Development, Growth & Differentiation
The Japanese Society of Developmental Biologists
Develop. Growth Differ. (2012)
doi: 10.1111/dgd.12020

Review Article

Neocortical neurogenesis is not really "neo": A new evolutionary model derived from a comparative study of chick pallial development

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The neocortex facilitates mammalian adaptive radiation by conferring highly sophisticated cognitive and motor abilities. A unique feature of the mammalian neocortex is its laminar structure in which similar neuronal subtypes are arranged in tangential layers and construct columnar circuits via interlaminar connections. The neocortical layer structure is completely conserved among all mammalian species, including monotremes and marsupials. However, this structure is missing in non-mammalian sister groups, such as birds and reptiles. The evolutionary origins of neocortical layers and cytoarchitectural borders have been the subject of debate over the past century. Using the chicken embryos as a model of evolutionary developmental biology (evo-devo model), we recently provided evidence suggesting that the evolutionary origin of layer-specific neuron subtypes predates the emergence of laminar structures. Based on this finding, we review the evolutionary conservation and divergence of neocortical development between mammals and non-mammals and discuss how the layered cytoarchitecture of the mammalian neocortex originated during evolution.

Key words: evolution, layer-specific subtype, neocortex, neural progenitor, pallium.

Chicken embryo as an evo-devo model to elucidate unique features of mammalian evolution

Unique mammalian features such as the mammary gland, endothermy, and highly developed brain functions, have likely facilitated the adaptive radiation of mammalian species in various environments (Wilson & Reeder 2005; Meredith *et al.* 2011). To understand the evolutionary history of mammals, it is important to address the molecular and cellular changes required for creating these unique mammalian features during evolution. For this purpose, comparative developmental studies between non-mammalian and mammalian animals are highly essential. According to phylogenetic studies of amniotes (Carroll 1988; Kumar & Hedges 1998; Hedges *et al.* 2006), mammals have diverged from the sauropsid lineage leading to the reptiles and birds over 300 million years ago (Fig. 1). This phylogenetic relationship indicates that reptiles and birds are the extant animals most closely related to mammals. As such, they can be successfully used as model organisms to investigate mammalian uniqueness. Among these species, the chicken is highly advantageous because of the available genomic information (Hillier *et al.* 2004) and experimental techniques, including embryonic manipulation and gene transfer (Le Douarin 1982; Yasugi & Nakamura 2000; Nakamura & Funahashi 2001; Pekarik *et al.* 2003). In this review, we introduce the phylogenetic conservation and differentiation of brain structures between mammals and birds, primarily using evidence from evolutionary developmental studies in chicken embryos.

Neocortical layer structure as a unique mammalian characteristic

The evolutionary origin of the mammalian neocortex has provoked significant researchers' attention over the past decades (Marin-Padilla 1978; Northcutt & Kaas 1995; Bock & Cardew 2000; Medina & Reiner 2000; Jarvis *et al.* 2005; Striedter 2005; Kaas 2007). The neocortex occupies a large portion of dorsal

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Received 10 September 2012; revised 18 October 2012; accepted 18 October 2012.

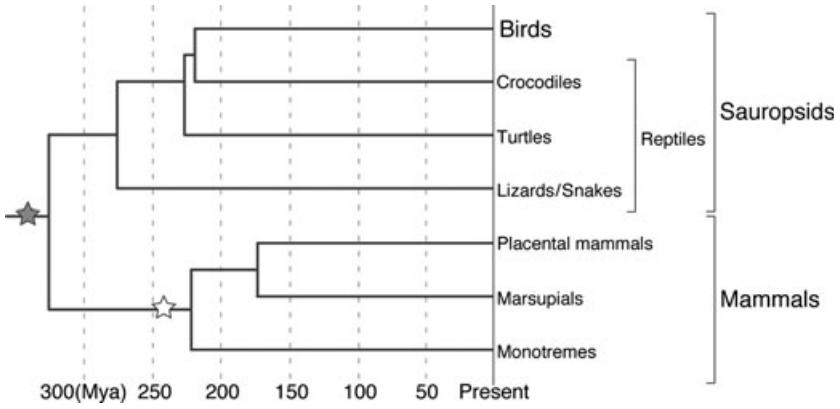

Fig. 1. Phylogenetic relationships of mammals and other amniotes. Molecular phylogenetic tree of the amniote groups indicates that the living animal groups closest to mammals are birds and reptiles. The layer-specific neuron subtypes in the neocortex originated from a common ancestor of mammals and sauropsids before the emergence of mammals (filled star), and the layered neocortex originated from a common ancestor of the all mammalian groups (open star).

telencephalon called the pallium. It is highly enlarged in some mammalian groups, including primates and cetaceans. This brain region has a characteristic laminar structure unique to mammals, in which similar types of neurons are tangentially arranged and form stratified layers parallel to the brain surface (Fig. 2A). This layered structure is completely conserved in all mammalian species including the monotremes and marsupials, but is not observed in the corresponding brain region of any non-mammalian species. The complete conservation of the layered neocortex among mammalian species implies that this structure provides adaptive benefits that have led to its selection by evolutionary constraints. In fact, it is widely accepted that the layered arrangement of neuronal subtypes in the neocortex provides the functional foundation for the construction of neural circuits that elicit higher-order cognitive functions (Kandel *et al.* 2000). The complete absence of this layered structure in non-mammalian pallia suggests that the layered neocortex was added to the pre-existing non-layered brain regions inherited from non-mammalian ancestors during early mammalian evolution (MacLean 1990; Northcutt & Kaas 1995). Because of its newly added nature, this portion of the brain is now referred to as the "neo"-cortex.

However, molecular expression studies of neocortical marker genes in non-mammalian pallia have challenged this traditional view of the neocortex being a newly added structure during mammalian evolution (Fernandez *et al.* 1998; Puelles *et al.* 2000). During

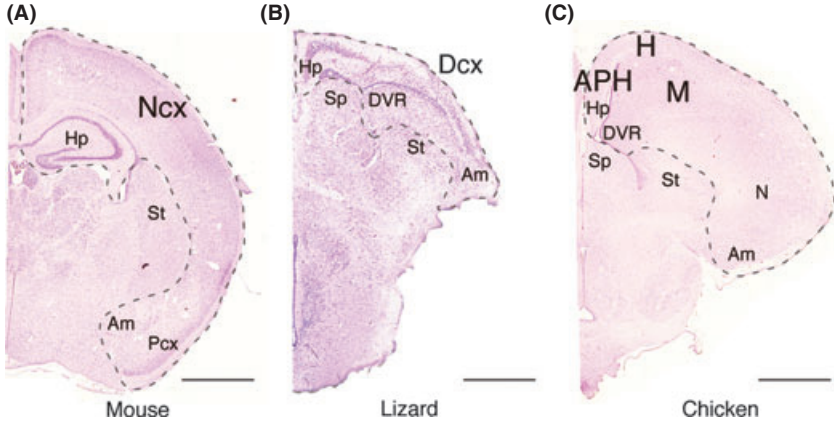

Fig. 2. Comparison of pallial cytoarchitecture among amniote groups. Forebrain cytoarchitectures stained with hematoxylin and eosin. The specimen from a mouse at postnatal day 7 (A), a lizard (Madagascar Ground Gecko, *Paroedura pictus*) reared by Drs Noro and Tamura (Noro *et al.* 2009) at embryonic day 50 (B), and a chick at embryonic day 14 (C). Dotted lines encircle the pallium in each panel. The mammalian neocortex (Ncx) and its homologues, the chick parahippocampal region (APH), hyperpallium (H) and mesopallium (M) and lizard dorsal cortex (Dcx), are labeled in larger fonts. Scale bars; 1.5 mm (A), 300 μm (B), 50 μm (C). Am, amygdala; DVR, dorsal ventricular ridge; Hp, hippocampus; N, nidopallium; Pcx, piriform cortex; Sp, septum; St, striatum.

mammalian development, combinatorial expression of transcription factors determines the neocortical fate of the dorsal telencephalon. Surprisingly, the same combination of transcription factors is expressed in non-mammalian pallia (Fernandez *et al.* 1998; Puelles *et al.* 2000). This evidence indicates that the non-mammalian pallium includes a homologous field of the mammalian neocortex. In fact, both mammals and birds use these homologous neocortical regions for similar cognitive and behavioral functions (Northcutt & Kaas 1995; Medina & Reiner 2000; Jarvis *et al.* 2005; Striedter 2005; Kaas 2007), despite the stark differences in their histological appearances (Fig. 2).

Reptilian species, such as lizards and turtles, possess a relatively simple structure in the pallium in which a single layer of pyramidal neurons spans throughout the structure (Fig. 2B). Axons from the thalamus are accumulated on both sides of this neuronal layer and synaptically connect with the dendrites of the pyramidal neurons (Butler & Hodos 2005; Ulinski 2007). This trilaminar cytoarchitecture resembles the sublaminar organization of the mammalian hippocampus. Because the hippocampus is generally accepted to be an evolutionarily older brain region, the reptilian dorsal cortex is often referred to as the primitive state of the neocortex (MacLean 1990; Butler & Hodos 2005). By contrast, birds have a more complex yet non-layered cytoarchitecture in their neocortical homologue. In these species, morphologically and functionally similar neurons are accumulated in several domains (Fig. 2C) (Medina & Reiner 2000; Puelles *et al.* 2000; Jarvis *et al.* 2005).

These recent tools have allowed researchers to settle several long-standing debates regarding the evolutionary origin of the neocortex. The emerging view is that both mammals and non-mammals commonly possess the same neocortical region defined by molecular expression and neurological functions. Nevertheless, there remains an important question whether both animal groups share homologous neuron types and neural circuits within the pallium. Furthermore, understanding how these animals construct species-specific cytoarchitecture from the same set of genes remains an ongoing question.

Layer-specific neuron subtypes in the mammalian neocortex

The layered neocortex of mammalian species consists of a huge variety of neuron subtypes that can be classified into two major categories: excitatory and inhibitory subtypes. Neocortical excitatory neurons, which are the major focus of this review, are further subclassified into multiple layer-specific subtypes according to the location of their cell bodies (Kandel *et al.* 2000; Molyneaux *et al.* 2007). The mammalian neocortex is traditionally subdivided into six layers from deepest layer 6 to the most superficial layer 1. Each neocortical layer is occupied by the neurons sharing similar characteristics, such as morphology, gene expression, and axon projection targets (Fig. 3A) (Kandel *et al.* 2000). The upper layers (UL; layer 2 and 3) contain neurons exhibiting pyramidal morphology with long apical dendrites reaching to layer 1, and characteristic axon connection with other neocortical neurons. The neurons projecting through the corpus callosum to the contralateral neocortex reside mainly in the UL. Layer 4 neurons are the major recipient of thalamic afferents, which are the primary source of neural input into the neocortex. The deep layers (DL; layer 5 and 6) contain pyramidal neurons that project efferent axons to extracortical targets. More specifically, layer 5 neurons send descending axons to various brainstem regions, including the superior colliculus, pons, and spinal cord, whereas layer 6 neurons mainly project to the thalamic nuclei. These wiring principles construct a stereotyped information flow; thalamic input is received by neurons in the central layer (layer 4), subsequently transmitted to and processed by the UL (layer 2/3) neurons, and finally DL (layer 5 and 6) neurons output the processed information to various targets outside the neocortex (Fig. 3A). Because of this stereotyped information flow across layers, mammalian neocortical neurons are assembled into radially oriented columns of local circuits. This scheme of functional operation in layer-specific neuron subtypes is basically conserved among all mammalian species.

