Identification of multipotent progenitors in the embryonic mouse kidney by a novel colony-forming assay

Kenji Osafune1,2,3, Minoru Takasato2,4, Andreas Kispert5, Makoto Asashima2,3 and Ryuichi Nishinakamura1,4,6,*

Renal stem or progenitor cells with a multilineage differentiation potential remain to be isolated, and the differentiation mechanism of these cell types in kidney development or regeneration processes is unknown. In an attempt to resolve this issue, we set up an in vitro culture system using NIH3T3 cells stably expressing Wnt4 (3T3Wnt4) as a feeder layer, in which a single renal progenitor in the metanephric mesenchyme forms colonies consisting of several types of epithelial cells that exist in glomeruli and renal tubules. We found that only cells strongly expressing Sall1 (Sall1-GFPhigh cells), a zinc-finger nuclear factor essential for kidney development, form colonies, and that they reconstitute a three-dimensional kidney structure in an organ culture setting. We also found that Rac- and JNK-dependent planar cell polarity (PCP) pathways downstream of Wnt4 positively regulate the colony size, and that the JNK pathway is also involved in mesenchymal-to-epithelial transformation of colony-forming progenitors. Thus our colony-forming assay, which identifies multipotent progenitors in the embryonic mouse kidney, can be used for examining mechanisms of renal progenitor differentiation.

KEY WORDS: Progenitor, Kidney, Colony-forming assay, Sall1, Wnt, PCP, JNK, Rho, Mouse

INTRODUCTION

Mammalian adult kidney, metanephros, is formed by reciprocally inductive interaction between two precursor tissues derived from the intermediate mesoderm, the metanephric mesenchyme and the ureteric bud. The ureteric bud induces the metanephric mesenchyme to differentiate into the epithelia of glomeruli and renal tubules, endothelial and stromal cells (Saxen, 1987). Inductive signals have been vigorously investigated, and several factors have been elucidated that trigger epithelialization of metanephric mesenchyme in explant culture system; the members of Wnt family (Herzlinger et al., 1994; Kispert et al., 1998), leukemia inhibitory factor (LIF) (Barasch et al., 1999; Plisov et al., 2001), and transforming growth factor B2 (TGFb2) (Plisov et al., 2001). These studies have also suggested the presence of clonal cells in mesenchymal rudiments, which sequentially form renal condensation, comma (C)- and S-shaped bodies, and terminally epithelia of glomeruli and renal tubules, and the existence of single epithelial precursors responding to LIF was demonstrated in mesenchyme (Barasch et al., 1999). One previous report suggested retrospectively the presence of multipotent cells in embryonic kidneys, demonstrating that cells in several portions of nephron were derived from a single stem cell using lacZ gene transduction with retrovirus into a single cell of mesenchyme (Herzlinger et al., 1992). However, none has isolated prospectively the renal progenitor cells with a multilineage differentiation potential from the embryonic kidney, and none has examined their differentiation mechanisms in a single cell culture. There has been a lack of assay systems that specifically identify renal progenitors, as in cases of the neurosphere method for neural stem cells (Reynolds et al., 1992) and the colony assay for hematopoietic progenitors (Pluznik and Sachs, 1965; Bradley and Metcalf, 1966).

We previously generated mice in which the green fluorescence protein gene (GFP) was knocked into the locus of Sall1 (Sall1-GFP mice), a zinc finger nuclear factor that is expressed in the metanephric mesenchyme and that is essential for kidney development (Nishinakamura et al., 2001; Takasato et al., 2004). Sall1 is also expressed in the subventricular zone of the central nervous system and progress zones of limb buds, where neural and mesenchymal stem cells reside, respectively, leading to speculation that Sall1 might have some association with stem cells in several organs, including the kidney.

Targeted disruption of Wnt4 results in kidney agenesis and impairs mesenchymal-to-epithelial transformation (Stark et al., 1994), and co-culture with 3T3Wnt4 induces tubulogenesis in the mesenchyme rudiment in organ culture (Kispert et al., 1998), suggesting both essential and sufficient roles of Wnt4 for epithelial differentiation of metanephric mesenchyme. Recently, Wnt9b expressed in the ureteric bud was shown to function upstream of Wnt4 (Carroll et al., 2005). Thus, we attempted to set up assay systems that can identify and characterize the progenitor cells with multipotent differentiation potential from uninduced metanephric mesenchyme using Wnt4 signal. Wnt genes are known to regulate multiple cellular functions using at least three intracellular signaling branches: the β-catenin pathway (canonical pathway), in which stabilized β-catenin interacts with members of the lymphoid enhancer factor/T cell factor (LEF/TCF) family of transcription factors and activates gene expression in the nucleus (Wodarz and Nusse, 1998; Miller et al., 1999); the planar cell polarity (PCP) pathway, which involves Jun N-terminal kinase (JNK) and the Rho family of small guanosine triphosphatases (GTPases) and which directs cytoskeletal rearrangements, coordinated polarization within the plane of epithelial sheets, and morphogenetic movements during development (Veenman et al., 2003; Wallingford et al., 2002); and the Wnt/Ca2+ pathway, which leads to release of intracellular calcium and is implicated in Xenopus ventralization and in the

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Accepted 24 October 2005
regulation of embryonic cell movements (Miller et al., 1999; Veeman et al., 2003; Wallingford et al., 2002). Mechanisms by which Wnt pathways mediate cellular effects in kidney development are poorly understood.

In this study, we established a novel colony-forming assay system using 3T3-expressing Wnt4 to identify renal progenitors in the metanephric mesenchyme. Combining our colony-forming assay with flow cytometry, we found that these progenitors could be enriched by using Sall1 as a marker. We also examined the effects of Wnt downstream branches on the renal progenitors.

