Ascl1 expression defines a subpopulation of lineage-restricted progenitors in the mammalian retina

Joseph A. Brzezinski, 4th1, Euiseok J. Kim2*, Jane E. Johnson2 and Thomas A. Reh1,†

SUMMARY

The mechanisms of cell fate diversification in the retina are not fully understood. The seven principal cell types of the neural retina derive from a population of multipotent progenitors during development. These progenitors give rise to multiple cell types concurrently, suggesting that progenitors are a heterogeneous population. It is thought that differences in progenitor gene expression are responsible for differences in progenitor competence (i.e. potential) and, subsequently, fate diversification. To elucidate further the mechanisms of fate diversification, we assayed the expression of three transcription factors made by retinal progenitors: Ascl1 (Mash1), Ngn2 (Neurog2) and Olig2. We observed that progenitors were heterogeneous, expressing every possible combination of these transcription factors. To determine whether this progenitor heterogeneity correlated with different cell fate outcomes, we conducted Ascl1- and Ngn2-inducible expression fate mapping using the CreERTM/LoxP system. We found that these two factors gave rise to markedly different distributions of cells. The Ngn2 lineage comprised all cell types, but retinal ganglion cells (RGCs) were exceedingly rare in the Ascl1 lineage. We next determined whether Ascl1 prevented RGC development. Ascl1-null mice had normal numbers of RGCs and, interestingly, we observed that a subset of Ascl1+ cells could give rise to cells expressing Math5 (Atoh7), a transcription factor required for RGC competence. Our results link progenitor heterogeneity to different fate outcomes. We show that Ascl1 expression defines a competence-restricted progenitor lineage in the retina, providing a new mechanism to explain fate diversification.

INTRODUCTION

The retina comprises seven principal cell types: rod and cone photoreceptors, amacrine, bipolar and horizontal interneurons, Müller glia and retinal ganglion cells (RGCs). Retroviral lineage-tracing studies in rodents have shown that all of these cell types derive from a common multipotent progenitor population (Turner and Cepko, 1987; Turner et al., 1990), though fate-restricted progenitors were not observed. Nonetheless, the time of permanent cell cycle exit (‘birthdate’) for each cell type follows a stereotypical pattern (Carter-Dawson and LaVail, 1979; La Vail et al., 1991; Rapaport et al., 2004; Sidman, 1961; Young, 1985). This change in production of the different cell types over the period of retinogenesis has led several investigators to propose that the competence (potential) of progenitors changes over time (Reh and Kljavin, 1989; Watanabe and Raff, 1990), which probably depends on the combination of genes expressed by progenitors (Livesey and Cepko, 2001). Attempts to link directly heterogeneity in progenitors to differences in competence have failed to identify transcription factors that define restricted retinal progenitor populations.

One family of transcription factors that has been shown to be important in the regulation of cell fate is the basic helix-loop-helix (bHLH) family. Three of these transcription factors, Olig2, Ngn2 (Neurog2) and Ascl1 (Mash1), are expressed in subpopulations of progenitor cells throughout the nervous system, including the retina (Guillemot and Joyner, 1993; Jasoni and Reh, 1996; Jasoni et al., 1994; Lu et al., 2000; Nakamura et al., 2006; Shibasaki et al., 2007; Sommer et al., 1996; Takebayashi et al., 2000). Previous studies concluded that these factors are made by retinal progenitors; however, no study has yet analyzed whether these factors are expressed in overlapping or distinct progenitor populations, i.e. whether they indeed define progenitor heterogeneity.

To address this, we first examined Olig2, Ascl1 and Ngn2 expression in progenitors. We found cells that expressed every single, double and triple combination of these factors in the developing retina, consistent with the hypothesis that these factors define progenitor heterogeneity. To determine whether this transcription factor heterogeneity corresponded to different fate outcomes in the progenitors, we conducted Ascl1- and Ngn2-inducible expression fate mapping using the CreERTM/LoxP system (Metzger and Chambon, 2001; Metzger et al., 1995). We found that Ascl1 and Ngn2 gave rise to very different distributions of retinal cells. Ascl1-expressing cells can give rise to all major types of retinal cells, though RGCs were not significantly represented. Interestingly, we found that Ascl1+ cells could express the RGC competence factor Math5 (J. A. Brzezinski, 4th, PhD thesis, University of Michigan, 2005) (Mu et al., 2005; Yang et al., 2003), but this subpopulation of cells did not adopt RGC fate. Together, our results link gene expression heterogeneity in retinal progenitors to different fate choice outcomes: Ascl1 expression defines a competence-restricted lineage in the retina.

MATERIALS AND METHODS

Animals and tamoxifen administration

All animals were used in accordance with University of Washington and UT Southwestern IACUC approved protocols. To trace the lineage of Ascl1+ progenitors, we used the Ascl1CreERT2 knock-in mouse strain in

1Department of Biological Structure, University of Washington, Seattle, WA 98195, USA. 2Department of Neuroscience, UT Southwestern Medical Center, Dallas, TX 75390, USA.

