CHARACTERIZATION OF PRGF-DERIVED FIBRIN SCAFFOLD INTERACTOME BY 2DE AND LC-MS/MS

E. Anitua [(1)], M. Azkargorta [(2)], E. Rodríguez-Suárez [(2)], I. Iloro [(2)], I. Escobés [(2)], N. Alkorta [(3)], J. Casado-Vela [(4)], R. Prado [(1)], G. Orive [(1)], F. Elortza [(2)].

[(1)] BTI, [(2)] CIC bioGUNE, [(3)] UPV/EHU, [(4)] I. de investgaciones Biomédicas Alberto Sols.

Tissue regeneration is a complex cascade of biological events regulated by multiple signaling networks. Even if its exact regulatory mechanisms remain to be elucidated, several cytokines and growth factors are known to be involved in this process.

"*Plasma rich in growth factors*" (PRGF) is an autologous technology used with the aim of helping regenerative processes. Initially used in dental implant surgery, its areas of application have importantly diversified in the last few years. Nowadays PRGF is successfully used in the treatment of chronic ulcers, facial surgery and sport medicine, among others.

Comprehensive characterization of the protein composition of this clot could shed light into the mechanisms involved in the regeneration-aiding properties of PRGF, and eventually may open potential new ways for the optimization of its performance.

For this purpose, the interactome of a fibrin scaffold derived from activated PRGF was characterized following both 2DE and LC-MS/MS-based strategies. The clot was processed in order to get rid of the most abundant proteins and gain focus into scarce proteins that may account for the helping of regeneration described. A protein-releasate obtained by centrifugation and acetonitrile-based extraction was analyzed as mentioned. Our results provide knowledge into the protein collection present in PRGF-derived fibrin scaffold, and underline the advantages of using complementary methods for the characterization of protein catalogues.