

The Recovery Process of Murine Tracheal Epithelium Injured by 5-FU and Its Microarray Analysis

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摘要

Background and objective Although there are increasing reports on localization of tracheal stem cells, the mechanism of proliferation and differentiation of tracheal stem cells remains unclear. **Methods** In this study, we developed an ex vivo model of murine tracheal epithelial injury and regeneration induced by 5-FU. The regeneration process of murine tracheal epithelium was observed and analyzed by morphological, immunofluorescence and microarray methods. **Results** After treatment with 5-FU, the differentiated mature cells were dead and desquamated. Only a few cells remained in G0 phase and located on the basement membrane. After being put back in normal culture media, the cells became flat, cubic and restored as pseudostratified epithelium at last. These G0 phase cells were ABCG2 positive. We detected the differences of stem cell genes between normal tracheal epithelial cells and regenerated epithelial cells at 24 h and 48 h after injured by 5-FU using stem cell differentiation gene microarray. At 24 h, 8 genes were up-regulated and 31 genes were down-regulated. At 48 h, 5 genes were up-regulated and 42 genes were down-regulated. **Conclusion** The differently expressed genes were mainly associated with cell cycle regulation, intercellular junction, FGF, BMP, Notch and Wnt signaling pathways, which suggested these alterations might be closely associated with the proliferation and differentiation of tracheal stem cells.






关键词

Trachea; Stem cells; Differentiation; Microarray; Signaling pathway


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
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