*Present address: Neurobiology Section, Division of Biological Sciences, University of California, San Diego, CA 92093, USA. 1Author for correspondence (tomreh@uw.edu)

Accepted 6 June 2011
which CreER<sup>TM</sup> replaces endogenous Ascl1 (Kim et al., 2011a; Kim et al., 2011b). To track the expression of Ascl1, we used a previously characterized mouse knock-in line in which the coding region of Ascl1 was replaced by a nuclear localized GFP element (Leung et al., 2007). Both Ascl1<sup>GFP<sup>+/</sup></sup> and Ascl1<sup>CreERT2</sup> mice have all of the 5' and 3' regulatory elements intact and GFP (or Cre) expression matches Ascl1 expression (Leung et al., 2007). Heterozygous Ascl1<sup>GFP<sup>+/</sup></sup> mice were intercrossed to generate wild-type, heterozygous and Ascl1<sup>GFP<sup>-</sup></sup>/GFP<sup>-null</sup> mice, which did not survive past birth. To track Math5 expression we used Math5<sup>Sce<sup>-</sup></sup> knock-in mice (Yang et al., 2003). For the Ngn2 lineage, the coding region of Ngn2 was replaced by CreER<sup>TM</sup> (Ngn2<sup>Sce<sup>-</sup>ERT2<sup>TM</sup></sup>) (Ma and Wang, 2006; Zirlinger et al., 2002).

To monitor Cre activity, we used a dual reporter mouse line Gt(ROSA)26Sortm2(ACTB-tdTomato,-EGFP)Luo<sup>/H11032</sup>, Jackson Stock 007576, i.e. m<sub>TmG</sub> that ubiquitously expressed membrane-localized tomato until recombination, at which point it expressed membrane-localized GFP (Muzumdar et al., 2007) from a CMV-β-actin enhancer/promoter element inserted into the ROSA26 locus. To induce recombination, pregnant mice were given 2 mg tamoxifen (T5648, Sigma, St Louis, MO, USA; 10 mg/ml in corn oil) intraperitoneally at both embryonic day (E) 12.5 and E13.5, at which point it expressed membrane-localized GFP (Muzumdar et al., 2007) from a CMV-β-actin enhancer/promoter element inserted into the ROSA26 locus. To induce recombination, pregnant mice were given 2 mg tamoxifen (T5648, Sigma, St Louis, MO, USA; 10 mg/ml in corn oil) intraperitoneally at both embryonic day (E) 12.5 and E13.5, at which point it expressed membrane-localized GFP (Muzumdar et al., 2007) from a CMV-β-actin enhancer/promoter element inserted into the ROSA26 locus. To induce recombination, pregnant mice were given 2 mg tamoxifen (T5648, Sigma, St Louis, MO, USA; 10 mg/ml in corn oil) intraperitoneally at both embryonic day (E) 12.5 and E13.5, at which point it expressed membrane-localized GFP (Muzumdar et al., 2007) from a CMV-β-actin enhancer/promoter element inserted into the ROSA26 locus. To induce recombination, pregnant mice were given 2 mg tamoxifen (T5648, Sigma, St Louis, MO, USA; 10 mg/ml in corn oil) intraperitoneally at both embryonic day (E) 12.5 and E13.5, at which point it expressed membrane-localized GFP (Muzumdar et al., 2007) from a CMV-β-actin enhancer/promoter element inserted into the ROSA26 locus. To induce recombination, pregnant mice were given 2 mg tamoxifen (T5648, Sigma, St Louis, MO, USA; 10 mg/ml in corn oil) intraperitoneally at both embryonic day (E) 12.5 and E13.5, at which point it expressed membrane-localized GFP (Muzumdar et al., 2007) from a CMV-β-actin enhancer/promoter element inserted into the ROSA26 locus. To induce recombination, pregnant mice were given 2 mg tamoxifen (T5648, Sigma, St Louis, MO, USA; 10 mg/ml in corn oil) intraperitoneally at both embryonic day (E) 12.5 and E13.5, at which point it expressed membrane-localized GFP (Muzumdar et al., 2007) from a CMV-β-actin enhancer/promoter element inserted into the ROSA26 locus. To induce recombination, pregnant mice were given 2 mg tamoxifen (T5648, Sigma, St Louis, MO, USA; 10 mg/ml in corn oil) intraperitoneally at both embryonic day (E) 12.5 and E13.5, at which point it expressed membrane-localized GFP (Muzumdar et al., 2007) from a CMV-β-actin enhancer/promoter element inserted into the ROSA26 locus. To induce recombination, pregnant mice were given 2 mg tamoxifen (T5648, Sigma, St Louis, MO, USA; 10 mg/ml in corn oil) intraperitoneally at both embryonic day (E) 12.5 and E13.5, at which point it expressed membrane-localized GFP (Muzumdar et al., 2007) from a CMV-β-actin enhancer/promoter element inserted into the ROSA26 locus. To induce recombination, pregnant mice were given 2 mg tamoxifen (T5648, Sigma, St Louis, MO, USA; 10 mg/ml in corn oil) intraperitoneally at both embryonic day (E) 12.5 and E13.5, at which point it expressed membrane-localized GFP (Muzumdar et al., 2007) from a CMV-β-actin enhancer/promoter element inserted into the ROSA26 locus.

