Gene Profiling Implicates Oviducts in Ovarian Cancer Genesis

A better understanding of how ovarian cancer progresses, including early markers for detection, could help reduce mortality from this often deadly disease. A group of researchers at Cornell University in Ithaca, N.Y., led by Patricia A. Johnson, Ph.D., used microarray technology to compare gene expression in ovarian tissue from normal chickens with that of tissue from chickens with this cancer. Hens, which have a high incidence of ovarian cancer, are the only known spontaneous animal model of ovarian cancer.

In their analysis of differentially expressed genes, the researchers discovered that 10 of the top 25 genes up-regulated in ovarian tumors are oviduct-related. These genes are expressed in early- and late-stage tumors, as well as in the oviduct, but not in the ovarian surface epithelium (OSE). This finding is noteworthy because, despite the fact that this cancer is a heterogeneous disease comprising a variety of cell subtypes, the OSE has traditionally been viewed as the common site of ovarian tumor origin. This study joins others in calling that view into question.

Estrogen is thought to promote ovarian tumor progression by regulating cell proliferation, motility, and invasion. The researchers found that several oviduct-related genes they identified are regulated by estrogen.

In an article to be published in Hormones & Cancer,* the researchers say their identification of up-regulated, oviduct-related genes in ovarian tumors gives evidence that at least some of these tumors do not originate in the OSE. Their finding that oviduct-related genes appear to be regulated by estrogen highlights the importance of estrogen signaling in these tumors.

The researchers propose that the secretions of a number of these genes are candidate serum biomarkers for ovarian cancer. ■