The subtype-specific characteristics of neocortical neurons are determined by the genes that are specifically expressed in each subtype. Currently, dozens of genes are known to be expressed in a layer-specific manner in the developing neocortex (Lein *et al.* 2007; Molyneaux *et al.* 2007; Zeng *et al.* 2012). Among them, some key transcription factors that have a fate-determining role for layer-specific phenotypes have been identified (Molyneaux *et al.* 2007; Leone *et al.* 2008). For example, Ctip2 is specifically expressed in layer 5 neurons and confers the property of descending to the brainstem (Arlotta *et al.* 2005). Tbr1 and Sox5, which are expressed in layer 6 neurons, instruct neurons to project to the thalamus (Hevner *et al.* 2001; Kwan *et al.* 2008; Lai *et al.* 2008; Leone *et al.* 2008; Bedogni *et al.* 2010; McKenna *et al.* 2011). Satb2 is expressed mainly by UL neurons and a minor fraction of layer 5 neurons (Britanova *et al.* 2005, 2008; Szemes *et al.* 2006; Alcamo *et al.* 2008; Gyorgy *et al.* 2008). Expression of this transcription factor

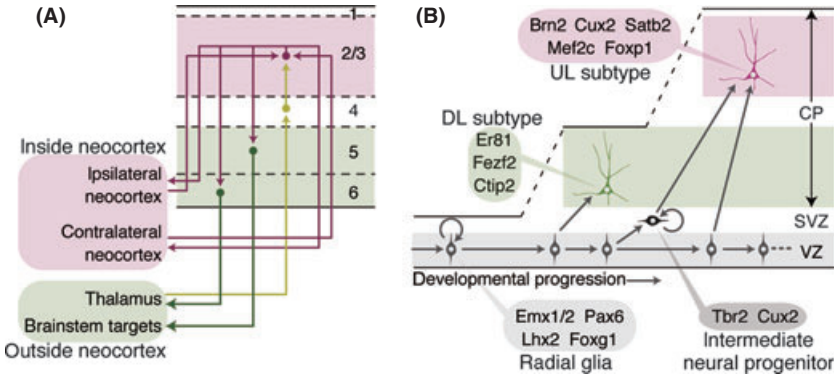

Fig. 3. Layer-specific neuron subtypes and their development in the mammalian neocortex. Characteristic connectivity among layer-specific neuron subtypes in the mammalian neocortex. (A) UL (upper layer; layer 2/3) subtypes are connected within the neocortex and to DL (deep layer; layer 5 and 6) subtypes that project outside the neocortex, such as the thalamus and brainstem targets. The primary input into the neocortex comes from the thalamus and terminates at layer 4. The developmental program of the layer-specific subtypes in the mammalian neocortex (B). Neural progenitors in the ventricular zone (VZ) amplify themselves by symmetric divisions and subsequently start to generate neurons in the stereotyped DL-to-UL temporal order. The newly generated layer-specific subtypes migrate radially to the destined laminar position in the cortical plate (CP). The intermediate neural progenitors that reside in the subventricular zone (SVZ) mainly produce the UL subtypes. The transcription factors in balloons are the specific marker genes for each cell type. Panel A is modified with permission from (Suzuki & Hirata 2012).

promotes interhemispheric projection to the contralateral neocortex through the corpus callosum.

Specification of layer-specific neuron subtypes during mammalian neocortical development

The molecular mechanisms of neocortical layer-specific neuron specification have been rapidly elucidated using rodent models (Fig. 3B). First, the neocortical field is established in the dorsal part of the rostral neural tube by expression of a specific combination of transcription factors (Muzio & Mallamaci 2003; Mallamaci & Stoykova 2006). Genetic studies in mice have revealed that Emx1/2, Pax6, Lhx2, and Foxg1, play essential roles in assigning the neocortical identity to neuroepithelial cells in the dorsal telencephalon (Qiu *et al.* 1996; Stoykova *et al.* 1996; Yoshida *et al.* 1997; Muzio & Mallamaci 2003). For example, in Pax6 mutant mice, the putative neocortical field is partly replaced by the ventral telencephalon (Stoykova *et al.* 1996; Stenman *et al.* 2003). At this stage, the neocortical primordium consists of neuroepithelial cells that apicobasally elongate and bridge the ventricular and pial surfaces. The neuroepithelial cells massively proliferate by symmetric divisions and expand the future neural progenitor pool for subsequent neurogenesis. In the next stage, the neuroepithelial cells initiate neuron production by changing the division mode from symmetric to asymmetric (Sahara & O'Leary 2009). These cells (which are at this point regarded as neural progenitors) are maintained for multiple rounds of asymmetric divisions to generate a variety of neuron subtypes throughout neocortical neurogenesis (Noctor *et al.* 2001, 2004; Temple 2001) (Fig. 3B).

Neocortical progenitors in principle produce only excitatory neurons, while inhibitory neurons originate from the ventral subpallium and secondarily translocate to the neocortex (Anderson *et al.* 1997; Gorski *et al.* 2002). The subpallial origin of inhibitory neurons is highly evolutionarily conserved among several vertebrate groups (Cobos *et al.* 2001; Metin *et al.* 2007; Carrera *et al.* 2008; Tanaka *et al.* 2011; Tanaka & Nakajima 2012). For excitatory neurons, it has been widely accepted that all layer-specific subtypes are generated by the same neocortical progenitor source (Temple 2001; Molyneaux *et al.* 2007). Both *in vivo* and *in vitro* experiments assure that a single neocortical progenitor generates multiple layer-specific subtypes. For example, in cell lineage tracing, a single progenitor generates clonally-related neurons that are radially distributed across the neocortical layers (Luskin *et al.* 1988; Price & Thurlow 1988; Walsh & Cepko 1990; Kornack & Rakic 1995; Reid *et al.* 1997; Noctor *et al.* 2001; Costa & Hedin-Pereira 2010). Preferential synaptic connections among these clonally related neurons are suggested to be the developmental basis for constructing the radial columnar unit of neural circuits (Yu *et al.* 2009, 2012; Li *et al.* 2012; Ohtsuki *et al.* 2012). Once the neural progenitors are dissociated and cultured, they divide and produce multiple layer-specific subtypes (Shen *et al.* 2006). Of particular interest is that even neocortical progenitors derived from embryonic stem cells have the same

neurogenetic potential for producing multiple layer-specific subtypes (Gaspard *et al.* 2008). Taken together, most of the neocortical progenitors have the multipotency to generate all of the layer-specific excitatory subtypes of the mammalian neocortex.

The most intriguing feature of neocortical neurogenesis is the dependence on developmental timing. Neuron subtypes located in the deeper layer are generated earlier than those in the upper layer. This process obviously requires a developmental "timer," by which the neocortical progenitors keep track of the temporal progression from the initiation of neurogenesis. According to the recorded time, the subtype fates of their daughter neurons are determined when the daughters are undergoing their final mitosis (McConnell 1991; McConnell & Kaznowski 1991). As development progresses, neocortical progenitors get older and their multipotency is progressively restricted (Frantz & McConnell 1996; Desai & McConnell 2000). Thus, the maximum multipotency to generate all layer-specific subtypes is inherent in progenitor cells only at the onset of neurogenesis. As time goes on, the progenitors gradually lose the potential to generate deeper layer subtypes and are only capable of producing upper layer subtypes. Because of this process, neocortical progenitors do not continue producing a single neuron subtype, but rather sequentially change their daughter subtypes.

Although the molecular mechanism underlying the progenitor "timer" is largely unknown, transcriptional regulations are implicated in the temporal control of neurogenesis. (Hanashima *et al.* 2004; Molyneaux *et al.* 2005; Fukumitsu *et al.* 2006; Hirabayashi *et al.* 2009; Mutch *et al.* 2009; Hirabayashi & Gotoh 2010; Kishi *et al.* 2012). For example, Fezf2 is specifically expressed in neurons generated at early time points (Chen *et al.* 2005a,b; Molyneaux *et al.* 2005; Rouaux & Arlotta 2010) and induces expression of the layer 5-specific transcription factor Ctip2 (Arlotta *et al.* 2005). In neurons generated earlier than layer 5 neurons, the expression of Fezf2 is suppressed by Tbr1 and Sox5 that provide layer 6 characteristics in neurons (Hevner *et al.* 2001; Kwan *et al.* 2008; Lai *et al.* 2008; Leone *et al.* 2008; Bedogni *et al.* 2010; McKenna *et al.* 2011). The expression of layer 5-specific Ctip2 is suppressed in later generated neurons by Satb2, the UL fate determinant (Alcamo *et al.* 2008; Britanova *et al.* 2008; Chen *et al.* 2008). Interestingly, interaction networks of these transcription factors seem to be evolutionarily conserved, at least among mammals (Kang *et al.* 2011; Shim *et al.* 2012).

Although the multipotent nature of the neocortical progenitor is widely accepted, an exceptional progenitor subpopulation in the neocortical ventricular zone was recently reported (Franco *et al.* 2012). This subpopulation is marked by the expression of the transcription factor Cux2, which is also expressed in differentiated UL neurons. The lineage tracing experiment in mice clearly demonstrated that these Cux2-expressing progenitors appear at the very early timing of embryonic day 10.5 (E10.5), are maintained through several rounds of symmetric divisions for a few days, and subsequently start selectively producing the UL subtype at the later timing. The next important question would be how much such lineage restriction in the progenitor pool contributes to generation of neocortical layer-specific subtypes.

