

Deep sequencing analysis of the developing mouse brain reveals a novel microRNA.

ABSTRACT

Background: MicroRNAs (miRNAs) are small non-coding RNAs that can exert multilevel inhibition/repression at a post-transcriptional or protein synthesis level during disease or development. Characterisation of miRNAs in adult mammalian brains by deep sequencing has been reported previously. However, to date, no small RNA profiling of the developing brain has been undertaken using this method. We have performed deep sequencing and small RNA analysis of a developing (E15.5) mouse brain. **Results:** We identified the expression of 294 known miRNAs in the E15.5 developing mouse brain, which were mostly represented by let-7 family and other brain-specific miRNAs such as miR-9 and miR-124. We also discovered 4 putative 22-23 nt miRNAs: mm_br_e15_1181, mm_br_e15_279920, mm_br_e15_96719 and mm_br_e15_294354 each with a 70-76 nt predicted pre-miRNA. We validated the 4 putative miRNAs and further characterised one of them, mm_br_e15_1181, throughout embryogenesis. Mm_br_e15_1181 biogenesis was Dicer1-dependent and was expressed in E3.5 blastocysts and E7 whole embryos. Embryo-wide expression patterns were observed at E9.5 and E11.5 followed by a near complete loss of expression by E13.5, with expression restricted to a specialised layer of cells within the developing and early postnatal brain. Mm_br_e15_1181 was upregulated during neurodifferentiation of P19 teratocarcinoma cells. This novel miRNA has been identified as miR-3099. **Conclusions:** We have generated and analysed the first deep sequencing dataset of small RNA sequences of the developing mouse brain. The analysis revealed a novel miRNA, miR-3099, with potential regulatory effects on early embryogenesis, and involvement in neuronal cell differentiation/function in the brain during late embryonic and early neonatal development.

Keyword: MicroRNA; Mouse brain; Animal embryo; Brain; Genetics.