MATERIALS AND METHODS
In vitro colony-forming assay
Metanephric mesenchyme of embryonic day (E) 11.5 mice was isolated surgically from embryonic kidney rudiment. The mesenchyme was incubated in 0.05% trypsin-EDTA at 37°C for 10 minutes and then transferred to DMEM with 10% fetal calf serum. Mesenchymal cells were then mechanically dissociated by gentle aspiration through repeated pipetting. Metanephros of E14.5 and 17.5 embryos was incubated in 1 mg/ml Dispase (Invitrogen) at 37°C for 30 minutes then mechanically dissociated by repeated pipetting. NIH3T3 cells stably expressing Wnt3a, Wnt4 and lacZ (Kispert et al., 1998) were mitotically inactivated with mitomycin C before use. Single mesenchymal cells were sorted by FACS Vantage (Becton Dickinson) and plated onto these feeder cells at a low density (5 × 10^3 cells/well of 6-well plates), then cultured in DMEM/F12 with 5% knockout serum replacement (Invitrogen), 10 µg/ml insulin, 6.7 µg/ml sodium selenite, 5.5 µg/ml transferrin, 1×10^-7 mol/dextransmine, 10 mM/l nicotinamide, 2 mM/l l-glutamine, 50 µM/l β-mercaptoethanol, 5 mM/l HEpes and penicillin/streptomycin.

RT-PCR
Primers used for PCR were as follows:
- Pax2, 5'-AGGCGATCTGCCGAAATGAC-3' and 5'-CTCCGCTTCTCTCCTAC3';
- Lin1 (Lhx1 – Mouse Genome Informatics), 5'-TGGACCTTCTCCTGGAAC-3' and 5'-TGTTCCTTCTTGCCAGACCTG-3';
- Eya1, 5'-CCTGCTGACCTTCTTGATGAGACAGATCTAAC-3' and 5'-AAGCTGTAGCTTCACCA-3';
- Sall1 (Sall1 - Mouse Genome Informatics), 5'-CTCTGAGTGGTCTTCCGTC-3' and 5'-GTACAGCCTTCTCCTGGA-3';
- Wnt5, 5'-ACCCAGGCTCAATAAAGA-3' and 5'-GCTGAAGGCTTCTTCACTTG-3';
- Fos all, 5'-GAATTGTTGATGACGCTGGTGC-3' and 5'-GATGAGCATTGCGCCAGATT-3';
- glial cell line derived neurotrophic factor (Gdnf); 5'-CCCGAAGGATATCCTGGACCACA-3' and 5'-TAGCCTCAACCCCAATGCT-3';
- integrin o8, 5'-GGCGGAAAGTGCAGTCTCAAA-3' and 5'-GAAGGAGACATTCCGGAGTG-3';
- integrin α3, 5'-CGGCCTGTGTCACATATCTC-3' and 5'-CGCAGATTGTTCCACAGCAG-3';
- cell adhesion molecule (Ncam), 5'-AGCTGGGCTTCTAGTCCCTG-3' and 5'-CTATGGTGCTCCTGCTCTTT-3';
- E-cadherin (cadherin 1 – Mouse Genome Informatics), 5'-CACACGGACCTTGAGTCCAC-3' and 5'-GAAATGTGTCAGGCGACATC-3';
- podoplanin, 5'-CTCTAGGGCCAGCAACCTCTC-3' and 5'-GCTCTTCTAGGGCCGAGACCTT-3';
- podocalyxin-like, 5'-ACTCATTGCGGCGTCTCCA-3' and 5'-AAAATCCTCAGTGGCTGTTGA-3';
- aquaporin 1 (Aqp1), 5'-CTCTCACAGTACCTCTC-3' and 5'-ACAGTGCCCCTGCAGTCTTT-3';
- chloride channel 5 (Clcn5), 5'-TGAGACGGTGCTTCTCCCT-3' and 5'-GGCAAGAAAGACCGCAATG-3';
- cubulin (intrinsic factor cobalamin receptor), 5'-CAACCTTGACCCTGTTACT-3' and 5'-GACTGACGTCCTCTGAGAG-3';
- Na/K-2Cl co-transporter 2 (Ncc2; Slc12a1 – Mouse Genome Informatics), 5'-CATGGCATTCTCTCTCAGTG-3' and 5'-GCGAGGGCAACTATTTCTCG-3';
- Clec2 (Clec2k – Mouse Genome Informatics), 5'-CCTCTCACTCTGCTGTTG-3' and 5'-AACAGTGCCGAGGCTA-3';
- gene expression analysis by FACS Vantage (Becton Dickinson) and plated onto these feeder cells. NIH3T3 cells stably expressing Wnt3a, Wnt4 and lacZ (Kispert et al., 1998) were mitotically inactivated with mitomycin C before use. Single mesenchymal cells were sorted by FACS Vantage (Becton Dickinson) and plated onto these feeder cells at a low density (5 × 10^3 cells/well of 6-well plates), then cultured in DMEM/F12 with 5% knockout serum replacement (Invitrogen), 10 µg/ml insulin, 6.7 µg/ml sodium selenite, 5.5 µg/ml transferrin, 1×10^-7 mol/dextransmine, 10 mM/l nicotinamide, 2 mM/l l-glutamine, 50 µM/l β-mercaptoethanol, 5 mM/l HEpes and penicillin/streptomycin.

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Retroviral infection

The cDNA clones of the active mutant form of β-catenin (pUC-\textit{EF-1α}-\textit{β-catenin\textsuperscript{\textminus 8,76AA}}) (Miyaegishi et al., 2000), the full length of rat axin (p\textit{RSKS-rAxin}) (Ikeda et al., 1998), and both constitutively-active and dominant-negative mutant forms of human \textit{Rac1} and \textit{RhoA} with N-terminus flag tag [p\textit{CAGIP-flag-Rac1} (Val), p\textit{CAGIP-flag-Rac1} (Asn), p\textit{CAGIP-flag-RhoA} (Val), p\textit{CAGIP-flag-RhoA} (Asn)] were subcloned into retroviral vector p\textit{MY-153EGFP} (Kitamura et al., 2003). To produce recombinant retrovirus, these plasmid vectors were transfected into the virus packaging cell line PLAT-E (Moriai et al., 2000) using FuGENE (Roche), and supernatant from the transfected cells was collected to infect cells of the metanephric mesenchyme. The viral supernatant was centrifuged at 20,000 \(g\) overnight at 4°C to concentrate the virus. To infect mesenchymal cells with the retrovirus, dissociated mesenchymal cells were resuspended into the concentrated virus supernatant with adding polybrene. The suspension was centrifuged 1400 \(g\) for 4 hours at room temperature. After washing with PBS, mesenchymal cells were plated onto 3T3 feeder cells.

