (7). Fbln1-deficient embryos examined at stages 16.5–18.5 dpc also exhibit hypoplastic thymus with 100% penetrance. This observation further implicates Fbln1 importance in NCC migration due to the fact that the thymus is derived from the third pharyngeal arch (23) and is dependent on neural crest-derived mesenchymal cells.

The extracellular matrix protein FN has also been implicated in affecting migration of NCC populations (24, 25). This role has been shown to be in part through interactions with α5β1 integrin. Conditional β1 integrin gene deletion in NCCs causes severe developmental alterations of the peripheral nervous sys-
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Genotyping of a single heterozygote cross of Fgf8 and Fbln1 mice

Mouse heterozygotes for Fgf8 were crossed with Fbln1 heterozygote mice, and animals were genotyped at 4 weeks of age. The number of animals for the double heterozygote animals was lower than the expected Mendelian ratio as indicated by the boldface number. The \( \chi^2 \) statistics test was used to calculate a \( p \) value to determine significant deviation from normal expected Mendelian genotypic ratios. Animals with a \((-/-)\) genotype for the Fgf8 allele (boldface symbol) were embryonic lethal and were neither expected to survive nor observed and were not included in the calculation. \( \chi^2 \) test was significant at \( \chi^2 = 0.041 \).

Genotype (Fgf8) (Fbln1)  | % expected* | % observed | No. expected* | No. observed
---|---|---|---|---
(+/-) (+/-) | 25% | 28% | 37 | 42
(+/-) (+/-) | 25% | 29% | 37 | 43
(+/-) (+/-) | 25% | 37% | 37 | 39
(+/-) (+/-) | 25% | 16% | 37 | 24
Total | 100% | 100% | 148 | 148

* Data were based on the total number of offspring obtained.

Genotyping of Fgf8/Fbln1 double heterozygote mouse cross

Mouse heterozygotes for both Fgf8 and Fbln1 were crossed together, and animals were genotyped at 4 weeks of age. The number of animals observed for the double heterozygote animals was lower than the expected Mendelian ratio as indicated by the boldface number. The \( \chi^2 \) statistics test was used to calculate a \( p \) value to determine significant deviation from normal expected Mendelian genotypic ratios. Animals with a \((-/-)\) genotype for the Fgf8 allele (boldface symbol) were embryonic lethal and were neither expected to survive nor observed and were not included in the calculation. \( \chi^2 \) test was significant at \( \chi^2 = 0.010 \).

Genotype (Fgf8) (Fbln1)  | % expected* | % observed | No. expected* | No. observed
---|---|---|---|---
(+/-) (+/-) | 12% | 15% | 21 | 28
(+/-) (+/-) | 22% | 26% | 43 | 50
(+/-) (+/-) | 22% | 26% | 43 | 51
(+/-) (+/-) | 44% | 33% | 86 | 64
Total | 100% | 100% | 193 | 193

* Data were based on the total number of offspring obtained.

Genotyping of Fgf8/Fbln1 double heterozygote mouse cross

Mouse heterozygotes for both Fgf8 and Fbln1 were crossed together, and animals were genotyped at 16.5 dpc. The number of animals observed for the double heterozygote animals was lower than the expected Mendelian ratio as indicated by the boldface number. The \( \chi^2 \) statistics test was used to calculate a \( p \) value to determine significant deviation from normal expected Mendelian genotypic ratios. Animals with a \((-/-)\) genotype for the Fgf8 allele (boldface symbol) were embryonic lethal and were neither expected to survive nor observed and were not included in the calculation. \( \chi^2 \) test was significant at \( \chi^2 = 0.039 \).

Genotype (Fgf8) (Fbln1)  | % expected* | % observed | No. expected* | No. observed
---|---|---|---|---
(+/-) (+/-) | 8% | 14% | 4 | 7
(+/-) (+/-) | 17% | 20% | 8 | 10
(+/-) (+/-) | 8% | 12% | 4 | 6
(+/-) (+/-) | 17% | 24% | 8 | 12
(+/-) (+/-) | 33% | 20% | 16 | 10
(+/-) (+/-) | 17% | 8% | 8 | 4
Total | 100% | 100% | 49 | 49

Table 2

Table 3

Table 4

might be regulated through partnership with FN along the migration paths from the hindbrain.

