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Adherens junction domains are split by asymmetric division of embryonic neural stem cells

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INTRODUCTION

Neural stem cells (NSCs) are able to self-renew and are multipotent. Before the onset of neurogenesis (embryonic day (E)11 in the mouse), they undergo symmetric proliferative divisions, with one NSC giving rise to two daughter stem cells to increase the size of the progenitor pool. As neurogenesis proceeds (E11–E17), they switch to an asymmetric neurogenic mode of division to generate one stem cell (Kosodo et al, 2004; Gotz & Huttner, 2005). The sub-apical junctional complexes—that is, adherens junctions (AJs)—seem to be partitioned along with the apical plasma membrane, as evidenced by the distribution during division of the AJ-enriched polarity protein PAR3 (Kosodo et al, 2004). As a result, AJ components have been considered to provide a mechanism for localization of fate determinants and regulation of their inheritance (Gotz & Huttner, 2005). However, such a model in which AJs are unequally inherited during asymmetric division cannot explain how the daughter cell that has not inherited any AJ retains its apical attachment. Here, we explain this discrepancy by showing the presence of distinct domains within the AJs that separate adhesion and putative fate-determining molecules, which are inherited differentially during cell division.

RESULTS AND DISCUSSION

Planar asymmetry of N-cadherin distribution in NSCs

N-cadherin is a crucial structural component of neuroepithelial AJs (Kadowaki et al, 2007). By stabilizing the Delta ligand of Notch receptors at the plasma membrane (Mizuhara et al, 2005) and by controlling the cytoplasmic pools of β- and αE-catenin, which are molecules implicated in Wnt and Shh signalling (Chenn & Walsh, 2002; Lien et al, 2006), N-cadherin might regulate the balance between symmetrical and asymmetrical division. A role for N-cadherin in fate determination would predict an appropriate
partitioning of the protein in the two daughter cells on mitosis—that is, equal inheritance in symmetrical divisions but unequal inheritance in asymmetrical divisions. Therefore, we examined the distribution of N-cadherin in SOX2-positive neocortical progenitors (Fig 1; supplementary Fig S1A online). We observed that the protein accumulates apically at sites of contact between NSCs undergoing mitosis and the processes of neighbouring cells (Fig 1A; Chenn et al., 1998). This accumulation represents AJs at the most apical end of the lateral plasma membrane, as evidenced by partial colocalization with actin filaments organized in a belt next to the ventricle. In addition, the protein is present in a broader distribution within the lateral membrane. Closer examination of dividing cells rounded up next to the ventricle showed that N-cadherin forms an apical crescent, but remains absent from the apical plasma membrane identified with the apical marker prominin 1 (Fig 1B). Within this crescent, we observed a lateral gradient in the distribution of N-cadherin in some dividing cells (Figs 1B and 2A), showing planar asymmetry in these cells.

No link between cadherin distribution and cell fate
As most of the mitotic cells show a vertical cleavage plane (73 out of 84 cells; supplementary Fig S2 online), the planar asymmetry in N-cadherin distribution predicts that two daughter cells might inherit different amounts of the protein at the time of division (Fig 2). To test this, we compared the fraction of N-cadherin accumulated in the lateral membranes of the two daughter cells at the end of mitosis by measuring the ratio of their fluorescence intensities (Fig 2B; supplementary information online). We found that in nearly half of the divisions, one of the two daughter cells inherits a larger fraction of the protein i.e. at least 1.5-fold more protein in almost 50% of cases, median value 1.4, n = 30 at E10 and n = 85 at E14; Fig 2A,B). We ruled out the possibility that this is only a consequence of oblique cleavage planes, as most of the divisions with differential partitioning of N-cadherin (ratios equal to or higher than 1.5) were vertical (n = 33 out of 41) rather than oblique (n = 7 out of 41; supplementary Fig S2 online).

This differential partitioning of N-cadherin was observed at all stages examined (E10 and E14), irrespective of the predominant mode of division (Fig 2B). To investigate any correlation with the mode of division (as would be expected if the hypothesis that N-cadherin has a role in fate determination is correct), we plotted the relative inheritance of the protein against the predicted fate of the daughter cells (Fig 2C; supplementary Fig S3 online). Cell fate was predicted by following the partitioning of the apical plasma membrane (Kosodo et al., 2004; supplementary Fig S3 online) or the presence of green fluorescent protein (GFP) expression in NSCs committed to neurogenic divisions using the TIS21-GFP knock-in mouse embryos (Haubensak et al., 2004; Fig 2C). In both cases, we found no difference in the distribution of N-cadherin ratios between the various types of division, as indicated by the absence of statistically significant differences between median values of 1.3 (n = 29) and 1.6 (n = 23) when prediction is made by inheritance of the apical membrane (supplementary Fig S3 online), or between median values of 1.5 (n = 34) and 1.3 (n = 27) when prediction is made by the TIS21-driven GFP expression (Fig 2C). Cells arising from symmetrical and asymmetrical divisions are therefore equally likely to inherit different amounts of N-cadherin, from which we conclude that the differential inheritance of N-cadherin observed in some dividing cells is not related to the fate of the daughter cells.