Immunocytochemistry and lectin staining

The colonies formed on 3T3Wnt4 feeder were fixed with 4% paraformaldehyde in PBS for 20 minutes at 4°C. After washing with PBS, PBS containing 2% skimmed milk and 0.1% Triton-X was incubated as a blocking solution for 1 hour at room temperature. The fixed dishes were incubated with primary antibodies overnight at 4°C followed by incubating with secondary antibodies for 1 hour at room temperature. The following antibodies were used: rabbit anti-Pax2 (Babco), rabbit anti-WT1 (Santa Cruz), mouse anti-E-cadherin (Becton Dickinson), rabbit anti-AQP1 (Chemicon), and rabbit anti-phosphorylated JNK1 and 2 (Biosource). Rhodamine-conjugated anti-rabbit IgG (H+L) and anti-mouse IgG (Chemicon) were used as secondary antibodies. To examine the expression of a proximal renal tubule-specific marker, fluorescein isothiocyanate (FITC)-conjugated \textit{Lotus Tetragonobulus} lectin (LT; Vector Labs) was used. After each step, the cultured cells were washed three times with PBS containing 0.1% Triton-X. For detection of Sall1, mesenchymal cells derived from \textit{Sall1-GFP} heterozygote embryos were cultured on 3T3 feeder and subjected to GFP immunostaining procedure using rabbit anti-GFP (Molecular Probes). Rhodamine-conjugated peanut agglutinin (PNA; Vector Labs) staining was done as described (Gilbert et al., 1994). Organ culture tissues were fixed with 4% paraformaldehyde in PBS for 1 hour at 4°C and incubated in PBS including 0.1% saponin (Sigma) for 1 hour at 37°C, then the same staining procedure was carried out. Staining with rabbit anti-secreted frizzled-related protein 2 (sFRP2; Santa Cruz) and FITC-conjugated \textit{Dolichos biflorus} agglutinin (DBA; Vector Labs) were also used on sections of paraffin-embedded explants to examine the effect of reagents on tubule formation and branching, respectively.

RESULTS

In vitro colony formation from E11.5 metanephric mesenchyme

We cultured single cells from the metanephric mesenchyme of E11.5 embryos, using 3T3Wnt4 as a feeder layer in a serum-free condition. The metanephric mesenchyme of transgenic mice ubiquitously expressing enhanced green fluorescence protein (EGFP; Okabe et al., 1997) was used to distinguish mesenchyme-derived cells from feeder cells, and single cells sorted by flow cytometry were cultured at a low cell density on 3T3Wnt4. This culture condition resulted in the formation of sheet-like colonies not formed on 3T3lacZ (Fig. 1A, upper panels), while scattered fibroblast-like cells were observed in both conditions (Fig. 1A, lower panels, arrows). Colonies were not formed in the presence of frizzled (Fz)-Fc chimeric protein, a Wnt inhibitor, thus confirming an essential role of Wnt4 for colony formation (Fig. 1B). Colonies were not formed by culturing in the conditioned medium from 3T3Wnt4 without feeder cells (data not shown). Colonies were also formed on 3T3Wnt3a, but not in feeder-free conditions using a purified recombinant Wnt3a protein (data not shown). These data suggested the requirement of other signals from 3T3 cells, in addition to the Wnt signals for the colony formation. In the presence of serum, colonies were not formed even on 3T3Wnt4, and some factors in the serum might prevent colony formation (data not shown). When colonies on 3T3Wnt4 were dissociated and plated onto fresh feeder cells at day 10 of culture, few colonies were obtained, and maintenance of these colonies could not be achieved (data not shown). When we tried colony-formation by using polycarbonate filters, which separate mesenchymal cells from the feeder layer, colonies were formed but the number of colonies formed was much smaller than that formed by directly culturing on feeder cells (data not shown).

