Asymmetric neurogenic commitment of retinal progenitors is regulated via the Notch endocytic pathway

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Abstract During brain development, progenitor cells need to balance proliferation and differentiation in order to generate different neurons in the correct numbers and proportions. Currently, the patterns of multipotent progenitors' division that lead to neurogenic entry and the factors that regulate them are not fully understood. We here use the zebrafish retina to address this gap, exploiting the possibilities for quantitative live-imaging. We show that early neurogenic progenitors arise from asymmetric divisions. Notch regulates this asymmetry as when inhibited, symmetric divisions producing two neurogenic progenitors occur. Surprisingly, Notch does not act through an apicobasal activity gradient as previously suggested but through asymmetric inheritance of Sara-positive endosomes. Further, the resulting neurogenic progenitors show cell biological features different from multipotent progenitors, raising the possibility that an intermediate state of progenitors exists in the retina. Our study thus opens new insights into the regulation of proliferative and differentiative events during central nervous system development.

Introduction

During central nervous system (CNS) development in vertebrates, the balance between proliferation and differentiation is crucial to generate the different types of neurons in the correct numbers and proportions. This in turn ensures functionality of the neural tissue as it is the prerequisite for correct neuronal connectivity and circuit formation. Multipotent progenitors are key to maintain this balance. They first grow in number through a phase of active proliferation (Fish et al., 2006; Homem et al., 2015) which is followed by neurogenesis onset. At neurogenesis onset, subsets of progenitors become neurogenic, consequently leave the cell cycle and differentiate into neurons (Götz and Huttner, 2005; Agathocleous and Harris, 2009). Expectedly, impairment of the intricate balance between proliferation and differentiation can lead to severe defects of brain development and is associated with numerous human diseases, including microcephaly and tumour formation (Fish et al., 2006; Thornton and Woods, 2009). Thus, understanding the parameters that differ between cells primed for continued proliferation versus cells that enter the neurogenic program is of utmost importance to comprehend brain development in health and disease.

Previous studies using the mammalian neocortex showed that at the onset of neurogenesis multipotent progenitors start dividing asymmetrically, generating one radial glial cell and one neuron or a basal progenitor and thereby balancing the ratio between differentiation and proliferation at early neurogenesis stages (Chenn and McConnell, 1995; Huttner and Brand, 1997; Götz and Huttner, 2005; Shen

et al., 2006; Shitamukai and Matsuzaki, 2012). Once a sufficient number of progenitors is produced, final symmetric consumptive neuronal divisions deplete the progenitor pool (Miyata et al., 2004; Noctor et al., 2004). Similarly to the mammalian cortex, asymmetric divisions have also been shown to be important for the maintenance of the progenitor pool before its final depletion in the fore- and hindbrain of the teleost Danio rerio (zebrafish) (Alexandre et al., 2010; Dong et al., 2012). Thus, the division modes responsible for the generation of the first neurons in different parts of the nervous system are relatively well explored, despite the fact that many questions are still open. What is much less understood, however, is how neurogenic progenitors first arise from the multipotent progenitors. Especially in the retina, the tissue that upon maturation enables the perception of visual information, this question has not yet gathered sufficient attention. Here, division patterns have mainly been investigated at later stages when the emergence of the seven different neurons that ensure retinal functionality has already commenced (Poggi et al., 2005; He et al., 2012; Kechad et al., 2012; Suzuki et al., 2013). It was shown that these late neurogenic divisions can be asymmetric, generating two neurons of different fate. However, how multipotent progenitors enter the neurogenic path in the first place, what type of division patterns and what regulation pathways these initial fate decisions entail is not yet well explored.

Asymmetric divisions leading to the formation of neurons in the CNS have often been linked to the asymmetric inheritance of different cellular components. Examples of differentially inherited components are the basal process (Saito et al., 2003; Okamoto et al., 2013), the apical domain (Bultje et al., 2009; Alexandre et al., 2010) and polarity components (Paolini et al., 2015; Zhao et al., 2020). In addition, different signalling pathways including Wnt (Hirabayashi et al., 2004) and very prominently Notch (Dorsky et al., 1995, 1997; Cayouette et al., 2001; Ohtsuka et al., 2001; Dong et al., 2012) have been shown to be involved. Notch for example can regulate the asymmetry of fate decisions through the asymmetric inheritance of Notch signalling endosomes, as shown in the zebrafish spinal cord and forebrain (Kressmann et al., 2015; Zhao et al., 2020). In the vertebrate retina, Notch signalling maintains progenitors in a proliferative state through lateral inhibition (Henrique et al., 1997; Jadhav et al., 2006). It was previously suggested that Notch drives neurogenic commitment of multipotent progenitors via an extracellular gradient along the apicobasal axis of the elongated neuroepithelial cells (Murciano et al., 2002; Del Bene et al., 2008). It was postulated that when nuclei travel along the apicobasal axis during the cell cycle (a phenomenon termed interkinetic nuclear migration, IKNM (Sauer, 1935; Baye and Link, 2007; Norden et al., 2009)), they are exposed to different Notch signalling levels, that in turn influence the progenitors' probability to enter the neurogenic program (Murciano et al., 2002; Baye and Link, 2007; Del Bene et al., 2008). However, the division patterns of retinal progenitors that lead to neurogenic entry and their possible links to Notch signalling were not fully explored.

We here investigate the division patterns that give rise to the neurogenic progenitors, one cell cycle before the generation of post-mitotic neurons. We find that divisions generating neurogenic progenitors are almost always asymmetric and that sister cells do not enter the same lineage. While Notch is involved in the generation of this asymmetry, it does not act via an apicobasal activity gradient. Instead, we provide evidence that Notch signalling acts through the asymmetric inheritance of Sara-positive endosomes. We further show that these first neurogenic progenitors differ in their cell biological features from multipotent progenitors, indicating that they are an intermediate cell type *en route* to differentiation.

Results

Ath5 positive neurogenic progenitors arise from asymmetric divisions

To understand how neurogenic progenitors emerge from multipotent progenitors in the developing zebrafish retina, we asked how the earliest neurogenic progenitors arise, by symmetric or asymmetric division patterns or a mixture of the two. To follow these earliest neurogenic progenitors, we made use of the well-established fact that they express the transcription factor *ath5* (*atoh7*) (Poggi et al., 2005; Zolessi et al., 2006) and we traced their origin by mosaically labelling cells in zebrafish embryos with an Ath5-driven reporter construct (Icha et al., 2016a). We followed the onset of the Ath5 signal using light-sheet imaging from the beginning of neurogenesis at 28 hpf (hours post fertilization) (Hu and Easter, 1999; Schmitt and Dowling, 1999; Martinez-Morales et al., 2005) as previously described (Icha et al., 2016b). To backtrack progenitors that began to express Ath5 (from here on referred to as 'Ath5 positive progenitors') (*Figure 1*A, *Supplementary Figure 1*A), we labelled the plasma membrane and/or the nucleus of the same cells using hsp70:mKate2-ras or hsp70:H2B-RFP constructs (*Figure 1*B). We backtracked sister cells of divisions giving rise to at least one Ath5 positive neurogenic progenitor and analysed their division patterns (*Figure 1*C,C').

Tracing of 38 multipotent progenitor divisions from 9 embryos (*Figure 1*B, *Video 1*) revealed that 92% of these divisions were asymmetric, generating one Ath5 positive (Ath5+) progenitor and one Ath5 negative (Ath5-) progenitor (*Figure 1*C,C',D). Only 8% of Ath5+ cells were generated by symmetric division, producing two Ath5+ cells (*Figure 1*C',D). Following Ath5- sister cells for another cell cycle showed that all cells divided again, but none of the daughter cells started expressing Ath5 (n=5 divisions, N=2 embryos) (*Supplementary Figure 1*B,C, *Video 1*). This suggests that Ath5- sister cells enter a different lineage than their Ath5+ counterpart. Together, these data provide first direct evidence that neurogenic progenitors in the retina emerge from asymmetric divisions, indicating that cellular asymmetry plays an important role in the selection of progenitors that enter neurogenic programs.

Inhibition of Notch signalling affects the pattern of divisions generating Ath5 positive progenitors

To understand the asymmetry of divisions producing Ath5+ progenitors at the molecular level, we set out to investigate the signalling factors involved. One promising candidate that drives asymmetric divisions in many neurogenic lineages is the Notch pathway (Bultje et al., 2009; Egger et al., 2010; Kechad et al., 2012; Kressmann et al., 2015). In the retina, Notch signalling has been shown to maintain progenitors in the proliferative state thus inhibiting neurogenesis (Bao and Cepko, 1997; Jadhav et al., 2006; Kechad et al., 2012; Maurer et al., 2014; Sato et al., 2016). We therefore tested whether and how Notch depletion influenced the asymmetry of divisions generating Ath5+ progenitors using two established Notch inhibitors, the γ-secretase inhibitors LY411575 (*Figure 1*E,F) and DAPT (*Supplementary Figure 1*D) (Ninov et al., 2012; MacDonald et al., 2015). In line with the reports that Notch signalling supresses neurogenesis and thereby Ath5 expression onset (Maurer et al., 2014), we found that both Notch inhibitors led to an increase in the number of Ath5+ cells at 36 hpf and 48 hpf (*Figure 1*E,F). The increase of Ath5+ cells was accompanied by a striking reduction in tissue thickness (*Figure 1*G, G') and retinal diameter (*Figure 1*G, G'') compared to controls at 48 hpf. This retinal size reduction indicated that indeed the balance between proliferation and differentiation in the retina was disturbed upon Notch inhibition, leading to tissue-wide consequences.