Organization of AJs in membrane domains
Previous observations that the polarity protein PAR3 is inherited by only one of the two daughter cells in asymmetric divisions have suggested the hypothesis that unequal AJ partitioning determines their fate (Kosodo et al., 2004). However, we find no correlation between N-cadherin distribution and fate. In addition, the distribution of the zona occludens protein ZO1, as followed by time-lapse imaging, shows that this component of the AJ is also inherited by the two daughter cells in most cases (Konno et al., 2004). One possible explanation for this discrepancy regarding N-cadherin and ZO1 being inherited by both daughter cells but PAR3 by only one daughter cell could be the differential partitioning of junctional proteins during division. Therefore, we examined the micro-organization of AJs by investigating a panel of proteins already resolved by electron microscopy to be junctional proteins (Aaku-Saraste et al., 1996; Manabe et al., 2002; Takekuni et al., 2003). These were two junctional proteins, ZO1 (part of the AJ rather than tight junctions in the neuroepithelium; Aaku-Saraste et al., 1996) and afadin (the cytoplasmic partner of nectin adhesion molecules), and the two PAR complex polarity proteins PAR3 and PAR6.
aPKC. As expected for proteins concentrated at the AJ, their distribution appears as a discrete line along the ventricle (supplementary Fig S1B online) and they accumulate at the most apical end of the lateral plasma membrane, where they form ring-like structures (Fig 3; supplementary Fig S4 online). N-cadherin was perfectly colocalized with β-catenin (supplementary Fig S4B online) and was used as a general marker for all neuroepithelial cadherins. The organization of actin filaments in a belt at the apical pole of polarized cells is commonly used to position the AJ, and consequently was used as a reference point to position the various membrane proteins along the apico-basal axis (Fig 3A; supplementary Fig S4A online). This helped to identify three membrane domains within the AJ: ZO1 and afadin were positioned centrally, the apical part was enriched in PAR3/aPKC and the basal part in N-cadherin (Fig 4F). This configuration was confirmed when N-cadherin was used as the point of reference instead of actin (Fig 3B; supplementary Fig S4B online), as we observed a partial colocalization of N-cadherin with the afadin/ZO1 rings and an absence of colocalization with the PAR3/aPKC rings. As the PAR3/aPKC-enriched domain occupies the most apical position, we tested and ruled out the possibility that it belongs to the apical plasma membrane rather than the AJ by showing no overlap with the apical marker prominin 1 (Fig 3A). Notably, the organization of the AJ was found to be identical irrespective of the brain region, developmental stage or cell-cycle phase (data not shown). The apico-lateral plasma membrane stratification that we report suggests that neuroepithelial AJs show a higher degree of organization than described previously (Manabe et al., 2002; Ghosh et al., 2008). Studies on other epithelial tissues have revealed two subdivisions of AJs, with PAR3 co-localized with cadherins but distinct from aPKC (Afonso & Henrique, 2006). Our work reveals that cadherin complexes can be separated from the two polarity proteins and suggests the existence of at least three functionally distinct microdomains within the AJ structure.