To characterize the molecular profiles of the colonies, genes expressed in the metanephric mesenchyme were examined by RT-PCR using RNA from the colonies together with 3T3Wnt4 (Fig. 1C). All the mesenchymal genes examined (\textit{Pax2}, \textit{Lim1}, \textit{Eya1}, \textit{Sall1}, \textit{WT1}, \textit{Hoxa1}, \textit{Gdnf}, integrin α8, integrin α3, \textit{Ncam}, \textit{E-cadherin} and \textit{K-cadherin}) were expressed, and the expression continued to day 20 (Fig. 1C, lanes 3-5). By contrast, when cultured on 3T3lacZ, the expression of these genes was below the detection level (lanes 7-9). The expression of ureteric bud markers (\textit{Ret} and \textit{Hoxb7}) were not detected in mesenchyme separated from ureteric bud, suggesting that the separation was successful (lane 1). To determine the potential for differentiation within the colonies, markers for terminally differentiated epithelia in glomeruli (podocyte), proximal or distal tubules, and the loop of Henle were also examined (glomeruli: \textit{α-actinin-4}, CD2-AP, P-cadherin, podoplanin and podocalyxin; proximal tubule: \textit{Aqp1}, \textit{ClC5}, cubilin, megalin and \textit{Sglt1}; Henle’s loop: \textit{Bnr1} and \textit{Nkcc2}; Henle’s loop or distal tubule: \textit{Clck2}, polycystin 2, and \textit{Romk2}; distal tubule: \textit{ENaC}, Na/Ca exchanger and polycystin 1. These markers encode: (1) cytoskeletal or structural proteins: \textit{α-actinin-4}, CD2-AP, P-cadherin, podoplanin and podocalyxin; (2) transcription factor: \textit{Bnr1}; (3) water or ion channels: \textit{Aqp1}, \textit{ClC5}, \textit{Clck2}, \textit{Romk2}, \textit{Enac}, and polycystin 1 and 2; and (4) transporters: cubilin, megalin, \textit{Sglt1}, \textit{Nkcc2} and Na/Ca exchanger. As shown in Fig. 1C, almost all the genes examined were expressed at day 20 on 3T3Wnt4 (lane 5), while these markers were not expressed on 3T3lacZ (lanes 7-9). To ascertain that these genes were expressed by the colony-forming cells, colonies were formed from GFP transgenic mesenchyme, and cells expressing GFP were separated from feeder layers by using flow cytometry sorting. RT-PCR using RNA from these cells suggested that the marker genes examined were indeed expressed by colony-forming cells (lane 10). Furthermore, we made use of immunocytochemistry and found that \textit{Pax2} (Fig. 1D-F), E-cadherin (Fig. 1G-I), \textit{Sall1} (Fig. 1J.K), and \textit{Aqp1} (Fig. 1L.M) were expressed on colonies. The expression of \textit{Pax2} and \textit{E-cadherin} was not detected on immunocytochemistry at day 3, and was subsequently upregulated by day 10, which was consistent with the result of RT-PCR (Fig. 1D,E,G,H). These data suggest that dissociated cells from the metanephric mesenchyme form colonies on 3T3Wnt4 feeder cells in serum-free conditions, and that these colonies contain differentiated epithelia expressing marker genes for epithelia in glomeruli (podocyte), proximal or distal tubules, and the loop of Henle.

Colonies are derived from a single multipotent renal progenitor

To confirm that these colonies were derived from a single cell, each single cell sorted from the EGFP transgenic mesenchyme was cultured in an individual well of 96-well plates coated with 3T3Wnt4. The sheet-like colony was found in 166 wells out of a total of 1632 (10.2%) from three independent experiments (Fig. 2A).
To examine the multilineage differentiation of single cell-derived colonies, RT-PCR was done for 22 independent wells containing a colony at day 20. The representative data from three colonies are shown in Fig. 2B (lanes 1-3). Although variation existed between colonies, all the colonies expressed markers for each of the three segments: glomerular podocytes, proximal and distal tubules, and the loop of Henle. Double staining using PNA and LTL, specific to glomerular podocytes and the proximal renal tubule, respectively, showed that adult kidney (8 weeks old) contained three kinds of cells; single-positive for PNA (those in the glomerulus); single-positive for LTL (those in the proximal renal tubule); and double-negative for LTL or PNA (Fig. 2C, left panel). Similarly, a single cell-derived colony at day 20 contained these three kinds of cells (Fig. 2C, right panel). With a combination of LTL and E-cadherin, at least three cell types were observed in adult kidney (Fig. 2D, left panel) and in a single cell-derived colony (right panel): cells strongly expressing only E-cadherin characteristic of distal renal tubules (Fig. 2D, arrows), and LTL-positive or -negative cells, with a faint expression of E-cadherin in the cell boundary. These results suggest that a colony was derived from a single progenitor, with multipotent differentiating capacity into epithelial cells in glomeruli, proximal and distal tubule, and the loop of Henle.

Colony-forming progenitors exist in the Sall1-GFP<sup>high</sup> subpopulation of the metanephros

We next attempted to identify prospectively the renal progenitor cells using Sall1-GFP knock-in mice (Takasato et al., 2004). As Sall1 is expressed in mesenchyme-derived tissues, GFP was detected in the mesenchyme around the ureteric bud at E11.5 in the Sall1-GFP<sup>heterozygous</sup> mouse (Fig. 3A, arrows). At E17.5, GFP-expressing cells were observed in the mesenchyme near the surface, as well as in C- or S-shaped bodies, and parts of renal tubules (Fig. 3B). By flow-cytometrical analysis, these subpopulations were fractionated based on the expression of Sall1-GFP; Sall1-GFP<sup>high</sup>,...
Sall1-GFPlow and Sall1-GFPnegative (Fig. 3C), and cells in these subpopulations were separated by flow cytometry sorting to be characterized using RT-PCR. As shown in Fig. 3D, Sall1-GFPhigh cells expressed Sall1 and Pax2. Sall1-GFPlow cells expressed markers of stroma (Foxd1, previously known as Bf2), endothelia (Flk1 and VE-cadherin), and blood cell (Cd45), in addition to Sall1 and Pax2. Sall1-GFPnegative cells expressed Flk1 and Cd45. The markers of fully differentiated renal epithelia were not expressed in these three populations. These data suggested that cells of stromal lineage were included in cell populations weakly expressing Sall1 and that those of hemangiogenic lineage were included in both Sall1-GFPlow and Sall1-GFPnegative populations. Then, the numbers of the colony-forming progenitors in each subpopulation were examined using the low-density culture on 3T3Wnt4 (Fig. 3E). At E11.5, colonies were formed exclusively from the Sall1-GFPhigh population, and not from Sall1-GFPlow or Sall1-GFPnegative populations. At E14.5 and 17.5, colonies were also formed only from Sall1-GFPhigh subpopulations, but the frequency of colony-forming progenitors decreased as gestation proceeded. These results indicate that renal progenitors with multipotent differentiating capacity are included in cell populations strongly expressing Sall1 throughout gestation periods.

