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Commentary

Role of Proteomics and Metabolomics in the Personalized Management of Wound Healing

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DESCRIPTION

Proteomics and metabolomics are powerful tools that can be used to monitor wound healing. Proteomics is the study of the structure and function of proteins in biological systems, while metabolomics is the study of the metabolites present in a biological system. During wound healing, various proteins and metabolites are involved in the process of tissue repair and regeneration. By analysing the changes in the levels and activities of these proteins and metabolites, researchers can gain insights into the molecular mechanisms underlying wound healing. Proteomics can be used to identify and quantify the proteins that are involved in wound healing. This can be done using techniques such as two-dimensional gel electrophoresis, mass spectrometry, and protein microarrays. By comparing the protein profiles of healthy and wounded tissues, researchers can identify the proteins that are specifically unregulated or down regulated during wound healing [1].

Metabolomics can be used to identify the metabolites that are involved in wound healing. This can be done using techniques such as Nuclear Magnetic Resonance (NMR) spectroscopy and mass spectrometry. By comparing the metabolite profiles of healthy and wounded tissues, researchers can identify the metabolites that are specifically altered during wound healing. Together, proteomics and metabolomics can provide a comprehensive view of the molecular changes that occur during wound healing. This information can be used to develop new therapies and treatments for wound healing, as well as to monitor the progress of wound healing in patients. The complex process of soft tissue and bone wound healing involves both internal and external influences, many distinct proteins being one of them, which control cellular differentiation and adaptation. Nowadays, effort was concentrated on bone regeneration and replacement. The need for innovative bio functional materials grows as a result of demographic pyramid changes and the resulting rise in associated comorbidities (such as diabetes and vascular disorders). Wound Fluid (WF) study gives a clear understanding of the local extracellular milieu surrounding a wound [2].

A number of proteins, particularly those linked to oxidative stress, growth factors, cytokines, and proteases, have been discovered in WF in latest days. These proteins can be used as predictive and diagnostic tools by helping to identify and categorise the impact on various stages of the wound healing process. However, the molecular basis that cause wound healing disruption is not well known, and none of the possible biomarkers for deregulated wound healing have been proven in clinical routine diagnostics too far. Hence, molecular identification of the contributing variables and how they interact is highly desirable. Often used in assessments on wound healing are immunoblotting, microbial arrays, and enzyme immunoassays. One of the promising methods for obtaining thorough profiling data that can be utilised for diagnosis or for finding prospective molecular diagnostic/prognostic indicators that do indicate differences from undisturbed wound healing is mass spectrometry-based proteomics. Proteomics has already been used to explore fluids from a range of different tissues, such as skin, brain, liver, bone, and eye in conjunction with micro dialysis [3].

However, technical aspects such as the great complexity, low sample volume (few micrograms), low protein concentration in wound fluids, the presence of salts and metabolites, and especially the large excess of serum proteins compared to other proteins such as mediator proteins have confined proteome investigations to only a few dozen high abundant proteins. Although numerous strategies are discussed, there is yet no proven method for reliably and effectively extracting protein from wound fluids. Low molecular weight proteins, which are sampled using diffusion and ultrafiltration, can be recovered using one of the well-established procedures known as micro dialysis. The incision receives an insertion of a semipermeable membrane that looks like a blood capillary [4].

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A deoxygenated blood that has a similar ionic strength to the wound fluid is used to continually perfuse this probe with a flow of a few microliters per minute. As an alternative, wound switching, occlusive dressings, porous dextranomer beads, capillary tubes, or paper strips can be used to measure WF intermittently. These techniques result in a bigger amount of protein being collected, but the wound fluid also contains salts and metabolites, and the protein concentration is rather low, necessitating extra cleaning and enrichment procedures for proteomic analysis. Proteomic explorations are problematic because of the low protein quantities and concentrations. Adsorption-based protein sampling using microdialysis catheters makes it possible to gather, concentrate, and purify enough proteins for a proteome analysis to identify over 600 proteins in various disorders [5].

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