The increase of Ath5+ progenitors observed upon Notch inhibition could arise from two not mutually exclusive scenarios: Ath5+ progenitors could emerge prematurely by asymmetric divisions that absorb multipotent progenitors too early, or an increase in symmetric divisions giving rise to two Ath5+
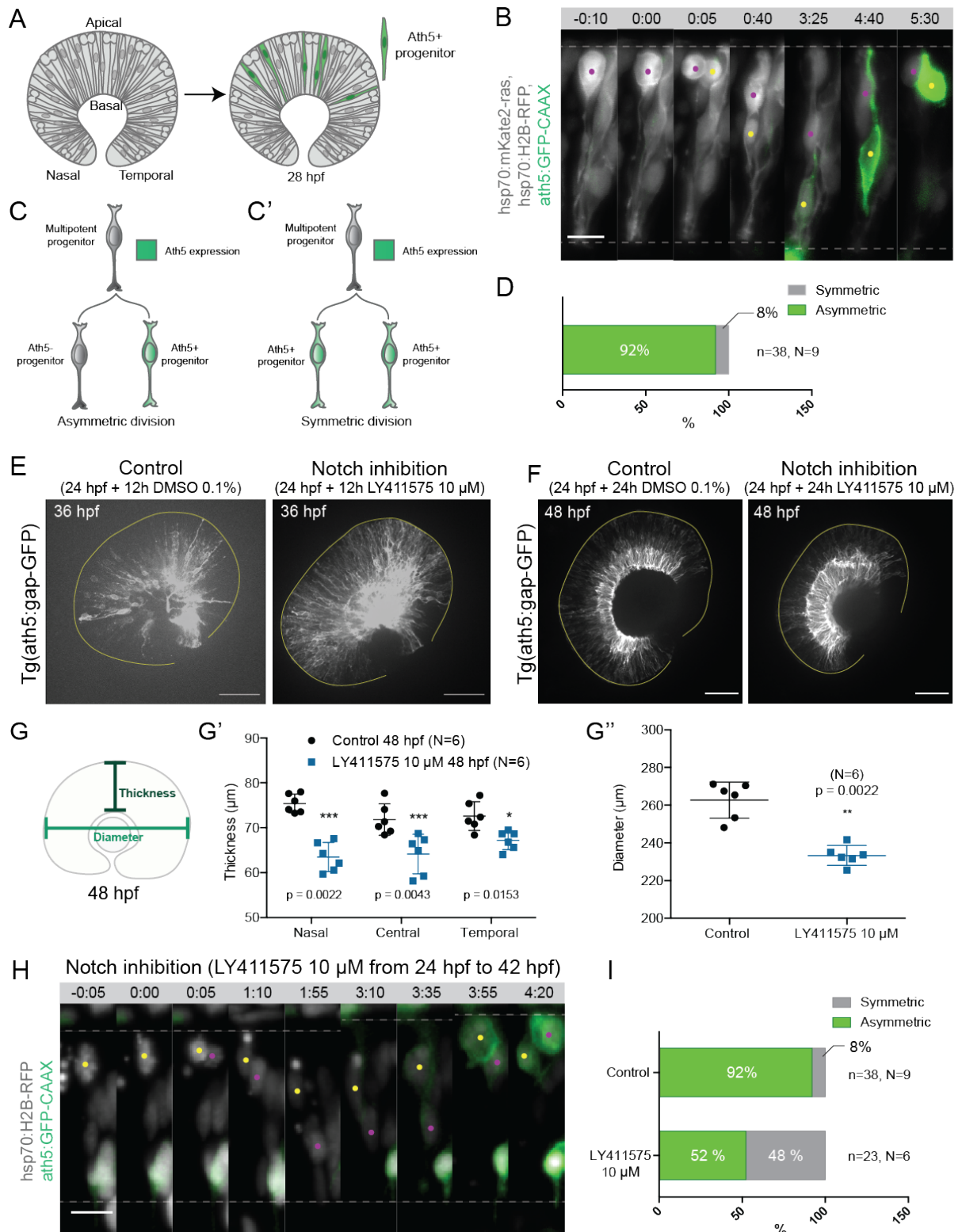
Figure 1. Asymmetric cell divisions generate Ath5+ progenitors in a Notch-dependent manner. (A) Schematic of mosaic Ath5 expression in the retina (green) at 28 hpf. Injection of ath5:GFP-CAAX construct at 1-cell stage. (B) Example of an asymmetric division of multipotent progenitors with regards to Ath5 expression onset. hsp70:H2B-RFP (nuclei, grey), hsp70:mkate2-ras (cell membrane, grey), ath5:GFP-CAAX (Ath5, green). Dashed lines show apical and basal sides of retinal neuroepithelium. Scale bar, 10 μm. Magenta and yellow dots label sister cells. (C-C') Schematics of multipotent progenitor cells dividing asymmetrically (C) or symmetrically (C') with regards to Ath5 expression. (D) Distribution of asymmetric vs symmetric divisions observed in live imaging experiments. N = number of embryos, n = number of divisions. (Continued on the following page)

Figure 1. (From previous page) (E) Ath5+ cells (grey) at 36 hpf in control (left) vs Notch inhibition (right). Scale bar, 50 μm. The yellow line delimits the apical side of the retinal neuroepithelium. (F) Ath5+ cells (grey) at 48 hpf in control (left) vs Notch inhibition (right). Scale bar, 50 μm. The yellow line delimits the apical side of the retinal neuroepithelium. (G) Schematic of retinal neuroepithelium measurements at 48 hpf, G' retinal thickness control vs Notch inhibition, G'' retinal diameter control vs Notch inhibition. Mann-Whitney test used for comparison. Vertical bars represent standard deviation. (H) Example of a symmetric division upon Notch inhibition. hsp70:H2B-RFP (nuclei, grey), ath5:GFP-CAAX (Ath5, green). Dashed lines show apical and basal borders of retinal neuroepithelium. Scale bar, 10 μm. Magenta and yellow dots label sister cells. (I) Distribution of asymmetric vs symmetric divisions observed in live imaging experiments in Notch inhibition compared to controls.

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progenitors could occur that would result in less progenitors entering another cell cycle, thus also depleting the pool of remaining progenitors prematurely (*Figure 1*C, C'). To explore these possibilities, live imaging of LY411575 treated embryos was performed (*Figure 1*H). Compared to controls, Notch inhibition led to a significant increase in symmetric neurogenic divisions that generated two Ath5+ progenitors (48% compared to 8% in controls, *Figure 1*I, *Video 2*). Thus, Notch signalling regulates the asymmetry of the division that produces neurogenic Ath5+ progenitors. Interference with Notch and thereby this division asymmetry influences neurogenesis patterns and tissue maturation in the developing retina.

Ath5 positive progenitors generally translocate more basally than Ath5 negative sister cells but a spatial bias is not observed at the cell population level

The selection of the sister cell that enters the neurogenic program could be regulated by differential exposure to the extracellular environment that hosts different fate determinants as shown for other systems (Yamashita and Fuller, 2005; Knoblich, 2008). It was previously reported that Notch RNA is distributed in a graded manner along the cell's apicobasal axis with more Notch RNA detected towards apical positions in the retinal neuroepithelium (Del Bene et al., 2008). This finding led to the idea that distinct Notch signaling milieus exist along the apicobasal axis of the retinal neuroepithelium and that these could influence neurogenic outcome due to nuclear movement along this axis during IKNM (Murciano et al., 2002; Baye and Link, 2007; Del Bene et al., 2008). Based on these studies, we asked whether the observed cell division asymmetry that generates Ath5+ progenitors (*Figure 1*C) could be explained by differential translocation depths between Ath5+ and Ath5- sister cells. To this end, we compared trajectories of Ath5+ and Ath5- sister cells after division (*Figure 2*A). We found that indeed one sister cell soma always translocated more basally than the other (*Figure 2*B), with an average difference of 10.11 $\pm$ 7.292 μm between the maximal basal positions (n=35 divisions, N=9 embryos) (*Figure 2*C). In 78% of sister cells, the more basally translocating sister cell started expressing Ath5 (27/35 divisions) (*Figure 2*D) while in 22% of divisions this pattern was reversed and it was the Ath5- cell that positioned the soma more basally (*Figure 2*E). In the latter case however, the difference between maximum basal position of sister cells was on average less prominent than in the reverse scenario (difference of 6.048 $\pm$ 3.559 μm when Ath5- soma is most basal compared to 11.31 $\pm$ 7.712 μm when Ath5+ soma is most basal) (*Figure 2*F).

To probe whether a basal positioning threshold could be defined that predicts the onset of Ath5 expression, all trajectories were pooled and their overlap was analysed (*Figure 2*G, H). To our surprise, this analysis showed a significant overlap of trajectories and of maximum basal positions for Ath5+ and Ath5- somas without clearly distinct Ath5+ and Ath5- zones (*Figure 2*G,H,I, *Supplementary Figure 2*A). The measurement of the average depth occupied by somas of Ath5+ and Ath5- cells (integral mean, *Supplementary Figure 2*B) further confirmed that the two populations did not occupy distinguishable basal positions.
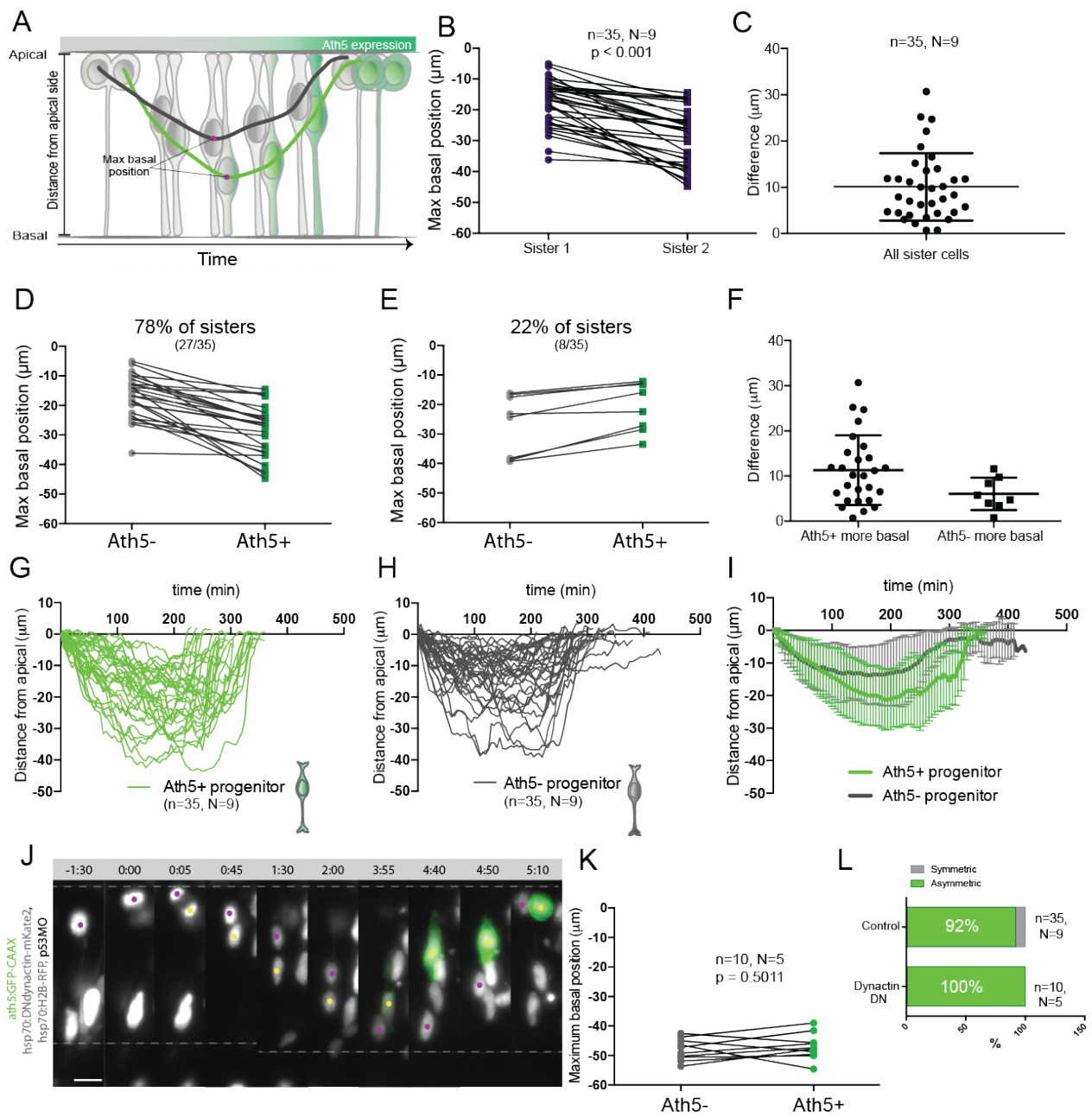
Figure 2. Asymmetry of division generating Ath5+ progenitors is independent of basal soma positioning in the neuroepithelium. (A) Schematic of progenitor cell soma moving along the apicobasal axis between divisions. (B) Maximum basal position of sister cells. Paired t-test was used to compare sister cells. Line connects sister cells. (C) Difference in maximum basal position between sister cells. Vertical error bars represent standard deviation. (D) Maximum basal position of sister cells in cases in which Ath5+ sister cell translocates more basally (27/35, 78%). (E) Maximum basal position of sister cells in cases in which Ath5- sister cell translocates more basally (8/35, 22%). (F) Difference in maximum basal position between sister cells, comparing Ath5+ and Ath5- cells at most basal positions. (G) Ath5+ progenitor trajectories between divisions. Start = 0 min, mitosis of mother cell. End, onset of cell rounding. (H) Ath5- progenitor trajectories between divisions. Start = 0 min, mitosis of mother cell. End, onset of cell rounding. (I) Mean + standard deviation of Ath5+ and Ath5- progenitor pooled tracks from panels G (Ath5+, green) and H (Ath5-, grey). (J) Asymmetric division upon DN-dynactin overexpression. hsp70:H2B-RFP (nuclei, grey), hsp70:DNdynactin-mKate2 (dynactin, grey) ath5:GFP-CAAX (Ath5, green). Scale bar, 10 μm. Dashed lines show apical and basal side of the neuroepithelium. Magenta and yellow dots label sister cells. (K) Maximum basal position of sister cells upon dynactin inhibition. Paired t-test to compare sister cells. (L) Percentage of asymmetric and symmetric divisions observed upon disruption of dynactin function compared to control.

