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**Citation**

**Published Version**
doi:10.1371/journal.pgen.1000809

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Kidney Development in the Absence of Gdnf and Spry1 Requires Fgf10

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Abstract

GDNF signaling through the Ret receptor tyrosine kinase (RTK) is required for ureteric bud (UB) branching morphogenesis during kidney development in mice and humans. Furthermore, many other mutant genes that cause renal agenesis exert their effects via the GDNF/RET pathway. Therefore, RET signaling is believed to play a central role in renal organogenesis. Here, we re-examine the extent to which the functions of Gdnf and Ret are unique, by seeking conditions in which a kidney can develop in their absence. We find that in the absence of the negative regulator Spry1, Gdnf, and Ret are no longer required for extensive kidney development. Gdnf−/−;Spry1−/− or Ret−/−;Spry1−/− double mutants develop large kidneys with normal ureters, highly branched collecting ducts, extensive nephrogenesis, and normal histarchitecture. However, despite extensive branching, the UB displays alterations in branch spacing, angle, and frequency. UB branching in the absence of Gdnf and Spry1 requires Fgf10 (which normally plays a minor role), as removal of even one copy of Fgf10 in Gdnf−/−;Spry1−/− mutants causes a complete failure of ureter and kidney development. In contrast to Gdnf or Ret mutations, renal agenesis caused by concomitant lack of the transcription factors Etv4 and Etv5 is not rescued by removing Spry1, consistent with their role downstream of both RET and FGFRs. This shows that, for many aspects of renal development, the balance between positive signaling by RTKs and negative regulation of this signaling by SPRY1 is more critical than the specific role of GDNF. Other signals, including FGF10, can perform many of the functions of GDNF, when SPRY1 is absent. But GDNF/RET signaling has an apparently unique function in determining normal branching pattern. In contrast to GDNF or FGF10, Etv4 and Etv5 represent a critical node in the RTK signaling network that cannot be bypassed by reducing the negative regulation of upstream signals.

Introduction

Signaling by the secreted protein GDNF through the RET receptor tyrosine kinase (RTK) and the GFRζ1 co-receptor plays a central role in the initiating event of kidney development, the outgrowth of the ureteric bud (UB) from the Wolffian duct (WD) into the metanephric mesenchyme (MM). They are also important for the subsequent growth and branching of the UB to form the renal collecting duct system. This is apparent not only from the lack of UB development in Gdnf, Ret, and Gfra1 mutants in mice [1–5] and humans [6], but also from the observation that most of the other genes whose absence causes renal agenesis are upstream regulators of Gdnf or Ret expression [7]. We have recently reported that expression in the UB of the ETS transcription factors Etv4 and Etv5 is upregulated by GDNF/RET signaling, and that Etv4−/−;Etv5−/− double homozygous mice fail to develop kidneys. Thus, the effects of GDNF/RET signaling on UB branching morphogenesis are largely transduced via ETV4 and ETV5 [8].

The mechanism by which GDNF/RET signaling induces epithelial branching remains to be fully elucidated. In the WD, it initially promotes cell movements that precede and lead to the formation of the UB [9], and it then induces UB outgrowth from the duct [10,11]. In the UB tips, it increases cell proliferation [12,13], a likely prerequisite for branching. Furthermore, because GDNF is capable of acting as a chemoattractant for cultured kidney cells [14,15], it has been suggested that GDNF may act as a chemoattractant for UB tips in vivo, thereby promoting and patterning their branching [10,11,16].

Here, we have further investigated the role of GDNF/RET signaling by identifying conditions under which the kidney can develop in the absence of either GDNF or RET. To achieve this, we employed a null allele of Sprouty1 (Spry1), a negative feedback inhibitor of RTK signaling, which modulates the response to GDNF during kidney development. Spry1−/− mutants show a pervasive defect in the development of the ureteric tree, including formation of supernumerary buds from the WD, which develop into multiplex ureters and kidneys, and an increase in the number and diameter of UB branches in the developing kidneys [17,18]. The molecular mechanism of Sprouty protein function is incompletely understood. Engineered expression of Sprouty in
cells leads to inhibition of signaling through the MAP kinase (MAPK) pathway, but effects have also been observed on the PI3K and PLCγ signaling pathways downstream of RTKs [19,20].

