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# Researchers find possible genetic link for pelvic floor disorders

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University of Utah researchers have identified a region of the human genome that may contribute to the development of pelvic floor disorders such as pelvic organ prolapse and stress urinary incontinence, according to a study published this week in the *American Journal of Human Genetics*.

Kristina Allen-Brady, Ph.D., and colleagues at the University of Utah School of Medicine analyzed the DNA of 70 women from 32 families with at least two cases of pelvic floor disorders (PFD) and found significant evidence for a gene that predisposes to PFD on chromosome 9.

"PFDs are a major public health concern for women of all ages," says Allen-Brady, research assistant professor of genetic epidemiology in biomedical informatics and lead author of the study. "Previous research has found that women with urinary incontinence are more likely to have family members with incontinence, but the genetic factors that predispose to PFD are not well understood."

An estimated one-third of all U.S. women are affected by some type of PFD, such as pelvic organ prolapse (POP) or urinary incontinence, during her lifetime. The pelvic floor refers to the network of muscles, ligaments, and connective tissues that keeps all of a woman's pelvic organs in place. PFDs occur when these muscles and tissues weaken or are injured. One in nine women will undergo surgery for PFD, and one-third of these women will require repeated surgeries.

Risk factors such as childbirth, increased age, smoking, and obesity may contribute to PFD, but they do not fully explain the development of these disorders. To better understand the genetics of PFD, Allen-Brady and her colleagues identified 32 families which included at least two closely-related female relatives affected by POP. In POP, the uterus, bladder, or other pelvic organ drops down and protrudes abnormally because supporting tissues are weakened.

The researchers studied DNA from a total of 70 women who received treatment, usually surgery, for moderate-to-severe POP. Genetic analysis of this DNA showed significant evidence that genes located in a region of the genome called chromosome 9q21 may be inherited together in related women who have POP.

"This is the largest collection of families with POP that has been reported to date," says Allen-Brady. "Although it is premature to suggest that all PFDs have a common genetic predisposition, our study shows significant evidence that the chromosome 9q21 region may be linked to the development of PFD in families where multiple women are affected."

The researchers are in the process of collecting and analyzing DNA from other families that seem to be at high risk for PFDs in order to strengthen their conclusions. Although PFDs are likely a disease caused by both genetic and environmental factors, further evidence that the chromosome 9q21 region is linked to PFD can direct efforts at narrowing down and identifying a gene that is responsible for disease development.

Confirmation of genetic susceptibility could provide insight into the underlying disease process of PFD and potential ways to prevent this common condition.

Source: University of Utah Health Sciences (news : web)