Characterization of transcript levels for matrix molecules and proteases in ruptured human anterior cruciate ligaments. [1]

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Abstract	An improved understanding of cellular responses during normal anterior cruciate ligament (ACL) function or repair is essential for clinical assessments, understanding ligament biology, and the implementation of tissue engineering strategies. The present study utilized quantitative real-time RT-PCR combined with univariate and multivariate statistical analyses to establish a quantitative database of marker transcript expression that can provide a "blueprint" of ACL wound healing. Selected markers (collagen types I and III, biglycan, decorin, MMP-1, MMP-2, MMP-9, and TIMP-1) were assessed from 33 torn ACLs harvested during reconstructive surgery. Trends were observed between postinjury period and marker expressions. Significant correlations between marker expression existed and were most prominent between collagen types I and III. Canonical correlation analysis established a relationship between patient demographics and a combination of all marker expressions. The currently observed trends and correlations may assist in identifying appropriate tissue samples and provide a baseline information of marker expression level that can support in vitro optimization of environmental cues for ligament tissue engineering application.
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