Genetic risk for uterine fibroids discovered

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Uterine fibroids are the most common type of pelvic tumors in women and are the leading cause of hysterectomy in the United States. Researchers from Brigham and Women's Hospital (BWH) are the first to discover a genetic risk allele (an alternative form of a gene) for uterine fibroids in white women using an unbiased, genome-wide approach. This discovery will pave the way for new screening strategies and treatments for uterine fibroids.

The study will be published online on October 4, 2012 in *The* American Journal of Human Genetics.

The research team, led by Cynthia Morton, PhD, BWH director of the Center for Uterine Fibroids and senior study author, analyzed genetic data from over 7,000 white women. The researchers detected genetic variants that are significantly associated with uterine fibroid status in a span of three genes including FASN which encodes a protein called FAS (fatty acid synthase).

Moreover, additional studies revealed that FAS protein expression was three times higher in uterine fibroid samples compared to normal myometrial tissue (muscle tissue that forms the uterine wall). Over-expression of FAS protein is found in various types of tumors and is thought to be important for tumor cell survival.

"Our discovery foretells a path to personalized medicine for women who have a genetic basis for development of uterine fibroids," said Morton. "Identification of genetic risk factors may provide valuable insight into

medical management."

Study samples used were from various cohort studies, such as the Finding Genes for Fibroids study and the Women's Genome Health Study at BWH.

Uterine fibroids may lead to abnormal vaginal bleeding, infertility, pelvic pain and pregnancy complications. Uterine fibroids are found in more than 75 percent of women of reproductive age.

Provided by Brigham and Women's Hospital