It was previously found that removing one Spry1 allele corrected the renal hypoplasia in Gdnf+/− heterozygous mice, and that removing one Gdnf allele corrected the abnormal UB branching in Spry1−/− mice. These findings demonstrated that the balance between GDNF and SPRY1 levels is critical for normal kidney development [17,18]. We have now further tested this idea by examining the consequences of eliminating Gdnf and Spry1 (or all Ret and Spry1). Surprisingly, such doubly homozygous mutant mice developed two large and well-formed kidneys, each with a single, normally-positioned ureter. Thus, in the absence of GDNF/RET signaling, other factors must be able to support normal UB outgrowth and extensive UB branching, but only when SPRY1 is absent. We provide in vivo, genetic evidence that FGF10 is one such factor, consistent with the previous observation that exogenous FGFs are capable of inducing budding by the Wolffian duct in organ culture [21]. However, our data also reveal that the specific pattern of UB branching is abnormal in Ret−/−;Spry1−/−; and Gdnf−/−;Spry1−/− double mutant kidneys. Therefore, although endogenous FGF10 and perhaps other factors can promote extensive UB branching, GDNF appears to serve a unique role in the patterning of UB branching morphogenesis. Finally, we show that, unlike the rescue of Gdnf or Ret mutations, the lack of both Etv4 and Etv5 cannot be overcome by removing Spry1. Thus, these two transcription factors represent a critical link in a signaling network downstream of Ret and other RTKs.

Figure 1. Loss of Spry1 rescues kidney development in Gdnf−/− or Ret−/− mice. (A–E,H) excretory systems dissected from newborn mice of the indicated genotypes shown in whole mount. Note that the ureter in the Spry1−/− mutant is greatly expanded (black asterisk) and the kidneys are cystic (red asterisk). (F,G) H&E stained sections showing histology of cortex and nephrogenic zone in control (Spry1+/−) and Gdnf−/−;Spry1−/− kidneys, revealing a normal overall organization with well-differentiated glomeruli (*). (I,J) PAS-stained sections of wild-type and Ret−/−;Spry1−/− double mutant kidneys, showing normal overall organization with renal cortex, medulla, and outer nephrogenic zone. Abbreviations: Ad, adrenal gland; Bl, bladder; Co, cortex; Ki, kidney; Me, medulla, NZ, nephrogenic zone; Ur, ureter. Scale bars 1 mm in A-E and H, 100 μm in F,G,J.
doi:10.1371/journal.pgen.1000809.g001
Results

Kidney development in the absence of Gdnf and Spry1, or Ret and Spry1

Gdnf−/+ newborn (P0) mice display ~80% renal agenesis and ~20% severe renal hypoplasia [1–3] (n = 20) (Figure 1A and 1B) (for statistical purposes, we count each of the two potential kidneys as a separate sample [22]). In contrast, we found that newborn Gdnf−/−;Spry1−/− (abbreviated GGSS) mice displayed only 11% renal agenesis (n = 18) and 89% of kidneys were normally shaped and only slightly smaller than controls (cross-sectional area 70±11% of wild-type) (Figure 1E). Unlike Spry1−/− mice (Figure 1D), GGSS newborns never showed hydroureter, although the bladder was often filled with urine (Figure 1E), indicating that the ureters were correctly connected to the bladder, and thus suggesting that the site of outgrowth of the UB from the WD had been normal [23,24].

These observations raised the possibility that in the absence of Gdnf and Spry1, kidney development was supported by another GDNF-family ligand, such as Neurturin, which is expressed in the developing kidney [25]. To investigate this possibility we generated Ret−/−;Spry−/− (RRSS) newborn mice, as RET is the common signaling receptor for all GDNF family ligands[26]. Whereas Ret−/− newborn mice display renal agenesis (~70%) or severe renal hypoplasia (~30%) (Figure 1C), 88% of the RRSS double mutants (n = 26) developed fairly large and well-formed kidneys (cross-sectional area 73±15% of wild-type) with apparently normal ureters (Figure 1H). Histological analysis of GGSS and RRSS kidneys indicated that the overall organization into renal papilla, medulla, cortex, and nephrogenic zone was essentially normal, with well differentiated collecting ducts, nephron epithelia and glomeruli in both double mutant genotypes (Figure 1F, 1G, 1I, and 1J and data not shown). Consistent with these findings, many podocalyxin-positive glomeruli were observed in the cortex of double mutant kidneys, although they were reduced in number (52±6% of wild-type in P0 RRSS mutants) (Figure 2A and 2B).

