H13 The Role of Proteomics for the Forensic Estimation of Postmortem Interval (PMI): A Preliminary Experimental Study

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After attending this presentation, attendees will be able to describe the application of proteomics for the estimation of time of death.

This presentation will impact the forensic science community by describing an operative experimental model used in order to analyze the PMI from the exact moment of death.

Proteomics is a branch of molecular biology that allows the systematic identification of the proteome from a quantitative and qualitative point of view. There are several studies in the literature that have analyzed animal or human biological samples using proteomic methods at different times since death. Regarding humans, no study has analyzed human samples from the exact time of death (time zero). Therefore, not knowing the exact time of death, studies were conducted in which the PMI analyzed was roughly calculated and was not known with certainty. In addition, before discovery, the corpse was exposed to various extrinsic factors, such as temperature or humidity. Therefore, proteomic analysis could be strongly influenced or altered by exposure to thermal variations of the sample.

This presentation introduces the operating model of an experimental study currently underway at the Department of Legal Medicine of the University of Catanzaro. The model is based on taking peripheral blood samples from patients who died at the intensive care unit, following an operation. The study was approved by the Ethics Committee of the University. The informed consent was signed by family members before the death of the patient. Samples were taken according to predefined time intervals, starting from the exact time of death (time zero) and up to two hours after the death. Samples were immediately centrifuged to extract plasma and stored at -80°C and were subjected to proteomic analysis by western blot and mass spectrometry at the Proteomic Laboratories of the University of Catanzaro. Although the experimental study is still ongoing, consistent results both with the time interval examined and the data already known in the literature are expected. In fact, a review of literature on this topic has already revealed that several proteins can undergo not only quantitative changes in terms of increase or reduction directly proportional to the PMI investigated, but also qualitative changes. According to the scientific evidence available in the literature, the expected results of the study are related to the search for quantitative and/or qualitative alterations from the exact moment of death of some markers, already showing time-dependent variations such as: (1) ubiquitous cellular proteins, like High Mobility Group Box 1 (HMGB1), and (2) specific organ proteins (muscle proteins due to progressive degradation, such as Cardiac Troponin I and T (cTn I and cTnT) and proteins related to brain damage, such as Glial Fibrillary Acidic Protein (GFAP) or talin).[1-4]

The proposed model is the first to conduct proteomic investigations on human biological samples from the exact moment of death without exposing the corpse to temperature variations or other extrinsic factors.

Finally, this operating model is intended to: (1) identify the possible role in the estimation of PMIs of new potential protein biomarkers expressed in peripheral blood from the exact moment of death; (2) verify and evaluate in detail the variation of the proteomic profile of markers already known in the literature; and, (3) focus on the analysis of the so-called “early PMI” for forensic purposes.

Reference(s)

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