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Commentary

Can We Find Breast Cancer via Salivary Fluid Glycosylation Analyses?

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Already decades ago, researchers found a correlation between altered glycosylation and the development of primary breast cancer cells. At that time changes in glycosylation were measured by the binding of peanut agglutinin (PNA), *Helix pomatia*, or *Ulex europaeus* I (UEA) lectins to cellular structures like alpha-*N*-acetylgalactosamine residues, for example, the Thomsen-nouvelle (Tn) epitope or blood group A antigen (Calafat and Janssen, 1984).

A coherence between staining of paraffin embedded tissues with HPA and the development of breast cancer could be shown (Fukutomi et al., 1989). HPA staining was regarded as a predictor for long-term prognosis (Brooks and Leathem, 1991). Another scientific approach was the analysis of glycosylation via *Datura stramonium* agglutinin (DSA)-Sepharose column, in which was shown that metastasized carcinomas contain two times more DSA-binding oligosaccharides than the normal mammary gland, while primary carcinomas contain an intermediate amount (Hiraizumi et al., 1992).

Only a few years later, the Tn and Thomsen–Friedenreich (T) epitopes were recognized as auto-immunogenic pan-carcinoma antigens, playing a role in breast cancer cell invasion (Springer, 1997) CA15-3, a highly glycosylated MUC1 epitope and serum marker, was also recognized to have functions in human breast disorders (Burchell et al., 1983). In the following years, more and more modifications of glycosylation structures became known, having to do with breast cancer, for example 2,6 sialylation, which contributes to altered cell adhesion (Lin et al., 2002).

More than ten years ago, dentists described the idea to find breast cancer via salivary fluid analyses (Paige and Streckfus, 2007). Only 4 years later, the first studies described glycosylation changes in the salivary fluid of breast cancer patients (Ozturk et al., 2011).

In a recent study in *EBioMedicine*, Zheng Li and colleagues systematically investigated and assessed the alterations of salivary glycosylation patterns and the possibility of these patterns as biomarkers for diagnosis of early-stage breast cancer (Liu et al., 2018). Alterations of salivary glycosylation patterns were probed using lectin microarrays and blotting analysis from 337 patients with benign breast cyst or tumor (BB) or breast cancer and 110 healthy humans. Their diagnostic models were constructed by a logistic stepwise regression in the retrospective cohort. The diagnostic models were constructed based on a total of 37 lectins with 9 lectins (PNA, PHA-E + L, UEA-I, PWM, MAL-I, NPA, BS-I, PTL-II and PHA-E) that exhibited significant alterations of salivary glycosylation-patterns, which achieved better diagnostic powers for the diagnosis of BB and breast cancer in the validation cohort. The diagnostic model of breast cancer exhibited a high accuracy in the double-blind cohort.

This study could contribute to the screening for patients with early-stage breast cancer based on precise alterations of salivary glycosylation patterns. As the authors stated, saliva is a mirror of body health and an indicator of the composition of various substances such as hormones, enzymes and drugs. Saliva contains many disease markers which reflect the state of health of not only the salivary glands and oral cavity, but also the whole body. In conclusion, the present study investigated the correlation of alterations in salivary protein glycosylation related to breast cancer and compare different or similar alterations of protein glycosylation patterns between healthy volunteers, benign breast tumor patients and breast cancer patients.

Disclosure

The author declared no competing interests.

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