Despite their apparently functional kidneys, GGSS and RRSS mice did not survive beyond 3–4 days after birth, presumably because removing Spry1 does not correct the multiple defects in the nervous system caused by lack of Gdnf or Ret [26].

UB branching is extensive, but abnormally patterned, in Gdnf−/−;Spry1−/− and Ret−/−;Spry1−/− kidneys

As GDNF/RET signaling is important for UB growth and branching, we crossed into the mutant backgrounds a Hoxb7/myrVenus transgene, which fluorescently labels the WD and UB lineage [27], to visualize UB branching in vivo or in cultured kidneys. In P0 wild-type kidneys, branching UB tips are numerous and regularly spaced over the kidney surface (Figure 3A). In Spry1−/− kidneys, the UB tips are likewise evenly spaced, but abnormally swollen (Figure 3D). In contrast, although there were numerous UB tips on the surface of GGSS and RRSS kidneys, indicating that the UB had branched very extensively even in the absence of Gdnf or Ret, the tips were irregularly and less densely arrayed, elongated, and abnormally shaped (Figure 3B and 3C). We also examined the kidneys at E15.5, when branching is less complex and the kidneys are small enough to image by confocal microscopy and perform 3D reconstruction (Figure 3E–3P). Volume rendering of the Hoxb7/myrVenus-positive UB tree showed that the double mutants had extensively branched, but the spacing and the branching geometry of UB tips was irregular (Figure 3F and 3G). In such samples, the points where UB tips connect to nephrons could be mapped in three dimensions, and were found to be essentially normal in GGSS mutants (Figure 2C–2J), indicating that the double mutant UB tips produce the factors necessary to connect to the nephrons. Higher magnification 3D reconstructions revealed a characteristic pattern of UB branching in wild-type kidneys (Figure 3I–3M), where successive branch generations occur at regular intervals, mostly at right angles to the parental branches (yellow dashed lines). In contrast, this regular pattern was rarely observed in GGSS or RRSS kidneys, where instead the UB tips were highly irregular in shape, orientation, and branching frequency (Figure 3J, 3K, 3N, and 3O). Spry1−/− UB tips resembled the wild type, except for an increased tip diameter (Figure 3L and 3P), indicating that the branching abnormalities in RRSS and GGSS are not due simply to lack of Spry1.

To examine the initial branching events, we explanted the WD, ureter and kidney at E12.5. Consistent with what was observed in newborn GGSS and RRSS mutants, the ureter and kidney were
nearly always present (88%, n = 26 and 100%, n = 16, respectively). In contrast, few Gdnf/2 or Ret/2 mutants had ureter and kidney at this stage (20%, n = 30 and 8%, n = 12, respectively). In none of the GGSS or RRSS mutants were duplicated ureters present, as they are in many Spry1/2 mutants. UB branching was somewhat delayed in the GGSS and RRSS kidneys compared to controls (Figure 4A versus Figure 4D, 0 hours; and data not shown). Several of the wild type, Spry1/−/−, and GGSS E12.5 kidneys were cultured to examine the subsequent branching events. While the GGSS kidneys branched extensively in culture, some of the tips elongated abnormally without branching (Figure 4D, asterisks) and some tips grew too slowly (Figure 4D, arrowheads), resulting in an irregularly patterned tree. Thus, while GDNF/RET signaling is not required for the UB to undergo extensive growth and branching when Spry1 is also absent, it is necessary to impose a regular pattern on UB branching.

Figure 3. Extensive but irregular UB branching in Gdnf/−/−; Spry1/−/− and Ret/−/−; Spry1/−/− double mutant kidneys. (A−D) Newborn stage kidneys, all carrying the Hoxb7/myrVenus transgene to label the UB branches. Each panel shows a high magnification view of the kidney surface, revealing the shape and organization of branching UB tips; insets show the entire kidney in whole mount. Wild-type kidneys (A) have evenly spaced UB tips with a regular branching pattern, whereas Gdnf−/−;Spry1−/− (B) and Ret−/−;Spry1−/− (C) double mutant kidneys have highly irregular branching. Spry1−/− kidneys (D) have regularly branched, but swollen UB tips. (E−P) 3D volume rendering of E15.5 kidneys. (E−H) Whole kidneys from embryos of the indicated genotypes, carrying Hoxb7/myrVenus. (I−P) Higher power views of two representative surface regions of each genotype. The 3D images were generated from confocal Z-stacks, using Volocity (E−H) or ImageJ (I−P). The yellow dashed lines indicate an interpretation of the branching patterns. While most UB branches in the wild-type (I,M) and Spry1−/− (L,P) kidneys show a reiterative pattern of terminal bifurcation, with branches forming at right angles to their predecessors, most UB branches in the double mutants (J,K,N,O) fail to conform to this pattern, and instead display a variety of abnormal shapes and branching patterns.