These results show that while basal translocation differs between sister cells for which the Ath5+ cell usually occupied more basal positions, overall basal position was not a clear readout for Ath5 expression onset as Ath5+ progenitors were found along the apicobasal axis.

Asymmetric neurogenic commitment is independent of maximum basal position

The large overlap between basal positioning of Ath5+ and Ath5- sister cell soma argued against a direct link between basal translocation and neurogenic commitment. To show this more directly, we eliminated the difference of basal translocation between sister cells by equalizing their translocation pattern after apical division. To achieve this, we used a heat shock inducible dominant negative version of dynactin (Norden et al., 2009), as dynactin downregulation has been shown to induce increased basal translocation of retinal progenitor cell soma (Del Bene et al., 2008; Norden et al., 2009) (*Figure 2*J). Heat shock expression of the hsp70:DNdynactin-mKate2 construct led to the translocation of both sister cell somas to greater and almost identical basal positions compared to controls (*Figure 2*K, *Video 3*, *Supplementary Figure 2*E). However, despite the fact that both sister cell somas reached very basal positions, only one became Ath5+ while the other remained Ath5- (n=10, N=5) (*Figure 2*L, *Video 3*).

These results show that the asymmetry of neurogenic commitment is not linked to differential somal translocation of sister cells along the apicobasal axis.

Notch pathway components are uniformly distributed along the apicobasal axis of the retinal neuroepithelium

Our results so far argue against a graded effect of Notch signalling on the asymmetry of divisions producing Ath5+ progenitors. Thus, we probed whether the previously reported Notch gradient at the RNA level (Del Bene et al., 2008) was also found at the level of the signalling proteins.

We performed immunostaining against two components of the Notch pathway, the receptor Notch1b and the ligand DeltaC. We found that both Notch pathway components were uniformly distributed along the apicobasal axis of the retinal neuroepithelium (*Figure 3*A,A',A" and *Figure 3*B,B', *Supplementary Figure 3*). We further analysed the distribution of Notch signalling activity using two previously established reporter lines: Tg(her4.1:mcherry-CreERT2), a marker for the gene her4, a direct Notch target (Takke et al., 1999), and Tg(Tp1bglob:H2BmCherry), a marker for a secondary Notch target (Souilhol et al., 2006). This analysis confirmed that Ath5- cells that display active Notch can occupy diverse positions along the apicobasal axis of the neuroepithelium (*Figure 3*C,D and *Video 4*). Interestingly, we noticed that Ath5+ progenitors never express Tp1 or her4 (*Figure 3*C,D, arrowheads), while Ath5- cells express both markers. Thus Ath5+ and Ath5- sister cells experience different levels of Notch signalling activation, independently of the basal position of cell soma.

Overall, these results combined with the fact that asymmetric Ath5 expression onset persisted even when both sister cell somas translocated very basally, argue that Notch signalling does not act via an apicobasal signalling gradient for setting up the asymmetry of divisions leading to neurogenic commitment.

Basal somal translocation of Ath5 positive progenitors depends on a combination of basal process inheritance and stabilized microtubules

While we show that somal positioning along the apicobasal axis does not influence the asymmetry of divisions that produce Ath5+ progenitors, we nevertheless found differences in basal translocation potential between Ath5+ and Ath5- sister cells. In the majority of cases the cell that later starts
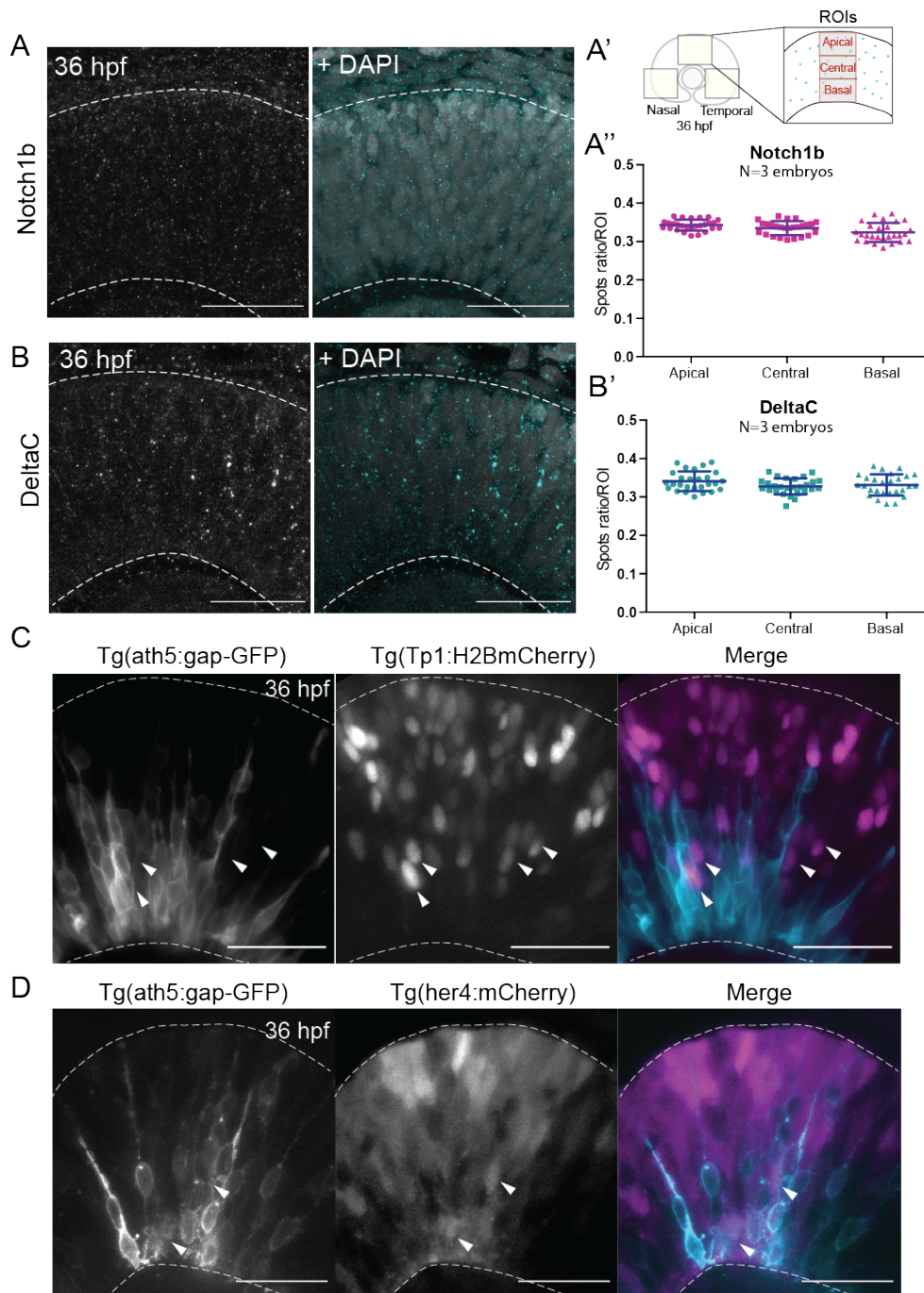
Figure 3. Notch signaling components are uniformly distributed along the apicobasal axis of the retinal neuroepithelium. (A) Staining 36 hpf embryos for Notch1b. Dashed lines show apical and basal side of retinal neuroepithelium. Scale bar, 30 μm. DAPI labels nuclei. (A') Schematic of ROIs along the apicobasal axis used to measure the DeltaC and Notch1b spots ratio. (A") Spot ratio distribution for Notch1b along the apicobasal axis. Unpaired t-test with Welch's correction. P-values: central vs apical, p = 0.0896; basal vs central, p = 0.0630; basal vs apical, p = 0.012. (B) Staining 36 hpf embryos for DeltaC. Dashed lines show apical and basal side of retinal neuroepithelium. Scale bar, 30 μm. DAPI labels nuclei. (B') Spot ratio distribution for DeltaC along the apicobasal axis. Unpaired t-test with Welch's correction. P-values: central vs apical, p = 0.0759; basal vs central, p = 0.6697; basal vs apical, p = 0.3053. (C) Imaging of retina expressing TP1:H2BmCherry (magenta) and ath5:gap-GFP (cyan) at 36 hpf. Scale bar, 30 μm. Arrows show TP1 positive Ath5 negative cells. Dashed lines show apical and basal side of retinal neuroepithelium. (D) Imaging of retina expressing her4:mCherry (magenta) and ath5:gap-GFP (cyan) at 36 hpf. Scale bar, 30 μm. Arrows show her4 positive Ath5 negative cells. Dashed lines show apical and basal side of retinal neuroepithelium.

expressing Ath5 (Ath5+ progenitor) translocated more basally (*Figure 2*D). We thus asked what other factors could facilitate this more basal translocation pattern of Ath5+ progenitors.

