Graphene-Protein Interactions Mapped using Quartz Crystal Microbalance with Dissipation Monitoring (QCM-D)

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Graphene-based materials have shown significant potential for biomedical applications including biosensors, cell scaffolds and drug delivery. However, the interaction of complex biomacromolecules like proteins with graphene and its derivatives, graphene oxide (GO) and reduced (r)GO, remains poorly understood. Here, we demonstrate that the quartz-crystal microbalance with dissipation monitoring (QCM-D) technique can be used to systematically study the interaction dynamics of a typical protein, bovine serum albumin (BSA), with graphene materials of varying degrees of functionalisation. We find significant differences in molecular orientation and confirmation, mass adsorption and biochemical functionality of BSA on different graphene surfaces, determined by both the population of functional groups of GO and the protein concentration. The dominant forces during the adsorption of biomolecules onto GO and rGO are shown to be hydrophilic and hydrophobic interactions, respectively. The GO surface yielded higher BSA adsorption than both rGO and control standard gold electrodes due to the high density of functional groups. The biochemical functionality of adsorbed BSA was investigated through the interaction with its anti-BSA antibody counterpart. BSA on GO can retain its binding sites while, in contrast, a denatured ad-layer of BSA forms on the rGO followed by further binding of active BSA molecules, depending on the concentration of the protein. Intermediate conformations are observed for partially-reduced GO. These results also suggest that QCM-D is a viable readout technique for graphene-based biosensors. This QCM-D approach could be further extended to study the interaction of a host of biomolecules and their assemblies, including whole cells, with 2-dimensional materials.

References

[1] M.-S. Chae et al., Biosens. Bioelectron., vol. 92, 2017, pp. 610–617
[2] D. Meléndrez, et al, Nanoscale, vol. 10, no. 5, 2018, pp. 2555–2567.

Figures

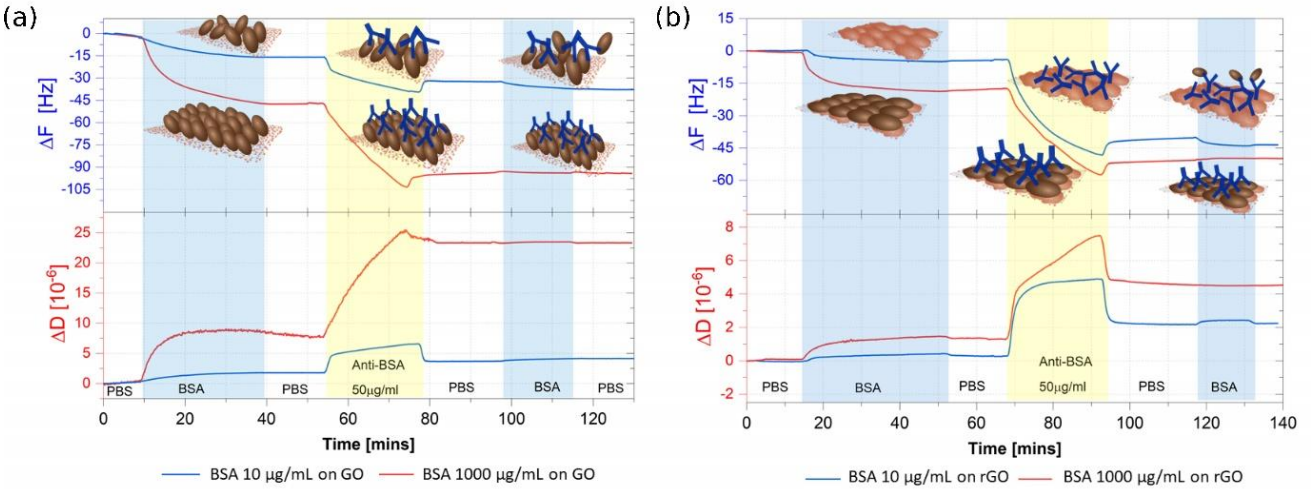

Figure 1: QCM-D monitoring of BSA and anti-BSA interaction on (a) GO and (b) rGO5.