Development 138 (16)
Ascl1\(^{GFP/+}\) line of mice (Leung et al., 2007). Ascl1-GFP expression in heterozygous knock-in mice was consistent with earlier reports on Ascl1 expression in the mouse retina (Brown et al., 1998; Guillemot and Joyner, 1993; Hufnagel et al., 2010). We observed Ascl1-GFP expression in nuclei in the progenitor zone of the central retina at E12.5 (Fig. 1A). At E13.5, Ascl1-GFP expression had spread towards, but not yet reached, the far periphery (Fig. 1B). At E14.5, Ascl1-GFP extended to the far peripheral retina and GFP+ nuclei were absent from the ganglion cell layer (GCL) (Fig. 1C-E). The majority of Ascl1-GFP cells co-expressed Sox2, a pan-progenitor marker (71.9±4.12% s.d.) (Fig. 1C-E, Fig. 2D-E), but only a small fraction of the Sox2 progenitor population made Ascl1-GFP (25.6±3.99% s.d.) (Fig. 2E). The fraction (~28%) of the Ascl1-GFP+ cells that did not express Sox2 probably represents transient persistence of GFP in postmitotic cells derived from Ascl1+ progenitors; however, we cannot exclude the possibility that some postmitotic cells transiently express Ascl1. Similarly, only a subset of Sox2+ and Sox9+ progenitors expressed Olig2 (14.1±3.57% s.d.) and Ngn2 (17.2±3.10% s.d.), respectively (Fig. 2E).

To determine whether these transcription factors were expressed in the same retinal progenitor cells, we compared the expression of Ascl1-GFP with that of Ngn2 and Olig2. At E12.5 and E13.5, the Ngn2 expression domain extended further peripherally than Ascl1-GFP (Fig. 1A, B) and three populations of cells were present: Ascl1-GFP+, Ngn2+ and cells that expressed both markers (Fig. 1A, B). At E14.5, we observed similar numbers of cells expressing Olig2 or Ngn2, whereas about 50% more expressed Ascl1-GFP (Fig. 1F-L, Fig. 2A). Interestingly, we found that all seven molecularly distinct populations of cells existed in the retina at E14.5 (Fig. 1F-L, Fig. 2C). The most abundant population expressed solely Ascl1-GFP (19.3±4.49 s.d. cells per 100 \(\mu m\)) (Fig. 2C). Some of these Ascl1-GFP-only cells are likely to be postmitotic; however, this single labeled population was larger than the Ascl1-GFP+, Sox2-negative population identified in parallel experiments (7.75±1.58 s.d. cells per 100 \(\mu m\)) (Fig. 2D), indicating that most of the Ascl1-GFP-only cells are progenitors. The six other population combinations were less common (about three to nine cells per 100 \(\mu m\)), but when pooled (31.2 cells per 100 \(\mu m\)) accounted for 50% more cells than Ascl1-GFP-only (Fig. 2C). Of the cells that made Ascl1-GFP, it was equally likely that they co-expressed Ngn2 or Olig2 (Fig. 2B). A slightly smaller fraction of the Ascl1-GFP+ population expressed all three markers (20.1±4.75% s.d.) (Fig. 2B). Examining three transcription factors, we found considerable progenitor heterogeneity in our snapshots of retinal development at E14.5 and E18.5 (see Fig. S1 in the supplementary material).

Ascl1+ progenitors form a fate-restricted lineage
The above results indicate that there is considerable heterogeneity in the progenitor population with respect to bHLH gene expression. One way to assess whether these progenitor populations are equivalent is to determine whether they generate different lineages. The lineages of Ngn2+ progenitor cells have already been analyzed.

**Fig. 1. Retinal progenitor transcription factor expression heterogeneity.** (A, B) E12.5 (A) and E13.5 (B) Ascl1\(^{GFP/+}\) mouse retinas stained for Ascl1-GFP (nuclear; green) and Ngn2 (red). Ascl1-GFP expression starts centrally and spreads towards the periphery with age (leading edge marked with arrowheads). (C-E) E14.5 retinas stained for Sox2 (red) and Ascl1-GFP (green). A small number of Ascl1− GFP+ cells do not express Sox2 (arrowhead; enlarged in inset). (F-L) Ascl1-GFP (green), Olig2 (gray) and Ngn2 (red) staining of the E14.5 retina. Cells that express Ascl1-GFP only; Olig2 only; Ngn2 only; Ascl1-GFP and Olig2; Ascl1-GFP and Ngn2; Olig2 and Ngn2; and all three transcription factors (arrows; enlarged in inset) are observed. (M) Ascl1-GFP, Olig2 and Ngn2 expression in E14.5 Ascl1\(^{GFP/+}\) null retinas is similar to control (L). A co-expressing cell is enlarged in inset. GCL, ganglion cell layer; L, lens; O, optic nerve head. Scale bars: 100 \(\mu m\) for A, B; 50 \(\mu m\) for C-M; 10 \(\mu m\) for higher magnification insets.
(Ma and Wang, 2006), but this type of analysis has not been reported for Ascl1+ progenitors. To determine the potential of Ascl1+ cells we conducted a conditional expression fate-mapping experiment utilizing Ascl1CreERT2/++ knock-in mice (Kim et al., 2011a; Kim et al., 2011b), crossed to reporter mice that express membrane localized GFP only after Cre-based recombination. Tamoxifen was used to induce CreERT2 localization to the nucleus and cause recombination. We injected tamoxifen at E12.5 and E13.5 to ensure that the earliest cohort of Ascl1+ cells would be represented in the lineage and to increase the total number of cells that underwent recombination. We immunostained adult retinas from reporter mice lacking Ascl1-Cre (Ascl1+/++) as a control and did not detect any GFP+ cells. No GFP+ cells in Ascl1CreERT2/++ mice were detected if tamoxifen was not administered (data not shown). We observed GFP+ cells distributed in all layers of the retina in E12.5/E13.5 Ascl1CreERT2/++ lineage-traced mice (Fig. 3B-M, see Fig. S2 in the supplementary material). GFP+ cells were often found in small groups (clumps) or in isolation (Fig. 3B-M). We observed GFP+ cells in peripheral retina, which strongly suggests that recombination events occur at the leading edge of the Ascl1 expression domain. However, we did not observe GFP+ cells in the far peripheral retina, consistent with the lack of Ascl1 expression in that domain at E12.5 and E13.5, indicating that CreER activity was neither protracted nor delayed.