To this end, we compared basal translocation kinetics of Ath5+ and Ath5- progenitor soma and performed mean square displacement (MSD) analysis. This analysis revealed that Ath5+ basal somal translocation is more directed than that of Ath5- soma (*Figure 4*B), a finding confirmed by directionality ratio analysis (*Supplementary Figure 2*C). Furthermore, Ath5+ sister cell soma showed a higher average velocity during basal translocation (*Supplementary Figure 2*D), indicating that Ath5+ progenitors translocate more efficiently towards the basal side.

It was previously shown that the inheritance of the basal process allows progenitors and emerging neurons to translocate soma and nucleus more efficiently to the basal side in neuroepithelia of the neocortex and the retina (Saito et al., 2003; Icha et al., 2016a). We thus asked whether basal process inheritance was correlated with efficient basal displacement of Ath5+ soma (*Figure 4*A). Indeed, in 15 out of 16 cell pairs analysed, the cell that inherited the basal process initially translocated its soma more basally (*Figure 4*C). However, only in 10/16 cases (60%), that cell also became the Ath5+ progenitor (*Figure 4*D). Thus, it was possible that additional factors were responsible for the more efficient basal somal translocation of Ath5+ cells. It was previously shown that stabilized microtubules emanating from the apically positioned centrosome, facilitate somal translocation of emerging retinal ganglion cell, the first neurons born in the retina (Icha et al., 2016a). To test whether stabilized microtubules are also present in Ath5+ progenitors, we stained for acetylated tubulin in Tg(ath5:gap-GFP/RFP) embryos (Zolessi et al., 2006) at stages before and during Ath5+ progenitors emergence, 24 hpf, 28 hpf, 32 hpf and 36 hpf (*Figure 4*E). This revealed that at 24 hpf, the developmental stage prior to neurogenesis onset, acetylated tubulin was seen only in the primary cilium of progenitor cells (*Figure 4*E, top left). However, once neurogenesis started, acetylated tubulin was also observed in the apical process of progenitors cells (*Figure 4*E top right and bottom left, 28 and 32 hpf) as well as in retinal ganglion cells at 36 hpf (*Figure 4*E bottom right), as previously reported (Icha et al., 2016a).

To examine whether these stabilized microtubules were directly involved in the basal somal translocation of neurogenic progenitors, we backtracked Ath5+ progenitors overexpressing the microtubule-destabilizing protein Stathmin-1 using a hsp70:Stathmin1-mKate2 construct (*Figure 4*F, *Video 5*) (Icha et al., 2016a). Soma of Ath5+ progenitors expressing Stathmin-1 did not translocate as basally as soma of control cells (*Figure 4*I,K). In contrast, the basal somal translocation of Ath5- progenitors was not affected (*Figure 4*H,J), indicating that only progenitors that enter the neurogenic state use stabilised microtubules for basal somal translocation.

This experiment further confirmed that Ath5 expression onset is independent of somal positioning along the apicobasal axis. While both sister cells remained at very apical positions after division, only one cell became an Ath5+ progenitor (*Figure 4*G, 10/10 divisions). This is the opposite scenario to the dominant negative dynactin condition in which cell nuclei translocated more basally (*Figure 4*J,K), but the asymmetry of Ath5 expression onset persisted in both independently of sister cell basal or apical positions (*Figure 2*L, *Video 3*, *Video 5*). Together, these two results strengthen our argument that neurogenic commitment occurs independently of basal somal translocation in asymmetric divisions.

Overall, these experiments showed that the greater basal somal translocation of Ath5+ progenitors is driven by a combination of basal process inheritance and the presence of apically enriched stabilized microtubules, as seen in other examples of neuronal basal somal translocation in CNS development (Yuasa et al., 1996; Umeshima et al., 2007; Cooper, 2013; Sakakibara et al., 2014; Icha et al., 2016a).
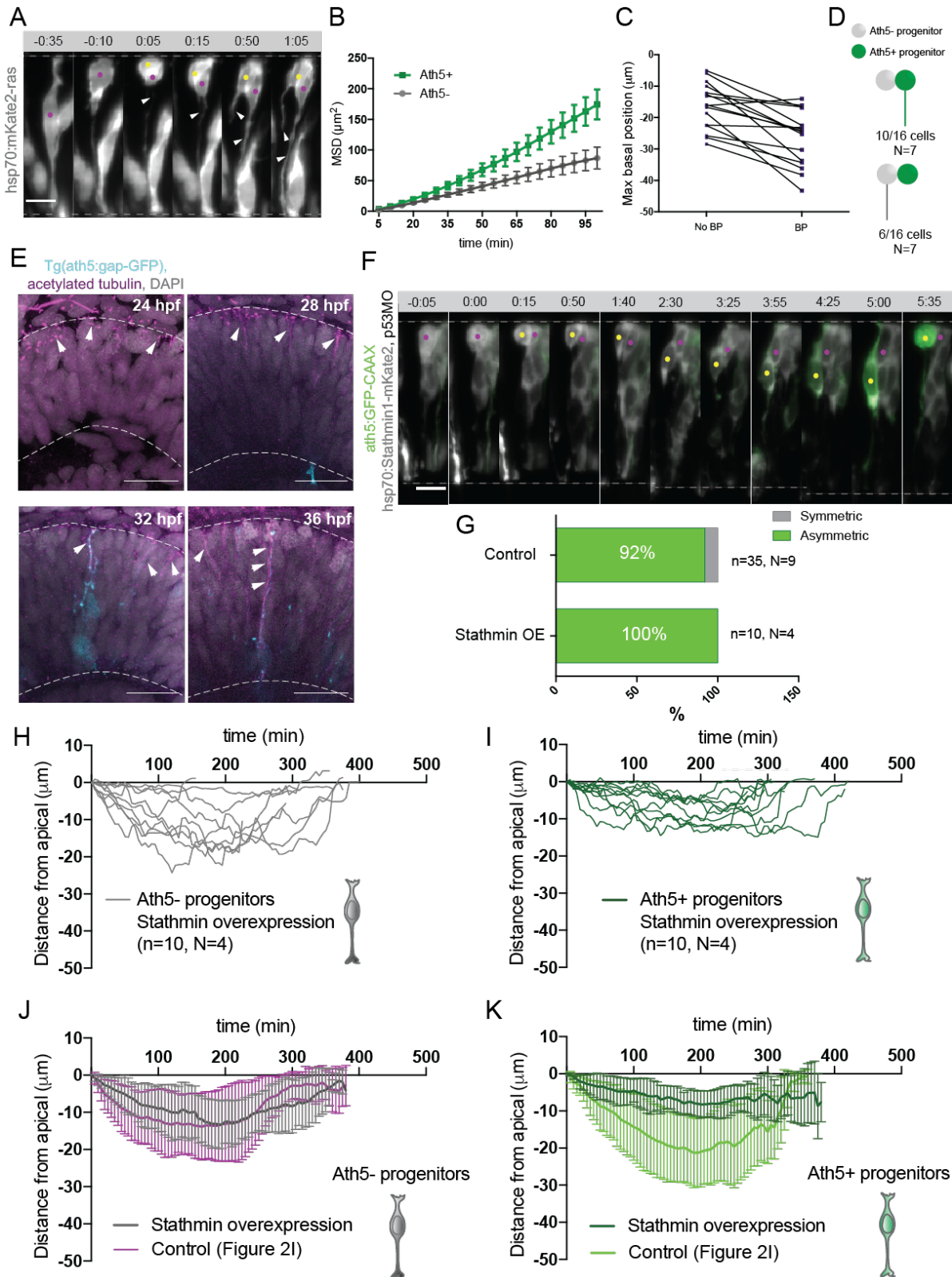
Figure 4. Basal soma translocation of Ath5+ progenitors is facilitated by basal process inheritance and stabilized microtubules. (A) Asymmetric inheritance of basal process during progenitor division. hsp70:mKate2-ras labels cell membrane (grey). Arrowheads: basal process. Scale bar, 10 μm. Magenta and yellow dots label sister cells. Dashed lines show apical and basal side of retinal neuroepithelium. (B) MSD for Ath5+ and Ath5- progenitors. MSD is calculated for basal translocation within the first 100 min after mitosis of the mother cell. Data from Figure 2G and 2H. (Continued on the following page)

Figure 4. (From previous page) (C) Maximum basal position of sister cells not inheriting the basal process (No BP) vs inheriting the basal process (BP) after division. (D) Proportion of Ath5+ and Ath5- progenitors inheriting the basal process. (E) Acetylated tubulin staining (magenta) of Tg(ath5:gap-GFP, cyan) with nuclei labeled by DAPI (grey) at 24 hpf (upper left panel), 28 hpf (upper right), 32 hpf (bottom left) and 36 hpf (bottom right). Scale bar, 30 μm. Arrows indicate acetylated tubulin staining in the primary cilium (upper left), retinal progenitors (upper right and bottom left) and retinal ganglion cells (bottom right). Dashed lines show apical and basal side of retinal neuroepithelium. (F) Example of basal translocation of progenitors upon Stathmin1 overexpression induced at 28 hpf. hsp70:Stathmin1-mKate2 (stathmin, grey), ath5:GFP-CAAX (Ath5, green). Scale bar, 5 μm. Magenta and yellow dots label sister cells. Dashed lines show apical and basal side of retinal neuroepithelium. (G) Percentage of asymmetric and symmetric divisions observed upon Stathmin1 overexpression compared to control. (H) Ath5- progenitor trajectories between divisions upon Stathmin1 overexpression. Start = 0 min, mitosis of mother cell. End, onset of cell rounding. (I) Ath5+ progenitor trajectories between divisions upon Stathmin1 overexpression. Start = 0 min, mitosis of mother cell. End, onset of cell rounding. (J) Mean and Standard Deviation of Ath5- progenitor trajectories in control (magenta) and Stathmin1 overexpression (grey). (K) Mean and Standard Deviation of Ath5+ progenitor trajectories in control (light green) and Stathmin1 overexpression (dark green).