Inside-out neuronal arrangement in the mammalian layered neocortex

The "inside-out" organization of the neocortex refers to the fact that younger subtypes reside in the more superficial layers while older subtypes reside in the deeper layers. This organization requires an additional migration mechanism. Neurons are generated in the ventricular zone and subsequently migrate radially into the appropriate layer position. In order to construct the "inside-out" pattern, the later-born neurons must pass through the older siblings located in the deeper layers and occupy the appropriate upper layers. Although the mechanisms that govern the inside-out neuronal migration are still unclear, reelin signaling has been implicated to play a role (Tissir & Goffinet 2003). The reelin mutant mouse *reeler* shows aberrant neocortical architecture, in which the spatial order of the layers is somehow inverted (D'Arcangelo *et al.* 1995). The signaling protein reelin is secreted by Cajal-Retzius neurons that are located in the most superficial layer 1 (Ogawa *et al.* 1995) and generated at the earliest timing of neocortical neurogenesis before production of layer 2–6 neurons as an exception to the "inside-out" rule (Marin-Padilla 1978). The radially migrating newborn neurons recognize this signaling protein by specific membrane receptors and settle into the correct position (Nadarajah & Parnavelas 2002; Tissir & Goffinet 2003), although it is still unclear how this signal can precisely determine the neurons positioning.

The reelin gene is encoded in the genomes of all vertebrates, and its expression has been confirmed even in the non-layered pallia of non-mammalian vertebrates (Bernier *et al.* 1999, 2000; Costagli *et al.* 2002; Pérez-Costas *et al.* 2002; Tissir *et al.* 2003; Cabrera-Socorro *et al.* 2007). However, the relatively scarce expression of reelin protein in non-mammalian pallia compared with the mammalian neocortex has raised the possibility that the increased amount of this protein contributes to the evolutionary emergence of the

layered neocortex (Bar *et al.* 2000; Nomura *et al.* 2009). More detailed analyses of the molecular functions of reelin signaling in both the mammalian neocortex and the non-mammalian pallia will be required to elucidate the significance of this signaling pathway in the evolutionary diversification of pallial structures.

Conservation of neocortical neuron subtypes in the avian pallium

The evolutionary history of acquiring the layered neocortex in mammalian lineage remains a mystery. As we have discussed, a complex series of molecular and cellular mechanisms are required for neocortical layer formation. Did all of these mechanisms arise at the same time when the layered neocortex emerged during early mammalian evolution? Or were some of the mechanisms already inherent in ancient mammals when they began this unique pallial development? Comparative analyses in the avian pallium have provided meaningful insights to tackle these questions.

There has been debate as to whether non-mammalian homologues share a neuronal repertoire with the mammalian neocortex (Northcutt & Kaas 1995; Medina & Reiner 2000; Butler & Hodos 2005; Jarvis *et al.* 2005; Striedter 2005; Kaas 2007; Suzuki & Hirata 2012). Although several attempts have been made to define neuronal subtypes in various non-mammalian pallia based on connectional, morphological, and molecular expression similarities with the mammalian neocortex (Marin-Padilla 1978; Jarvis *et al.* 2005), to date there is no consensus about the cell-level homology between the mammalian layer-specific subtypes and the pallial subtypes present in non-mammals. A recent molecular expression study provides more conclusive evidence that the neocortical neuronal subtypes in fact exist in the avian pallium (Nomura *et al.* 2008; Suzuki *et al.* 2012). After the mid-neurogenetic stage, the orthologues of mammalian DL markers Er81, Fezf2, and CTIP2, are all expressed by neurons in the medial domains of the chick pallium (Fig. 4A). Anatomically, the small restricted medial domain called the area parahippocampalis (APH) is the core region, and the DL marker expressing neurons further spread over the adjacent apical part of the hyperpallium (HA). The UL marker genes Cux2, Satb2, Mef2c, FOXP1, and Brn2 initiate expression mainly in the lateral pallial domain named the mesopallium and the densocellular part of hyperpallium (HD) at a slightly later stage. Thus, the avian pallium houses the neuron subtypes molecularly corresponding to the mammalian DL and UL subtypes in its medial and lateral domains, respectively (Fig. 4A,B).

The cellular homologies are also supported by axon projection patterns. The medial DL domain HA in the avian pallium contains neurons that project outside of the pallium and reach the brainstem, similar to mammalian layer 5 neurons (Karten *et al.* 1973; Reiner & Karten 1983; Veenman *et al.* 1995; Wild & Williams 2000; Suzuki *et al.* 2012). The lateral UL domain mesopallium contains neurons that are interconnected within the pallium, as is commonly observed in mammalian UL neurons (Bradley *et al.* 1985; Shimizu *et al.* 1995; Atoji & Wild 2012; Suzuki *et al.* 2012). However, there is a minor difference. The corpus callosum is an axon tract specific to placental mammals (Mihrshahi 2006). Therefore, this interhemispheric projection is conspicuous in mammalian UL neurons but is missing in avian UL neurons. With the exception of this difference, molecular and projection analyses agree that the chick DL and UL neurons are equivalent to the DL and UL neurons of the mammalian neocortex. The middle domain located between the medial DL and lateral UL domains is one of the major recipient regions of thalamic afferents (Shimizu *et al.* 1995; Csillag & Montagnese 2005). From this functional analogy, this domain is suggested to correspond to the mammalian neocortical layer 4 located between the DL and UL, although expression of a layer 4 marker Rorb in this domain is not observed (Atoji & Karim 2012).

Conservation of subtype specification mechanisms in the mammalian neocortex and the avian pallium

How are neocortical subtypes generated in the avian pallium? Birthdate analysis of chick pallial neurons has revealed that the DL subtypes differentiate earlier than the UL subtypes as observed in mammalian neocortical development (Suzuki *et al.* 2012). The same sequential order of neurogenesis in both mammals and chicks suggests that they use similar temporal specification mechanisms for generating neuron subtypes. Indeed, when the chick pallial progenitors are dissociated and cultured in a clonal density, they generate DL subtypes and then UL subtypes in a sequential manner (Suzuki *et al.* 2012). These results indicate that neural progenitors in the avian pallium possess the mammalian-type developmental program, by which a single progenitor sequentially generates layer-specific subtypes one by one from deeper to upper layer subtypes. Taken together, the mammalian neocortex and the avian pallium share not only the same neuronal repertoire, but also the same generation program.

Further evidence indicates that the gene regulatory network responsible for specifying layer-specific

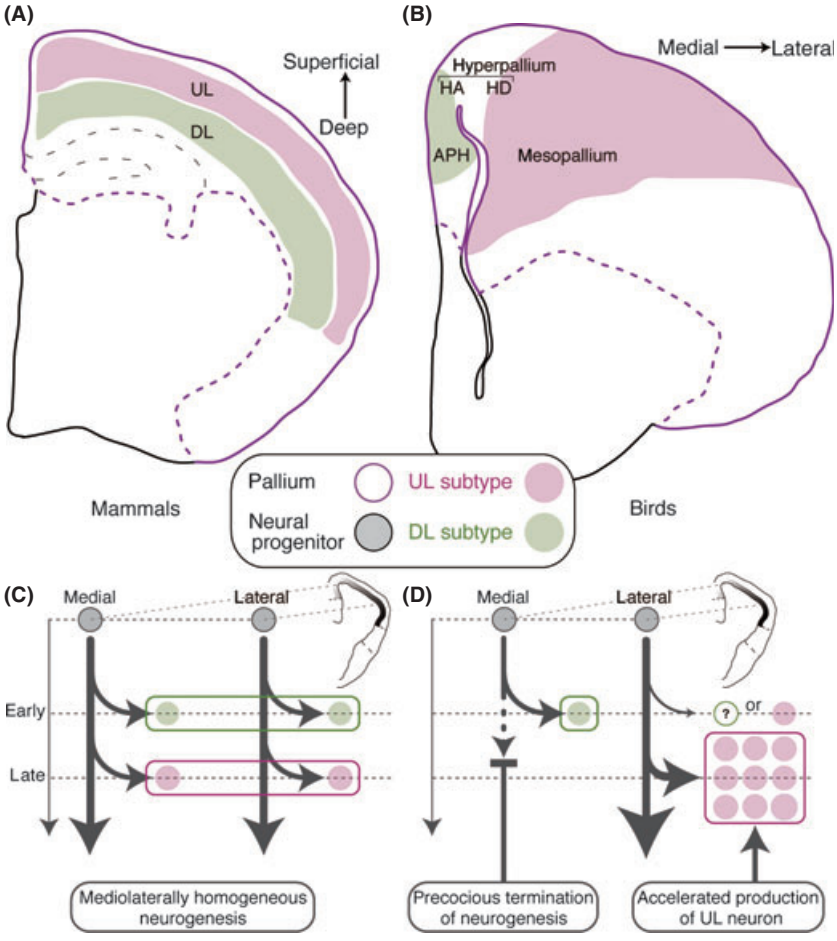

Fig. 4. Phylogenetic differences in the spatial arrangement and generation program of layer-specific subtypes. DL (deep layer) and UL (upper layer) subtypes are tangentially distributed throughout the mammalian neocortex (A). In the avian pallium, these subtypes are not arranged in layers but separately localized at the medial and lateral domains (B). The spatiotemporal generation programs of layer-specific subtypes in the mammalian neocortex (C) and the avian pallium (D). The vertical axis from the top to the bottom indicates the developmental progression. The horizontal axis denotes the mediolateral axis of the neocortex (or pallium). Neurogenesis proceeds virtually homogeneously in the medial and lateral regions in the mammalian neocortex (C). On the other hand, in the avian pallium, neurogenesis is highly biased along the mediolateral axis; the neuron production terminates precociously before UL subtype is generated in the medial region but explosively occurs in the lateral region at the later time (D). APH, area parahippocampalis; H, hyperpallium; HA, apical part of hyperpallium; HD, densocellular part of hyperpallium. All panels are reproduced with permission from (Suzuki & Hirata 2012; Suzuki *et al.* 2012).

subtypes is at least in part conserved between mammals and birds. During mammalian neocortical development, the UL determinant Satb2 inhibits transcription of the DL determinant Ctip2. Likewise, in the chick pallium, overexpression of Satb2 suppresses endogenous Ctip2 expression, suggesting that the genetic interactions between these genes are conserved between mammals and birds (Suzuki *et al.* 2012). Moreover, a recent study demonstrated that the cis-regulatory sequence of Fezf2 responsible for specific expression in layer 5 is conserved among amniotes (Shim *et al.* 2012). Because other regulatory interaction between layer-specific transcription factors remain unexplored in non-mammals, further research is necessary to elucidate which parts of the gene network are conserved or diversified between mammals and non-mammals.

