

**PROFILING OF NORMAL HUMAN LEG LYMPH PROTEINS USING
THE 2-D ELECTROPHORESIS AND SELDI-TOF MASS
SPECTROPHOTOMETRY APPROACH**

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ABSTRACT

The parenchymatous cells are supplied by nutrients transported in fluid from blood across the capillary wall. This fluid, called tissue fluid (TF), contains proteins originating from plasma as well as those synthesized and secreted by tissue cells. The protein composition of TF remains largely unknown. The TF which has entered lymphatics is called lymph (L). Harvesting L and measuring its proteins concentrations and identifying them provide an insight into biochemical processes in the TF. Here we describe our initial evaluation of the normal human prenodal L protein profile of m.w. 2.5 to 12.5kDa using the ProteinChip SELDI MS system and compare it with that of plasma (P) protein. This is the first study in the literature providing evidence for the presence of the so far non-identified proteins in L as well as proteins identified in L but absent from P and conversely present in P but not in L. Evident differences between paired L and P samples have been found, along with similarities. Thirteen proteins were detected in P and seven in L in the region of 2.5 to 12.5 kDa. Five identical proteins, although of different relative intensity, were found in L and P. The proteins specific for L but not P had m.w. of 7070 and 8619 ion values. P proteins absent from L were of 3890, 3969, 4078, 6863, 7676, 7778, 7847 and 7937 ion values. In addition to detecting some so far unknown proteins in L, these preliminary findings throw a new light on our understanding of the mechanism of transcapillary transport of low m.w. proteins. They challenge the commonly accepted notion of unlimited free diffusion of peptides across the capillary membrane.