Asymmetric inheritance of Sara-positive endosomes affects the asymmetry of neurogenic commitment

We conclude that the greater basal translocation of progenitors that start expressing Ath5 was driven by a combination of basal process inheritance and a stabilized microtubule network. However, these findings do not yet explain how Notch signalling is involved in the asymmetry of neurogenic commitment independently of a Notch activity gradient. It was shown that Notch signalling components can segregate asymmetrically during division of the mother cell in other systems (Le Borgne and Schweisguth, 2003; Dong et al., 2012; Kechad et al., 2012; Coumailleau et al., 2009), which leads to the inheritance of different levels of Notch by the two daughter cells. In particular, Sara-positive endosomes (Sara endosomes) that carry active Notch signalling via the endocytosis of Delta receptors and Notch ligands were shown to be involved in asymmetric neurogenic fate decisions in the Drosophila sensory organ precursor and the zebrafish spinal cord (Coumailleau et al., 2009; Kressmann et al., 2015).

To test whether Sara-endosomes could also be involved in divisions generating Ath5 positive progenitors, we assessed whether Sara endosomes are present in retinal progenitors at stages at which Ath5+ progenitors emerge. Embryos were injected with mRFP-Sara mRNA and stained for Notch1b and DeltaC. We found that these components indeed co-localise in retinal progenitors (*Figure 5*A,A' and *Figure 5*B,B'). To understand whether Sara-endosomes are asymmetrically distributed between progenitors upon division as suggested elsewhere (Coumailleau et al., 2009; Kressmann et al., 2015), we injected mRFP-Sara RNA into membrane labelled Tg(actb1:HRAS-EGFP) embryos. At all developmental stages analysed, 24 hpf, 28 hpf and 36 hpf, asymmetric distribution of Sara-endosomes was observed in dividing cells (*Figure 5*C). Cells mainly contained 1 to 3 endosomes and rarely more than that (*Supplementary Figure 4*A, n = 25 dividing cells, N = 7 embryos). In most cases one of the two sister cells inherited all endosomes (*Supplementary Figure 4*B, suggesting that the majority of Sara endosome related Notch signalling is dispatched to only one sister cell. Light-sheet live imaging confirmed asymmetric distribution of Sara endosomes during multipotent retinal progenitor divisions (*Figure 5*D, D').

These experiments indicated that Notch signalling is asymmetrically partitioned through Sara-positive endosomes. Thus, Sara endosomes inheritance could mediate asymmetric neurogenic commitment in the retina. Our finding that Ath5+ progenitors never displayed active Notch signalling (*Figure 3*C,D) is in agreement with this notion. Combined, these findings argue that the depletion of Sara endosomes is linked to Ath5+ fate. We propose that Sara endosomes are mostly inherited by the Ath5- cell, which
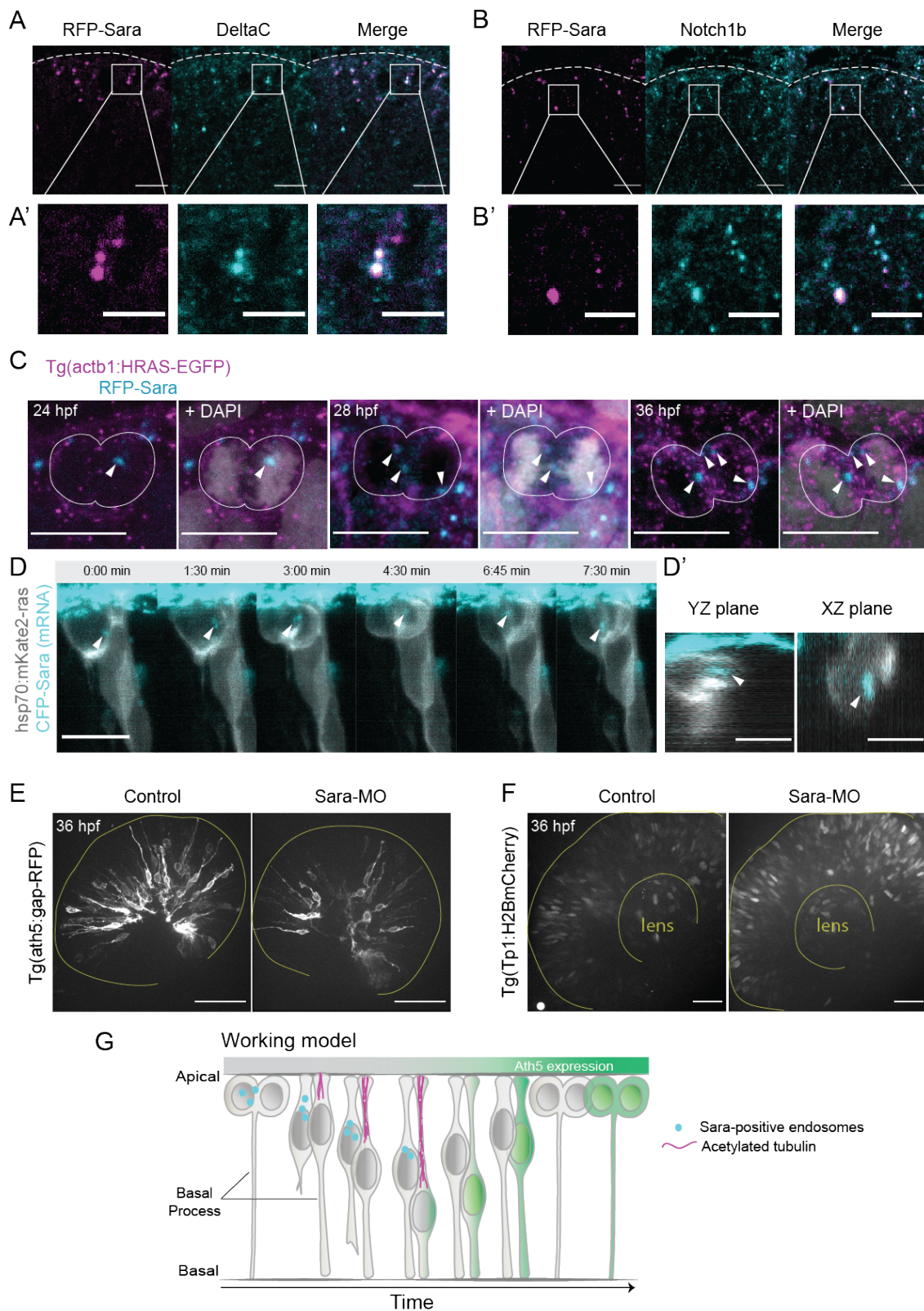
Figure 5. Sara-positive endosomes affect the asymmetry of divisions generating Ath5+ progenitors. (A) Colocalization of Sara-positive endosomes (RFP-Sara, magenta) and DeltaC staining (cyan). Scale bar, 10 μm. Dashed line represents the apical side. (A') Close-up of colocalization. Scale bar, 5 μm. (Continued on the following page)

Figure 5. (From previous page) (B) Colocalization of Sara-positive endosomes (RFP-Sara, magenta) and Notch1b staining (cyan) and. Scale bar, 10 μm. Dashed line represents the apical side. (B') Close-up of colocalization. Scale bar, 5 μm. (C) Asymmetric distribution of Sara-positive endosomes in dividing progenitor cells in fixed samples at 3 different stages, 24 hpf, 28 hpf and 36 hpf. Tg(actb1:HRAS-EGFP) (membrane, magenta), RFP-Sara (Sara-positive endosomes, cyan), DAPI (chromatin, grey). Scale bar, 10 μm. (D) Asymmetric distribution of Sara-positive endosomes in dividing cells in live samples at 32 hpf. hsp70:mkate2-ras (membrane (grey), CFP-Sara (Sara-positive endosomes, cyan). Scale bar, 10 μm. Arrowheads point to the endsosomes (D') YZ (left) and XZ (right) view of sister cells (grey) and Sara endosomes (cyan) at minute 3:00. Scale bar, 10 μm. Arrowheads point to the endsosomes. (E) Ath5+ cells (grey) in retinal neuroepithelium at 36 hpf in control (left) and Sara knockdown (Sara-MO, right). Scale bar, 50 μm. The yellow line delimits the apical side of the retinal neuroepithelium. (F) TP1+ cells (grey) at 36 hpf in control (left) and Sara morpholino knockdown (right). Scale bar, 30 μm. The yellow line delimits the apical side of the retinal neuroepithelium and the lens. (G) Scheme recapitulating the main findings and working model for Sara-positive endosomes inheritance and its role in asymmetric divisions.

retains high Notch signalling and thus stays in the proliferative state (see working model in *Figure 5*G and cell in *Supplementary Figure 4*D, *Video 6*). To further test the involvement of Sara endosomes in asymmetric neurogenic commitment, we depleted the Sara protein using an established Sara splice morpholino (Kressmann et al., 2015).

We found that the number of Ath5+ cells was greatly reduced compared to controls upon Sara inhibition, leading to the presence of fewer neurons (*Figure 5*E, *Supplementary Figure 4*C). At the same time, the number of Tp1-positive cells increased (*Figure 5*F), suggesting an increase in active Notch signalling in both daughter cells as postulated by our working model (*Figure 5*G). This is the opposite scenario to what we observed upon Notch signalling inhibition which lead to the generation of more neurogenic progenitors through an increase in symmetric neurogenic divisions (*Figure 1*E,H,I). In contrast, depletion of Sara led to more symmetric proliferative divisions generating two Ath5- cells.

Overall, these results suggest that Sara-mediated intracellular Notch signalling is necessary to create asymmetries in Notch activity among progenitors, thereby selecting the progenitors that enter the neurogenic path.

Discussion

We here used long-term live imaging to explore the emergence of neurogenic progenitors in the vertebrate retina. Our study reveals that early neurogenic commitment arises via asymmetric divisions of multipotent retinal progenitors that generate one Ath5+ neurogenic progenitor and one Ath5- progenitor that will enter a different lineage. This asymmetry is regulated by Notch signalling and is important to ensure the balance between proliferating cells and cells entering differentiation routes at early stages of neurogenesis. Interference with the division asymmetry leads to premature or delayed differentiation. We provide evidences that Notch does not act through an apicobasal activity gradient as previously proposed but via the endocytic pathway. *Figure 5*G summarises our main findings and presents a working model.

Our quantitative imaging approach showed that progenitor divisions that generate the earliest retinal neurogenic progenitors, Ath5 positive progenitors, are reproducibly asymmetric. This approach allowed us to investigate whether and how the asymmetry is influenced by Notch signalling. Our finding that Notch inhibition leads to more symmetric neurogenic divisions producing two neurogenic progenitors explains the increase in the total number of neurons at the linage level, adding to previous findings that probed this issue at the tissue level (Austin et al., 1995; Ahmad et al., 1997). We show that this increase in symmetric divisions leads to the premature exhaustion of multipotent progenitors.