Mediolateral specialization of neurogenetic patterns in the avian pallium

Despite the conserved neurogenetic programs between the mammalian neocortex and the avian pallium, layer-specific subtypes in the avian pallium are not arranged in tangential layers, but are instead separately localized in the medial and lateral domains

(Fig. 4A,B). The mediolateral separation of the DL and UL markers is recognizable early in development when the layer-specific subtypes are actively generated. This observation has led to the assumption that these subtypes are generated from spatially distinct progenitor pools. Consistent with this speculation, the focal labeling of the chick pallial ventricular zone demonstrated that DL and UL subtypes originate from distinct medial and lateral populations of pallial progenitors (Suzuki *et al.* 2012). Thus, newly differentiated pallial neurons simply migrate radially but do not tangentially translocate along the mediolateral axis, although they substantially disperse along the rostrocaudal direction (Szele & Cepko 1996; Striedter & Beydler 1997; Striedter *et al.* 1998). This is consistent with a previously proposed model, which stated that the avian pallium is composed of neuronal compartments, and that the neurons in each compartment are derived from a domain in the ventricular zone demarcated by distinct genetic codes (Medina & Reiner 2000; Redies & Puelles 2001). The spatially distinct origins of the DL and UL subtypes in the chick pallium are highly contrasted with the common origin of both subtypes in the mammalian neocortex.

The segregated production of DL and UL subtypes in the avian pallium seemingly contradicts the observation that both DL and UL subtypes are generated from a multipotent pallial progenitor *in vitro* (Suzuki *et al.* 2012). In fact, in culture conditions, the chick medial and lateral progenitors behave very similarly and exhibit almost equivalent neurogenetic potential to generate DL and UL subtypes (Suzuki *et al.* 2012). This seeming contradiction has been reconciled by the discovery of spatially regulated pallial neurogenesis *in vivo* by extrinsic factors. In contrast to the relatively homogeneous neurogenesis in the mammalian neocortex (Fig. 4C), chick pallial neurogenesis is highly spatiotemporally biased (Fig. 4D). While the early neurogenesis that gives rise to DL subtypes occurs fairly uniformly along the entire mediolateral axis, the later neurogenesis that produces UL subtypes almost exclusively occurs in the lateral region. One reason for this is the precocious termination of neurogenesis in the medial region before the active production of UL subtypes. Another reason is that neurogenesis is enhanced in the lateral region during the later stage. In this regard, one notable finding is that the intermediate neural progenitors (also named basal progenitor), which are implicated to UL subtype generation in mammals (Kriegstein *et al.* 2006), develop only in the lateral region of the chick pallium at the later timing (Cheung *et al.* 2007; Suzuki *et al.* 2012). In this way, a spatial regulation of the conserved neocortical neurogenetic program can drive mediolateral patterning in the avian pallium.

The abovementioned study could imply that neurogenesis in the mammalian neocortex can be regarded as the default state that is unleashed from extrinsic control to exhibit its full multipotency. However, this simple explanation is insufficient, as other types of extrinsic control of neurogenesis in the mammalian neocortex have been observed. Cajal-Retzius neurons originate from only a few restricted regions outside the neocortex and migrate into the neocortex during normal development (Takiguchi-Hayashi *et al.* 2004; Bielle *et al.* 2005; Yoshida *et al.* 2006; Hanashima *et al.* 2007). However, when neocortical progenitors are cultured *in vitro*, progenitors from any part can generate Cajal-Retzius neurons prior to producing other layer-specific subtypes (Shen *et al.* 2006; Gaspard *et al.* 2008). Thus, even in the mammalian neocortex, the earliest round of the layer-fate specification still seems to be restricted by some extrinsic factors.

Potential extrinsic factors responsible for constructing animal group-specific pallial structures

What kinds of extrinsic signals regulate neurogenesis in the chick pallium? The mediolateral axis of the pallium is determined by morphogen signals secreted from several distinct sources in the forebrain, such as the cortical hem (Grove *et al.* 1998; Grove & Fukuchi-Shimogori 2003; Subramanian & Tole 2009), the antihem (Kim *et al.* 2001; Frowein *et al.* 2002; Assimacopoulos *et al.* 2003; Faedo *et al.* 2010), and the ventral midline (Campbell 2003). Under the influence of these morphogen signals, some genes exhibit a mediolaterally-graded expression in the neocortex (Grove & Fukuchi-Shimogori 2003; Muzio & Mallamaci 2003; Mallamaci & Stoykova 2006; Mangale *et al.* 2008). Although the expression patterns of these genes are largely conserved among amniotes (Puelles *et al.* 2000; Butler & Hodos 2005; Kaas 2007), a small number of genes are expressed differently between mammals and birds. In mammals, among LIM-homeodomain (LIM-HD) genes, Lhx1 and 5 are specifically expressed in the cortical hem, whereas Lhx2 is expressed in the neocortex excluding the hem. These region-specific expressions of the LIM-HD genes control the regional identity of pallial derivatives (Zhao *et al.* 1999; Peng & Westerfield 2006; Hébert & Fishell 2008; Mangale *et al.* 2008). However, the chick hem does not express Lhx1, but uniquely express Lhx2 and shares the Lhx5 expression with the mammalian hem (Abellan *et al.* 2010). Considering the importance of the cortical hem as a morphogen source, the

different combination of LIM-HD codes in the chick hem could result in different morphogen signals from their mammalian counterparts, thereby affecting the mediolateral patterning of the pallium. In addition, the cortical hem is a source of reelin-expressing Cajal-Retzius neurons in mammals (Takiguchi-Hayashi *et al.* 2004; Yoshida *et al.* 2006; Hanashima *et al.* 2007) and in birds (Nomura *et al.* 2008). Therefore, it is possible that the Cajal-Retzius neurons in mammals and birds possess different properties (Abellan *et al.* 2010).

Another candidate region for creating animal group-specific differences is the antihem. The antihem, also called the ventral pallium (Puelles 2011), is the boundary region between the dorsally positioned pallium and the ventrally located subpallium. The antihem secretes signaling proteins and generates special cell types that regulate neocortical development, as does the cortical hem (Assimacopoulos *et al.* 2003; Medina *et al.* 2004; Bielle *et al.* 2005; Subramanian *et al.* 2009; Griveau *et al.* 2010; Teissier *et al.* 2010). The antihem has been posited to play a role in the phylogenetic divergence of pallial structure because this region shows notable morphological differences between mammals and non-mammals (Molnár & Butler 2002; Molnár *et al.* 2006). This region uniquely differentiates as the dorsal ventricular ridge (DVR; a tissue protrusion adjacent to the antihem) in non-mammalian amniotes such as birds and reptiles, and contains highly elaborated neural circuitry, particularly in some avian species (Karten 1997; Medina & Reiner 2000; Butler & Hodos 2005; Jarvis *et al.* 2005; Striedter 2005; Kaas 2007). The elaboration of DVR is remarkably well correlated with the massive selective neurogenesis occurring in the lateral region of the avian pallium (Suzuki *et al.* 2012).

The evolutionary roles of the antihem have been pointed out in several studies. The first study details the divergent expression of the transcription factor Dbx1. This gene is expressed in the antihem progenitors in mammals but not in birds (Bielle *et al.* 2005; Nomura *et al.* 2008). Dbx1-expressing progenitors are another prominent source of Cajal-Retzius neurons (Bielle *et al.* 2005; Griveau *et al.* 2010). Possibly because this source is absent in birds, the avian pallium possesses fewer Cajal-Retzius neurons than the mammalian neocortex. Interestingly, avian antihem progenitors still retain the potential to generate reelin-expressing Cajal-Retzius neurons when Dbx1 is exogenously expressed in the antihem (Nomura *et al.* 2008). Furthermore, the resulting augmentation in reelin protein enhances the elongation of radial processes of neural progenitors in the avian pallium (Nomura *et al.* 2008). This observation is important because the long, straight, radial processes are considered as a marked characteristic of the mammalian neocortex and to contribute to the mammalian-like coordinated radial migration of newly differentiated neocortical neurons. The structure is also functionally important for cell fate decisions during asymmetric progenitor division (Miyata *et al.* 2001; Fishell & Kriegstein 2003; Huttner & Kosodo 2005; Kosodo & Huttner 2009; Tsunekawa *et al.* 2012).

In mammals, Dbx1-expressing antihem progenitors produce another intriguing neuron population that tangentially migrates into the neocortex. These cells distribute over the neocortex and express the same layer-specific markers as the surrounding neurons, but are eventually eliminated by apoptosis around the time of birth (Teissier *et al.* 2010). Surprisingly, when these neurons are killed prematurely using a genetically induced toxin, the cortical thickness is significantly reduced. This finding suggests that these neurons play an important neurogenesis-promoting role during normal neocortical development. An important yet unanswered question is whether a Dbx1-deficient avian antihem can generate this transient neuron population. If not, the resulting development could lead to a neurogenetic pattern distinct from that of mammals.

The antihem also functions as a source of several morphogens, such as fibroblast growth factor (FGF)-related proteins (Faedo *et al.* 2010), EGF-related proteins (Assimacopoulos *et al.* 2003) and Wnt-related proteins (Kim *et al.* 2001; Frowein *et al.* 2002), some of which can provide positional information along the mediolateral axis in the pallium. Considering the huge morphological divergence in the antihem among animal groups, these potential morphogens may provide good candidates for the extrinsic factors that support animal group-specific neurogenetic patterns in the pallium.

Hypothetical evolutionary emergence of the layered neocortex and its developmental mechanism

Finally, we discuss how mammals have acquired a multilayered neocortex from comparative views on the avian pallium. Considering that the non-layered chick pallium possesses the mammalian-type neocortical neurogenetic program, this program was likely acquired from a common ancestor of both mammals and birds (Fig. 1). This suggests that when ancestral mammals first innovated the unique layered arrangement of neuron subtypes, they had simply renovated the pre-existing program by changing its extrinsic regulation. This change allowed mammals to take full advantage of the program to allocate multiple

layer-specific subtypes homogeneously across the entire neocortex. The complete conservation of layered neuronal arrangement among all the mammalian species suggests that this evolutionary event occurred early in the mammalian lineage and prior to the branching of monotremes (Rowe *et al.* 2011). The resulting layered neocortex likely provided strong functional benefits to mammalian species and was therefore completely retained during mammalian adaptive radiation and became larger and more complex in primates.

It is somewhat peculiar that birds retain the mammalian-type neocortical neurogenetic program even though its use is complexly restricted. This is possibly because this neurogenetic program confers a general advantage for all animals and is therefore protected throughout evolution. One obvious advantage of this program is that it can efficiently generate a huge variety of neuron subtypes from a limited variety of neural progenitors. In fact, even invertebrates use a similar strategy in neurogenesis to produce a stereotyped cell lineage of diverse neuron types from a single neural progenitor (Bossing *et al.* 1996; Schmid *et al.* 1999; Isshiki *et al.* 2001; Jacob *et al.* 2008). Therefore, the sequential generation of multiple subtypes from a single progenitor likely represents a basic strategy for all animal kingdoms to maximize the variety of neuron subtypes under limited conditions.