When we assayed the cell types present in E12.5/E13.5 Ascl1 lineage-traced animals at 19-21 days of age, we found that all of the principal cell types in the retina were well represented except the ganglion cells (Fig. 3H-P, see Table S1 in the supplementary material). Co-labeling for calbindin to mark horizontal and amacrine cells (Fig. 3H,I), Pax6 to label amacrine (among other) cells (Fig. 3J), Otx2 to mark photoreceptors and bipolar cells (see Fig. S2 in the supplementary material), or Sox9 to label Müller glia (data not shown) confirmed that all these cell types were present in the Ascl1 lineage; however, the vast majority of the cells in the ganglion cell layer were displaced amacrine cells as shown by: (1) the lack of labeling by ganglion cell-specific markers pan-Brn3 (Brn3a, b, c), Brn3a/b (in tandem) or Neurofilament-M (NFM) (Fig. 3B-D) (Nixon et al., 1989; Xiang et al., 1995); (2) the inability to label the cells with retrograde uptake of biotinylated dextran (Fig. 3E) (Farah and Easter, 2005); or (3)
the presence of AP2α staining, which specifically labels the bulk of displaced amacrine cells (Fig. 3G) (Bassett et al., 2007). In our analysis of the Ascl1 lineage, we identified only seven RGCs in the 3115 GFP+ cells sampled (see Table S1 in the supplementary material). The paucity of ganglion cells in the Ascl1 lineage was not due to lack of production at this age; we conducted a birthdating analysis and found that 14% of cells that exited the cell cycle at E13.5 adopted RGC fate (see Fig. S3, Table S2 in the supplementary material). If we conservatively assume that RGCs should be generated at their adult frequency (0.6%) (Jeon et al., 1998) at the time of tamoxifen injection, then the probability of observing at least seven RGCs in our sample size is 0.00181 (binomial distribution, see Table S3 in the supplementary material), demonstrating that RGCs are significantly under-represented in the

Fig. 3. The E12.5/E13.5 Ascl1 lineage. Tamoxifen was administered at E12.5 and E13.5 and mice were examined as adults. (A) A control animal lacking the Ascl1-Cre (Ascl1+/-) transgene. There is a fibrous GFP antibody-specific background in the ganglion cell layer (GCL; arrow) and inner plexiform layer (IPL). (B-P) Examples of Ascl1CreERT2/+ lineage-traced cells (isolated or in clumps) (green or gray) with cell-type specific labeling in A-J (red). (B-J) Displaced amacrine (dA), inner nuclear layer (INL) amacrine (A), rods (R) and horizontal cells (H) are seen. (K-P) Examples of cones (C), rods, bipolar cells (B), amacrine cells and Müller glia (M) seen in the Ascl1 lineage. (B-G) Cells in the GCL are labeled by pan-Brn3 (Brn3*), Brn3a/b, Neurofilament-M (NFM) or with retrograde uptake of biotinylated dextran to label retinal ganglion cells (RGCs), and with AP2α to label displaced amacrine cells (all in red). Nearly all GCL cells are label-negative displaced amacrine cells. (H-J) Horizontal and amacrine cells are co-labeled with calbindin (red) or Pax6 (red). Arrowheads denote outer segments of photoreceptors. Scale bars: 50 μm for A-C, H-P; 25 μm for D-G; 10 μm for insets.
Ascl1 lineage. Only five of the ten animals we examined had GFP+ RGCs. Indeed, the RGC frequency (0.322±0.488% s.d.) was not statistically different from zero (t-test, P>0.05) (see Fig. S4 in the supplementary material). Thus, although an occasional ganglion cell was seen in some Ascl1 lineage-traced mice, we can conclude that the Ascl1 lineage effectively lacks RGCs.

In addition to the absence of ganglion cells in the Ascl1 lineage, the relative numbers of cells in the E12.5/E13.5 Ascl1 lineage was different from the normal adult mouse retina (Jeon et al., 1998). Horizontals, cones and amacrines were over-represented whereas rods were under-represented (see Fig. S4 in the supplementary material). Thus, although an occasional ganglion cell was seen in some Ascl1 lineage-traced mice, we can conclude that the Ascl1 lineage effectively lacks RGCs.