The mechanism by which FBLN1 affects FGFR8 functions/signaling needs further investigation. It is plausible to suggest that FBLN1 sequesters FGFR8 in the extracellular matrix and prevents it from binding to its receptor as demonstrated by our immunohistochemistry and signaling experiments. Moreover, preventing its enzymatic degradation helps in maintaining FGFR8 activity in tissues that would be later released by a yet unknown mechanism. We can only speculate at this moment about the significance of FGFR8 sequestration by FBLN1 because we have not identified the presence of another receptor system for this complex. It is possible that fibulin-1 might hand off the FGFR8 molecule stored extracellularly to the FGFR receptor after a certain signal is initiated in a manner similar to extracellular proteoglycans storage of FGF2 and its release to the FGFR receptor by the activity of certain heparinases (29).

We were unable to find any report indicating that FBLN1 binds to the promoter region of any gene, thus affecting its expression. However, FBLN1 promoter sequences have been characterized and found to contain Sp1- and Sp3-binding sites, which are active in regulating the expression of FBLN1 (30). In contrast, the regulation of the FGFR8 gene is more complicated. Marinić et al. (31) identified the enhancers of FGFR8 gene expression in mammalian embryogenesis as elements interspersed within unrelated genes (220-kb region) upstream of the start site that act only on FGFR8 according to their position within this region and not their sequence.

We speculate that FBLN1 might be acting at an upstream effector of the FGFR8 signaling pathway such as sonic hedgehog. We have evidence that FBLN1 binds to the sonic hedgehog with high affinity and that FBLN1 affects sonic hedgehog expression. We hypothesize that FBLN1 might be affecting FGFR8 at the level of sonic hedgehog as well as a direct interaction to maintain its presence and availability for NCC survival. Although there is a high degree of redundancy in FGFR protein family signaling, it appears that the interaction of FBLN1 and FGFR8 is not compensated by other members of the FGFR family (mainly FGFR3 (32) and FGFR4 (33)) to rescue the double heterozygote embryos. Moreover, the interaction of FBLN1
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and FGF8 might be unique because the FBLN1/FGF2 interaction did not have any effects on cell signaling.

Recently, two reports in the literature have implicated proteoglycans in the proper development of the heart and outflow tract. The first report described the development of the DeGeorge syndrome-like phenotype in mice deficient in the heparan sulfate-generating enzyme GlcNAc N-deacetylase/GlcN N-sulfotransferase 1 (NDST1) (34) similar to those exhibited by FGF8 (16) and Fbln-1 (7) null mice. In the second report mutations in the glycosyltransferase enzyme Ext1 result in outflow tract defects that can be reversed using FGF8 (35). It is interesting to speculate that proteoglycans, FBLN1, which is involved proteoglycan processing (9, 36), and FGF8 all play a cooperative role in the maintenance and guidance of NCC to ensure proper cell migration and population in the second heart field and outflow tract for proper development.

We propose that FBLN1 is required for FGF8-dependent NCC guidance and/or survival in the hindbrain by sustaining FGF8 signaling through protection from enzymatic degradation in the extracellular matrix milieu. Preventing NCC death in the hindbrain by maintaining FGF8 signaling ensures that adequate numbers of NCCs migrate and populate the secondary heart field and pharyngeal arches for proper development.

Experimental Procedures

Cells—P19 cells (37) were kindly provided by Dr. Kyu-Ho Lee (Medical University of South Carolina) and used to test the effects of FBLN1 (38) on FGF8 gene expression.

Antibodies—Polyclonal antibody Rb2954 recognizes all FBLN1 variants. Monoclonal antibodies 3A11, which recognizes FBLN1 variants A–D with epitope mapping to the N-terminal anaphylatoxin region, and 5D12, which recognizes FBLN1C variant, were described earlier (38). Anti-pERK1/2 monoclonal antibody (clone 20G11) and anti-ERK2 were purchased from Cell Signaling. Monoclonal and polyclonal antibodies against FGF8 as well as FGF8b protein (carrier-free) were purchased from Cell Signaling. Antibodies against FGF8 and FGF8b were immobilized on a 96-well ELISA plate (Nunc) overnight at 4 °C in Tris-buffered saline (TBS, pH 8.0) buffer. Wells were then rinsed and blocked with 5% nonfat milk, the blots were incubated overnight in Tris-buffered saline containing 100 nM FBLN1, 3) with 0.2 g/ml monoclonal antibody (clone 20G11) and secondary horseradish peroxidase (HRP)-conjugated antibody at 0.5 µg/ml in TBS containing 0.5% gelatin or monoclonal anti-fibulin-1 antibody (3A11) and secondary horseradish peroxidase (HRP)-conjugated antibody at 0.2 µg/ml for 2 h at room temperature. Color development was done using ultra-3,3,5,5-tetramethylbenzidine reagent (Thermo, Pierce) as per the manufacturer’s instructions.

