New Gene Identification That Affects Risk of Ovarian Cancer

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 Ovarian cancer is one of the leading causes of cancer deaths among women. According to the CDC, about “21,000 women in the United States were diagnosed with ovarian cancer in 2013” (Sandoiu). As part of the genomic study OncoArray Consortium, 12 new variants of a gene associated with the inheritance of ovarian cancer were discovered (Sandoiu). In addition to finding these new variants, 18 previously discovered ones were confirmed; this research has increased the known genetic risk of developing ovarian cancer to 6.5% (Sandoiu). This means that doctors are more likely to identify if a person has the genes that increase their risk for developing this specific cancer, and provide them with the resources to detect any cancer earlier on. Therefore, this new medical achievement can be life-saving.

 The genetic variants that were discovered were also found to be common variants, meaning that some women have the risk of carry multiple variants. Contrary to what some may think, this does not actually have a large effect on increasing the risk of developing ovarian cancer (Phelan, et al). Even so, it allows doctors to detect these multiple variants and keep an eye out for cancer symptoms early on.

 Catching ovarian cancer in its early stages helps to increase the chances of survival for women who are diagnosed. According to the Cancer Research UK, “more than 90% of women diagnosed with the earliest stage of ovarian cancer survive their disease for at least 5 years compared to around 5% for women diagnosed with the most advanced stage of disease” (Cancer Research UK). The newfound discovery of the different genetic variants that can lead to the hereditary development of ovarian cancer means that doctors are more likely to detect these genes. Once they are detected, action can be taken to catch ovarian cancer in its earlier stages, exponentially increasing the ability to save thousands of women.

References:

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