Closing remarks

The evolutionary origin of the mammalian layered neocortex has long been debated. In part, this debate has been difficult to resolve because it is impossible to collect information about internal structure of soft brain tissue from fossil specimens of ancient animals. Although the mammalian neocortex and the non-mammalian counterparts exhibit completely different structures in the adult, the embryonic primordia show more similar structures. This indicates that the developmental process plays a key role in constructing animal group-specific brain structures. Therefore, the evolutionary developmental approach is promising for elucidating the evolutionary origin of the layered neocortex. The chicken, one of the non-mammalian animals located in the sister phylogenetic position to mammals, can be a powerful model organism because of the abundant and sophisticated experimental techniques available to researchers. Our developmental study of the chick pallium revealed that the neurogenetic program encoded in neural progenitors is fundamentally conserved between the mammalian neocortex and the chick pallium (Suzuki & Hirata 2012; Suzuki *et al.* 2012). This finding revised the conventional idea that the layered neocortex suddenly emerged during early evolution of mammals. It alternatively proposes that the layered neocortex evolved through a series of changes in the developmental process. In the revised model, the neocortical neurogenetic program originated in a common ancestor of mammals and birds, and mammals modified the neurogenetic regulation to fully benefit from the program and establish the layered architecture of the neocortex. In the future, the same approach using the chicken embryos as a model organism will undoubtedly uncover additional mysteries of neocortical evolution.

Acknowledgments

We thank T. Kawasaki, T. Gojobori, Y. Murakami, Y. Hiromi, K. Emoto, K. Sumiyama, T. Nomura and S. Aizawa for comments and encouragement. I. K. S was a NIG Postdoctoral Research Fellow.

References

Abellan, A., Menuet, A., Dehay, C., Medina, L. & Retaux, S. 2010. Differential expression of LIM-homeodomain factors in Cajal-Retzius cells of primates, rodents, and birds. *Cereb. Cortex* **20**, 1788–1798.

Alcamo, E., Chirivella, L., Dautzenberg, M., Dobreva, G., Fariñas, I., Grosschedl, R. & McConnell, S. K. 2008. Satb2 regulates callosal projection neuron identity in the developing cerebral cortex. *Neuron* **57**, 364–377.

Anderson, S. A., Eisenstat, D. D., Shi, L. & Rubenstein, J. L. 1997. Interneuron migration from basal forebrain to neocortex: dependence on Dlx genes. *Science* **278**, 474–476.

Arlotta, P., Molyneaux, B. J., Chen, J., Inoue, J., Kominami, R. & Macklis, J. D. 2005. Neuronal subtype-specific genes that control corticospinal motor neuron development in vivo. *Neuron* **45**, 207–221.

Assimacopoulos, S., Grove, E. A. & Ragsdale, C. W. 2003. Identification of a Pax6-dependent epidermal growth factor family signaling source at the lateral edge of the embryonic cerebral cortex. *J. Neurosci.* **23**, 6399–6403.

Atoji, Y. & Karim, M. R. 2012. Expression of the neocortical marker, RORbeta, in the entopallium and field L2 of adult chicken. *Neurosci. Lett.* **521**, 119–124.

Atoji, Y. & Wild, J. M. 2012. Afferent and efferent projections of the mesopallium in the pigeon (*Columba livia*). *J. Comp. Neurol.* **520**, 717–741.

Bar, I., Lambert De Rouvroit, C. & Goffinet, A. M. 2000. The evolution of cortical development. An hypothesis based on the role of the Reelin signaling pathway. *Trends Neurosci.* **23**, 633–638.

Bedogni, F., Hodge, R. D., Elsen, G. E., Nelson, B. R., Daza, R. a M., Beyer, R. P., Bammler, T. K., Rubenstein, J. L. R. & Hevner, R. F. 2010. Tbr1 regulates regional and laminar identity of postmitotic neurons in developing neocortex. *Proc. Natl Acad. Sci. USA* **107**, 13129–13134.

Bernier, B., Bar, I., D'Arcangelo, G., Curran, T. & Goffinet, A. M. 2000. Reelin mRNA expression during embryonic brain development in the chick. *J. Comp. Neurol.* **422**, 448–463.

Bernier, B., Bar, I., Pieau, C., Lambert De Rouvroit, C. & Goffinet, A. M. 1999. Reelin mRNA expression during embryonic

brain development in the turtle *Emys orbicularis*. *J. Comp. Neurol.* **413**, 463–479.
Bielle, F., Griveau, A., Narboux-Neme, N., Vigneau, S., Sigrist, M., Arber, S., Wassef, M. & Pierani, A. 2005. Multiple origins of Cajal-Retzius cells at the borders of the developing pallium. *Nat. Neurosci.* **8**, 1002–1012.
Bock, G., Cardew, G. & Novartis Foundation. 2000. *Evolutionary Developmental Biology of the Cerebral Cortex*. Wiley, Chichester, New York.
Bossing, T., Udolph, G., Doe, C. Q. & Technau, G. M. 1996. The embryonic central nervous system lineages of *Drosophila melanogaster*. I. Neuroblast lineages derived from the ventral half of the neuroectoderm. *Dev. Biol.* **179**, 41–64.
Bradley, P., Davies, D. C. & Horn, G. 1985. Connections of the hyperstriatum ventrale of the domestic chick (*Gallus domesticus*). *J. Anat.* **140**, 577–589.
Britanova, O., Akopov, S., Lukyanov, S., Gruss, P. & Tarabykin, V. 2005. Novel transcription factor Satb2 interacts with matrix attachment region DNA elements in a tissue-specific manner and demonstrates cell-type-dependent expression in the developing mouse CNS. *Eur. J. Neurosci.* **21**, 658–668.
Britanova, O., De Juan Romero, C., Cheung, A., Kwan, K. Y., Schwark, M., Gyorgy, A., Vogel, T., Akopov, S., Mitkovski, M., Agoston, D., Sestan, N., Molnár, Z. & Tarabykin, V. 2008. Satb2 is a postmitotic determinant for upper-layer neuron specification in the neocortex. *Neuron* **57**, 378–392.
Butler, A. B. & Hodos, W. 2005. *Comparative Vertebrate Neuroanatomy : Evolution and Adaptation*. Wiley-Interscience, Hoboken, NJ.
Cabrera-Socorro, A., Hernandez-Acosta, N. C., Gonzalez-Gomez, M. & Meyer, G. 2007. Comparative aspects of p73 and Reelin expression in Cajal-Retzius cells and the cortical hem in lizard, mouse and human. *Brain Res.* **1132**, 59–70.
Campbell, K. 2003. Dorsal-ventral patterning in the mammalian telencephalon. *Curr. Opin. Neurobiol.* **13**, 50–56.
Carrera, I., Ferreiro-Galve, S., Sueiro, C., Anadon, R. & Rodriguez-Moldes, I. 2008. Tangentially migrating GABAergic cells of subpallial origin invade massively the pallium in developing sharks. *Brain Res. Bull.* **75**, 405–409.
Carroll, R. L. 1988. *Vertebrate Paleontology and Evolution*. Freeman, New York, NY.
Chen, B., Schaevitz, L. R. & McConnell, S. K. 2005a. Fezl regulates the differentiation and axon targeting of layer 5 subcortical projection neurons in cerebral cortex. *Proc. Natl Acad. Sci. USA* **102**, 17184–17189.
Chen, B., Wang, S. S., Hattox, A. M., Rayburn, H., Nelson, S. B. & McConnell, S. K. 2008. The Fezf2-Ctip2 genetic pathway regulates the fate choice of subcortical projection neurons in the developing cerebral cortex. *Proc. Natl Acad. Sci. USA* **105**, 11382–11387.
Chen, J. G., Rasin, M. R., Kwan, K. Y. & Sestan, N. 2005b. Zfp312 is required for subcortical axonal projections and dendritic morphology of deep-layer pyramidal neurons of the cerebral cortex. *Proc. Natl Acad. Sci. USA* **102**, 17792–17797.
Cheung, A. F., Pollen, A. A., Tavare, A., Deproto, J. & Molnar, Z. 2007. Comparative aspects of cortical neurogenesis in vertebrates. *J. Anat.* **211**, 164–176.
Cobos, I., Puelles, L. & Martinez, S. 2001. The avian telencephalic subpallium originates inhibitory neurons that invade tangentially the pallium (dorsal ventricular ridge and cortical areas). *Dev. Biol.* **239**, 30–45.
Costa, M. R. & Hedin-Pereira, C. 2010. Does cell lineage in the developing cerebral cortex contribute to its columnar organization? *Front. Neuroanat.* **4**, 26.
Costagli, A., Kapsimali, M., Wilson, S. W. & Mione, M. 2002. Conserved and divergent patterns of Reelin expression in the zebrafish central nervous system. *J. Comp. Neurol.* **450**, 73–93.
Csillag, A. & Montagnese, C. 2005. Thalamotelencephalic organization in birds. *Brain Res. Bull.* **66**, 303–310.
D'Arcangelo, G., Miao, G. G., Chen, S.-C., Scares, H. D., Morgan, J. I. & Curran, T. 1995. A protein related to extracellular matrix proteins deleted in the mouse mutant reeler. *Nature* **374**, 719–723.
Desai, A. & McConnell, S. 2000. Progressive restriction in fate potential by neural progenitors during cerebral cortical development. *Development* **127**, 2863–2872.
Faedo, A., Borello, U. & Rubenstein, J. L. 2010. Repression of Fgf signaling by sprouty1-2 regulates cortical patterning in two distinct regions and times. *J. Neurosci.* **30**, 4015–4023.
Fernandez, A. S., Pieau, C., Reperant, J., Boncinelli, E. & Wassef, M. 1998. Expression of the Emx-1 and Dlx-1 homeobox genes define three molecularly distinct domains in the telencephalon of mouse, chick, turtle and frog embryos: implications for the evolution of telencephalic subdivisions in amniotes. *Development* **125**, 2099–2111.
Fishell, G. & Kriegstein, A. R. 2003. Neurons from radial glia: the consequences of asymmetric inheritance. *Curr. Opin. Neurobiol.* **13**, 34–41.
Franco, S. J., Gil-Sanz, C., Martinez-Garay, I., Espinosa, A., Harkins-Perry, S. R., Ramos, C. & Muller, U. 2012. Fate-restricted neural progenitors in the mammalian cerebral cortex. *Science* **337**, 746–749.
Frantz, G. & McConnell, S. 1996. Restriction of late cerebral cortical progenitors to an upper-layer fate. *Neuron* **17**, 55–61.
Frowein, J., Campbell, K. & Gotz, M. 2002. Expression of Ngn1, Ngn2, Cash1, Gsh2 and Sfrp1 in the developing chick telencephalon. *Mech. Dev.* **110**, 249–252.
Fukumitsu, H., Ohtsuka, M., Murai, R., Nakamura, H., Itoh, K. & Furukawa, S. 2006. Brain-derived neurotrophic factor participates in determination of neuronal laminar fate in the developing mouse cerebral cortex. *J. Neurosci.* **26**, 13218–13230.
Gaspard, N., Bouschet, T., Hourez, R., Dimidschstein, J., Naeije, G., van den Ameele, J., Espuny-Camacho, I., Herpoel, A., Passante, L., Schiffmann, S., Gaillard, A. & Vanderhaeghen, P. 2008. An intrinsic mechanism of corticogenesis from embryonic stem cells. *Nature* **455**, 351–357.
Gorski, J. A., Talley, T., Qiu, M., Puelles, L., Rubenstein, J. L. & Jones, K. R. 2002. Cortical excitatory neurons and glia, but not GABAergic neurons, are produced in the Emx1-expressing lineage. *J. Neurosci.* **22**, 6309–6314.
Griveau, A., Borello, U., Causeret, F., Tissir, F., Boggetto, N., Karaz, S. & Pierani, A. 2010. A novel role for Dbx1-derived Cajal-Retzius cells in early regionalization of the cerebral cortical neuroepithelium. *PLoS Biol.* **8**, e1000440.
Grove, E. A. & Fukuchi-Shimogori, T. 2003. Generating the cerebral cortical area map. *Annu. Rev. Neurosci.* **26**, 355–380.
Grove, E. A., Tole, S., Limon, J., Yip, L. & Ragsdale, C. W. 1998. The hem of the embryonic cerebral cortex is defined by the expression of multiple Wnt genes and is compromised in Gli3-deficient mice. *Development* **125**, 2315–2325.
Gyorgy, A., Szemes, M., De Juan Romero, C., Tarabykin, V. & Agoston, D. 2008. SATB2 interacts with chromatin-remodeling molecules in differentiating cortical neurons. *Eur. J. Neurosci.* **27**, 865–873.