Binding of FGF8b to FBLN1 Using Surface Plasmon Resonance—Reichert SR7000DC instrument was used to demonstrate that FGF8b and FBLN1 bind to each other with high affinity. Monoclonal antibody against FGF8 was immobilized on the surface of planar polyethylene glycol/carboxyl sensor chip using amine coupling chemistry and then FGF8b was passed over and captured by the antibody at room temperature in phosphate-buffered saline (PBS) containing 0.1% Tween 20 (PBST). Then 320 nM FBLN1 was injected over the antibody-captured FGF8b, and binding was recorded using a binding sensogram. Association (kₐ) and dissociation (kₐ) affinities as well as the affinity constant Kₛ were calculated.

Immunoprecipitation of FGF8b Using FBLN1-conjugated Sepharose—Placental FBLN1 was conjugated to cyanogen bromide-activated Sepharose at 1.15 mg/ml gel. Fifty microliters of the FBLN1-conjugated beads were mixed with 500 ng of FGF8b diluted in 5 µl of PBS. Twenty microliters of PBST containing 1 mM CaCl₂ was added and incubated overnight at 4 °C with end over end agitation. Tubes were then spun down, and supernatant was removed and mixed with 4× non-reducing sample buffer. The FBLN1-conjugated beads were rinsed three times with TBST, and 40 µl of 2× non-reducing sample buffer was added. Plain CL-4B-Sepharose beads were used as negative controls. Bound and unbound fractions were resolved on 4–12% NUPAGE gel (Novex, Life Technologies, Inc.). Proteins were transferred to polyvinylidene fluoride (PVDF) membrane and blocked with 5% nonfat milk. Proteins were visualized using monoclonal antibody against FGF8 at 0.2 µg/ml, HRP-conjugated secondary antibody at 0.1 µg/ml, and enhanced chemiluminescent (ECL+) reagent (GE Healthcare).

Detection of FGF8 in Purified FBLN1, Recombinant Fibulin-1C, and Recombinant Fibulin-1D Preparations—FBLN1, rFBLN1C, or rFBLN1D (2.73 µg/well) (39) was electrophoresed onto 4–12% NUPAGE gels. FGF8b was loaded at 50 ng/lane (positive control). After transfer onto PVDF membrane and blocking with 5% nonfat milk, the blots were incubated overnight at 4 °C with monoclonal antibody against FGF8 at 0.5 µg/ml and secondary anti-mouse horseradish peroxidase-conjugated IgG at 0.4 µg/ml. ECL+ reagent was used for detection. Blots were re-probed after stripping with 100 mM glycine buffer, pH 2.3, with either polyclonal antibody against fibulin-1 (Rb2954) or monoclonal antibody against FBLN1 (3A11) at 0.5 µg/ml. Secondary antibody was used at 0.4 µg/ml, and ECL reagent was used for chemiluminescent detection.