**Sall1-GFPhigh mesenchyme reconstitutes a three-dimensional structure in organ culture**

We next examined the in vitro differentiation capacity of three subpopulations in E11.5 mesenchyme by modifying organ culture of mesenchyme rudiments (Grobstein, 1953; Kispert et al., 1998). Sall1-GFPhigh, Sall1-GFPlow and Sall1-GFPnegative cells were separated by flow cytometry, aggregated to form a cell pellet by centrifugation and cultured on 3T3Wnt4 feeder cells in an organ culture setting. Starting from day 3 in culture, tubulogenesis was observed only in the aggregate of the Sall1-GFPhigh population (Fig. 4A, upper panels), while that from Sall1-GFPlow or Sall1-GFPnegative did not differentiate and disappeared by day 7 (Fig. 4A, lower panels; data of Sall1-GFPnegative, not shown). In sections of the Sall1-GFPhigh aggregate (Fig. 4B), many tubule- (t) and glomerulus-like structures (g) were observed, and the expression of markers for glomerular podocyte (Wt1, Fig. 1C, red) and proximal tubule (LTL, green) was confirmed by confocal microscopy. These data suggest that only Sall1-GFPhigh cells differentiate into renal epithelia in vitro in a three-dimensional setting, in addition to forming colonies.

**Colony size is affected by the absence of Sall1**

To investigate the role of Sall1 in colony formation, mesenchymal cells from Sall1+/+, Sall1+/- and Sall1–/– embryos at E11.5, which were obtained from intercrosses of Sall1-GFP mice, were plated on 3T3Wnt4 feeder cells at a low density. Ten days after culture, double immunostaining using anti-GFP and anti-E-cadherin antibodies was done to strengthen the green fluorescence and to examine the expression of E-cadherin, respectively (Fig. 5). The numbers of colonies formed were not significantly different among wild-type, heterozygous and homozygous mesenchyme, suggesting that colony-forming progenitors do exist and are not decreased in the absence of Sall1 (data not shown). Colonies derived from Sall1+/+ wild-type mesenchyme were not stained with GFP (Fig. 5A), while Sall1+/- and Sall1–/– colonies were positive for GFP (Fig. 5C,E, green), indicating that Sall1 itself is not required for Sall1 promoter activity. Colonies from all three groups (Sall1+/+, Sall1+/- and Sall1–/–) were also positive for E-cadherin (Fig. 5B,D,F), suggesting that differentiation (mesenchymal-to-epithelial transformation) may not be impaired in the absence of Sall1. Indeed, marker gene expression for terminally differentiated epithelia in glomeruli and renal tubules was not changed among Sall1+/+, Sall1+/- and Sall1–/– colonies (Fig. 5E,F), suggesting that differentiation (mesenchymal-to-epithelial transformation) may not be impaired in the absence of Sall1. Colony size was larger in E-cadherin (red, arrow, distal tubule marker) and with LTL (green). Scale bars: 50 μm.

**Table 1. Colonies derived from Sall1-mutant metanephric mesenchyme**

<table>
<thead>
<tr>
<th>Genotype</th>
<th>Embryos*</th>
<th>Area at day 10 (mean±s.d.) (μm²)</th>
<th>P</th>
</tr>
</thead>
<tbody>
<tr>
<td>+/+</td>
<td>2</td>
<td>16,118±7219</td>
<td>0.44</td>
</tr>
<tr>
<td>+/-</td>
<td>2</td>
<td>16,318±7473</td>
<td>&lt;0.001</td>
</tr>
<tr>
<td>–/-</td>
<td>2</td>
<td>5140±2071</td>
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*Number of embryos examined. P values were analyzed against wild type (+/+) using a t-test. Representative data from one experiment are shown.
required for generation or differentiation of renal progenitors, but the colony size is affected by Sall1 absence. This is consistent with our previous report that Sall1-deficient mesenchyme is competent with respect to epithelial differentiation tested by spinal cord recombination (Nishinakamura et al., 2001). In the spinal cord recombination experiments, Sall1-deficient mesenchyme was consistently smaller than wild-type mesenchyme, but this could be due to differences in the initial size of the mesenchyme. Using the colony-forming assay starting from a single cell, we now show that Sall1 is indeed required for the colony from the mesenchyme to develop into a normal size.

The PCP pathway regulates colony size and the differentiation of colony-forming cells

By combining the colony-forming assay set up in this study and gene transfer using retroviral vector pMY-IRES-EGFP (Morita et al., 2000; Kitamura et al., 2003), we observed EGFP expression in 12.9% of colony-forming progenitor cells (116 colonies expressing green fluorescence per total of 896 colonies formed from three independent experiments). Thus, the colony-forming assay in this study enables us to investigate direct effects of reagents and gene transduction on colony-forming progenitor cells, allowing us to examine the roles of Wnt and its downstream branches in kidney development. Positive immunostaining of the colonies for activated JNK1 and 2 indicated that the JNK branch of the PCP pathways (Boutros et al., 1998) may be activated downstream of Wnt4 (Fig. 6A). Indeed, the addition of two kinds of JNK inhibitor (JNKI1 and JNKI2) (Bonny et al., 2001; Bennett et al., 2001) gave rise to smaller colonies than did the control without reagents (Fig. 6B,C, colonies from EGFP transgenic mesenchyme, Table 2). The result of control experiments using the HIV-TAT peptide excluded the possibility that the effects of JNKI1 were derived from non-specific toxicity of the peptide constituting the inhibitor (Fig. 6B). We then investigated effects of both activation and inactivation of Rac1, one of the Rho family GTpases implicated in PCP pathways (Habas et al., 2003), on colony formation. Cells from wild-type E11.5 mesenchyme were transduced with both constitutively active (CA) and dominant-negative (DN) forms of Rac1 using the retroviral vector pMY-IRES-EGFP. Colonies consisting of cells expressing both EGFP and CA-Rac1 were larger than those transduced with pMY-IRES-EGFP controls (Fig. 6D, Table 3), suggesting positive effects on colony size. By contrast, the transduction of DN-Rac1 gave rise to smaller