doi:10.1371/journal.pgen.1000809.g003
Many tip-specific genes can be upregulated by exogenous GDNF, and their expression is reduced in a Ret hypomorphic mutant [8,12,30], suggesting that GDNF/RET signaling may be required to maintain the tip-specific pattern. However, we found that three tip-specific markers, Ret, Wnt11, and Etv4, all of which normally require wild-type levels of GDNF/RET signaling for expression in the UB, continued to be expressed in a tip-specific pattern in GGSS or RRSS double mutants (Figure 5A–5F). The trunk-specific marker Wnt7b [31] also retained its normal expression pattern in GGSS double mutants (Figure 5G and 5H), indicating that the lack of Wnt7b expression in the UB tip does not require GDNF/RET signaling. Therefore, there must be other, Ret-independent mechanisms that can establish and maintain tip/trunk differences in gene expression.

Figure 4. Abnormal branching of double mutant kidneys in organ culture. Kidneys of wild-type (A) and mutant genotypes (B–D), carrying Hoxb7/myrVenus, were excised at E12.5, cultured in vitro, and photographed at the indicated times. The Ret−/− Wolffian duct (B) failed to develop a ureter or kidney, while the Spry1−/− kidney (C) has multiple ureters (arrowheads), swollen UB tips and an enlarged common nephric duct (cnd). (D), in two examples of Gdnf−/−; Spry1−/− mutant kidneys, UB branching is retarded at E12.5, and subsequent branching in culture displays abnormal patterns (asterisks and arrowheads – see text) compared to wild-type.

doi:10.1371/journal.pgen.1000809.g004

Figure 5. Differential gene expression in tip and trunk domains is retained in Gdnf−/−;Spry1−/− and Ret−/−;Spry1−/− double mutant kidneys. Whole mount in situ hybridization for the UB tip markers Ret, Wnt11 and Etv4 and the trunk marker Wnt7b, in wild-type (A,C,E,G) and double mutant E12.5 kidneys (B,F and H, Gdnf−/−; Spry1−/−; D, Ret−/−;Spry1−/−). Solid arrows indicate UB tips and open arrows indicate trunks. Scale bars 100 µm.

doi:10.1371/journal.pgen.1000809.g005

Fgf10 cooperates with Gdnf to promote UB outgrowth and branching morphogenesis, and can largely compensate for the loss of Gdnf/Ret in the absence of Spry1.

We next sought to determine what signaling molecule(s) support ureteric bud outgrowth from the WD, and subsequent growth and branching, in the absence of Gdnf/Ret and Spry1. The observation that kidney development is rescued in Gdnf2/2 or Ret2/2 embryos only when Spry1 is absent suggests that the signaling responsible for the rescue must itself be negatively regulated by Spry1. Since Sprouty genes are negative regulators of RTK signaling, the rescue most likely occurs through a RTK. According to this reasoning, FGF signaling is a strong candidate. Genetic studies in the mouse have identified FGF7 and FGF10, signaling through FGFR2, as important factors for normal UB branching [32,33]; however, the effects of Fg7 or Fg10 knockouts (KOs) are far less severe than those caused by loss of Gdnf or Ret, indicating that these FGFs play a secondary role under normal conditions. Fg7 mRNA was not detected in the kidney before E14.5 [34],
whereas Fgf10, like Gdnf, is expressed in the MM at least as early as E10.5 (Figure 6A–6D), making Fgf10 a good candidate to participate in UB outgrowth and early branching morphogenesis. Fgf10−/− mice [35] have small kidneys at birth [33], and we found this to be reflected in reduced UB branching during kidney development (Figure 6E and 6F). The reduction in UB branching was comparable to that in kidneys lacking Fgf2 (or both Fgf1 and Fgf2) in the UB lineage [36], suggesting that FGF10 is the major FGF signaling through FGFR2 in the UB. Furthermore, this defect could be corrected by deletion of one Spry1 allele (Figure 6G), indicating that Spry1 negatively regulates FGF10 (as well as GDNF) signaling.