Hanashima, C., Fernandes, M., Hebert, J. M. & Fishell, G. 2007. The role of Foxg1 and dorsal midline signaling in the generation of Cajal-Retzius subtypes. *J. Neurosci.* **27**, 11103–11111.

Hanashima, C., Li, S. C., Shen, L., Lai, E. & Fishell, G. 2004. Foxg1 suppresses early cortical cell fate. *Science* **303**, 56–59.

Hébert, J. & Fishell, G. 2008. The genetics of early telencephalon patterning: some assembly required. *Nat. Rev. Neurosci.* **9**, 678–685.

Hedges, S. B., Dudley, J. & Kumar, S. 2006. TimeTree: a public knowledge-base of divergence times among organisms. *Bioinformatics* **22**, 2971–2972.

Hevner, R. F., Shi, L., Justice, N., Hsueh, Y., Sheng, M., Smiga, S., Bulfone, A., Goffinet, A. M., Campagnoni, A. T. & Rubenstein, J. L. 2001. Tbr1 regulates differentiation of the preplate and layer 6. *Neuron* **29**, 353–366.

Hillier, L. W., Miller, W., Birney, E., Warren, W., Hardison, R. C., Ponting, C. P., Bork, P., Burt, D. W., Groenen, M. A. M., Delany, M. E., Dodgson, J. B., Chinwalla, A. T., Cliften, P. F., Clifton, S. W., Delehaunty, K. D., Fronick, C., Fulton, R. S., Graves, T. A., Kremitzki, C., Laymand., D., Magrini, V., McPherson, J. D., Miner, T. L., Minx, P., Nash, W. E., Nhan, M. N., Nelson, J. O., Oddy, L. G., Pohl, C. S., Randall-Maher, J., Smith, S. M., Wallis, J. W., Yang, S. P., Romanov, M. N., Rondelli, C. M., Paton, B., Smith, J., Morrice, D., Daniels, L. & Tempest, H. G., Robertson, L., Masab, J. S., Griffin, D. K., Vignal, A., Fillon, V., Jacobbson, L., Kerje, S., Andersson, L., Crooijmans, R. P., Aerts, J., vander Poel, J. J., Ellegren, H., Caldwell, R. B., Hubbard, S. J., Grafham, D. V., Kierzek, A. M., McLaren, S. R., Overton, I. M., Arakawa, H., Beattie, K. J., Bezzubov, Y., Boardman, P. E., Bonfield, J. K., Croning, M. D., Davies, R. M., Francis, M. D., Humphray, S. J., Scott, C. E., Taylor, R. G., Tickle, C., Brown, W. R., Rogers, J., Buerstedde, J. M., Wilson, S. A., Stubbs, L., Ovcharenko, I., Gordon, L., Lucas, S., Miller, M. M., Inoko, H., Shiina, T., Kaufman, J., Salomonsen, J., Skjoedt, K., Wong, G. K., Wang, J., Liu, B., Wang, J., Yu, J., Yang, H., Nefedov, M., Koriabine, M., Dejong, P. J., Goodstadt, L., Webber, C., Dickens, N. J., Letunic, I., Suyama, M., Torrents, D., von Mering, C., Zdobnov, E. M., Makova, K., Nekrutenko, A., Elnitski, L., Eswara, P., King, D. C., Yang, S., Tyekucheva, S., Radakrishnan, A., Harris, R. S., Chiaromonte, F., Taylor, J., He, J., Rijnkels, M., Griffiths-Jones, S., Ureta-Vidal, A., Hoffman, M. M., Severin, J., Searle, S. M., Law, A. S., Speed, D., Waddington, D., Cheng, Z., Tuzun, E., Eichler, E., Bao, Z., Flicek, P., Shteynberg, D. D., Brent, M. R., Bye, J. M., Huckle, E. J., Chatterjee, S., Dewey, C., Pachter, L., Kouranov, A., Mourelatos, Z., Hatzigeorgiou, A. G., Paterson, A. H., Ivarie, R., Brandstrom, M., Axelsson, E., Backstrom, N., Berlin, S., Webster, M. T., Pourquie, O., Reymond, A., Ucla, C., Antonarakis, S. E., Long, M., Emerson, J. J., Betran, E., Dupanloup, I., Kaessmann, H., Hinrichs, A. S., Bejerano, G., Furey, T.S., Harte, R. A., Raney, B., Siepel, A., Kent, W. J., Haussler, D., Eyras, E., Castelo, R., Abril, J. F., Castellano, S., Camara, F., Parra, G., Guigo, R., Bourque, G., Tesler, G., Pevzner, P. A., Smit, A., Fulton, L. A., Mardis, E. R. & Wilson, R. K. 2004. Sequence and comparative analysis of the chicken genome provide unique perspectives on vertebrate evolution. *Nature* **432**, 695–716.

Hirabayashi, Y. & Gotoh, Y. 2010. Epigenetic control of neural precursor cell fate during development. *Nat. Rev. Neurosci.* **11**, 377–388.

Hirabayashi, Y., Suzki, N., Tsuboi, M., Endo, T. A., Toyoda, T., Shinga, J., Koseki, H., Vidal, M. & Gotoh, Y. 2009. Polycomb limits the neurogenic competence of neural precursor cells to promote astrogenic fate transition. *Neuron* **63**, 600–613.

Huttner, W. B. & Kosodo, Y. 2005. Symmetric versus asymmetric cell division during neurogenesis in the developing vertebrate central nervous system. *Curr. Opin. Cell Biol.* **17**, 648–657.

Isshiki, T., Pearson, B., Holbrook, S. & Doe, C. Q. 2001. Transcription factors which specify the temporal identity of their neuronal progeny. *Cell* **106**, 511–521.

Jacob, J., Maurange, C. & Gould, A. P. 2008. Temporal control of neuronal diversity: common regulatory principles in insects and vertebrates? *Development* **135**, 3481–3489.

Jarvis, E. D., Güntürkün, O., Bruce, L., Csillag, A., Karten, H., Kuenzel, W., Medina, L., Paxinos, G., Perkel, D. J., Shimizu, T., Striedter, G., Wild J. M., Ball, G. F., Dugas-Ford, J., Durand, S. E., Hough, G. E., Husband, S., Kubikova, L., Lee, D. W., Mello, C. V., Powers, A., Siang, C., Smulders, T. V., Wada, K., White, S. A., Yamamoto, K., Yu, J., Reiner A. & Butler, A. B. 2005. Avian brains and a new understanding of vertebrate brain evolution. *Nat. Rev. Neurosci.* **6**, 151–159.

Kaas, J. H. 2007. *Evolution of Nervous Systems : A Comprehensive Reference*, Elsevier Academic Press, Amsterdam; Boston.

Kandel, E. R., Schwartz, J. H. & Jessell, T. M. 2000. *Principles of Neural Science*. McGraw-Hill, Health Professions Division, New York.

Kang, H. J., Kawasawa, Y. I., Cheng, F., Zhu, Y., Xu, X., Li, M., Sousa, A. M. M., Pletikos, M., Meyer, K., Sedmak, G., Guennel, T., Shin, Y., Johnson, M. B., Krsnik, Ž., Mayer, S., Fertuzinhos, S., Umlauf, S., Lisgo, S. N., Vortmeyer, A., Weinberger, D. R., Mane, S., Hyde, T. M., Huttner, A., Reimers, M., Kleinman, J. E. & Šestan, N. 2011. Spatio-temporal transcriptome of the human brain. *Nature* **478**, 483–489.

Karten, H. J. 1997. Evolutionary developmental biology meets the brain: the origins of mammalian cortex. *Proc. Natl Acad. Sci. USA* **94**, 2800–2804.

Karten, H. J., Hodos, W., Nauta, W. J. & Revzin, A. M. 1973. Neural connections of the "visual wulst" of the avian telencephalon. Experimental studies in the piegon (*Columba livia*) and owl (*Speotyto cunicularia*). *J. Comp. Neurol.* **150**, 253–278.

Kim, A. S., Lowenstein, D. H. & Pleasure, S. J. 2001. Wnt receptors and Wnt inhibitors are expressed in gradients in the developing telencephalon. *Mech. Dev.* **103**, 167–172.

Kishi, Y., Fujii, Y., Hirabayashi, Y. & Gotoh, Y. 2012. HMGA regulates the global chromatin state and neurogenic potential in neocortical precursor cells. *Nat. Neurosci.* **15**, 1127–1133.

Kornack, D. R. & Rakic, P. 1995. Radial and horizontal deployment of clonally related cells in the primate neocortex: relationship to distinct mitotic lineages. *Neuron* **15**, 311–321.

Kosodo, Y. & Huttner, W. B. 2009. Basal process and cell divisions of neural progenitors in the developing brain. *Dev. Growth Differ.* **51**, 251–261.

Kriegstein, A., Noctor, S. & Martinez-Cerdeno, V. 2006. Patterns of neural stem and progenitor cell division may underlie evolutionary cortical expansion. *Nat. Rev. Neurosci.* **7**, 883–890.