Differential inheritance of AJ domains on division

The unequal distribution of these microdomains could provide an explanation as to how AJ components could be differentially inherited on asymmetric division. Therefore, we examined the partitioning of these microdomains in the progeny of NSCs (Fig 4). This partitioning was evaluated in anaphasic cells by predicting the orientation of the cleavage plane (Fig 4A; supplementary information online), and in telophasic cells based on fusion of the
cleavage furrow ingressing from basal to apical with the apico-lateral membrane (supplementary information online; Kosodo et al, 2004). The aPKC domain was inherited by both daughter cells on symmetric division when the apical membrane was bisected by the cleavage plane (27 out of 27 symmetric divisions; Fig 4C; supplementary 3D movie 2 online) and by only one of the two daughter cells on asymmetric division when the apical membrane was bypassed (26 out of 29 asymmetric divisions; Fig 4D; supplementary 3D movie 3 online). From these observations, we conclude that the aPKC domain always partitions with the apical membrane. In addition, we showed that differential inheritance of aPKC by the progeny is usually observed when one of the two daughter cells detaches from the ventricle and loses its polarity, as predicted by the TIS21 promoter-driven GFP expression identifying neurogenic divisions (11 cells with unequal aPKC out of 12 GFP positive; Fig 4E; supplementary 3D movies 4 and 5 online; Attardo et al, 2008). By contrast, we observed that in most of the divisions, the afadin central domain was inherited by both daughter cells (28 out of 30 cells), with only a small fraction showing a clear bypass of this domain (2 out of 30 cells; Fig 4B; supplementary 3D movie 1 online). These respective distributions of afadin and aPKC in the progeny at the time of division indicate that the AJ microdomains can be differentially inherited. Taken together, our observations therefore provide new evidence that the AJ is split, on asymmetric division, between the polarity and the adhesive microdomains (Fig 4F). We propose that the inheritance of adhesion molecules by both daughter cells, whatever the mode of division, will allow the retention of their apical processes next to the ventricle after mitosis is complete. This is not to say that the AJs will remain normal in the process that loses polarity proteins after asymmetrical division; indeed, given the proposed role of polarity proteins in the maintenance of AJs (Imai et al, 2006; Alfonso & Henrique, 2006; Cappello et al, 2006; Ghosh et al, 2008), the splitting away of these proteins from the adhesion molecules would be predicted to destabilize the AJ and might be responsible for the later detachment of the apical processes from the ventricle. In support of this, aPKC has not been detected in those apical processes involving detachment from the ventricle (Ghosh et al, 2008), and we observe that aPKC is inherited by the daughter stem cell whose apical membrane remains in contact with the ventricle.
Our model requires that the orientation of the cleavage plane is tightly regulated to split the adhesive and polarity domains. It follows that abnormal cleavage planes will increase the probability that one daughter cell does not inherit adhesion molecules and prematurely loses its apical attachment. In agreement with this, recent studies have described mispositioning of the progeny as a result of random cleavage planes (Morin et al., 2007; Konno et al., 2008; Yingling et al., 2008). The consequences of this abnormal cell positioning in neurogenesis are crucial questions that remain to be answered.

METHODS

Immunohistochemistry. Pregnant CD-1 mice were purchased from a UK supplier. Central nervous system embryonic tissues
were harvested in accordance with the Animals (Scientific Procedures) Act 1986. Tissues were fixed with 4% paraformaldehyde overnight at 4 °C and incubated in 30% sucrose before cryostat sectioning. Paraformaldehyde-fixed brains collected from E14 heterozygous embryos of the knock-in mouse line expressing GFP under the control of the TIS21 promoter were generously provided by W. Huttner.

Sections were treated with a blocking buffer containing Triton X100 detergent (0.5–1%) and bovine serum albumin (3%) for 1 h. Primary antibodies (supplementary Table 1 online) were incubated overnight in the blocking buffer without detergent at 20 °C. Appropriate AlexaFluor dye conjugated secondary antibodies (Molecular Probes, Invitrogen Ltd, Paisley, UK) were incubated for 1–2 h along with Hoechst for nuclei staining. Images were captured with a Leica SP1/SP2 or a Zeiss confocal.

**Prediction of cleavage plane positioning.** Cleavage plane orientation was determined according to the procedure described by Kosodo et al (2004), and is detailed in the supplementary information online section.

**Partitioning of N-cadherin and AJ microdomains.** To quantify the amount of N-cadherin fluorescence in each presumptive membrane territory (Fig 2), the 1.5–2.5-μm depth stack of 3–5 consecutive confocal sections showing the same chromosome morphology was projected as a sum of pixels and the fluorescence intensity evaluated in the sum-projected image with the integrated density function of the Image J software. The comparison of fluorescence intensities in the two presumptive membrane territories was expressed as the ratio of the sum of pixel values—that is, integrated density. The distribution of ratios was depicted for each population and the medians calculated for further analysis. The 3D reconstructed views provided in Figs 2 and 4 were built from lateral or en face views of z-stacks using the Velocity software.

**Positioning of AJ rings.** The relative positioning of AJ rings was evaluated using en face stacks of confocal images acquired at 0.12-μm intervals. Fluorescence intensity profile analyses along the z-axis were drawn using the Leica confocal software. 3D reconstructions were performed with stacks of images at 0.2-μm intervals acquired on cryosections of 30 μm depth using Imaris software (Bitplane, Zurich, Switzerland).

**Supplementary information** is available at EMBO reports online (http://www.emboreports.org)

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**CONFLICT OF INTEREST**

The authors declare that they have no conflict of interest.

**REFERENCES**


