Gene expression changes during murine postnatal brain development

ABSTRACT

The expression level of some genes expressed in the postnatal developing brain varies from newborn to adult development, and it is possible that these developmentalally regulated transcripts are molecular markers for the complex developmental process occurring in this area.

INTRODUCTION

The human brain is the largest organ in the body. During human development, it is divided into brainstem and neocortex, which are the two halves of the brain. The neocortex is responsible for most of our cognitive and motor functions, while the brainstem is responsible for most of basic sensory and motor functions. The human brain is made up of approximately 500 million neurons connected by a network of synapses. The brainstem is responsible for normal and abnormal functions, while the neocortex is responsible for all of the functions that make up most of our lives.

The human brain is divided into two sections: the neocortex and the thalamus. In the human brain, the neocortex is divided into an 'out' section called the thalamus, which is responsible for most of the functions of the brainstem, and an ' Most vertebrate organs and tissues experience development during embryogenesis, while postnatal changes are primarily related to growth. The CNS is unique in that postpostnatal development involves significant morphological development, cell differentiation, and acquisition of function. However, the molecular mechanisms behind these complex developmental processes remain unclear. We have conducted a recent experiment using DDRT-PCR to identify genes expressed in the murine postnatal developing brain. This analysis formed the basis for our investigation, and we produced RNA fingerprints representing genes transcribed at specific stages of brain development. We compared these fingerprinted genes at different timepoints during postpartum development: newborn (day 1), day 10, day 20 and adult (Day 42). We found that many genes were clearly regulated in wild-type mouse brains, thus we can use this data to help others can isolate specific transcripts regulating expression profiles limiting events. The selection of these fingerprints was based on the fact that they were all created using the same DDRT-PCR profiles and at least two different batches of RNA, and that each fingerprint displayed at most three developmentally regulated transcripts. We have placed at minimum three bands on each group of fingerprint to indicate the position of at or above the most obviously EDGE genes; we have found that LDLD genes are more likely to increase during brain development; our team has found several matched bands whose levels are decreasing with increasing time; and we now know which genes expressing peaks To verify that alterations in DDRT-PCR profiles are accurate, we performed downstream expression analyses on two cDNA fragments recovered, which were then analyzed for changes in expression levels. The overall approach used is illustrated in Figure 1 (and see). The northern blot expression profiles of both transcripts were formatted to replicate the original RDDHCP expression accounts with accuracy.

CONCLUSION

Remarkable conclusions The study of gene expression in the postnatal developing murine brain has revealed that only 1% of genes transcribed as

such have developmental regulation. The aim of this report is to enable individuals interested in these genes to selectively isolate certain transcripts without undergoing a comprehensive screening process. We have presented RNA fingerprints containing supplementary information to allow individual transcript identification. These fingerprint items are divided into three broad expression profiles, with 71 of them belonging to category C and the remaining ones being split between A and B (61). Furthermore, we can confirm that alterations in this profile reflect actual