

Similarities in gene expression profiles during in vitro aging of primary human embryonic lung and foreskin fibroblasts

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[Details](#)

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Abstract

Replicative senescence is of fundamental importance for the process of cellular aging, since it is a property of most of our somatic cells. Here, we elucidated this process by comparing gene expression changes, measured by RNA-seq, in fibroblasts originating from two different tissues, embryonic lung (MRC-5) and foreskin (HFF), at five different time points during their transition into senescence. Although the expression patterns of both fibroblast cell lines can be clearly distinguished, the similar differential expression of an ensemble of genes was found to correlate well with their transition into senescence, with only a minority of genes being cell line specific. Clustering-based approaches further revealed common signatures between the cell lines. Investigation of the mRNA expression levels at various time points during the lifespan of either of

the fibroblasts resulted in a number of monotonically up- and downregulated genes which clearly showed a novel strong link to aging and senescence related processes which might be functional. In terms of expression profiles of differentially expressed genes with age, common genes identified here have the potential to rule the transition into senescence of embryonic lung and foreskin fibroblasts irrespective of their different cellular origin.

Involved units

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Topics

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