Proteomic analysis of sera from patients with joint hypermobility syndrome

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Joint hypermobility syndrome (JHS) is a heritable connective tissue disorder mostly characterized by generalized joint hypermobility (excessive range of movement in joints), joint instability complications, minor skin changes, and chronic mild to severe pain. However, it has been unclear whether specific genetic factors are involved in the risk of developing the disorders in patients with JHS. Thus, interventions are limited to symptomatic treatments. In this study, in order to identify potential serum biomarkers for JHS, we investigated proteins with differential levels in sera from patients with JHS and in sera from control individuals by iTRAQ-MALDI-TOF/TOF-MS/MS. In the sera of patients with JHS, a total of 106 proteins with differential levels were identified, and they were further narrowed down to 6 proteins (p < 0.05, patient vs. control). Among the 6 proteins, proteins involved in the complement system including C1r, vitronectin (VTN), C9, and C4bPA were increased in sera from JHS patients compared with those in sera from controls. Western blot analyses verified increased levels of C1r and VTN in sera of JHS patients. The results indicate the possibility of a locally occurring inflammatory process in JHS patients. This study has been published by Watanabe et al., Proteomic analysis for the identification of serum diagnostic biomarkers for joint hypermobility syndrome. Int. J. Mol. Med. 37, 461-467, 2016.

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