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Insights into the epithelial mesenchymal transition phenotype in cancer of unknown primary from a global microRNA profiling study.

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Abstract

PURPOSE:

We sought to study the microRNA regulation of epithelial mesenchymal transition (EMT), the acquisition of migratory, mesenchymal-like properties of epithelial cells, in cancer of unknown primary (CUP).

PATIENTS AND METHODS:

We studied the global expression profile of 982 microRNAs by means of microarray technology in 68 CUP cases immunohistochemically characterised as EMT-positive (n = 5 by % of cells or n = 10 by a semiquantitative H-score) or EMT-negative.

RESULTS:

EMT-suppressive miRNAs such as miR-203 and members of the miR-200 family (miR-200a,b,c and miR-141) presented a 2.45 to 3.64-fold lower expression level in the EMT-positive cases without, however, reaching statistical significance. MiR-205, a squamous tissue-specific marker, was very variable in the data set. Excluding CUP cases with squamous cell histology, miR-205, miR-203 and the miR-200 family exhibited a trend of downregulation in EMT-positive cases. A similar pattern of miRNA expression was detected when the comparison took place between EMT-positive vs EMT-negative cases according to the H-score. Moreover, miR-203, miR-205 and miR-200c were numerically downregulated in those tumours with high expression of the EMT marker N-cadherin.

CONCLUSIONS:

The EMT-suppressive miR-203 and miR-200 family were consistently but non-significantly downregulated in CUP with the EMT phenotype. A larger study is warranted to further explore the role of microRNAs in CUP.