Kumar, S. & Hedges, S. B. 1998. A molecular timescale for vertebrate evolution. *Nature* **392**, 917–920.

Kwan, K. Y., Lam, M. M., Krsnik, Z., Kawasawa, Y. I., Lefebvre, V. & Sestan, N. 2008. SOX5 postmitotically regulates migra-

tion, postmigratory differentiation, and projections of subplate and deep-layer neocortical neurons. *Proc. Natl Acad. Sci. USA* **105**, 16021–16026.

Lai, T., Jabaudon, D., Molyneaux, B. J., Azim, E., Arlotta, P., Menezes, J. R. L. & Macklis, J. D. 2008. SOX5 controls the sequential generation of distinct corticofugal neuron subtypes. *Neuron* **57**, 232–247.

Le Douarin, N. 1982. *The Neural Crest*. Cambridge University Press, Cambridge, Cambridgeshire; New York.

Lein, E. S., Hawrylycz, M. J., Ao, N., Ayres, M., Bensinger, A., Bernard, A., Boe, A. F., Boguski, M. S., Brockway, Kevin S., Byrnes, E. J., Chen, L., Chen, L., Chen, T., Chin, M. C., Chong, J., Crook, B. E., Czaplinska, A., Dang, C. N., Datta, S., Dee, N. R., Desaki, A. L., Desta, T., Diep, E., Dolbeare, T. A., Donelan, M. J., Dong, H., Dougherty, J. G., Duncan, B. J., Ebbert, A. J., Eichele, G., Estin, L. K., Faber, C., Facer, B. A., Fields, R., Fischer, S. R., Fliss, T. P., Frensley, C., Gates, S. N., Glattfelder, K. J., Halverson, K. R., Hart, M. R., Hohmann, J. G., Howell, M. P.Jeung, D. P., Johnson, R. A., Karr, P. T., Kawal, R., Kidney, J. M., Knapik, R. H., Kuan, C. L., Lake, J. H., Laramee, A. R., Larsen, K. D., Lau, C., Lemon, T. A., Liang, A. J., Liu, Y., Luong, L. T., Michaels, J., Morgan, J. J., Morgan, R. J., Mortrud, M. T., Mosqueda, N. F., Ng, L. L., Ng, R., Orta, G. J., Overly, C. C., Pak, T. H., Parry, S. E., Pathak, S. D., Pearson, O. C., Puchalski, R. B., Riley, Z. L., Rockett, H. R., Rowland, S. A., Royall, J. J., Ruiz, M. J., Sarno, N. R., Schaffnit, K., Shapovalova, N. V., Sivisay, T., Slaughterbeck, C. R., Smith, S. C., Smith, K. A., Smith, B. I., Sodt, Andy J., Stewart, N. N., Stumpf, K., Sunkin, S. M., Sutram, M., Tam, A., Teemer, C. D., Thaller, C., Thompson, C. L., Varnam, L. R., Visel, A., Whitlock, R. M., Wohnoutka, P. E., Wolkey, C. K., Wong, V. Y., Wood, M., Yaylaoglu, M. B., Young, R. C., Youngstrom, B. L., Yuan, X. F., Zhang, B., Zwingman, T. A. & Jones, A. R. 2007. Genome-wide atlas of gene expression in the adult mouse brain. *Nature* **445**, 168–176.

Leone, D. P., Srinivasan, K., Chen, B., Alcamo, E. & McConnell, S. K. 2008. The determination of projection neuron identity in the developing cerebral cortex. *Curr. Opin. Neurobiol.* **18**, 28–35.

Li, Y., Lu, H., Cheng, P., Ge, S., Xu, H., Shi, S.-H. & Dan, Y. 2012. Clonally related visual cortical neurons show similar stimulus feature selectivity. *Nature* **486**, 118–121.

Luskin, M. B., Pearlman, A. L. & Sanes, J. R. 1988. Cell lineage in the cerebral cortex of the mouse studied in vivo and in vitro with a recombinant retrovirus. *Neuron* **1**, 635–647.

MacLean, P. D. 1990. *The Triune Brain in Evolution: Role in Paleocerebral Functions*. Plenum Press, New York.

Mallamaci, A. & Stoykova, A. 2006. Gene networks controlling early cerebral cortex arealization. *Eur. J. Neurosci.* **23**, 847–856.

Mangale, V. S., Hirokawa, K. E., Satyaki, P. R., Gokulchandran, N., Chikbire, S., Subramanian, L., Shetty, A. S., Martynoga, B., Paul, J., Mai, M. V., Li, Y., Flanagan, L. A., Tole, S. & Monuki, E. S. 2008. Lhx2 selector activity specifies cortical identity and suppresses hippocampal organizer fate. *Science* **319**, 304–309.

Marin-Padilla, M. 1978. Dual origin of the mammalian neocortex and evolution of the cortical plate. *Anat. Embryol. (Berl)* **152**, 109–126.

McConnell, S. K. 1991. The generation of neuronal diversity in the central nervous system. *Annu. Rev. Neurosci.* **14**, 269–300.

McConnell, S. K. & Kaznowski, C. E. 1991. Cell cycle dependence of laminar determination in developing neocortex. *Science* **254**, 282–285.

McKenna, W. L., Betancourt, J., Larkin, K. A., Abrams, B., Guo, C., Rubenstein, J. L. R. & Chen, B. 2011. Tbr1 and Fezf2 regulate alternate corticofugal neuronal identities during neocortical development. *J. Neurosci.* **31**, 549–564.

Medina, L., Legaz, I., González, G., De Castro, F., Rubenstein, J. & Puelles, L. 2004. Expression of Dbx1, Neurogenin 2, Semaphorin 5A, Cadherin 8, and Emx1 distinguish ventral and lateral pallial histogenetic divisions in the developing mouse claustroamygdaloid complex. *J. Comp. Neurol.* **474**, 504–523.

Medina, L. & Reiner, A. 2000. Do birds possess homologues of mammalian primary visual, somatosensory and motor cortices? *Trends Neurosci.* **23**, 1–12.

Meredith, R. W., Janečka, J. E., Gatesy, J., Ryder, O. A., Fisher, C. A., Teeling, E. C., Goodbla, A., Eizirik, E., Simão, T. L L., Stadler, T., Rabosky, D. L., Honeycutt, R. L., Flynn, J. J., Ingram, C. M., Steiner, C., Williams, T. L., Robinson, T. J., Burk-Herrick, A., Westerman, M., Ayoub, N. A., Springer, M. S. & Murphy, W. J. 2011. Impacts of the cretaceous terrestrial revolution and KPg extinction on mammal diversification. *Science* **334**, 521–524.

Metin, C., Alvarez, C., Moudoux, D., Vitalis, T., Pieau, C. & Molnar, Z. 2007. Conserved pattern of tangential neuronal migration during forebrain development. *Development* **134**, 2815–2827.

Mihrshahi, R. 2006. The corpus callosum as an evolutionary innovation. *J. Exp. Zool. B Mol. Dev. Evol.* **306**, 8–17.

Miyata, T., Kawaguchi, A., Okano, H. & Ogawa, M. 2001. Asymmetric inheritance of radial glial fibers by cortical neurons. *Neuron* **31**, 727–741.

Molnár, Z. & Butler, A. B. 2002. The corticostriatal junction: a crucial region for forebrain development and evolution. *BioEssays* **24**, 530–541.

Molnár, Z., Métin, C., Stoykova, A., Tarabykin, V., Price, D. J., Francis, F., Meyer, G., Dehay, C. & Kennedy, H. 2006. Comparative aspects of cerebral cortical development. *Eur. J. Neurosci.* **23**, 921–934.

Molyneaux, B., Arlotta, P., Hirata, T., Hibi, M. & Macklis, J. 2005. Fezl is required for the birth and specification of corticospinal motor neurons. *Neuron* **47**, 817–831.

Molyneaux, B., Arlotta, P., Menezes, J. & Macklis, J. 2007. Neuronal subtype specification in the cerebral cortex. *Nat. Rev. Neurosci.* **8**, 427–437.

Mutch, C. A., Funatsu, N., Monuki, E. S. & Chenn, A. 2009. Beta-catenin signaling levels in progenitors influence the laminar cell fates of projection neurons. *J. Neurosci.* **29**, 13710–13719.

Muzio, L. & Mallamaci, A. 2003. Emx1, emx2 and pax6 in specification, regionalization and arealization of the cerebral cortex. *Cereb. Cortex* **13**, 641–647.

Nadarajah, B. & Parnavelas, J. G. 2002. Modes of neuronal migration in the developing cerebral cortex. *Nat. Rev. Neurosci.* **3**, 423–432.

Nakamura, H. & Funahashi, J. 2001. Introduction of DNA into chick embryos by in ovo electroporation. *Methods* **24**, 43–48.

Noctor, S., Flint, A., Weissman, T., Dammerman, R. & Kriegstein, A. 2001. Neurons derived from radial glial cells establish radial units in neocortex. *Nature* **409**, 714–720.

Noctor, S., Martinez-Cerdeno, V., Ivic, L. & Kriegstein, A. 2004. Cortical neurons arise in symmetric and asymmetric division zones and migrate through specific phases. *Nat. Neurosci.* **7**, 136–144.

