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2-DE ANALYSIS OF SERA PROTEIN EXPRESSION PROFILES IN EARLY STAGES OF HUMAN NEONATAL DEVELOPMENT. A PRELIMINARY STUDY

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While survival of premature infants has greatly increased in the last decades, prematurity is still a major cause of mortality and subsequent physical and developmental disabilities despite advances in neonatal care. A correct evaluation of their postnatal growth is nowadays of primary concern, although optimal nutrition is not well-defined and their growth patterns differ markedly from that of full-term infants. Efforts to characterize the variables affecting neonatal outcomes have focused primarily on patient characteristics including birth weight, gender, race, gestational age, and markers of illness severity... but a detailed understanding at the protein level is still missing. Recent advances in human proteomics will open new perspectives in premature´ management. The human proteome, the protein counterpart to the genome, is dynamic and signals a precise physiologic state. Proteomic techniques like two-dimensional electrophoresis (2-DE) and mass spectrometry (MS) are pivotal in the identification of human sera proteins.

Human proteome development was studied from early neonatal stages to fulltime gestational development, using pooled sera of 232 neonates of the following weights at birth: <750g, n=6; 750-999g, n=27; 1000-1249g, n=33; 1250-1499g, n=35; 1500-1999g, n=38; 2000-2499g, n=30; 2500-3499g, n=38; >3500g, n=25. Blood samples were drawn into Vacutainer® SST tube and sera immediately frozen at -86 ºC until use. Protocols were optimized for sera preparation, and first (IEF, pH 4-7) and second dimension separations (SDS-PAGE, 18cm). Samples were run in triplicate and gel images analyzed with Proteomweaver (Bio-Rad®). Different time-course protein patterns were recognized with several differential peaks, at extremely low birth weight (401-999g), very low (1000-1499g), low (1500-2499g), and normal birth weights (2500-3500g).

Identification and quantification of sera proteins and their time-course patterns will allow a new approach in neonatology, starting from the application of proteomic data to discover new protein biomarkers to finally reach a significant decrease of neonatal mortality rate.

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