Characterisation of microRNA expression in post-natal mouse mammary gland development.

BACKGROUND: The differential expression pattern of microRNAs (miRNAs) during mammary gland development might provide insights into their role in regulating the homeostasis of the mammary epithelium. Our aim was to analyse these regulatory functions by deriving a comprehensive tissue-specific combined miRNA and mRNA expression profile of post-natal mouse mammary gland development. We measured the expression of 318 individual murine miRNAs by bead-based flow-cytometric profiling of whole mouse mammary glands throughout a 16-point developmental time course, including juvenile, puberty, mature virgin, gestation, lactation, and involution stages. In parallel whole-genome mRNA expression data were obtained.

RESULTS: One third (n = 102) of all murine miRNAs analysed were detected during mammary gland development. MicroRNAs were represented in seven temporally co-expressed clusters, which were enriched for both miRNAs belonging to the same family and breast cancer-associated miRNAs. Global miRNA and mRNA expression was significantly reduced during lactation and the early stages of involution after weaning. For most detected miRNA families we did not observe systematic changes in the expression of predicted targets. For miRNA families whose targets did show changes, we
observed inverse patterns of miRNA and target expression. The data sets are made publicly available
and the combined expression profiles represent an important community resource for mammary gland
biology research. CONCLUSION: MicroRNAs were expressed in likely co-regulated clusters during
mammary gland development. Breast cancer-associated miRNAs were significantly enriched in these
clusters. The mechanism and functional consequences of this miRNA co-regulation provide new
avenues for research into mammary gland biology and generate candidates for functional validation.

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