Gene Expression Signature in Atherosclerosis: The Role of Antioxidants and Macrophage Phenotype

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Atherosclerosis is an inflammatory process, which is strongly related with redox impairment. Moreover, macrophages play a central role on disease development. Nowadays, is discussed the involvement of different macrophage phenotypes in disease progression; for instance, M1 (pro-inflammatory) and M2 (anti-inflammatory). Our aim is to compare gene expression networks between early and advanced human atherosclerosis plaques, and among baseline and foam cells from both, normal and atherosclerosis subjects. Two different datasets, GSE28829 and GSE9874, were selected from GEO platform [http://www.ncbi.nlm.nih.gov/geo/](http://www.ncbi.nlm.nih.gov/geo/), and 3 gene networks were built with STRING [http://string-db.org/](http://string-db.org/). Lastly, we performed statistical comparisons among groups of each dataset with 2 bioinformatics tools, ViaComplex [http://lief.if.ufrgs.br/pub/biosoftwares/viacomplex/](http://lief.if.ufrgs.br/pub/biosoftwares/viacomplex/) and GSEA [http://www.broadinstitute.org/gsea/index.jsp](http://www.broadinstitute.org/gsea/index.jsp). Antioxidants, M1 and M2 gene networks are significantly increased in advanced plaque (compared to early), in baseline macrophages from atherosclerosis subjects (compared to baseline from normal), and in foam cells from atherosclerosis (compared to baseline from atherosclerosis). However, just Antioxidants and M2 networks are raised in foam cells from normal (when compared to baseline from normal). Both, M1 and M2, are higher in foam from atherosclerosis (compared to foam from normal). Our data suggest that different from cancer, in atherosclerosis there is no M1/M2 macrophage polarization; actually, both phenotypes are enhanced, together antioxidants, what is a novel aspect to better understand the disease development, and can help to find new therapy targets. Key-words: antioxidants, atherosclerosis, macrophage. Support: CNPq, IBN-Net, MCT/CNPq INCT-TM.