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The use of salivary protein profiles as an *in vivo* model for studying breast cancer progression

Charles Streckfus
University of Texas School of Dentistry at Houston, USA

Purpose: The purpose of this study was twofold. The first objective was to compare salivary protein profiles among Her2-receptor-positive and -negative breast cancer patients and secondly, to support the theory for using salivary protein profile expression as a *in vivo* method for modeling breast cancer progression.

Methods: Two pooled saliva specimens underwent proteomic analysis. One pooled specimen was from women diagnosed with stage IIa HER2/neu-receptor-positive breast cancer patients (n=10) and the other was from women diagnosed with stage IIa HER2/neu-receptor-negative cancer patients (n=10). The pooled samples were trypsinized and the peptides labeled with iTRAQ reagent. Specimens were analyzed using an LC-MS/MS mass spectrometer.

Results: The results yielded approximately 71 differentially expressed proteins in the saliva specimens. There were 34 up-regulated proteins and 37 down-regulated proteins.

Biography

Charles F. Streckfus is currently a professor in the Department of Diagnostic & Biomedical Sciences at the University of Texas Dental Branch at Houston and formerly the Associate Dean of Research at the University of Mississippi Medical center Dental School. He received his Bachelor of Science degree in Biology from Johns Hopkins University and he graduated with a DDS degree from the University of Maryland School of Dentistry. Streckfus has published numerous peer-reviewed journal articles and invited to speak at many national and international conferences. He has received many honors and awards which include the the prestigious President's Award for Scientific Excellence, Presented by the International Society for Preventive Oncology, 6th International Symposium Predictive Oncology Intervention Strategies, Pasteur Institute, Paris France, February 12, 2002.

Charles.Streckfus@uth.tmc.edu