In line with our findings, it has been shown earlier that Notch is involved in asymmetric divisions that generate two different neurons or one neuron and one proliferative cell in other neural systems including the vertebrate spinal cord and mammalian neocortex (Mizutani et al., 2007; Nelson et al., 2013; Kressmann et al., 2015). For the early neurogenic progenitor divisions in the retina investigated here, it was speculated that Notch acts via a signalling gradient along the apicobasal axis of the neuroepithelium (Murciano et al., 2002; Del Bene et al., 2008). Two studies proposed that more basally translocating progenitors are more likely to become neurogenic, generating two neurons after the next division (Murciano et al., 2002; Baye and Link, 2007). This led to the hypothesis that Notch signalling acts mainly at the apical side of the neuroepithelium where it suppresses neurogenic fate. However, due to technical challenges at the time, these analyses could only take a small number of unrelated cells into consideration. We here analysed large cohorts of sister cells and tracked their basal translocation patterns and indeed found that the more basally translocating sister cell is more likely to enter the Ath5+ lineage. However, when the entirety of Ath5+ cells was taken into account, a significant overlap of basal positioning of Ath5+ and Ath5- cohorts was observed. In addition, the asymmetry of neurogenic commitment persisted when the translocation position of sister cells was levelled towards either the basal or the apical side. Together, this shows that somal position along the apicobasal axis of the retinal neuroepithelium does not influence asymmetric neurogenic commitment.

Instead, we present evidence that it is the asymmetric partitioning of Sara endosomes that drives the asymmetry of retinal progenitors divisions to enter the neurogenic pathway, as shown before in the Drosophila sensory organ precursor and the zebrafish spinal cord (Coumailleau et al., 2009; Kressmann et al., 2015). Ideally, we would have directly correlated Sara-positive endosomes inheritance with neurogenic or proliferative fate occurrence in numerous cells. However, this correlation could not be systematically quantified over several instances of asymmetric divisions in our system, due to its complexity and long timeframes between division and fate readout. Nevertheless, we could follow one division in which Sara endosomes where asymmetrically inherited and correlated the inheritance with sister cell fates. As expected, the cell inheriting all endosomes becomes the Ath5- progenitor and thus remains proliferative (*Supplementary Figure 4*D, *Video 6*) while the cell without Sara-endosomes starts Ath5 expression and thereby enters the neurogenic lineage (see working model *Figure 5*G and *Supplementary Figure 4*D, *Video 6*). This outcome is coherent with the fact that Ath5+ cells do not show active Notch signaling. These observations, combined with the finding that asymmetric inheritance is observed at stages at which asymmetric Ath5 decisions occur and that Sara knockdown impairs the balance between proliferation and neurogenesis in the Ath5 lineage, strongly argue that Notch signaling via Sara-positive endosomes is important for lineage asymmetry in the retina. The asymmetric distribution of Sara-positive endosomes most likely leads to the downregulation of Notch in one sister cell. This explains our observation that upon Sara knockdown more progenitors express active Notch signaling, as the Sara protein guides the asymmetric dispatch of these endosomes (Coumailleau et al., 2009). It should be noted that our systematic analysis not only enhances the understanding of Notch signalling in this particular neurogenesis event, but also shows the importance of quantitative approaches in developmental systems. Only due to the analysis of large cohorts of sister cells combined with a backtracking approach could we achieve the depth of data needed to exclude the role of a possible Notch gradient which led to the investigation of the Notch endocytic pathway. The advance of imaging techniques, image analysis algorithms and the possibility of performing backtracking studies in the retina are exciting emerging tools to follow similar questions in future studies on brain development. Such sophisticated studies will in turn promote our understanding of reproducibility and/or plasticity of lineage decisions at diverse developmental stages in different tissues of the central nervous system.

Despite the fact that basal position is not directly linked to Ath5+ fate commitment, we find that

the majority of progenitors entering the Ath5 lineage nevertheless translocate their soma more basally than their Ath5- sister. This observation argues that the more basal translocation of neurogenic Ath5+ progenitors is a consequence of neurogenic commitment, not the cause for it. We find that basal translocation of Ath5+ progenitors is linked to apically localized stabilized microtubules and basal process inheritance. This is remarkably similar to what has been shown for somal translocation events of retinal ganglion cells (Icha, Kunath, et al., 2016). In contrast, this is different to nuclear and thereby somal translocation during IKNM in multipotent progenitors, which has been shown to be caused by passive nuclear displacements (Norden et al., 2009; Kosodo et al., 2011; Leung et al., 2011). Thus, an interesting interpretation of these findings could be that Ath5+ progenitors constitute an intermediate cell type placed between multipotent progenitors and differentiating neurons at the level of cellular arrangements including cytoskeletal components. This is reminiscent of intermediate progenitors found in the mammalian neocortex (Haubensak et al., 2004; Miyata et al., 2004; Noctor et al., 2004). To our knowledge such intermediate progenitors have not yet been described in the retina, meaning that our finding opens the possibility of exciting future studies of this cell type. It will be interesting to probe how cytoskeletal changes could be linked to cell identity changes in the developing retina and beyond. Such studies will open new avenues to understand the biology of fate decisions downstream of transcription profiles towards the cell biological scale.

Asymmetric progenitor divisions are an important mean to maintain the balance between proliferation and differentiation in developing organs. To understand the regulation of these types of divisions and thereby embryogenesis as a whole, their investigation needs to span scales from the molecular to the cellular to the tissue level. Furthermore, investigations need to combine knowledge of cell type specific transcription factor profiles, the signalling factors involved in guiding fate decisions and the cell biological consequences that differentiation entails. The emerging possibilities of quantitative in vivo studies mentioned above in combination with the advent of single-cell sequencing data that is becoming more and more extensive (Wagner and Klein, 2020; Xu et al., 2020), opens new perspectives for an understanding of these phenomena at a previously unimaginable level. This, in combination with the continued use of the zebrafish as a model for quantitative developmental biology, has the potential to reveal general principles that can then be extended to other, often less accessible systems.

Materials and Methods

Zebrafish husbandry

Wild-type zebrafish were maintained at 26°C. Embryos were raised at 21°C, 28.5°C, or 32°C in E3 medium, which was changed daily. To prevent pigmentation, E3 medium was supplemented with 0.2 mM 1-phenyl-2-thiourea (Sigma-Aldrich) from 8 hours post fertilization (hpf). Animals were staged in hpf according to Kimmel et al. (1995). All animal work was performed in accordance with European Union directive 2010/63/EU, as well as the German Animal Welfare Act.

Transgenic lines

To visualize Ath5 neurogenic progenitors, the Tg(ath5:gap-GFP) and Tg(ath5:gap-RFP) (Zolessi et al., 2006) lines were used. To visualize Notch activity, the Notch reporter lines Tg(her4.1:mcherry-CreERT2) (Kroehne et al., 2011), Tg(her4:EGFP) (Yeo et al., 2007) and Tg(Tp1bglob:H2BmCherry) (Ninov et al., 2012) were used. To label cell membranes, the Tg(actb1:HRAS-EGFP) (Cooper et al., 2005) line was used. To visualise progenitors nuclei, Tg(hsp70:H2B-RFP) line was used (Dzafic et al., 2015).

Table 1. DNA constructs used in this study.

Plasmid	Concentration	Heat shock	Reference(s)
ath5:GFP-CAAX	15 ng/μl	–	(Kwan et al., 2007) (Icha et al., 2016a)
hsp70:H2B-RFP	10 ng/μl	37 °C, 15 min	(Strzyz et al., 2015)
hsp70:mKate2-ras	15 ng/μl	37 °C, 15 min	(Strzyz et al., 2015)
hsp70:Stathmin1-mKate2	15 ng/μl	39 °C, 10 min	(Taverna et al., 2016)
hsp70:mKate2-dynactin (1-811)	15 ng/μl	39 °C, 15 min	(Taverna et al., 2016)

DNA and RNA injections

To mosaically label cells in the zebrafish retina, DNA constructs were injected into 1 cell stage embryos. Injected volumes ranged from 0.5 to 1 nl. The amount of injected DNA ranged from 10 to 20 pg per embryo and did not exceed 40 pg even when multiple constructs were injected. See *Table 1* for details. pCS2 expression vectors containing CFP-Sara or mRFP-Sara were kindly provided by Marcos Gonzáles-Gaitán and published previously (Kressmann et al., 2015). The Sara mRNA was synthesized using the Ambion mMessage mMachine kit. To visualize SARA endosomes, 100 pg of CFP-SARA or mRFP-SARA where injected into one cell stage embryos for ubiquitous expression.

Heat shock of embryos

To induce expression of the heat shock promoter (hsp70)–driven constructs, embryos were incubated at 24 or 28 hpf in water bath at different temperatures (see *Table 1* for details). Imaging always started 3–4 hours after heat shock.

Morpholino experiments

To knock down gene function, the following amounts of morpholinos (Gene Tools) were injected into the yolk at 1-cell stage: 2,5 ng of a splice morpholino for the sara gene 5' -TGAACTAGAGACTTTA CCTTGCCAC-3', (Kressmann et al., 2015) and 2 ng of p53 MO, 5'- GCGCCATTGCTTTGCAAGAATTG-3' (Robu et al., 2007).

Blastomere transplantation

Donor embryos from the double transgenic line Tg(hsp70:H2B-RFP),Tg(her4:EGFP) and acceptor were dechorionated in pronase. At the high stage, cells from the animal pole of donors were transplanted into the acceptor wild type embryos. Transplanted embryos were grown at 32°C to recover for 4 hours, then moved to 28°C. The E3 medium was supplemented with 100 U of penicillin and streptomycin (Thermo Fisher Scientific). Transplanted embryos were heat shocked at 24 hpf for 15 minutes at 39°C and imaged from 28 hpf.

Drug treatments

Notch inhibitors DAPT (Sigma-Aldrich) and LY411575 (Sigma-Aldrich) were dissolved in DMSO and used at 50 μM and 10 μM concentration respectively and compared to DMSO only controls. Embryos were dechorionated and treated with the drugs at 28°C in E3 medium, either in a 24 multi-well plate or the light sheet microscope chamber for live imaging experiments. All treatments started at 24 hpf. For live imaging experiments, fish were pre-incubated with the drug for 4 hours and imaging started at 28 hpf.