Placental FBLN1 Protection of FGF8b from Enzymatic Degradation—In a total volume of 30 µl, 150 ng of FGF8b were incubated 1) alone, 2) with 1.4 µg of FBLN1, 3) with 0.2 µg of ADAM17/TACE, 4) with 1.4 µg of FBLN1 and 0.2 µg of ADAM17/TACE, or 5) with 5 mM EDTA. Incubation was performed at 4 °C and then 10 µl of non-reducing sample buffer was added, and the incubation reaction was run on 4–12% NUPAGE gel and immunoblotted for FGF8 as described above. Membrane was re-blotted with anti-ADAM17/TACE antibody at 0.2 µg/ml and detected using ECL prime chemiluminescent reagent (GE Healthcare).
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FGF8b Activation of Phospho-ERK1/2 (pERK1/2) Signaling Molecules—NIH 3T3 cells (1.0 \( \times 10^5 \)/well, 6-well plate) were cultured for 18 h in serum-containing medium and then switched to serum-free medium containing insulin, transferrin, and sodium selenite (ITS, Corning Glass) for another 30 h. Cells were then treated with 25 ng/ml FGF8b in the presence or absence of 1.5 \( \mu \)g of FBLN1 for 5 min, and the cell layer was then rinsed with cell rinsing buffer (Bio-Rad BioPlex reagent), and cells in each well were extracted with 300 \( \mu l \) of extraction buffer (Bio-Rad BioPlex phosphoprotein extraction reagent) containing enzyme inhibitors according to the manufacturer’s protocol. Basic fibroblast growth factor (FGF2, 25 ng/ml) was used as a control protein. Total protein in the cell extract was quantified using Pierce BCA assay (Thermo Scientific), and a total of 30 \( \mu \)g of protein was loaded in each well of a 4–12% NUPAGE gel. Proteins were transferred to PVDF membrane and blocked with 5% nonfat milk and visualized using antibodies against pERK1/2 and ECL+ as mentioned above. The immunoblot was re-probed with anti-total ERK2 as a loading control. A parallel experiment was also conducted to measure the levels of pERK1/2 in the NIH 3T3 cell extracts (5 \( \mu \)g of total protein/well in duplicate) of FGF8b treatment in the presence or absence of rFBLN1-C, rFBLN1-D, or FBLN1 using LumineX-based assay from Bio-Rad as per the manufacturer’s protocol.

Real Time qPCR Detection of FGF8 Transcripts in HT1080 Cells Transfected with FBLN1C and FBLN1D Coding Plasmids—TaqMan assay procedure (Roche Applied Science) was used to detect FGF8 mRNA expression in control (empty vector) and rFBLN1C- and rFBLN1D-transfected HT1080 cells. Briefly, hydrolysis probe 67 (human universal probe library, Roche Applied Science) was used with two primers listed in Table 1 to detect FGF8 message from stably transfected HT1080 cells (39). Total RNA was isolated from cells cultured on FN-coated 6-well plates in serum-free DMEM using the RNeasy plus kit (Qiagen). cDNA was made using iScript cDNA synthesis kit (Bio-Rad) according to the manufacturer’s protocol from 1 \( \mu \)g of total RNA. Twenty microliters of qPCR mixture was made according to the manufacturer’s instructions using FastStart Universal Probe Master (Roxy) containing 250 nM hydrolysis probe and 900 nM of each primer. The cycling parameters using a CFX96 thermo cycler (Bio-Rad) were 95 °C for 10 min, 40 cycles of 95 °C for 15 s, and 60 °C for 30 s. Primers specific for fibulin-1 variants C and D were also used to detect fibulin-1C and -1D transcripts (Table 1). Regular qPCR assay was used to detect FBLN1C and FBLN1D transcripts as well as the housekeeping genes. Cycling parameters using Bio-Rad’s iCycler was as follows: 95 °C for 3 min, 40 cycles of 95 °C for 10 s, 60 °C for 30 s, and 72 °C for 30 s with final extension at 72 °C for 7 min. Melting curve was run from 55 to 95 °C every 0.5 °C to verify the presence of a single amplicon in the reaction mixture. Expression data were analyzed using the PCR miner method (40).

Inhibition of FBLN1 in P19 Mouse Embryonal Teratocarcinoma Cells Using siRNA—Transfection of P19.CL6 cells was performed using nucleofection according to the manufacturer’s recommended procedure (Amaxa, Transfection Kit V, program C-020). Briefly, 2.0 \( \times 10^6 \) cells were transfected with 30 pmol of either FBLN1 or control Stealth RNAi siRNA (Life Technologies, Inc.). Cells were plated at 1.25 \( \times 10^5 \) cells/well of a 6-well tissue culture plate and allowed to attach in complete medium (a-minimal essential medium supplemented with 10% fetal bovine serum). At 0–5 days after electroporation, wells were extracted, and total RNA was prepared using the RNeasy kit (Qiagen). Quality of the total RNA was assessed using an Agilent system. The qPCR experiments for detecting FGF8, FBLN1C, FBLN1D, and the housekeeping genes B-actin, HPRT1, and WYHAX were conducted using Bio-Rad’s Evagreen qPCR master mix in a 25-\( \mu l \) total reaction volume using an iCycler qPCR machine (Bio-Rad). Cycling parameters were described above.