In addition to the absence of ganglion cells in the Ascl1 lineage, the relative numbers of cells in the E12.5/E13.5 Ascl1 lineage was different from the normal adult mouse retina (Jeon et al., 1998). Horizontals, cones and amacrines were over-represented whereas rods were under-represented (see Fig. S4 in the supplementary material). Thus, although an occasional ganglion cell was seen in some Ascl1 lineage-traced mice, we can conclude that the Ascl1 lineage effectively lacks RGCs.

We next examined the Ascl1 lineage after inducing Cre recombination at E17.5. There were more GFP+ cells seen in lineage-traced animals, correlating with a greater number of Ascl1+ cells at E17.5 compared with E13.5. GFP+ cells were seen in isolation and in small clumps, both in the central and far peripheral parts of the retina (Fig. 4B-L). Very few cells were observed in the GCL and none of them co-expressed pan-Brn3 (see Table S1 in the supplementary material). We observed few early-born cell types (cones, horizontals and displaced amacrines). These occurrences were almost always observed in the peripheral retina, where a small number of these cells are still being born on E17.5. Most of the cells in the E17.5 Ascl1 lineage were rods and amacrine cells (Fig. 4B-L). However, multicellular clumps that contained postnatally generated cell types, such as Müller cells and bipolar cells, were observed, indicating that some of the Ascl1+
progenitors continue to generate progeny for several days (Fig. 4B-L). Taken together, our data show that Ascl1 expression defines a population of competence-restricted progenitors in the retina. Ascl1 itself does not inhibit RGC competence. Our lineage studies show that Ascl1+ progenitors do not become RGCs. RGC development requires the transcription factor Math5 (Brown et al., 2001; Wang et al., 2001). Math5 is expressed in postmitotic cells and establishes RGC competence, but only a subset of Math5+ cells adopts RGC fate (J. A. Brzezinski, 4th, PhD thesis, University of Michigan, 2005) (Mu et al., 2005; Yang et al., 2003). In principle, Ascl1 could act by preventing the expression of Math5 in the Ascl1 lineage, thereby inhibiting RGC fate. Alternatively, Ascl1+ progenitors could give rise to Math5+ postmitotic cells and this subpopulation, owing to its previous expression of Ascl1, would be inhibited from RGC fate. To test these hypotheses, we crossed Ascl1GFP+ mice to Math5Cre+ mice and looked for overlap of GFP and Cre proteins, which both persist transiently after Ascl1 and Math5 expression terminates. We examined mice at E13.5 (the peak of RGC formation) and at E18.5 (the tail of RGC formation) for pan-Brn3 co-expression. At E13.5, 36% of the cells in the retina are pan-Brn3+ RGCs (see Fig. S3 in the supplementary material) and most of the Math5-Cre+ cells co-expressed pan-Brn3 (65.7±8.99% s.d.) (Fig. 5A-D,M,N). By contrast, we observed only one instance of an Ascl1-GFP+ cell that co-expressed pan-Brn3 (Fig. 5E-H,M,N, see Table S4 in the supplementary material). Nonetheless, we observed that many Ascl1-GFP+ cells co-expressed Math5-Cre at this age (31.0±11.1% s.d.) (Fig. 5A-D,M,N). The same was true at E18.5; by
this age, most Math5-Cre+ cells co-expressed Ascl1-GFP (59.11±17.98% s.d.) (Fig. 5M,N, see Fig. S7 in the supplementary material), but we did not detect Ascl1-GFP+/Brn3+ cells.

The fact that Ascl1+ progenitor cells can give rise to Math5-expressing cells, but not Brn3+ ganglion cells suggests that prior (or concurrent) Ascl1 expression prevents Math5+ cells from adopting RGC fate. If Ascl1 prevents Brn3 expression in the progeny of these progenitors, then the loss of Ascl1 should cause an increase in RGC number. To test this hypothesis, we examined the number of pan-Brn3+ RGCs at both E14.5 and E18.5 in Ascl1GFP/+ heterozygous and null retinas and found no differences at either age (Fig. S1 in the supplementary material). Thus, Ascl1 is not required for the repression of the RGC fate in this lineage and neither compensation nor cross-regulation by Ngn2 or Olig2 can explain this result.

