Researchers create molecular Braille to identify DNA molecules

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Researchers at UCLA and New York University have developed a method to detect sequence differences in individual DNA molecules by taking nanoscopic pictures of the molecules themselves.

The work is reported in the Journal of the Royal Society *Interface*.

Using the approach they call "Direct Molecular Recognition," the UCLA and NYU researchers used nanoparticles to turn the DNA molecules into a form of molecular braille that can be read in the scale of nanometers, or one billionth of a meter, using high-speed Atomic Force Microscopy (AFM).

The leaders of the study are: Jason Reed, a research professor, and Professor Jim Gimzewski, nanotechnology pioneer, both at UCLA's California Nanosystems Institute, and Professor Bud Mishra, genomics expert, at NYU's Courant Institute of Mathematical Sciences. This group believes the method will have many practical uses, such as super-sensitive detection of DNA molecules in genomic research and medical diagnostics as well as in identifying pathogens.

While there are a variety of techniques currently used for this purpose, they are time consuming, technically difficult, and expensive. They also require a significant amount of genetic material in order to make accurate readings and often require prior knowledge of the sample composition.

According to Mishra, to overcome these shortcomings, the team devised a "single-cell, single-molecule" method that would dispense with the complex chemical manipulations on which existing methods are based, and, instead, utilize the unique shapes of the molecules themselves as the method of identification. This approach has the benefits of being rapid and sensitive to the level of a single molecule.

Reed says that "the long term goal of our team's research is to dissect, understand, and control the biology of single cells in complex tissues, such as brain, or in malignant tumors. Furthering this body of work requires that we address an unsolved problem in single-cell molecular analysis: the lack of a method to routinely, reliably, and inexpensively determine global gene transcriptional activity."

In their paper, the team closely examined the potential use of this technique to quantify the activity of genes in living tissue, a method known as transcriptional profiling. They were able to show that their Direct Molecular Recognition technique could accurately quantitate the relative abundance of multiple DNA species in a mixture using only a handful of molecules – a result not achievable using other methods.

Provided by New York University

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