Nomura, T., Hattori, M. & Osumi, N. 2009. Reelin, radial fibers and cortical evolution: insights from comparative analysis of

the mammalian and avian telencephalon. *Dev. Growth Differ.* **51**, 287–297.
Nomura, T., Takahashi, M., Hara, Y. & Osumi, N. 2008. Patterns of neurogenesis and amplitude of Reelin expression are essential for making a mammalian-type cortex. *PLoS ONE* **3**, e1454.
Noro, M., Uejima, A., Abe, G., Manabe, M. & Tamura, K. 2009. Normal developmental stages of the Madagascar ground gecko Paroedura pictus with special reference to limb morphogenesis. *Dev. Dyn.* **238**, 100–109.
Northcutt, R. G. & Kaas, J. H. 1995. The emergence and evolution of mammalian neocortex. *Trends Neurosci.* **18**, 373–379.
Ogawa, M., Miyata, T., Nakajima, K., Yagyu, K., Seike, M., Ikenaka, K., Yamamoto, H. & Mikoshiba, K. 1995. The reeler gene-associated antigen on cajal-retzius neurons is a crucial molecule for laminar organization of cortical neurons. *Neuron* **14**, 899–912.
Ohtsuki, G., Nishiyama, M., Yoshida, T., Murakami, T., Histed, M., Lois, C. & Ohki, K. 2012. Similarity of visual selectivity among clonally related neurons in visual cortex. *Neuron* **75**, 65–72.
Pekarik, V., Bourikas, D., Miglino, N., Joset, P., Preiswerk, S. & Stoeckli, E. T. 2003. Screening for gene function in chicken embryo using RNAi and electroporation. *Nat. Biotechnol.* **21**, 93–96.
Peng, G. & Westerfield, M. 2006. Lhx5 promotes forebrain development and activates transcription of secreted Wnt antagonists. *Development* **133**, 3191–3200.
Pérez-Costas, E., Meléndez-Ferro, M., Santos, Y., Anadón, R., Rodicio, M. C. & Caruncho, H. J. 2002. Reelin immunoreactivity in the larval sea lamprey brain. *J. Chem. Neuroanat.* **23**, 211–221.
Price, J. & Thurlow, L. 1988. Cell lineage in the rat cerebral cortex: a study using retroviral-mediated gene transfer. *Development* **104**, 473–482.
Puelles, L. 2011. Pallio-pallial tangential migrations and growth signaling: new scenario for cortical evolution? *Brain Behav. Evol.* **78**, 108–127.
Puelles, L., Kuwana, E., Puelles, E., Bulfone, A., Shimamura, K., Keleher, J., Smiga, S. & Rubenstein, J. L. 2000. Pallial and subpallial derivatives in the embryonic chick and mouse telencephalon, traced by the expression of the genes Dlx-2, Emx-1, Nkx-2.1, Pax-6, and Tbr-1. *J. Comp. Neurol.* **424**, 409–438.
Qiu, M., Anderson, S., Chen, S., Meneses, J. J., Hevner, R., Kuwana, E., Pedersen, R. A. & Rubenstein, J. L. 1996. Mutation of the Emx-1 homeobox gene disrupts the corpus callosum. *Dev. Biol.* **178**, 174–178.
Redies, C. & Puelles, L. 2001. Modularity in vertebrate brain development and evolution. *BioEssays* **23**, 1100–1111.
Reid, C. B., Tavazoie, S. F. & Walsh, C. A. 1997. Clonal dispersion and evidence for asymmetric cell division in ferret cortex. *Development* **124**, 2441–2450.
Reiner, A. & Karten, H. J. 1983. The laminar source of efferent projections from the avian Wulst. *Brain Res.* **275**, 349–354.
Rouaux, C. & Arlotta, P. 2010. Fezf2 directs the differentiation of corticofugal neurons from striatal progenitors in vivo. *Nat. Neurosci.* **13**, 1345–1347.
Rowe, T. B., Macrini, T. E. & Luo, Z.-X. 2011. Fossil evidence on origin of the mammalian brain. *Science* **332**, 955–957.
Sahara, S. & O'Leary, D. D. 2009. Fgf10 regulates transition period of cortical stem cell differentiation to radial glia controlling generation of neurons and basal progenitors. *Neuron* **63**, 48–62.
Schmid, A., Chiba, A. & Doe, C. Q. 1999. Clonal analysis of Drosophila embryonic neuroblasts: neural cell types, axon projections and muscle targets. *Development* **126**, 4653–4689.
Shen, Q., Wang, Y., Dimos, J. T., Fasano, C. A., Phoenix, T. N., Lemischka, I. R., Ivanova, N. B., Stifani, S., Morrisey, E. E. & Temple, S. 2006. The timing of cortical neurogenesis is encoded within lineages of individual progenitor cells. *Nat. Neurosci.* **9**, 743–751.
Shim, S., Kwan, K. Y., Li, M., Lefebvre, V. & Sestan, N. 2012. Cis-regulatory control of corticospinal system development and evolution. *Nature* **486**, 74–79.
Shimizu, T., Cox, K. & Karten, H. J. 1995. Intratelencephalic projections of the visual wulst in pigeons (*Columba livia*). *J. Comp. Neurol.* **359**, 551–572.
Stenman, J., Yu, R. T., Evans, R. M. & Campbell, K. 2003. Tlx and Pax6 co-operate genetically to establish the pallio-subpallial boundary in the embryonic mouse telencephalon. *Development* **130**, 1113–1122.
Stoykova, A., Fritsch, R., Walther, C. & Gruss, P. 1996. Forebrain patterning defects in small eye mutant mice. *Development* **122**, 3453–3465.
Striedter, G. F. 2005. *Principles of Brain Evolution*. Sinauer Associates, Sunderland, MA.
Striedter, G. F. & Beydler, S. 1997. Distribution of radial glia in the developing telencephalon of chicks. *J. Comp. Neurol.* **387**, 399–420.
Striedter, G. F., Marchant, T. A. & Beydler, S. 1998. The "neostriatum" develops as part of the lateral pallium in birds. *J. Neurosci.* **18**, 5839–5849.
Subramanian, L., Remedios, R., Shetty, A. & Tole, S. 2009. Signals from the edges: the cortical hem and antihem in telencephalic development. *Sem. Cell Dev. Biol.* **20**, 712–718.
Subramanian, L. & Tole, S. 2009. Mechanisms underlying the specification, positional regulation, and function of the cortical hem. *Cereb. Cortex* **19**(Suppl 1), i90–i95.
Suzuki, I. K. & Hirata, T. 2012. Evolutionary conservation of neocortical neurogenetic program in the mammals and birds. *BioArchitecture* **2**, 0–1.
Suzuki, I. K., Kawasaki, T., Gojobori, T. & Hirata, T. 2012. The temporal sequence of the mammalian neocortical neurogenetic program drives mediolateral pattern in the chick pallium. *Dev. Cell* **22**, 863–870.
Szele, F. G. & Cepko, C. L. 1996. A subset of clones in the chick telencephalon arranged in rostrocaudal arrays. *Curr. Biol.* **6**, 1685–1690.
Szemes, M., Gyorgy, A., Paweletz, C., Dobi, A. & Agoston, D. V. 2006. Isolation and characterization of SATB2, a novel AT-rich DNA binding protein expressed in development- and cell-specific manner in the rat brain. *Neurochem. Res.* **31**, 237–246.
Takiguchi-Hayashi, K., Sekiguchi, M., Ashigaki, S., Takamatsu, M., Hasegawa, H., Suzuki-Migishima, R., Yokoyama, M., Nakanishi, S. & Tanabe, Y. 2004. Generation of reelin-positive marginal zone cells from the caudomedial wall of telencephalic vesicles. *J. Neurosci.* **24**, 2286–2295.
Tanaka, D. H. & Nakajima, K. 2012. GABAergic interneuron migration and the evolution of the neocortex. *Dev. Growth Differ.* **54**, 366–372.
Tanaka, D. H., Oiwa, R., Sasaki, E. & Nakajima, K. 2011. Changes in cortical interneuron migration contribute to the

evolution of the neocortex. *Proc. Natl Acad. Sci. USA* **108**, 8015–8020.

Teissier, A., Griveau, A., Vigier, L., Piolot, T., Borello, U. & Pierani, A. 2010. A novel transient glutamatergic population migrating from the pallial-subpallial boundary contributes to neocortical development. *J. Neurosci.* **30**, 10563–10574.

Temple, S. 2001. The development of neural stem cells. *Nature* **414**, 112–117.

Tissir, F. & Goffinet, A. M. 2003. Reelin and brain development. *Nat. Rev. Neurosci.* **4**, 496–505.

Tissir, F., Lambert De Rouvroit, C., Sire, J. Y., Meyer, G. & Goffinet, A. M. 2003. Reelin expression during embryonic brain development in *Crocodylus niloticus*. *J. Comp. Neurol.* **457**, 250–262.

Tsunekawa, Y., Britto, J. M., Takahashi, M., Polleux, F., Tan, S. S. & Osumi, N. 2012. Cyclin D2 in the basal process of neural progenitors is linked to non-equivalent cell fates. *EMBO J.* **31**, 1879–1892.

Ulinski, P. 2007. Visual cortex of turtles. In *Evolution of Nervous Systems*, Vol. **2** (ed. Jon HK) Oxford: Academic Press, pp. 195–203.

Veenman, C. L., Wild, J. M. & Reiner, A. 1995. Organization of the avian "corticostriatal" projection system: a retrograde and anterograde pathway tracing study in pigeons. *J. Comp. Neurol.* **354**, 87–126.

Walsh, C. & Cepko, C. L. 1990. Cell lineage and cell migration in the developing cerebral cortex. *Experientia* **46**, 940–947.

Wild, J. M. & Williams, M. N. 2000. Rostral wulst in passerine birds. I. Origin, course, and terminations of an avian pyramidal tract. *J. Comp. Neurol.* **416**, 429–450.

Wilson, D. E. & Reeder, D. M. 2005. *Mammal Species of the World : A Taxonomic and Geographic Reference*. Johns Hopkins University Press, Baltimore, MD.

Yasugi, S. & Nakamura, H. 2000. Gene transfer into chicken embryos as an effective system of analysis in developmental biology. *Dev. Growth Differ.* **42**, 195–197.

Yoshida, M., Assimacopoulos, S., Jones, K. R. & Grove, E. A. 2006. Massive loss of Cajal-Retzius cells does not disrupt neocortical layer order. *Development* **133**, 537–545.

Yoshida, M., Suda, Y., Matsuo, I., Miyamoto, N., Takeda, N., Kuratani, S. & Aizawa, S. 1997. Emx1 and Emx2 functions in development of dorsal telencephalon. *Development* **124**, 101–111.

Yu, Y., He, S., Chen, S., Fu, Y., Brown, K. N., Yao, X., Ma, J., Gao, K. P., Sosinsky, G. E., Huang, K. & Shi, S. 2012. Preferential electrical coupling regulates neocortical lineage-dependent microcircuit assembly. *Nature* **486**, 113–117.

Yu, Y. C., Bultje, R. S., Wang, X. & Shi, S. H. 2009. Specific synapses develop preferentially among sister excitatory neurons in the neocortex. *Nature* **458**, 501–504.

Zeng, H., Shen, E. H., Hohmann, J. G., Oh, S. W., Bernard, A., Royall, J. J., Glattfelder, K. J., Sunkin, S. M., Morris, J. A., Guillozet-Bongaarts, A. L., Smith, K. A., Ebbert, A. J., Swanson, B., Kuan, L., Page, D. T., Overly, C. C., Lein, Ed S., Hawrylycz, M. J., Hof, P. R., Hyde, T. M., Kleinman, J. E. & Jones, A. R. 2012. Large-scale cellular-resolution gene profiling in human neocortex reveals species-specific molecular signatures. *Cell* **149**, 483–496.

Zhao, Y., Sheng, H. Z., Amini, R., Grinberg, A., Lee, E., Huang, S., Taira, M. & Westphal, H. 1999. Control of hippocampal morphogenesis and neuronal differentiation by the LIM homeobox gene Lhx5. *Science* **284**, 1155–1158.