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Combining H-FABP and GFAP increases the capacity to differentiate between CT-positive and CT-negative patients with mild traumatic brain injury

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Mild Traumatic Brain Injury (mTBI) patients may have trauma-induced brain lesions detectable using CT scans. However, most patients will be CT-negative. There is thus a need for an additional tool to detect patients at risk. Combining several biomarkers into panels has become increasingly interesting for diagnoses and to enhance classification performance. The present study evaluated 13 proteins individually—H-FABP, MMP-1, MMP-3, MMP-9, VCAM, ICAM, SAA, CRP, GSTP, NKDA, PRDX1, DJ-1 and IL-10—for their capacity to differentiate between patients with and without a brain lesion according to CT results. The best performing proteins were then compared and combined with the S100B and GFAP proteins into a CT-scan triage panel. Patients diagnosed with mTBI, with a Glasgow Coma Scale score of 15 and one additional clinical symptom were enrolled at three different European sites. Patients were divided into two cohorts and further dichotomized into CT-positive and CT-negative groups. Single markers and panels were evaluated using Cohort 1. Four proteins—H-FABP, IL-10, S100B and GFAP—showed significantly higher levels in CT-positive patients. The best-performing biomarker was H-FABP, with a specificity of 32% (95% CI 23–40) and sensitivity reaching 100%. The best-performing two-marker panel for Cohort 1, subsequently validated in Cohort 2, was a combination of H-FABP and GFAP, enhancing specificity to 46% (95% CI 36–55). When adding IL-10 to this panel, specificity reached 52% (95% CI 43–61) with 100% sensitivity. These results showed that proteins combined into panels could be used to efficiently classify CT-positive and CT-negative mTBI patients.

Biography

Jean-Charles Sanchez has completed his PhD at Bukhingam University, UK and further professional carrier at the Faculty of Medicine, Geneva University. He is the Director of the Geneva Biomarker Center. He has published more than 200 papers in reputed journals and has been serving as an Editor in Chief and associated of several proteomics journal. He is the Founder of the Swiss Proteomics Society, the European Proteomics Association, Swiss-2Dservice and ABCDx.

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