**Ascl1+ and Ngn2+ progenitors give rise to distinct lineages**

Previous conditional expression fate-mapping experiments demonstrated that Ngn2+ progenitors can give rise to all retinal cell types, including RGCs (Ma and Wang, 2006). As Ascl1 and
Ngn2 have partially overlapping domains at several time points (Figs 1, 2, see Fig. S1 in the supplementary material), we tested whether differences in expression of these factors in progenitors leads to distinct lineages. We carried out lineage analysis of Ngn2CreERTM/+ mice after administering tamoxifen at E12.5/E13.5 and at E17.5. Adult control mice without Ngn2-Cre (Ngn2+/+) and Ngn2CreERTM/+ mice that did not receive tamoxifen lacked GFP+ cells (Fig. 6A) (data not shown). Ngn2CreERTM/+ mice given tamoxifen at E12.5/E13.5 had GFP+ cells in all layers of the retina and were typically seen in isolation or in clumps of two to three cells spanning the central and far peripheral retina (Fig. 6B-J). Most abundant in the E12.5/E13.5 Ngn2 lineage trace were cones, horizontals and amacrine cells (Fig. 6F-J). There were few rods, bipolars or Müller glia from this trace, which contrasts significantly with the Ascl1 lineage trace (χ² test, P<0.001) (Fig. 7A, see Table S1 in the supplementary material). Although the Ngn2 lineage was strongly biased towards cell fates born around the time of tamoxifen administration, RGCs formed only a small, though significant (t-test, P<0.01), fraction of the Ngn2 lineage.

In the E17.5 Ngn2 lineage trace, most of the cells we observed were rods, but a few early-born cell types were seen (e.g. RGCs and cones), primarily in peripheral parts of the retina (Fig. 6K-N). In contrast to the Ascl1 lineage, the latest generated cell types, bipolars and Müller glia, were nearly absent from the E17.5 Ngn2 lineage (χ² test, P<0.001) (Fig. 7B, see Table S1 in the supplementary material). As before, the E17.5 Ngn2 lineage distribution is highly biased towards the cell types born at the time of tamoxifen administration. Together, our data show that Ascl1 and Ngn2 lineages are distinct. First, RGCs are significantly more abundant in the Ngn2 lineage. Second, the Ngn2 lineage is more heavily biased towards cell types that exit the cell cycle shortly after tamoxifen treatment.

The differences in fate distributions suggested differential proliferative ability of the Ascl1+ and Ngn2+ progenitor populations. We counted the number of cells in clumps traced from both time points as an indirect measure of the proliferative ability of these progenitors. We plotted the frequency of clump sizes and observed a Pareto-like (L-shaped) distribution for both lineages at 15 cells for the Ascl1 lineage and nine cells for the Ngn2 lineage at E12.5/13.5 (12 and seven cells, respectively, at E17.5).
both time points (Fig. 7C,D). The average clump size was about twice as large in the Ascl1 lineage compared with the Ngn2 lineage at both time points (Mann-Whitney test, P<0.0001) (Fig. 7E). The high frequency of one- and two-cell clumps in the Ngn2 lineage (98.5%) suggests that Ngn2+ progenitors are typically in their last cell cycle.

As noted above, all populations of E18.5 progenitors were modestly decreased (~15-30%) in Ascl1\(^{-}\)/\(^{GFP}\)/\(^{GFP}\)-null retinas (see Fig. S1 in the supplementary material), consistent with a previous study that suggested that Ascl1 non-autonomously maintains the retinal progenitor pool (Nelson et al., 2009). We also found that E18.5 Ascl1\(^{-}\)/\(^{GFP}\)/\(^{GFP}\)-null explants cultured for 2 days in vitro (DIV) had 50% fewer EdU+ (S-phase) nuclei (progenitors) at the end of the culture period compared with heterozygous explants (see Fig. S8 in the supplementary material). Lastly, we examined E17.5 retinal explants cultured for 9 DIV and found that although Ascl1-null retinas were noticeably smaller, all seven principal retinal cell types were present (data not shown, see Figs S1, S9 in the supplementary material). Together these results suggest that Ascl1 is required for proliferation, which cannot be compensated for by Olig2 or Ngn2.

**DISCUSSION**

Here, we report that retinal progenitors are heterogeneous in their expression of the bHLH transcription factors Ascl1, Ngn2 and Olig2. This progenitor heterogeneity is reflected in differences in fate; Ascl1 and Ngn2 lineages are distinct from each other. The Ascl1+ progenitor cells do not significantly generate RGCs, but can give rise to the other six principal retinal cell fates. Ascl1 expression, therefore, defines a subpopulation of competence-restricted progenitors during retinal development. Interestingly, Ascl1 itself is not required to restrict RGC competence, suggesting a mechanism by which factors upstream of Ascl1 limit competence in the retina.

**Ascl1 defines a competence-restricted retinal lineage**

Ascl1+ progenitors did not significantly generate RGCs at any time point. Although we cannot formally rule out that a biologically relevant, rare RGC subtype(s) derives from the Ascl1 lineage, our data strongly argue against this possibility. First, Ascl1-GFP and pan-Brn3 co-expression data suggests that this putative subtype would have to be exceedingly rare during development (one cell or fewer per retina) (binomial distribution, \(P<0.00001\), see Table S5 in the supplementary material). Second, whereas Brn3a/b/c expression might not label all ganglion cell subtypes (Badea and Nathans, 2011), retrograde dextran uptake labels all RGCs; nonetheless, we did not observe a significant number of Brn3+ or dextran-labeled RGCs in the Ascl1 lineage.