Table 2. Effects of reagents on the area of colony

<table>
<thead>
<tr>
<th>Reagent</th>
<th>Area at day 10 (mean±s.d.)(μm²)</th>
<th>P</th>
</tr>
</thead>
<tbody>
<tr>
<td>Control (without reagents)</td>
<td>35,429±15,132</td>
<td></td>
</tr>
<tr>
<td>HIV-TAT peptide</td>
<td>38,198±11,357</td>
<td>0.25</td>
</tr>
<tr>
<td>JNK inhibitor 1</td>
<td>777±4520</td>
<td>&lt;0.001</td>
</tr>
<tr>
<td>Control (without reagents)</td>
<td>36,330±15,056</td>
<td></td>
</tr>
<tr>
<td>JNK inhibitor 2</td>
<td>668±2834</td>
<td>&lt;0.001</td>
</tr>
<tr>
<td>Y27,632</td>
<td>92,359±24,768</td>
<td>&lt;0.001</td>
</tr>
<tr>
<td>LiCl</td>
<td>568±2535</td>
<td>&lt;0.001</td>
</tr>
<tr>
<td>BIO</td>
<td>743±497</td>
<td>&lt;0.001</td>
</tr>
<tr>
<td>Dkk-1</td>
<td>31,998±12,566</td>
<td>0.147</td>
</tr>
</tbody>
</table>

n, number of colonies measured. P values were analyzed against control using a t-test. For each reagent, more than three independent experiments were performed. Representative data from one experiment are shown.
colonies than did the controls (Fig. 6D, Table 3). The numbers of colonies formed were not significantly changed either with the addition of inhibitors or with gene transduction (data not shown). These data indicate that Rac and JNK pathways positively regulate colony size.

By contrast, inactivation of the Rho/Rho-associated protein kinase (ROCK) pathway, another branch of PCP (Strutt et al., 1997; Winter et al., 2001; Habas et al., 2001; Habas et al., 2003), with the addition of ROCK inhibitor, Y27,632 (Uehata et al., 1997) (Fig. 6E, colonies from EGFP transgenic mesenchyme, Table 2), or the transduction of DN-RhoA increased the colony size (Fig. 6F, Table 3), while the activation with CA-RhoA decreased it (Fig. 6F, Table 3). Activation of β-catenin signaling both with the addition of two kinds of glycogen synthetase kinase (GSK)-3 inhibitors, lithium chloride (LiCl) (Klein and Melton, 1996) (Fig. 6G, colonies from EGFP transgenic mesenchyme, Table 2) and (2′-Bromoindirubin-3′-oxime (BIO) (Sato et al., 2004) (Table 2) and with the transduction of the active form of β-catenin (Fig. 6H, Table 3) gave rise to smaller colonies. However, inactivation of the β-catenin pathway with the addition of recombinant dickkopf homolog 1 (Dkk-1), a specific inhibitor of the β-catenin pathway (Glinka et al., 1998) and with the transduction of axin (Zeng et al., 1997) exerted no significant effects on colony formation (Tables 2, 3). These data suggest inhibitory roles of Rho/ROCK and β-catenin pathways in regulating colony size.

RT-PCR analysis showed that the expression of marker genes (E-cadherin, P-cadherin, podocalyxin, Aqp1, Clc5, Brn1, Nkcc2, ENaC and Clck2) was inhibited with the addition of JNK inhibitors (Fig. 6I). Although the addition of LiCl and JNK inhibitors resulted in a decreased size of colonies to the same extent, immunostaining confirmed that E-cadherin was lost with JNK inhibitors 1 and 2, but not with LiCl (Fig. 6J, colonies from EGFP transgenic mesenchyme). Thus, the JNK pathway is likely not only to regulate colony size but also to be involved in epithelialization (mesenchymal-to-epithelial transformation) of colony-forming progenitors.

### Table 3. Effects of gene transduction on the area of colony

<table>
<thead>
<tr>
<th>Gene transduced</th>
<th>n</th>
<th>Area at day 20 (mean±s.d.) (µm²)</th>
<th>P</th>
</tr>
</thead>
<tbody>
<tr>
<td>Control (vector)</td>
<td>23</td>
<td>49,666±32,111</td>
<td></td>
</tr>
<tr>
<td>CA-Rac1</td>
<td>12</td>
<td>83,990±52,619</td>
<td>0.01</td>
</tr>
<tr>
<td>DN-Rac1</td>
<td>24</td>
<td>23,045±22,791</td>
<td>&lt;0.001</td>
</tr>
<tr>
<td>CA-RhoA</td>
<td>12</td>
<td>25,658±19,205</td>
<td>&lt;0.005</td>
</tr>
<tr>
<td>DN-RhoA</td>
<td>21</td>
<td>89,723±49,989</td>
<td>0.001</td>
</tr>
<tr>
<td>Control (vector)</td>
<td>38</td>
<td>62,013±31,212</td>
<td></td>
</tr>
<tr>
<td>Active-β-catenin</td>
<td>20</td>
<td>23,241±21,685</td>
<td>&lt;0.001</td>
</tr>
<tr>
<td>Axin</td>
<td>22</td>
<td>65,352±27,675</td>
<td>0.34</td>
</tr>
</tbody>
</table>

n, number of colonies measured. P values were analyzed against control using a t-test. Data from three independent experiments is shown.
The PCP pathway is involved in tubulogenesis in organ culture

To examine if the results described above were consistent with kidney formation in vivo, we tested the effect of the reagents on whole metanephroi (Fig. 7A-E) and mesenchyme rudiments (F-J) in an organ culture setting. After 7 days of culture, the size of kidney structures was measured. As compared with the control explants cultured without reagents (Fig. 7A,F), the addition of JNK inhibitor 1 (Fig. 7B,G) and JNK inhibitor 2 (Fig. 7C,H) and LiCl (Fig. 7E,J) resulted in a decrease in the size of kidney structures developed, while the addition of ROCK inhibitor Y27,632 (Fig. 7D,I) gave rise to larger ones. These findings were observed both in whole kidney and in mesenchyme rudiments, and were confirmed statistically (Table 4). We also evaluated the effect of the reagents on tubule formation and branching of ureteric bud by staining with an antibody against secreted frizzled-related protein.

