1L-12
GLYCAN ANALYSIS OF THE SARS-COV-2 SPIKE GLYCOPROTEIN S1: LECTIN-BASED MICROARRAY AND MASS SPECTROMETRY APPROACHES

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A novel betacoronavirus named SARS-CoV-2 was identified as the causative agent of COVID-19, the disease affecting the lower respiratory tract manifesting as pneumonia in humans[1]. Coronavirus spike (S) glycoproteins promote entry into cells using ACE2 receptors and are the main target of antibodies, and vaccine development is focused to this principal as well. S glycoprotein comprises two functional subunits responsible for binding to the host cell receptor (S1 subunit) and fusion of the viral and cellular membranes (S2 subunit)[2]. S1 subunit is more exposed at the viral surface than S2 and is likely to be a subject of immune response.

Here we used two approaches, lectin-based microarray and mass spectrometry MALDI-TOF/TOF to reveal the glycan pattern on a recombinant SARS-CoV-2 spike glycoprotein S1 expressed in HEK293 mammalian cells. MALDI MS enabled detailed identification of presented N-glycan structures after their enzymatic release. Lectin-based microarray allowed determining the interactions of biologically accessible glycans with set of lectins, a special class of proteins selectively recognizing glycan structures, thus mapping the composition of glycan shell of S1 glycoprotein. The results obtained by both methods were in accordance. Our findings are in general in agreement as well with the data on glycan composition of SARS-CoV-2 S1 glycoprotein already reported[3–7].

The glycomic studies are very important regarding both the understanding of SARS-CoV-2 acting and the development of efficient vaccine targeting the spike glycoprotein.

Acknowledgment: APVV-17-0239, VEGA 2/0137/18, COST CA18132, H2020 ITN synBIOcarb, MZ SR 2019/7-CHÚSAV-4.

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1L-13
AFFINITY-BASED METHOD USING GLYCOPROTEIN MICROARRAY WITH LECTIN RECOGNITION FOR HIGH THROUGHPUT DETERMINATION OF GLYCOSYLATION IN CANCER

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Human body encounters various physiological and pathological states during the lifespan. Physiological changes for instance during various stages of growth, pregnancy, ageing along with environmental factors can amend the homeostasis of human body. Similarly, pathophysiology of complex human diseases like obesity, hypertenion, diabetes, cancer and many other diseases is a consequence of combined effect of genetic and environmental factors. Genetics predominantly governs the propogation of genes to the next generation as well as the embryonic development. Contrastingly the impact of internal and external elements such as environment, diet, lifestyle and so on, on the overal homeostasis of the subject and its anomalies is reflected in terms of various means like excretion of metabolites, serum component markers and molecular markers. Structural alterations in glycan composition represent one such promising molecular marker depicting disease specific changes. Gycans are not directly encoded by a genetic code as in case of proteins, rather they are ezymatically assembled by biosynthetic pathways. Hence, any physiological or pathological factors affecting such enzymatic activities can alter the final structure of glycans. Consequently, the glycan structure mediated biological outcomes are influenced by glycan structure modulations.

Glycan and lectin arrays in combination with other analytical tools serve as excellent means for high throughput determination of the changes in the glycosylation pattern. This can further help to understand the implications of alterations in glycan stucture during the pathophysiology of a partiular disease and thereby help in early diagnosis of a disease. Here we tried to demonstrate one such approach to decipher changes in glycan composition in case of patients (n = 150) diagnosed with various cancers using glycoprotein arrays. This will further help to understand the alterations occuring in glycans due to various oncologial onset and further propose a potential marker for early diagnosis.

Acknowledgments: H2020 ITN synBIOcarb, APVV SK-SRB-18-0028.

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