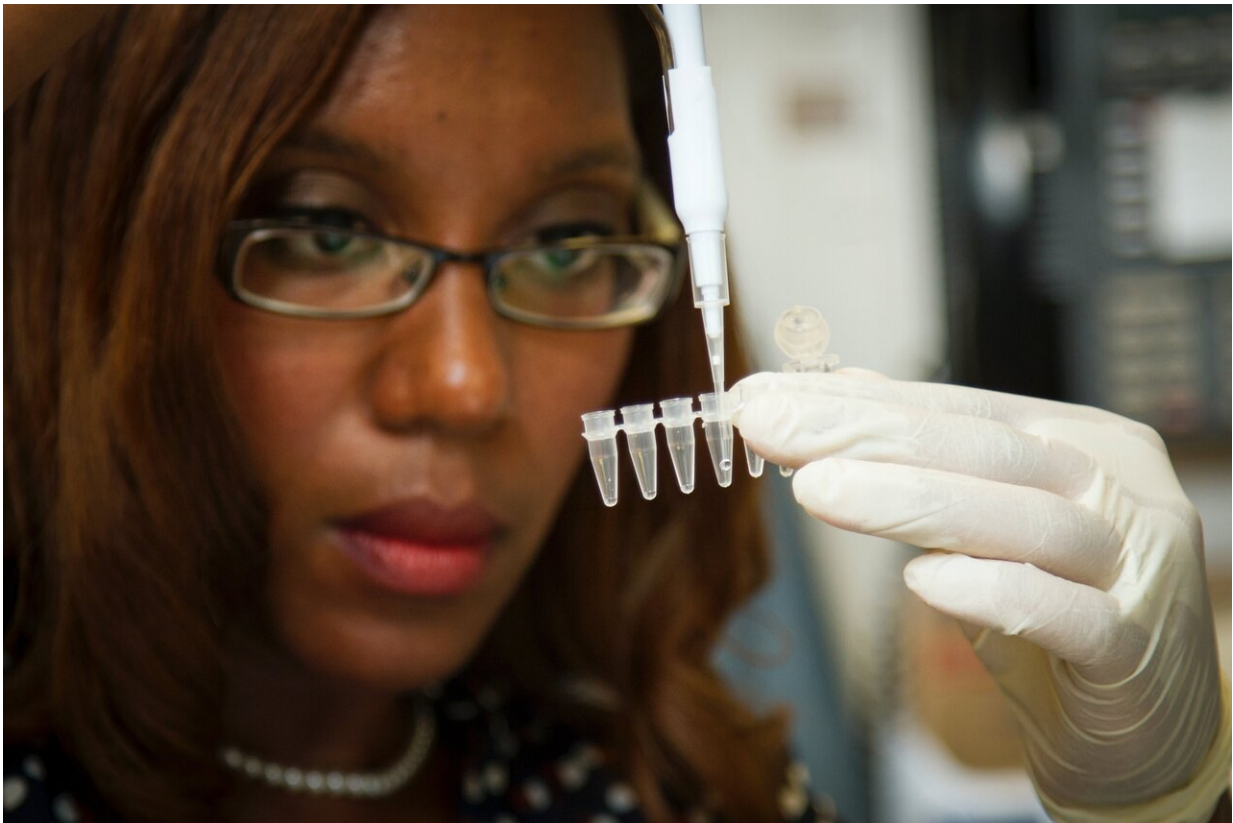


DNA methylation regulator QSER1 identified

April 9 2021, by Bob Yirka



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A team of researchers from a number of institutions in the U.S. has identified a DNA methylation regulator called QSER1. In their paper published in the journal *Science*, the group describes studying the valleys

of unmethylated DNA and their discovery of a new regulator. Tianpeng Gu and Margaret Goodell with the Baylor College of Medicine, have published a Perspectives piece in the same journal issue outlining prior research with DNA methylation and the work by the team on this new effort.

Methylation is a process that happens in biochemical systems—it involves the transfer of atoms from one material to another. DNA methylation is a process by which [methyl groups](#) are added to DNA molecules. When it happens, the sequence remains the same, but the activity promoted by the sequence can change. Quite often, such changes involve repressing transcription. DNA methylation was only recently found to be one of the major factors involved in epigenetics. Thus, it is still not well understood—most particularly in the way it behaves during the development of diseases.

Recent prior research has found that there are valleys of unmethylated DNA in the mammalian genome—a finding that suggests methylation is not involved in repressing transcription in the strands of DNA where they are located. Subsequent research showed that most of the valleys were connected to developmental regulators and that the size of the valleys (also described as canyons) was regulated by a push-and-pull system involving DNA methyltransferases and also ten-eleven translocation dioxygenases. In this new effort, the researchers found evidence of a protein with large amounts of serine and glutamine called QSER1. It's a component of the "push" part of the system—thus, it plays a role in restricting DNA methylation. They also found that it works with ten-eleven translocation dioxygenases by interfering with the binding process of DNMT3B and DNMT3A. In so doing, the proteins protect the DNA methylation canyons from hypermethylation.

The researchers were able to identify QSER1 by using the CRISPER gene editing tool to screen for regulators of DNA methylation. Gu and

Goodell suggest that future work involved in studying QSER1 should center on learning more about the relationship between QSER1 and ten-eleven translocation dioxygenases, perhaps using early embryos.

More information: Gary Dixon et al., "QSER1 protects DNA methylation valleys from de novo methylation," *Science* 09 Apr 2021: Vol. 372, Issue 6538, eabd0875. [DOI: 10.1126/science.abd0875](https://doi.org/10.1126/science.abd0875)

Tianpeng Gu, Margaret A. Goodell. "The push and pull of DNA methylation," *Science* 09 Apr 2021: Vol. 372, Issue 6538, pp. 128-129. [DOI: 10.1126/science.abh3187](https://doi.org/10.1126/science.abh3187)

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