Characterization of pluripotent cells by profiling microRNA expression pattern in human and mouse ES and iPS cells

その他のタイトル	ES、iPS細胞におけるmicroRNA発現パターンの解析による幹細胞のキャラクタリゼーション
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論文の内容の要旨

論文題目　Characterization of pluripotent cells by profiling microRNA expression pattern in human and mouse ES and iPS cells

(ES、iPS細胞におけるmicroRNA発現パターンの解析による幹細胞のキャラクタリゼーション)

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Abstract

Using quantitative PCR-based miRNA arrays, I have comprehensively analyzed the expression profiles of miRNAs in human and mouse embryonic stem (ES), induced pluripotent stem (iPS), and somatic cells. Immature pluripotent cells were purified using the SSEA-1 or SSEA-4 antibody and were used for miRNA profiling. Hierarchical clustering and consensus clustering by nonnegative matrix factorization showed two major clusters, human ES/iPS cells and other cell groups, as previously reported. Principal components analysis (PCA) that segregates miRNAs into these two groups identified miR-187, 299-3p, 499-5p, 628-5p, and 888 as new miRNAs that specifically characterize human ES/iPS cells. Detailed direct comparisons of miRNA expression levels in human ES and iPS cells showed that several miRNAs included in the chromosome 19 miRNA cluster were more strongly expressed in iPS cells than in ES cells. Similar analysis was conducted with mouse ES/iPS cells and somatic cells, and several miRNAs were suggested to be ES/iPS cell-specific, which have not been reported to be expressed in mouse ES/iPS cells. ES/iPS cells in humans and mice showed quite similar expression levels of miRNAs. Expression levels of miRNA showed drastic and different patterns of changes during embryoid body formation. In summary, my miRNA expression profiling, encompassing human and mouse ES and iPS cells, would give various perspectives in understanding the miRNA core regulatory networks which regulate the characteristics of pluripotent cells.