Immunofluorescence

All immunostainings were performed on whole-mount embryos fixed in 4% paraformaldehyde (Sigma-Aldrich) in PBS as previously described (Icha et al., 2016a). In brief, embryos were permeabilized with trypsin, blocked with goat or donkey serum 10% in PBS-Triton 0.8% and incubated with the primary antibody for 72 hours. The Notch1b (GTX48505, GeneTex) and DeltaC (zdc2, Abcam) antibodies were used at 1:100 dilution. The acetylated tubulin antibody (T6793, Sigma-Aldrich) was used at 1:250 dilution. Embryos were incubated for 48 hours with an appropriate fluorescently labeled secondary antibody (Molecular Probes) at 1:500 dilution and DAPI at 1:1000 dilution (Thermo Fisher Scientific).

Image acquisition

Laser scanning confocal microscopy (LSCM)

Fixed samples from immunostaining experiments were imaged with the Zeiss LSM 880 inverted point-scanning confocal microscope (Carl Zeiss Microscopy) using the 40x/1.2 C-Apochromat water immersion objective (Zeiss). Samples were mounted in 1% agarose in glass-bottom dishes (MatTek Corporation) and imaged at room temperature. The microscope was operated with the ZEN 2011 (black edition) software (Zeiss).

Spinning disk confocal microscopy (SDCM)

Confocal stacks for fixed samples for Notch inhibition and Sara knockdown experiments were taken using an Andor SDCM system (Andor), consisting of an Andor IX 83 stand equipped with a CSU-W1 scan head (Yokogawa) with Borealis upgrade and an Andor iXon Ultra 888 Monochrome EMCCD camera. 40x/1.25 or 60x/1.3 silicone objectives were used to acquire 50-80 μm z-stacks were recorded with 1 μm optical sectioning. Fixed samples were mounted in 1% agarose in glass-bottom dishes (MatTek Corporation) and imaged at room temperature. The microscope was operated by Andor iQ 3.6 software.

In vivo light sheet fluorescent imaging (LSFM)

Light sheet imaging started between 28 hpf and 30 hpf. Embryos were manually dechorionated and mounted in glass capillaries in 1% low-melting-point agarose as previously described (Icha et al., 2016b). The sample chamber was filled with E3 medium containing 0.01% MS-222 (Sigma-Aldrich) to immobilize embryos and 0.2 mM N-phenylthiourea (Sigma-Aldrich) to prevent pigmentation. Imaging was performed on a Zeiss Lightsheet Z.1 microscope (Carl Zeiss Microscopy) equipped with two PCO.Edge 5.5 sCMOS cameras and using a 20x/1.2 Zeiss Plan-Apochromat water-immersion objective at 28.5°C. Z-stacks spanning the entire retinal epithelium (70-100 μm) were recorded with 1 μm optical sectioning every 5 min for 15-20 hours using the double-sided illumination mode. Sara endosomes inheritance during cell division was imaged with 1 min time resolution and 0.5 μm optical sectioning. The system was operated by the ZEN 2014 software (black edition).

Image analysis

Images from live imaging experiments were cropped and averaged in ZEN Black and/or Fiji (Schindelin et al., 2012) and were corrected for drift using a Fiji plugin (Manual drift correction) created by Benoit Lombardot (Scientific Computing Facility, Max Planck Institute of Molecular Cell Biology and Genetics, Dresden, Germany).

Analysis of sister cell somal translocation

Ath5 progenitor divisions were identified and cells were backtracked to the previous cell division in order to identify cells giving rise to Ath5+ progenitors and the sister cell arising from the division. From

the point after division, the translocation of sister cells was tracked in 2D in maximum projected sub-stacks by following the center of the cell body in Fiji using the semi-automated ImageJ plugin MTrackJ (Meijering et al., 2012). MSDs and directionality ratios were calculated in the DiPer program (Gorelik and Gautreau, 2014), executed as a macro in Excel (Microsoft). To calculate the average instantaneous velocities, a custom-made scripts was written using Python 3 and can be found here.

Integral mean calculations

The integral mean $\hat{d}$ was computed using Python 3 (available here) as follows:

$$\hat{d} = \frac{I}{T} \tag{1}$$

Where T is the time length of each cellular trajectory and I is the area below the trajectory curve, calculated as:

$$I = \int_0^T \mathrm{depth}(t)\, \mathrm{d}t \tag{2}$$

Where deptht > 0.

Retinal size measurements

Retinal size was manually measured using 48 hpf retinas treated with LY411575 10 μM or equal volume of DMSO, as illustrated in *Figure 1*G. Thickness and diameter were measured in the central z plane of the nasal, central and temporal region of the retina, using the Fiji line tool.

Notch1b and DeltaC spatial distribution

Prior to analysis, a gaussian blur of 0.5 was applied to all the images. Apical, central and basal ROIs (560 μm^2) of the same dimensions were set for each image, dividing the length of the apicobasal axis by 3. Three central slices per embryo were analyzed in the nasal, central and temporal regions (*Figure 3*A"). SpotCounter plugin for Fiji (Spot counter, Nico Stuurman, ValelabUtils package) was used to measure the number of spots in each ROIs. The number of spots in each ROIs was then normalized by the total number of spots in the 3 ROIs of a slice.

Sara-positive endosome count

Prior to analysis, a gaussian blur of 0.5 was applied to all the images. Confocal z-stack of retinal progenitors were reconstructed in 3D using the volume renderer ClearVolume (Royer et al., 2015) for Fiji. The number of Sara-positive endosomes was manually counted in dividing cells from 3D reconstructions.

Statistical analysis

All Statistical tests used are indicated in the figure legend, as well as the definitions of error bars. All tests used were two-sided and 95% confidence intervals were considered. P values and sample sizes are noted in figure panels or figure legends. Data was analyzed using GraphPad Prism 6 or Python 3. Statistical analysis was performed using GraphPad Prism 6 and MATLAB.