Table 4. Effects of reagents on the area of organ culture

<table>
<thead>
<tr>
<th>Reagent</th>
<th>Whole metanephroi n 7</th>
<th>Area at day 7 (mean ± s.d.) (mm²)</th>
<th>P</th>
<th>Mesenchymal rudiments n 6</th>
<th>Area at day 7 (mean ± s.d.) (mm²)</th>
<th>P</th>
</tr>
</thead>
<tbody>
<tr>
<td>Control (without reagents)</td>
<td>1.717±0.381</td>
<td></td>
<td></td>
<td>1.912±0.200</td>
<td></td>
<td></td>
</tr>
<tr>
<td>HIV-TAT peptide</td>
<td>1.500±0.215</td>
<td>0.12</td>
<td></td>
<td>1.838±0.364</td>
<td>0.33</td>
<td></td>
</tr>
<tr>
<td>JNK inhibitor 1</td>
<td>1.020±0.325</td>
<td>&lt;0.005</td>
<td></td>
<td>0.651±0.131</td>
<td>&lt;0.001</td>
<td></td>
</tr>
<tr>
<td>JNK inhibitor 2</td>
<td>1.105±0.260</td>
<td>&lt;0.005</td>
<td></td>
<td>1.078±0.377</td>
<td>&lt;0.001</td>
<td></td>
</tr>
<tr>
<td>Y27,632</td>
<td>2.871±0.879</td>
<td>&lt;0.01</td>
<td></td>
<td>3.401±0.433</td>
<td>&lt;0.001</td>
<td></td>
</tr>
<tr>
<td>LiCl</td>
<td>0.716±0.070</td>
<td>&lt;0.001</td>
<td></td>
<td>1.270±0.238</td>
<td>&lt;0.001</td>
<td></td>
</tr>
</tbody>
</table>

n, number of explants measured. P values were analyzed against control by using a t-test. Data from five independent experiments each for whole metanephroi and mesenchyme rudiments are shown.
protein 2 (sFRP2; Fig. 7K-N, red), the gene expressed only in newly formed tubular epithelia (Lescher et al., 1998), and DBA (Fig. 7K, green), respectively. While some tubules expressing sFRP2 were found in explants treated with control HIV-TAT peptide (Fig. 7K,M, arrows), they were lost with JNK inhibitor 1 both in whole metanephroi (Fig. 7L) and in mesenchyme explants (Fig. 7N), suggesting the involvement of JNK pathways in mesenchymal-to-epithelial transformation in organ culture. By contrast, branching of ureteric bud was proportional to the size of explants, and there were no specific effects of the reagents observed on the ureteric bud itself (data not shown). These findings were consistent with the results observed in the colony-forming assay (Fig. 6, Table 2). Thus our colony-forming assay, which enables analysis at a single cell level, could be used for examining mechanisms of three-dimensional kidney development.

**DISCUSSION**

**Renal progenitors defined by colony-forming assay**

In this study, we provide evidence, using in vitro clonal analysis combined with flow cytometry, for the presence of progenitor cells in the fetal mouse kidney. Results of staining with PNA, LTL and E-cadherin, and of RT-PCR showed the differentiating capacity of a single Sall1-GFPhigh cell into glomerular epithelia (podocyte), proximal and distal tubule, respectively. In addition to lineage-marker expression, both glomerulus- and tubule-like structures were reconstituted by Sall1-GFPhigh cells, supporting their differentiation ability. A multipotent renal stem cell line has been isolated from E11.5 mesenchyme utilizing immortalization with T antigen of SV40 virus (Oliver et al., 2002). The cell line expresses marker genes of endothelia and smooth muscle cells with treatment of TGFβ1, in addition to gene expression of mesenchyme and renal epithelia. It has not been known, however, whether they normally resided in the fetal kidney or accidentally emerged by the influence of the process with immortalization. In our colony-forming system, gene expression of endothelia and smooth muscle cells was not observed, and expression of Foxd1 (BF2), a marker gene specific to stroma, a third cell population included in metanephros was not found (data not shown). Thus, it remains to be elucidated whether embryonic kidney contains stem cells that can differentiate into endothelium, smooth muscle or stroma in addition to epithelia of glomerulus and renal tubules.

The renal progenitors defined by our colony-forming assay are included in cell populations strongly expressing Sall1 throughout gestation periods, and they might continue to reside in the outer layer of embryonic kidney, where undifferentiated metanephric mesenchyme resides and strongly expresses Sall1 (Fig. 3B). As shown in Table 5, the total cell numbers of metanephros increased and the frequency of colony-forming Sall1-GFPhigh cells decreased as gestation proceeded. Interestingly, the calculated numbers of the colony-forming cells remained almost constant throughout gestation periods (400-800 cells/embryonic kidney). The amplification of these progenitors might not occur in the embryonic kidney. One interesting question is whether they continue to remain in the adult kidney. From 8-week-old mice, however, colonies were not formed under the same culture conditions (data not shown). Renal progenitors defined by our colony-forming assay might be lost by the time kidney development is complete.

**Table 5. Calculated number of colony-forming progenitors in embryonic kidney**

<table>
<thead>
<tr>
<th></th>
<th>E11.5</th>
<th>E14.5</th>
<th>E17.5</th>
</tr>
</thead>
<tbody>
<tr>
<td>Total cell number of kidney (×10⁵)</td>
<td>0.77±0.24</td>
<td>21.4±2.7</td>
<td>77.9±19.4</td>
</tr>
<tr>
<td>Sall1-GFPhigh cells in kidney (%)</td>
<td>23.6±1.7</td>
<td>46.3±2.1</td>
<td>44.5±0.9</td>
</tr>
<tr>
<td>Colony formation in Sall1-GFPhigh cells (%)</td>
<td>32.2±2.8</td>
<td>0.79±0.18</td>
<td>0.14±0.07</td>
</tr>
<tr>
<td>Calculated numbers of colony-forming cells*</td>
<td>585.1</td>
<td>782.7</td>
<td>485.3</td>
</tr>
</tbody>
</table>

*Numbers of colony-forming cells were calculated by multiplying the means of the three values above.

