Accepted Manuscript

Title: Charting the protomap of the human telencephalon

Authors: Gavin J. Clowry, Ayman Alzu'bi, Lauren F. Harkin, Subrot Sarma, Janet Kerwin, Susan J. Lindsay

PII: S1084-9521(17)30236-7
DOI: http://dx.doi.org/10.1016/j.semcdb.2017.08.033
Reference: YSCDB 2342

To appear in: *Seminars in Cell & Developmental Biology*

Received date: 18-5-2017
Accepted date: 15-8-2017

<AT>Charting the protomap of the human telencephalon

Gavin J Clowry[1,*] , Ayman Alzu'bi[1,2], Lauren F Harkin[3], Subrot Sarma[4], Janet Kerwin[2], Susan J Lindsay[,2]

<AU>Institutes of [1]Neuroscience and [2]Genetic Medicine, Newcastle University, Newcastle upon Tyne, the United Kingdom.##Email##gavin.clowry@ncl.ac.uk##/Email##
<AU>
<AFF>[3]School of Healthcare Science, Manchester Metropolitan University, the United Kingdom.
<AFF>[4]Department of Chemistry, Indian Institute of Technology, Mumbai, India

<PA>Institute of Neuroscience, Newcastle University, Framlington Place, Newcastle upon Tyne, NE2 4HH, the United Kingdom. Tel.:+44 191 208 5981.

<ABS-HEAD>Abstract

<ABS-P>The cerebral cortex is divided stereotypically into a number of functionally distinct areas. According to the protomap hypothesis formulated by Rakic neural progenitors in the ventricular zone form a mosaic of proliferative units that provide a primordial species-specific cortical map. Positional information of newborn neurons is maintained during their migration to the overlying cortical plate. Much evidence has been found to support this hypothesis from studies of primary cortical areas in mouse models in particular. Differential expansion of cortical areas and the introduction of new functional modules during evolution might be the result of changes in the progenitor cells. The human cerebral cortex shows a wide divergence from the mouse containing a much higher proportion of association cortex and a more complicated regionalised repertoire of neuron sub-types. To what extent does the protomap hypothesis hold true for the primate brain? This review summarises a growing number of studies exploring arealised gene expression in the early developing human telencephalon. The evidence so far is that the human and mouse brain do share fundamental mechanisms of areal specification, however there are subtle differences which could lead us to a better understanding of cortical evolution and the origins of neurodevelopmental diseases.

<KWD>Keywords:
Cerebral Cortex; Cortical arealisation; Development; Evolution; Ganglionic Eminences.

<H1>1. Introduction

Each individual, excepting those suffering a gross environmental or genetic insult, possesses a telencephalon built in development to the same plan. Different functional modules always appear in the same place, connections between areas are universal and the brain tissue architecture at the cellular level in each module is the same (1) however subtle differences in these parameters may underlie human diversity in intelligence and personality. Furthermore, this basic plan is shared by all mammalian species, for instance the medial ganglionic eminence (MGE) gives rise to certain classes of cortical interneuron, caudal ganglionic eminence (CGE) to others (2). Primary cortical areas occupy the same positions; primary motor cortex is always in the frontal lobe, visual cortex the occipital lobe, etc., however the relative amount of cortex occupied by each primary area can vary dramatically between species (3). Also, in primates and particularly human, there is a more complicated pattern of functional arealisation with a considerably larger proportion devoted to higher functioning association cortex (3-5).
It is generally accepted that the layout of the cerebral cortex is determined by the co-ordinated and compartmented expression of genes in time and space at the earliest stages of its development, prior to its connection with the sensory input that could drive its maturation (the protomap hypothesis) (6) although spontaneous thalamo-cortical activity may fine tune sensory cortex