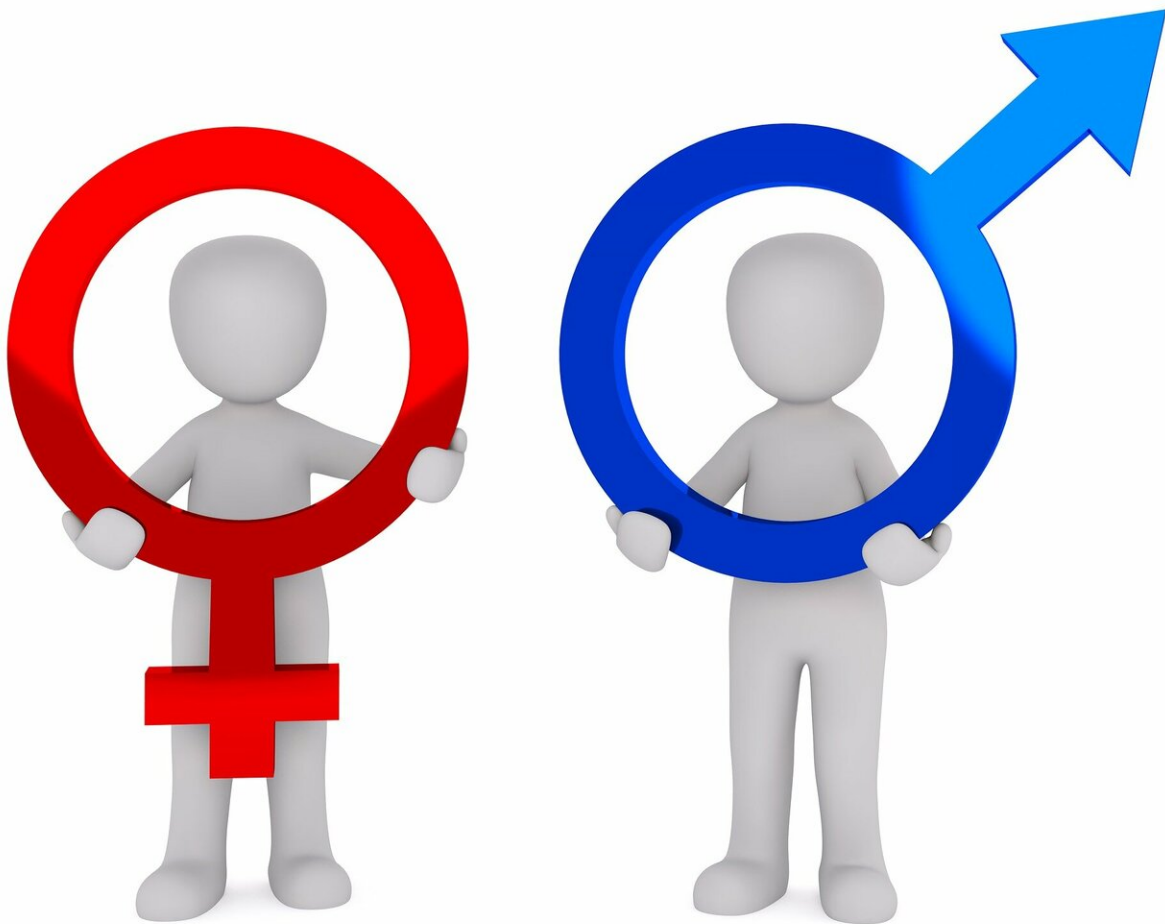


Researchers discover genome-wide variations in gene expression between male and female mammals

July 19 2019, by Bob Yirka



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A team of researchers affiliated with several institutions in the U.S. has discovered genome-wide variations in gene expression between male and female mammals. In their paper published in the journal *Science*, the group describes their RNA sequencing studies in several types of mammals and what they found.

Physiological differences between mammalian genders are quite often easy to spot—in addition to organs involved in reproduction, there are skeletal and facial hair differences, as well as height differences. Prior research and anecdotal evidence has also suggested there may be some differences in the way the brain works. But what about variations in [gene expression](#)? The researchers in this new effort report that very little research has been done in this area, which is a problem—recent studies have shown that there are many [gender](#)-based health issues. Women are more likely to suffer from autoimmune diseases, for example. And men are more likely to develop cardiovascular diseases.

To understand why such differences exist, medical scientists need to better understand gender-based variations in the genome. To learn more about gender-based gene expression, the researchers sequenced the RNA of both genders of four non-human mammals: rats, mice, macaques and dogs. As part of their efforts, they tested different tissues in each of the animals to ensure that each germ layer was represented. They also sequenced tissue from all of the most prominent organs. They then compared what they found to similar data collected from [human subjects](#) stored in the Genotype Tissue Expression Consortium database.

The researchers found examples of hundreds of conserved gender-biased gene expressions in each tissue. As just one example, they found that 12 percent of the gender differences related to average height in humans could be attributed to conserved gender-biased gene expression. They note that such findings are significant because they prove that gender biases in gene [expression](#) can lead directly to differences in traits.

The researchers also found evidence that suggested such gender-biased gene expressions came about relatively recently, evolutionarily speaking. They suggest this finding indicates that researchers need to pay particular attention to such differences when using non-human models to study gender-based differences in humans.

More information: Sahin Naqvi et al. Conservation, acquisition, and functional impact of sex-biased gene expression in mammals, *Science* (2019). [DOI: 10.1126/science.aaw7317](https://doi.org/10.1126/science.aaw7317)

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