**Figure 6.** Fgf10 expression and function in early ureter and kidney development. (A,B) In situ hybridization in transverse sections of E10.5 wild type embryos reveals that Fgf10 and Gdnf are expressed in metanephric mesenchyme (arrows). (C,D) Whole-mount in situ hybridization at E11.0 (dorsal view) shows that Fgf10 and Gdnf are expressed in metanephric mesenchyme (MM) surrounding the UB epithelium. The schematic diagram illustrates Fgf10 expression, with purple indicating where the hybridization signal was detected. (E–G) Visualization of Hoxb7/myrVenus shows (E) normal UB branching in an Fgf10+/− kidney, (F) reduced branching in an Fgf10−/− kidney, and (G) rescue of UB branching in an Fgf10−/− kidney when Spry1 dosage is reduced (Spry1+1/−). Scale bars, 100 μm. (H–J) Induction of ectopic budding from the Wolffian duct by FGF10. Dissected E10.5 urogenital regions were cultured with control PBS-soaked beads (H) or beads soaked in FGF10 (I,J) placed between the two Wolffian ducts (dotted yellow circles). FGF10 induces multiple ectopic UB outgrowths (marked by asterisks) in both control Gdnf+1/− (I) and Gdnf−/− (J) samples. Open arrowhead in H, Wolffian duct; arrows in H–I, normal ureteric buds.

doi:10.1371/journal.pgen.1000809.g006
To examine the relationship between FGF10 and GDNF in kidney development, we performed gain- and loss-of-function studies. FGF10-soaked beads placed next to the WD of E10.5 embryos induced the formation of multiple ectopic buds (Figure 6H and 6I), as do GDNF beads [10]. To test whether FGF10 induced the ectopic buds indirectly, by up-regulating Gdnf, we performed the same experiment in Gdnf−/− embryos, but the result was similar (Figure 6J). Therefore, FGF10 is capable of inducing UB outgrowth, presumably by acting directly on the WD. The role of Fgf10 was also examined by performing genetic crosses between Fgf10 and Gdnf KO mice, and examining UB formation at early stages (E11.5–12.5) and kidney development in late fetal or newborn mice. Fgf10 heterozygotes always had normal ureters and kidneys (Figure 7A and 7B), whereas Gdnf heterozygotes had a low frequency (7–10%) of defective UB outgrowth or renal agenesis (Figure 7A). However, in Fgf10+−;Gdnf−/− double heterozygotes, 81% of the UBs were missing or severely delayed at E11.5–E12.5 (e.g., Figure 7A and 7C–7E), and 58% of kidneys were absent at E17.5–P0 (e.g., Figure 7A, 7F, and 7G), roughly equivalent to what is observed in Gdnf null homozygotes with normal Fgf10 dosage (Figure 7A). Furthermore, although renal agenesis was rare in Fgf10 homozygotes (15%), removing one Gdnf allele (Fgf10−/−;Gdnf+/−) caused 100% agenesis (e.g., Figure 7A and 7H). Thus, while the consequences of deleting both Fgf10 alleles in a wild-type background are relatively mild, in a Gdnf−/− background the loss of even one Fgf10 allele causes more severe defects, and loss of both Fgf10 alleles is catastrophic, indicating that Fgf10 and Gdnf normally cooperate to promote UB outgrowth from the WD.

To ask if it is Fgf10 that rescues kidney development in Gdnf−/−;Spry1−/− mice, we next examined Gdnf−/−;Spry1−/−;Fgf10+/− mice in which Fgf10 gene dosage was reduced. We found that removal of either one or both Fgf10 alleles resulted in 100% renal agenesis (Figure 8). These data conclusively demonstrate that Fgf10 supports the extensive kidney development that occurs in Gdnf−/−;Spry1−/− mice.

Expression of the ETS transcription factors ETV4 and ETV5 in the UB in vivo requires normal levels of GDNF/RET signaling, and they can also be upregulated in kidney cultures by exogenous FGF10, suggesting that they function downstream of both RET and FGF2 [8]. If ETV4 and ETV5 are needed to transduce both FGF10, suggesting that they function downstream of both RET and they can also be upregulated in kidney cultures by exogenous Etv5

