Gene Expression and Protein Analysis in Ruptured Human Achilles Tendons – A Comparison Between Ruptured and Healthy Area
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Purpose: We studied the extracellular matrix (ECM) of 19 humans’ ruptured Achilles tendons, comparing the tissue composition of specimens taken from area close to the rupture with specimens taken from an apparently healthy area in the same tendon. The hypothesis was that the metabolism of these molecules is altered in patients with Achilles tendon rupture.

Methods: We compared the gene expression and the protein localization of the main ECM molecules (collagen type I, decorin and versican) including enzymes involved in their metabolism as matrix metalloproteases (MMP2 and 9) and tissue inhibitory of metalloproteinase (TIMP 1 and 2) using a real time RT-PCR, zymography and FACE analysis.

Results: The gene expression of proteoglycans core protein, collagen type I, MMPs and TIMPs was more represented in the area close to the tendon rupture (p<0.05). The expression of MMPs was confirmed by zymography analysis, showing a marked increase of gelatinolytic activity in area close to the tendon rupture (p<0.05). The chemical composition of tendon changes showing that in the healthy area the carbohydrate content is higher than the ruptured area (p<0.05).

Conclusions: In the ruptured area, the tenocytes tried to restore the normal ECM pattern increasing the core protein synthesis but without a normal production. Our data support the hypothesis that, in human tendons, the tissue in the area of rupture undergoes marked rearrangement at molecular levels based on the MMP2 activity, and support the role of MMPs in the tendon pathology.