TOTAL INTERNAL REFLECTION ELLIPSOMETRY STUDY OF SARS-COV-2 OMICRON SPIKE PROTEIN AND POLYCLONAL ANTIBODIES INTERACTION

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It has been over two years since the detection of the SARS-CoV-2 Omicron variant, characterized by the highest number of mutations [1]. The vaccines provided a protection in the form of antibodies produced by the body against the original strain but understanding how the antibodies interact with other variants is of great importance. In this study, we investigated the interactions between specific polyclonal human antibodies and the Spike protein of SARS-CoV-2 Omicron variant. To assess whether the vaccines generated a higher amount of antibodies against this variant, we analyzed the blood serums of two individuals: one vaccinated against the wild-type SARS-CoV-2, and the other unvaccinated but recovered after the COVID-19 infection.

The use of total internal reflection ellipsometry provided a non-destructive, label-free, and highly sensitive approach [2]. This optical method employs surface plasmon resonance and allows real-time monitoring of interactions between molecules on the sensing surface of a biosensor and kinetics measurements. Such measurements were performed to determine the surface mass density formed on the sensing surface after the immunocomplex formation of specific polyclonal human antibodies to the Spike protein of SARS-CoV-2 Omicron variant by the use of mathematical modeling [3].

In this study, a self-assembling monolayer comprised of 11-mercaptoundecanoic acid molecules was utilized to immobilize the Spike protein onto the gold surface of a sensor disc. During the analysis, multiple dilutions of blood serums were prepared, and differences between the blood serums taken from vaccinated and unvaccinated individuals were observed. Notably, a higher amount of mass was formed on the sensing surface after the interaction between the SARS-CoV-2 Omicron Spike protein and the antibodies in blood serum taken from an individual who was vaccinated against the wild-type strain.

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