**Figure 7. Fgf10 and Gdnf cooperate to support UB outgrowth and kidney development.** (A) Frequency of the failure of UB outgrowth at E11.5–12.5, and renal agenesis or hypoplasia at E17.5–P0. (B) Normal T-stage UB in an Fgf10+/− embryo at E11.5. (C–E) Three examples of UB formation or lack thereof in Fgf10+/−;Gdnf+/− E11.5 embryos. In (C), the UB is slightly retarded, in (D), the UB is severely delayed, and in (E) the UB is absent. (F–H), normal kidneys in wild-type and renal agenesis or hypoplasia in compound Fgf10+/−;Gdnf−/− embryos at P0. The wild-type in (F) has two normal kidneys, the double heterozygote in (G) has renal agenesis on one side and a hypoplastic kidney on the other, and the Fgf10+/−;Gdnf+/− example in (H) has bilateral agenesis. Ad, adrenal; Ki, kidney; Go, gonad. n = number of (potential) kidneys.

doi:10.1371/journal.pgen.1000809.g007
In a wild-type background (i.e., in the presence of SPRY1), GDNF/RET signaling is essential for the positioning and normal outgrowth of the UB from the WD. Not only does the UB usually fail to emerge in Ret−/− or Gdnf−/− mice, but when it does, its position is often abnormal, resulting in the lack of a normal connection to the bladder [37]. Furthermore, ectopic expression of Gdnf causes ectopic UBs to form along the WD [38–40]. This led to the model that the specific domain of Gdnf expression in the nephrogenic cord is critical for positioning the UB in the correct location [5,16]. However, in the absence of SPRY1, mice lacking GDNF or RET make a normal UB that develops into a normal kidney [41,42], also contribute to the normal positioning of the UB. Unlike Gdnf−/− or Ret−/− ureteric buds on a wild-type (Spry1+/+) background, which grow and branch minimally if at all, the double mutant UBs (GGSS or RRSS) grew and branched extensively, leading to a kidney that was often close to normal in size, with an extensive collecting duct system, normal overall histoarchitecture and large numbers of nephrons connected to the collecting ducts. Therefore, GDNF/RET signaling does not have a unique ability to induce UB branching, including the predominant terminal bifurcations, nor is it required for the UB tips to induce nephrogenesis. As in the case of UB outgrowth from the WD, it appears that other factors are potentially redundant with GDNF in their ability to promote UB branching. Since loss of Fgf10 in a Gdnf−/−;Spry1−/− double mutant background eliminated initial UB outgrowth, it could not be determined to what extent FGF10 contributes to later UB branching in the absence of GDNF. However, the reduced UB branching in Fgf10−/− kidneys shows that FGF10 normally contributes significantly to UB branching, and is likely to be at least one of the factors that can promote this process in GGSS or RRSS double mutant mice. Other factors that might also be involved include HGF and EGF [43].
It was recently reported that the effects of a Ret-Y1062F point mutation, which causes renal agenesis or hypoplasia similar to that observed in Ret knockout mice, can be rescued by removal of Spry1 [44]. The double mutant mice had kidneys of normal size, with normal glomerular number. The Y1062F mutation abolishes signaling through the PI3K-AKT and RAS-MAPK pathways, but does not affect signaling through PLC-γ or other pathways that potentially act downstream of RET (e.g., SRC) [45]. The authors speculated that in the double mutants, the ERK MAPK pathway might be activated by RET via an alternative pathway involving PLC-γ, allowing kidney development to proceed normally, and they did not suggest that other signaling molecules might substitute for GDNF under these conditions. However, in our Ret−/−; Spry1−/− double null mutant mice, the ability of RET to signal through alternative pathways was eliminated, which revealed the ability of other signaling molecules, including FGF10, to support kidney development in the absence of RET or GDNF.

Based on our findings, we propose a model (Figure 10) in which GDNF, FGF10 and probably other signaling molecules expressed in the MM signal through their cognate receptor tyrosine kinases in the UB epithelium to collectively promote budding from the Wolffian duct and subsequent growth and branching during kidney development. RET and FGFR2 (and probably other RTKs) activate a series of shared downstream signaling pathways, including RAS-MAPK, PI3K-AKT and PLC-γ-Ca++ [46], which together support UB branching morphogenesis. Spry1 expression is upregulated by these signals, and SPRY1 then provides negative feedback by regulating one or more of the shared signaling pathways downstream of RET and FGFR. In early kidney development, GDNF is the predominant signal, while FGF10 is much weaker (presumably due to lower expression) (Figure 10A).

