Oral cancer secretome: Identification of cancer-associated proteins

Type: Article

Abstract:

This study aims to identify cancer-associated proteins in the secretome of oral cancer cell lines. We have successfully established four primary cell cultures of normal cells with a limited lifespan without human telomerase reverse transcriptase (hTERT) immortalization. The secretome of these primary cell cultures were compared with that of oral cancer cell lines using 2DE. Thirty five protein spots were found to have changed in abundance. Unambiguous identification of these proteins was achieved by MALDI TOF/TOF. In silico analysis predicted that 24 of these proteins were secreted via classical or nonclassical mechanisms. The mRNA expression of six genes was found to correlate with the corresponding protein abundance. Ingenuity Pathway Analysis (IPA) core analysis revealed that the identified proteins were relevant in, and related to, cancer development with likely involvements in tumor growth, metastasis, hyperproliferation, tumorigenesis, neoplasia, hyperplasia, and cell transformation. In conclusion, we have demonstrated that a comparative study of the secretome of cancer versus normal cell lines can be used to identify cancer-associated proteins.

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