Retroviral lineage-tracing studies have shown that all seven retinal cell types derive from a common progenitor population (Turner and Cepko, 1987; Turner et al., 1990). However, throughout most of retinal development, several cell types are being formed concurrently (La Vail et al., 1991; Rapaport et al., 2004; Sidman, 1961; Young, 1985). This implies that retinal progenitor cells form a heterogeneous population that expresses different intrinsic factors and responds differentially to extrinsic cues (Livesey and Cepko, 2001; Taylor and Reh, 1990). Previous studies have demonstrated that Ascl1 is expressed in a subset of retinal progenitors, and proposed that Ascl1 expression defines a particular stage in the progenitor cells (Jasoni and Reh, 1996; Jasoni et al., 1994). Our Ascl1 lineage-tracing experiment confirmed this proposal, as Ascl1+ progenitors significantly generated all retinal cell types except for RGCs. This is the first molecularly defined progenitor population that has competence to form all but one cell type in the retina. Analogously, Ascl1+ cells give rise to a competence-restricted lineage in the spinal cord (Battiste et al., 2007), forebrain (Parras et al., 2002) and other regions of the CNS (Kim et al., 2008).

Although lineage-restricted progenitors have not been previously shown to exist in the mouse retina in vivo, it has been shown that committed precursors exist in the fish retina. Raymond and colleagues first demonstrated that many of the rod photoreceptors in the teleost retina are generated through a committed rod precursor (Raymond and Rivlin, 1987). More recently, immature horizontal cells in the inner nuclear layer of the zebrafish retina have been shown to undergo a mitotic division to generate two horizontal cells (Godinho et al., 2007). In Ath5-GFP transgenic zebrafish, GFP is made by cells in their terminal division such that one daughter becomes a ganglion cell and the other adopts a different neural fate (Poggi et al., 2005). This cell is somewhat different from the committed horizontal and rod precursors, but nevertheless suggests that, in fish, there is something unique about progenitor cells in their last cell division. Our results suggest that Ngn2 expression might mark mouse progenitors in their final mitotic division since nearly all of the traced cells were found in one- to two-cell clumps and because their cell fates were strongly biased towards those born at the time of tamoxifen treatment. However, we did not find any clear pattern to the types of progeny generated in two-cell clumps in the Ngn2 or Ascl1 lineages (data not shown) (Ma and Wang, 2006). This appears to be true in vitro as well, where single isolated progenitors that undergo their final mitotic division in culture do not show a bias towards generating cells of the same identity (Gomes et al., 2011).

Our study demonstrates that the E12.5/E13.5 Ascl1 and Ngn2 lineages are quite distinct from each other and from retroviral lineages traced at the same time points (see Figs S4, S10 in the supplementary material) (Turner et al., 1990). However, these lineage-tracing techniques are quite different from each other. First, only progenitors can be infected and labeled by retroviruses, but it is possible for Ascl1- and Ngn2-Cre to persist transiently and catalyze recombination in newly postmitotic cells. Thus, the average clump size in the Ascl1 and Ngn2 lineages should be lower than that in the retroviral lineages, but the maximum clump size should be similar. Second, although clumps seen in the E12.5/E13.5 Ascl1 and Ngn2 lineage traces were sparsely distributed, we cannot be certain they were clones. Thus, we might be overestimating the number of progeny that Ascl1+ and Ngn2+ cells generate.

A major difference between these three lineage traces was the clump/clone size distribution. Whereas some retroviral clones were larger than 50 cells (Turner et al., 1990), we did not observe any clumps in the Ascl1 lineage that contained more than 15 cells and no clumps in the Ngn2 lineage that contained more than nine cells (see Fig. S10 in the supplementary material). Most of the clumps in the Ascl1 and Ngn2 lineages contained one or two cells (82.4% and 98.5%, respectively), but only a small fraction of retroviral clones (~33%) contained one or two cells. These differences in the clump/clone size distributions strongly suggest the following model (Fig. 8). Retinal progenitors that do not express Ascl1 or Ngn2 can undergo a large number of mitotic divisions, whereas progenitors that express Ascl1 undergo few mitotic divisions and those that express Ngn2 are in their last cell cycle. This model is consistent with observations in other regions of the CNS, where it has been proposed that Ngn2-expressing progenitors in the spinal cord are in their last cell division (Helms et al., 2005) and that Ascl1
In response to increases in cAMP, whereas those from early retina. For example, progenitor cells from late retina differentiate (Shibasaki et al., 2005) (Mu et al., 2005; Yang et al., 2003). How are Ascl1 and Ngn2 mutants have increased glia at the expense of neurons, whereas overexpression of these factors drives neurons (Akagi et al., 2004; Cai et al., 2000; Nelson et al., 2009; Tomita et al., 2000; Tomita et al., 1996). A third possibility is that these transcription factors differentially regulate progenitor cell cycle dynamics; our lineage data show that Ascl1+ and Ngn2+ cells have different proliferative and fate potentials. Perhaps a combination of Ascl1 and Ngn2 reach a threshold and induce terminal differentiation. Alternatively, Ascl1, but not Ngn2, might autonomously promote proliferation of progenitors by activating cell-cycle genes (Castro et al., 2011). Lastly, these transcription factors might differentially activate cell non-autonomous signaling mechanisms. Previously, we have shown that Ascl1-null mice express lower levels of the Notch ligands Dll1 and Dll3 in progenitors, resulting in diminished Notch signaling within the retina (Nelson et al., 2009). One consequence of reduced Notch signaling might be a progressive depletion of progenitors, a phenotype that we observed in Ascl1-null mice. Notch ligand reduction is not observed in Ngn2-deficient retinas, demonstrating a difference between these transcription factors in sustaining Notch signaling and the progenitor pool (Nelson et al., 2009; Ohsawa and Kageyama, 2008).