It remains to be elucidated whether embryonic kidney contains stem cells that can differentiate into endothelium, smooth muscle or stroma in addition to epithelia of glomerulus and renal tubules. The renal progenitors defined by our colony-forming assay are included in cell populations strongly expressing Sall1 throughout gestation periods, and they might continue to reside in the outer layer of embryonic kidney, where undifferentiated metanephric mesenchyme resides and strongly expresses Sall1 (Fig. 3B). As shown in Table 5, the total cell numbers of metanephros increased and the frequency of colony-forming Sall1-GFPhigh cells decreased as gestation proceeded. Interestingly, the calculated numbers of the colony-forming cells remained almost constant throughout gestation periods (400-800 cells/embryonic kidney). The amplification of these progenitors might not occur in the embryonic kidney. One interesting question is whether they continue to remain in the adult kidney. From 8-week-old mice, however, colonies were not formed under the same culture conditions (data not shown). Renal progenitors defined by our colony-forming assay might be lost by the time kidney development is complete.
Analysis of gene function in kidney development by colony-forming assay

The knowledge of gene function in kidney development has mainly been obtained from analyses using knockout mice, while experimental systems that investigate gene function in individual cells of metanephros have been lacking. By setting up a novel system combining colony formation from a single cell and gene transduction using a retroviral vector, our culture system enables the direct observation of effects of reagents and gene transduction on colony-forming progenitor cells. As similar results were obtained from organ culture experiments (Fig. 7), it is less likely that the cellular behavior observed in our colony-assay system might be artifactual.

Mice lacking the constituent genes involved in downstream branches of Wnt signaling pathways often show early embryonic lethality, such as Rac1 (Sugihara et al., 1998), Jnk1 and Jnk2 (Kuan et al., 1999), β-catenin (Haegel et al., 1995), axin (Zeng et al., 1997), and their functions in kidney morphogenesis remain largely unknown. Using our culture system, functions of these genes in metanephros development were elucidated. Furthermore, experiments for colony formation from mesenchyme of Sall1-mutant embryos demonstrated the roles of Sall1 for the colony size. Thus, the colony-assay system set up in this study can also be applied to the analysis of genetic mouse models.

Roles of PCP pathway in kidney development

Among downstream branches of Wnt4 signal, we found that Rac- and JNK-dependent PCP pathways positively regulated the colony size and the differentiation of colony-forming cells. This result is compatible with several previous reports (Du et al., 1995; Ungar et al., 1995). Activation of the β-catenin pathway, which is polarized movement during embryonic development regulated by the PCP pathway (Du et al., 1995; Ungar et al., 1995). Activation of the β-catenin signaling was not detected at various stages of differentiation of the metanephric mesenchyme, which was examined using transgenic mice expressing the lacZ reporter genes under the control of β-catenin/TCF responsive elements (Maretto et al., 2003). Furthermore, activation of the β-catenin pathway is implicated in epithelial-to-mesenchymal transition during mesoderm formation in embryonic development and tumorigenesis (Polakis, 2000; Bienenstock and Clevers, 2000), which is opposite to the process we examined in this study: mesenchymal-to-epithelial transformation. Thus it may be possible that PCP pathways, not the β-catenin pathway, play central roles as downstream branches of Wnt4 for epithelial differentiation of metanephric mesenchyme.

We demonstrated that Rac1 and RhoA play positive and negative roles for the regulation of colony size, respectively. The Rho family of small GTPases is known to be implicated in cell proliferation by the regulation of cell cycle progression, in addition to its effects on the cytoskeleton (Etienne-Manneville and Hall, 2002). Antagonism, or the opposing activities, between two Rho GTPases have been noted in some cell types (Luo, 2000; Gu et al., 2005). For instance, a hematopoietic-specific Rho GTPase, RhoH, negatively regulates both growth and actin-based function of hematopoietic progenitors via suppression of Rac-mediated signaling (Gu et al., 2005). Similarly, our data suggested the possibility that Rac1 and RhoA might antagonistically regulate the growth of progenitors in kidney development. Recently the roles of the JNK pathway in epithelial morphogenesis have been noted both in Drosophila and in mice (Xia and Karin, 2004). Our data also suggested the essential roles of JNK pathways in epithelialization, as well as in regulation of colony size. Common mechanisms regulating epithelial morphogenesis might underlie these processes. The PCP pathways, including the Rho family of small GTPases and JNK, control several developmental processes, mainly by regulating cell cytoskeletons, such as the polarity of hairs on the epidermal cells of Drosophila wings, the arrangement of ommatidial cells of Drosophila eyes, the polarity of stereocilia in the inner ears of mammals, and convergent extension in Xenopus and zebrafish (Veeman et al., 2003; Wallingford et al., 2002). In addition to these processes, we provide a novel hypothesis of the involvement of the PCP pathways in kidney development.

In summary, we set up a novel colony-forming assay by which we demonstrated the presence and the frequency of multipotent progenitor cells in embryonic kidneys. This assay would serve as a useful tool for analyzing differentiation mechanisms in the kidney at a single cell level, taking advantage of the facility of gene transfer.

We thank Dr M. Okabe for providing EGFP transgenic mice, Dr A. Kidachi for pBSKS+rAxin, Dr A. Nagafuchi for pUC-EF-1α-β-catenin250-3HA, Dr H. Koido for pCAGIP-flag-Rac1 and RhoA, Dr T. Kitamura for pMY/ires-EGFP and PLAT-E, Y. Morita for technical support for FACS, and Dr C. Kobayashi for critically reading the manuscript. This work was partly supported by the Ministry of Health, Labor, and Welfare of Japan.

References