Expression of Etv4 and Etv5 is upregulated by these signals, thus controlling transcription of downstream genes required for UB growth and branching. Loss of Gdnf (Figure 10B) causes renal agenesis because in the presence of SPRY1 the level of FGF10 signaling via FGFR2 is not sufficient to produce the necessary responses, such as an appropriate level of Etv4 and Etv5 expression. Normally, loss of Fgf10 has relatively mild consequences because of the high level of GDNF signaling. When Spry1 is absent there is no brake on signaling via FGFR2 (Figure 10C), and GDNF can be removed without causing renal agenesis, due (at least in part) to the effects of FGF10, and to the restoration of Etv4/Etv5 expression; however, UB branching pattern is abnormal. If Fgf10 is also removed (Figure 10D) any remaining factors are insufficient to rescue kidney development, resulting in renal agenesis. In the absence of Etv4 and Etv5, removal of Spry1 is unable to rescue kidney development (Figure 10E). This suggests that Etv4 and Etv5 normally mediate the combined effects of several RTKs (RET, FGFR2 and probably others), and therefore elevated RTK signaling due to lack of SPRY1 cannot bypass the requirement for these transcription factors.

The main abnormality observed in the Ggss and Rrss double mutant kidneys was in the specific pattern of branching. Instead of the regular terminal bifurcations in wild-type kidneys, which typically occur at right angles to the previous branching event, the double mutant branching UB tips were heterogeneous in shape, typically occur at right angles to the previous branching event, the double mutant branching UB tips were heterogeneous in shape, orientation, branch angle and frequency of branching. The defects were distinct from those caused by loss of Spry1 alone, which causes the UB tips to swell but does not alter branch orientation or tip spacing. Therefore, it appears that these specific defects in branching pattern are a consequence of the loss of GDNF/RET signaling, and reflect a function that cannot be replaced by FGF10 or other factors present in the double mutant kidneys.

Figure 10. Model: GDNF and FGF10 cooperate to promote ureteric bud branching morphogenesis, via Etv4 and Etv5, while Sprouty1 regulates signaling downstream of both RET and FGFR2. (A) In wild-type, GDNF/RET signaling plays a major role and FGF10/FGFR2 a minor role in promoting UB outgrowth and branching morphogenesis. The response to these signals is modulated by SPRY1, leading to a normal kidney at birth (right panel). The transcription factors ETV4 and ETV5 are downstream effectors of GDNF and FGF10 signaling. (B) In the absence of GDNF, there is presumably less SPRY1 produced (indicated by smaller text), but FGF10 is insufficient to overcome negative regulation by SPRY1, causing reduced downstream signaling to induce UB budding and branching (indicated by thinner arrows), one manifestation of which is a severe reduction in Etv4/Etv5 expression [8]. Consequently, renal agenesis or severe hypoplasia is observed. (C) When GDNF and SPRY1 are both absent, the lack of negative regulation of signaling by FGFR2 allows for Etv4/Etv5 expression, UB branching, and kidney development; however, the pattern of UB branching is altered, suggesting a unique role of GDNF in this process. (D) When FGF10 and GDNF are both absent, there is too little RTK signaling, even in the absence of negative regulation by SPRY1, to allow UB outgrowth from the Wolffian duct, resulting in renal agenesis (whether Etv4/Etv5 would be expressed is not known, as there is no ureter or kidney to analyze). (E) Renal agenesis in Etv4−/−; Etv5−/− mice is not rescued by loss of Spry1, showing that increased RTK signaling is insufficient for kidney development in the absence of Etv4 and Etv5 (dashed arrow). The observation that ureters develop in Etv4+Etv5+Spry1 triple mutants suggests that UB out-
growth, but not later branching, can occur independently of Etv4/ Etv5. Insets in a and c show the pattern of branching UB tips in stage P0 wild-type and double mutant kidneys. doi:10.1371/journal.pgen.1000809.g010

How may GDNF/RET signaling influence the specific pattern of UB branching? One possibility is that GDNF in the metanephric mesenchyme acts as a chemoattractant to direct the growth of the UB tips toward local foci of GDNF expression [10,14,16], similar to the way in which FGF10 is thought to direct the branching of the developing lung epithelium [47,48].