**Ascl1 is not required to restrict RGC competence**

The bHLH transcription factor Math5 is required for RGC formation (Brown et al., 2001; Wang et al., 2001). Math5 is required for RGC competence, but only a small subset of Math5+ cells adopts RGC fate (J. A. Brzezinski, 4th, PhD thesis, University of Michigan, 2005) (Mu et al., 2005; Yang et al., 2003). How are Ascl1+ cells prevented from becoming RGCs? First, Ascl1 might repress Math5 and prevent RGC competence. This is unlikely as we saw numerous Ascl1+/Math5+ co-labeled cells and Math5 expression is unchanged in Ascl1-null mice (Hufnagel et al., 2010; Nelson et al., 2009). Second, Ascl1 might restrict RGC competence independently of Math5. This also seems unlikely because Ascl1 mutant mice had normal numbers of RGCs during development. Ngn2+ cells, which can give rise to Math5+ cells and RGCs,

**Progenitor heterogeneity correlates with different fate outcomes**

Previous studies have demonstrated progenitor heterogeneity in the retina. For example, progenitor cells from late retina differentiate in response to increases in cAMP, whereas those from early embryonic stages do not (Taylor and Reh, 1990). Analogously, EGF and related EGFR ligands are mitogenic for late progenitors, but not early ones (Anchan et al., 1991; Lillien and Cepko, 1992). Progenitors are heterogeneous in their expression of the cyclin-dependant kinase inhibitors p57kip2 and p27kip1 (Dyer and Cepko, 2001). In our experiments, we found that all seven distinct single, double and triple bHLH transcription factor combinations were represented, along with Sox2+ progenitors that did not express Ascl1, Ngn2 or Olig2. In single-cell gene expression-profiling experiments, roughly similar fractions of progenitors expressed Ascl1, Ngn2 or both factors (Trimarchi et al., 2008). Although we have not analyzed the Olig2 lineage, at least two populations of cells, Ascl1+ and Ngn2+, have different fate and proliferative potentials. Thus, progenitor heterogeneity correlates with different fate choice outcomes in the retina.

How do Ascl1, Ngn2 and Olig2 regulate cell diversity in the retina? One model proposes that different bHLH transcription factors bias retinal progenitor cells, or their postmitotic progeny, to specific cell fates (Ohsawa and Kageyama, 2008); each factor (or combination of factors) is instructive for a specific cell fate. This seems unlikely for Ascl1 and Ngn2, as mice deficient in these transcription factors are able to generate all of the seven principal retinal cell types (Akagi et al., 2004; Hufnagel et al., 2010; Skowronska-Krawczyk et al., 2009; Tomita et al., 2000). Alternatively, these factors could bias progenitors towards neural fates. Ascl1 and Ngn2 mutants have increased glia at the expense of neurons, whereas overexpression of these factors drives neurons (Akagi et al., 2004; Cai et al., 2000; Nelson et al., 2009; Tomita et al., 2000; Tomita et al., 1996). A third possibility is that these transcription factors differentially regulate progenitor cell cycle dynamics; our lineage data show that Ascl1+ and Ngn2+ cells have different proliferative and fate potentials. Perhaps a combination of Ascl1 and Ngn2 reach a threshold and induce terminal differentiation. Alternatively, Ascl1, but not Ngn2, might autonomously promote proliferation of progenitors by activating cell-cycle genes (Castro et al., 2011). Lastly, these transcription factors might differentially activate cell non-autonomous signaling mechanisms. Previously, we have shown that Ascl1-null mice express lower levels of the Notch ligands Dll1 and Dll3 in progenitors, resulting in diminished Notch signaling within the retina (Nelson et al., 2009). One consequence of reduced Notch signaling might be a progressive depletion of progenitors, a phenotype that we observed in Ascl1-null mice. Notch ligand reduction is not observed in Ngn2-deficient retinas, demonstrating a difference between these transcription factors in sustaining Notch signaling and the progenitor pool (Nelson et al., 2009; Ohsawa and Kageyama, 2008).
engineered to co-express Ascl1 were still able to make Math5 and become RGCs (Hufnagel et al., 2010). Also, overexpression of Ascl1 in chicken retina did not change the number of RGCs (Mao et al., 2009). Third, it is possible that Ascl1, Ngn2 and/or Olig2 function redundantly to repress RGC formation. This is consistent with the paucity of RGCs in our Ascl1 and Ngn2 lineages traces and with our Ascl1, Ngn2 and Olig2 expression data. In support of this possibility, there is a modest increase in the number of RGCs and amount of Math5 expression in Ascl1/Ngn2 double knockout mice (Akagi et al., 2004). Lastly, another factor might restrict RGC competence to promote cell fate diversification in the retina. 2010). However, unlike retinas have extra RGCs. This raises the possibility that the factors upstream of, or redundant with, Ascl1 restrict RGC competence to promote cell fate diversification in the retina.


