Endocrinol Diabetes Nutr. 2022;69(Espec Cong 2):90

Endocrinología, Diabetes y Nutrición

24 - PROTEOMIC PROFILE IN THYROID CANCER CELLS AND THEIR EXOSOMES TO DETERMINE TUMOR AGGRESSIVENESS

P. Morales-SÁnchez[1,2], L. Rodal-Bravo[3], A. Montero-Calle[5], M.P. LÓpez-Molina[3], M.F. Fraga[2,7,8], E. Delgado-Álvarez[1,2,6], R. Barderas[5] and A. de la Vieja[3,4]

[1]Endocrinology, Nutrition,Diabetes and Obesity (ENDO). Health Research Institute of the Principality of Asturias (ISPA). Oviedo.[2] Spanish Biomedical Research Network in Rare Diseases (CIBERER). Instituto de Salud Carlos III (ISCIII). Madrid.[3]Endocrine Tumor Unit (UFIEC). Instituto de Salud Carlos III (ISCIII). Madrid.[4]Spanish Biomedical Research Network in Cancer (CIBERONC). Instituto de Salud Carlos III (ISCIII). Madrid.[5]Funtional Protein Unit (UFIEC). Instituto de Salud Carlos III (ISCIII). Madrid.[6] Department of Medicine. University of Oviedo.[7]Department of Organisms and Systems Biology (B.O.S.). University of Oviedo.[8] Cancer Epigenetics and Nanomedicine Laboratory. (CINN-CSIC)-(IUOPA)-(ISPA). Oviedo.[9]Endocrinology and Nutrition Service. Central University Hospital of Asturias. Oviedo.

Resumen

Although the exact causes are not known, differentiated thyroid cancer (DTC: follicular and papillary thyroid cancer) might become dedifferentiated (POOR), leading to poorly differentiated thyroid cancer and ultimately anaplastic thyroid cancer. These last two are relatively rare but are more aggressive and likely to be associated with lymph node and distant metastases. Exosomes are secreted by almost all cells and involved in intercellular communication. They play an essential role in regulation of tumour environment and contribute to oncogenesis. Therefore, the aim of this work was to characterize protein expression patterns in thyroid *in vitro* models and their secretome, to discuss the role in thyroid tumorigenesis. Cell lines (CLs) were divided into DTC (n = 5) and POOR (n = 9). To collect exosomes, CL supernatants were ultracentrifuged. Protein isolation was performed using RIPA, TMT-11-Plex-based quantitative proteomics was done, followed by LC-MS/MS and analyzed with MaxQuant. IRS/TMM-normalization and differential expression (DE; log2FC ? 1,5, p-value ? 0,05) were performed in RStudio. Biological networks were identify by KEGG analyses. Differentially expressed proteins in the POOR_DTC comparison were established: 1) CLs 12 up and 1 downregulated; 2) exosomes: 2 up and 3 downregulated. No common differential protein was found. However, when all possible comparisons were made between CLs (87) and exosomes (62), there were 12 in common. In exosomes, KEGGs found were pentose-phosphate pathway, fructose-mannose metabolism, and glycolysis/gluconeogenesis were dysregulated. In CL, the complement and coagulation cascade, one carbon pool by folate, galactose metabolism, and SNARE interactions in vesicular transport were found to be altered. CLs secrete exosomes into the medium that contain proteins involved in pathways related to oncogenesis. Furthermore, the proteomic profile of exosomes from patient sera could determine tumour aggressiveness and should be further investigated.