We have previously argued against such a model for several reasons [40]. First, the distribution of Gdnf mRNA in the MM is extremely diffuse; however, it remains possible that the protein is more limited in its spatial distribution than the mRNA. Second, we found that kidneys developed rather normally in Gdnf null mice in which Gdnf was misexpressed in the UB epithelium, suggesting that it is the presence, but not the location, of GDNF that is important [40]. However, the specific pattern of UB branching was not closely examined in those mutant/transgenic mice, and it remains possible that they had subtle branching defects similar to the Ggss and Rrss double mutant kidneys. Methods to locally and precisely manipulate the pattern of Gdnf expression will be needed to better test this model. If not through chemoattraction, then GDNF/RET signaling must in some other manner influence the specific pattern of growth and branching of the UB tips.

Methods

Ethics statement

All work on animals was conducted under PHS guidelines and approved by the relevant Institutional Animal Care and Use Committees.

Mouse strains

Ret [4], Gdnf [3], Sply1 [17], Fgft0 [35], Etv4 [49], Etv5 [50] and HoxB7/myrVenus [27] mutant mice have been described. These mice were maintained on a mixed background (129S1/SvJ:CS7BL/6). Embryo stage was estimated by considering noon of the day of the vaginal plug as embryonic day (E) 0.5, and more accurate staging was determined by counting somites. PCR genotyping of mice and embryos was done as described previously [3,4,8,17,35].

Whole-mount in situ hybridization

Whole-mount and section RNA in situ hybridization and detection of β-galactosidase activity were performed as described previously [38,51] using digoxigenin-UTP-labeled anti-sense riboprobes.

Histological analysis and nephron counting

Newborn mice were sacrificed according to Institutional and NIH guidelines. Whole kidneys and urogenital tracts were dissected in PBS. Kidney cross-sectional area was determined from whole-mount photographs of 28 wt, 16 Ggss and 12 Rrss P0 kidneys using ImageJ. For histological analysis, 7–10 μm sections were prepared from paraffin-embedded samples fixed in 4% paraformaldehyde (PFA). Dec-waxed sections were stained with either haematoxylin and cosin (H&E) or Periodic Acid Schiff (PAS). To count glomeruli, five evenly-spaced sections across each kidney (two wild-type and four Rrss mutants) were stained with podocalyxin, and the number of glomeruli per section was averaged for each kidney.

Metanephric kidney explant cultures and immunohistochemistry

Intermediate mesoderm or metanephric kidneys were dissected from E10.5 to E14.5 embryos in PBS +Ca +Mg (Invitrogen). Explants were cultured at 37°C in DMEM/F12 (Invitrogen) supplemented with Glutamax, 100 U/ml penicillin, 100 μg/ml streptomycin, and 10% fetal bovine serum in a 5% CO2, humidified atmosphere at the medium-air interface on Costar Transwell filters (0.4 μm). After culture, explants were fixed in 4% PFA. For immunostaining, explants were incubated with goat anti-podocalyxin antibodies (R&D Systems), followed by Cy2 or Cy3 anti-goat Ig (Jackson ImmunoResearch). Images were captured on a Zeiss Axio Observer Z1.

For FGF bead experiments, posterior intermediate mesoderm was dissected from embryos at the 29 to 33 somite stage in Hanks Balanced Salt Solution, with 1% FBS. Two heparin acrylic beads (Sigma) soaked in FGF10 (R&D Systems), reconstituted in PBS at 1mg/ml or in PBS were inserted between the WDs, and rudiments were cultured on Whatman Nuclepore Track-Etch Membrane filters (8 micron pore size) in 44% F12, 44% DMEM, 10% FBS, 1% glutamine, 1% Penstrep at the air-liquid interphase for 48–55 hours. Samples were fixed in cold 100% methanol and stained with anti-pan cytokeratin antibody (Sigma C9687).

Confocal imaging and 3D analysis

E15.5 metanephric kidneys were dissected in PBS and fixed overnight in 4% PFA. After clearing using FocusClear (CelExplorer), kidneys were mounted in MountClear (CelExplorer) and scanned using a Leica LS5 confocal microscope, and 3D rendering was performed using Volocity software.

Acknowledgments

We thank Scott Simonet (Amgen) for the Fgft0 KO mice, Mariano Barbacid for the Gdnf KO mice, Silvia Arber for the Etv4 KO mice, Ken Murphy for the Etv5 KO mice, and Albert Basson for stimulating and fruitful discussions.

Author Contributions

Conceived and designed the experiments: OM GRM FC. Performed the experiments: OM CC DH UG LW VD. Analyzed the data: OM CC DH UG LW VD VD. Contributed reagents/materials/analysis tools: JDL. Wrote the paper: GRM FC.

References