



MicroRNA expression profiling studies on bronchopulmonary dysplasia: a systematic review and meta-analysis

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ABSTRACT. Over the past several years, several microRNA (miRNA) expression profiling studies have been carried out on bronchopulmonary dysplasia (BPD) in mammalian lung tissues. The most effective way to identify these important miRNAs is to systematically search for similar signatures identified in multiple independent studies. Accordingly, a meta-analysis was conducted to review published miRNA expression profiling studies that compared miRNA expression profiles between BPD lung tissues and normal lung tissues. A vote-counting strategy that considered the total number of studies and time points reporting differential expression was applied. Furthermore, cut-off criteria of statistically significant differentially expressed miRNAs as defined by the author and their predicted target genes, if available, as well as the list of up- and down-regulated miRNA features, were collected and recorded. Results of the meta-analysis revealed that four up-regulated miRNAs (miRNA-21, miRNA-34a, miRNA-431, and Let-7f) and one down-regulated miRNA (miRNA-335) were differentially expressed in BPD lung tissues compared with normal groups. In addition, eight miRNAs (miRNA-146b, miRNA-29a, miRNA-503, miRNA-411,

miRNA-214, miRNA-130b, miRNA-382, and miRNA-181a-1*) were found to show differential expression not only in the process of normal lung development, but also during the progress of BPD. Finally, several meaningful target genes (such as the HPGD and NTRK genes) of common miRNAs (such as miRNA-21 and miRNA-141) were systematically predicted. These specific miRNAs may provide clues of the potential mechanisms involved in BPD. Further mechanistic and external validation studies are needed to confirm the clinical significance of these miRNAs in the development of BPD.

Key words: MicroRNA; Profiling; Bronchopulmonary dysplasia; Meta-analysis