Step forward for antigen-based therapies



Research published this week in the *Journal of the American Chemical Society (JACS)* could prove an important milestone in the journey towards antigen therapies to target specific diseases.

Reliable information on the structure of triple DNA helices in gas phase has been notoriously hard to gather, but researchers from the Institute for Research in Biomedicine (IRB Barcelona) and the Barcelona Supercomputing Centre (BSC) have managed to characterise such molecules for the first time. It has taken the team more than ten years to complete a map of gas phase DNA structures, which they achieved with a combination of experimental data from mass spectrometry and computational simulations.

"Until now these special DNA structures were almost impossible to detect and it was not known whether they preserved structural memory in solution when they were evaporated," explained Dr Modesto Orozco, principal investigator at IRB Barcelona and Director of Life Sciences at the BSC. "With this study we have characterised this structure and demonstrated that it maintains a surprising memory of its previous biological environment - aqueous solution - in which it is normally very difficult to characterise."

The work carried out may have a significant impact on the future of antigen-based therapies, as the difficulty of detecting triple helix structures is considered one of the main factors holding such therapies back.

"Demonstration that the structure is maintained in gas phase will allow these DNA structures to be detected more easily", Orozco pointed out. Although many gene therapy drugs have been under development for years, none are available on the market as yet.

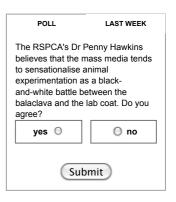
The results could also have implications for the use of X-ray free-electron laser (XFEL) technology in structural resolution techniques. Orozco went on to say that "If our calculations are correct XFEL could be used to obtain structural data in gas phase about the behavior of a molecule in its natural biological environment and XFEL would become a very powerful tool to resolve the structure of macromolecules."

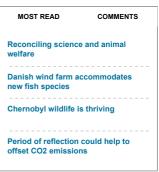
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