Acknowledgments

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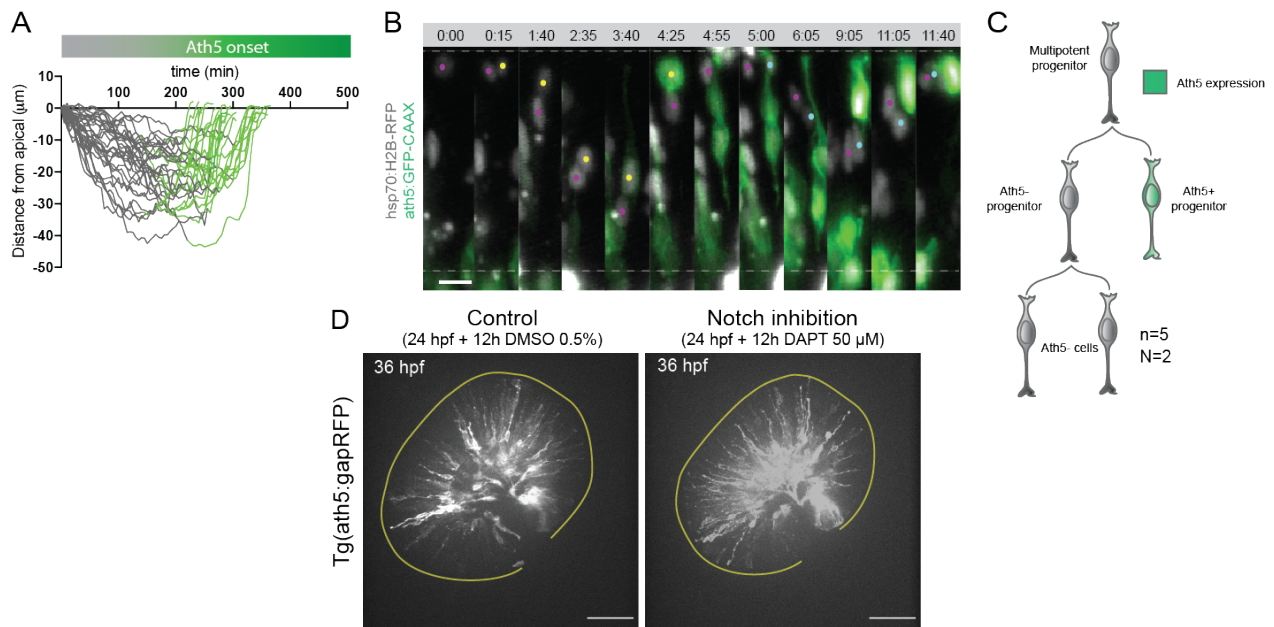
Supplementary Figure 1. The Ath5- sister cell does not enter the Ath5 lineage in the next cell cycle. (A) Onset of Ath5 expression (green) in Ath5+ progenitors between divisions. (B) Example of Ath5- sister cell followed to next division. hsp70:H2B-RFP (nuclei, grey), ath5:GFP-CAAX (Ath5, green). Scale bar, 10 μm. (C) Schematics of lineage tree of Ath5- cell. (D) Ath5+ cells (grey) at 36 hpf in control (left) and upon Notch inhibition (right) with DAPT 50 μM. Scale bar, 50 μm. The yellow line delimits the apical side of the retinal neuroepithelium.
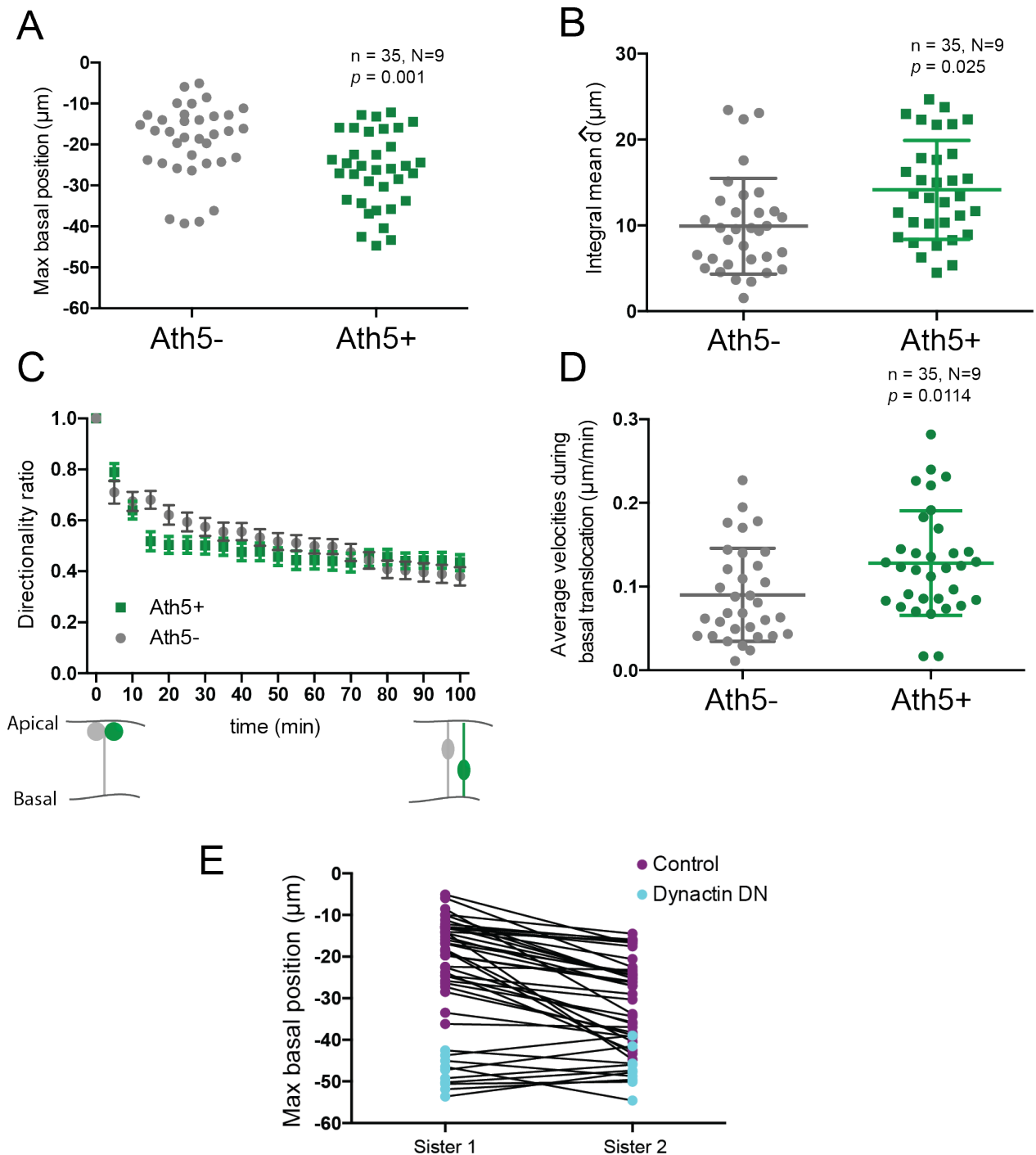
Supplementary Figure 2. Ath5- and Ath5+ progenitor populations spatially overlap during translocation between division. (A) Maximum basal position of Ath5- and Ath5+ cells. Unpaired t-test with Welch's correction. (B) Integral mean of Ath5- and Ath5+ cells. Vertical bars represent standard deviation. Kolmogorov-Smirnov test. (C) Directionality ratio of Ath5+ and Ath5- progenitors cell soma for basal translocation. Data from Figure 2 D-E. Error bars represent SEM. (D) Average velocity of Ath5+ and Ath5- cell bodies between 0 and 100 min, corresponding to basal translocation. Vertical bars represent standard deviation. Unpaired t-test. (E) Comparison between maximum basal position of sister cells in control (purple dots) and dynactin dominant negative (dynactin DN, cyan dots) from figures 2B and 2K, respectively. Line connects sister cells.
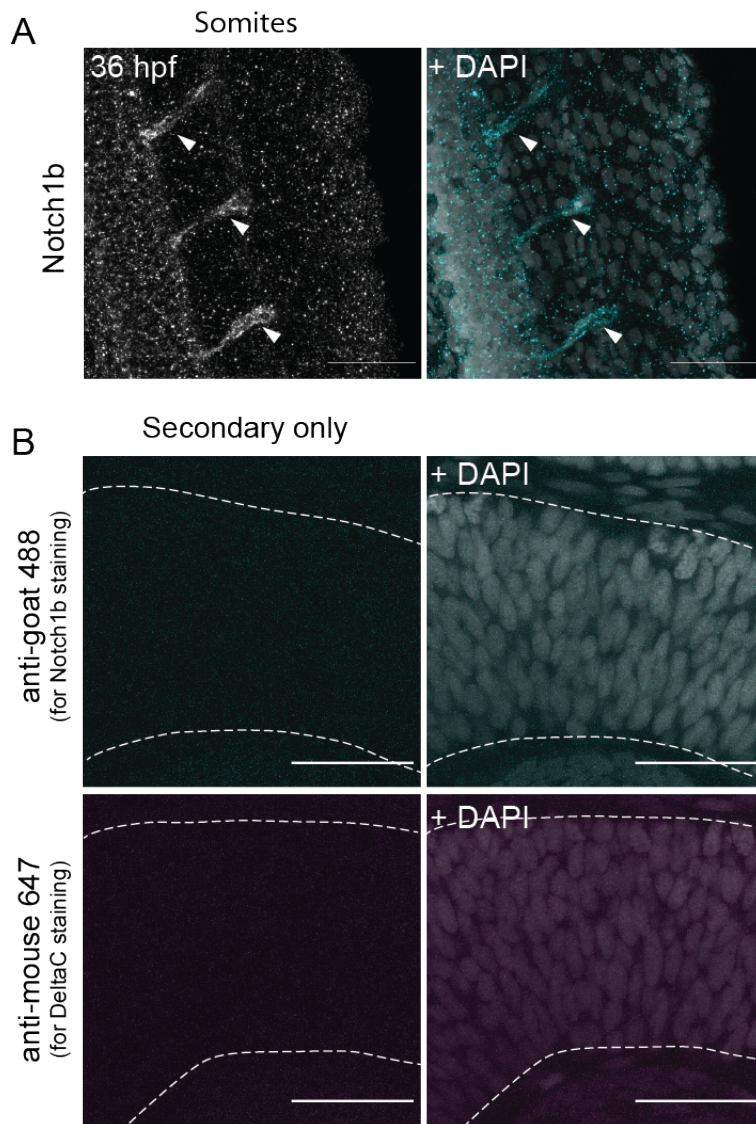
Supplementary Figure 3. Controls for Notch1b and DeltaC stainings in the retinal neuroepithelium. (A) Staining 36 hpf embryos for Notch1b in the tail. Arrowheads indicate positive staining on the somites. Scale bar, 50 μm. DAPI labels nuclei. (B) Staining 36 hpf embryos with secondary used for Notch1b (upper row) and DeltaC (lower row) stainings. Dashed lines indicate apical and basal side of the retinal neuroepithelium. Scale bar, 30 μm. DAPI labels nuclei.
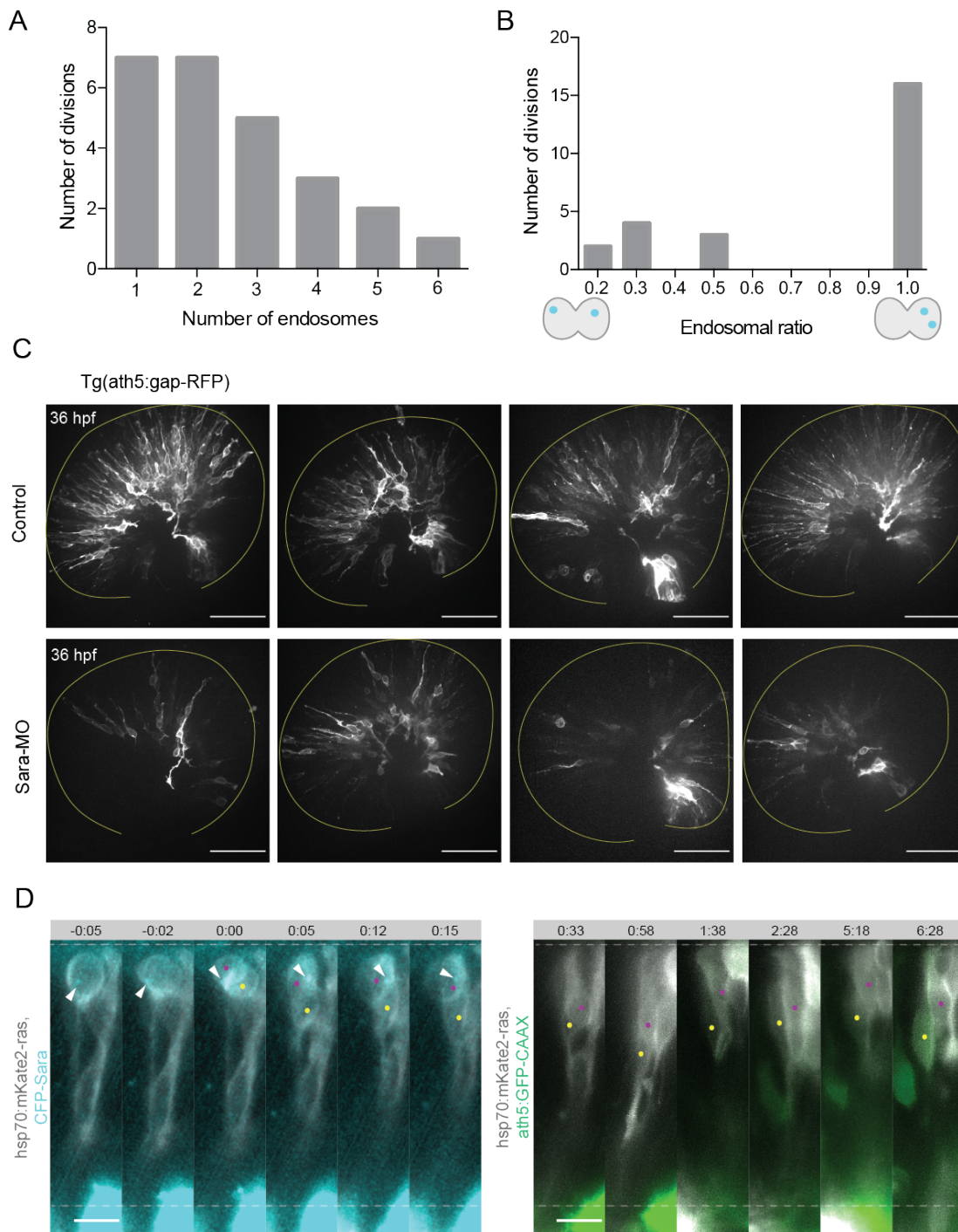
Supplementary Figure 4. Sara-positive endosomes are asymmetrically distributed during cell division. (A) Number of endosomes within dividing cells. n = 25 cells, 7 embryos. (B) Histogram of endosomal ratio between dividing cells. n = 25 cells, 7 embryos. (C) Ath5+ cells in retinal neuroepithelium at 36 hpf in control (upper row) and Sara knockdown (lower row) with 2.5 ng/embryo of Sara morpholino. Scale bar, 50 μm. The yellow line delimits the apical side of the retinal neuroepithelium. (D) Example of an asymmetric inheritance of Sara-positive endosomes (left) within asymmetric division of multipotent progenitors generating Ath5+ progenitors (right). hsp70:mkate2-ras (cells membrane, grey), CFP-Sara (Sara-positive endosomes, cyan), ath5:GFP-CAAX (Ath5, green). Dashed lines show apical and basal borders of retinal neuroepithelium. Scale bar, 10 μm. Magenta and yellow dots label sister cells. White arrow points to the Sara-positive endosome.