Immunofluorescence Detection of Fgf8 and Fbln1—Immunodetection of both Fgf8 and Fbln1 proteins was performed on histological sections of mouse hearts at 10.5 dpc. Embryos were harvested at 10.5 dpc and fixed in 4% paraformaldehyde and embedded in paraffin. Sections were cut, rehydrated, and then treated for 1 min at high temperature with citrate-based antigen retrieval solution (Vector Laboratories). Sections were then blocked with 1% bovine serum albumin and incubated overnight with monoclonal antibody against FGF8 at 10 \( \mu g/ml \) and with polyclonal anti-FBLN1 IgG (RB1323) at 15 \( \mu g/ml \) at 4 °C. After three rinses with PBS, the sections were incubated with Alexa 633-conjugated anti-mouse IgG and FITC-conjugated anti-rabbit IgG (Jackson Immunoresearch) for 2 h at room temperature. Sections were rinsed three times in TBST and mounted in mounting media containing propidium iodide. Control sections were incubated with purified IgG instead of the primary antibodies. Sections were analyzed using a Leica TCS SP5 Confocal AOBs microscope system (Leica Microsystems Inc., Exton, PA). Images were taken at the same laser power and gain settings compared to IgG control sections.

Generation of Fgf8 Mutant—The Fgf8-deficient mouse strain used in this work was generated from an Fgf8-deficient mouse strain containing a non-hypomorphic conditional allele and maintained in 50% each of C57BL6 and SV129 strain background. This mouse strain has been previously described and was generously provided to us by Dr. Anne Moon (19). The Fgf8 conditional allele contains a loxP site 5’ to exon 4, and a flippase recognition target (Frt)-flanked Neo and loxP site in the 3’ untranslated region. The loxP sites were positioned within the Fgf8 allele such that Cre recombinase, when expressed, deletes exons 4 and 5, creating a nonfunctional allele. A total of 38 blastocysts were received and implanted in surrogate females at the Gene Targeting and Knock-out Mouse Facility, Medical University of South Carolina. Upon reaching reproductive maturity, a female mutant mouse containing the Fgf8 conditional allele was mated with a male C57BL/6-Tg(Zp3-Cre)-93Knw/J (strain JR 003651). This is a transgenic mouse in which Cre recombinase expression is controlled by the promoter sequence from the mouse zona pellucida 3 (Zp3) gene and directs expression in the growing oocyte prior to completion of the first meiotic division. Initial genotypic analyses examined offspring from matings between Fgf8 heterozygous mice (Fgf8+/-) and Fbln1 heterozygous mice (Fbln1+/-). The \( \chi^2 \) test statistic was used to calculate a \( p \) value by comparing the calculated values to the \( \chi^2 \) distribution to determine significant delineation from
normal Mendelian genotypic ratios. Subsequent genotypic analyses examined offspring from matings between compound heterozygous mice for both Fgf8 and FBLN1 (Fgf8+/−/Fbln1+/−).

Genotyping—The genotypes of offspring were determined from tail tip genomic DNA by PCR. To detect the wild-type Fbln1 allele, PCR was performed using Fbln1 genotyping primers (Table 1). To detect the mutated Fbln1 allele, the Fbln1 genotyping reverse primer was used with a CD4 primer (Table 1). Cycling parameters for PCR were as follows: 30 cycles of 95 °C for 30 s, 55 °C for 30 s, and 72 °C for 1 min. The expected size for the amplicon produced from the wild-type Fbln1 allele is 308 bp. The expected size for the amplicon produced from the hypomorphic conditional Fgf8 allele, PCR was performed using Fgf8 wild-type allele primers. The expected size for the amplicon produced from the wild-type Fgf8 allele is 214 bp. To detect the wild-type and non-hypomorphic conditional Fgf8 allele, PCR was performed using Fgf8 recombinant mutant allele primers. The expected size for the amplicon produced from the wild-type allele is 314 bp. To detect the wild-type and non-hypomorphic conditional Fgf8 allele, PCR was performed using Fgf8 recombinant mutant allele primers. The expected size for the amplicon produced from the recombinant null allele is 300 bp. The PCR cycling parameters for the detection of all Fgf8 alleles were 30 cycles of 95 °C for 30 s, 60 °C for 30 s, and 72 °C for 1 min.

Author Contributions—W. O. T. conducted and analyzed all the experiments presented in Figs. 1–6 and wrote the manuscript. V. M. F. conducted the experiments that generated the double knock-out mouse and did the genotyping of mice. C. B. K. conducted the experiments presented in Figs. 1–6 and wrote the manuscript. V. M. F. and C. B. K. also wrote the manuscript.

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