Epithelial ovarian cancer is a major health care problem for women. Most patients present with advanced stage disease. All patients are treated with surgery and then combination chemotherapy. There has been difficulty in identifying clinically useful biomarkers in this disease. However, the recent genomic characterization of epithelial ovarian cancers has provided new opportunities for the development of biomarkers that will likely result in better diagnosis, detection, and treatment of the disease.

For high-grade serous tumors, there is a profound abnormality in DNA repair (from mutations in p53 and BRCA1or2) that result in few actionable mutations but massive gain and loss of DNA. These deletions and amplifications contain many genes that are over or under-expressed and could be potential biomarkers. For other ovarian tumors such as endometrioid tumors, clear cell, and mucinous tumors, each have specific mutations and genomic abnormalities that can be used as diagnostic biomarkers.

The development of an accurate early detection assay for ovarian cancer has been an important goal for many years. We have developed an affymetrix-based virtual array to identify genes that encode proteins that are likely found in the blood. Combing this approach with high through-put proteomic analysis using proximal fluids such as ovarian cysts has identified a list of plasma based biomarkers which excellent early detection candidates.

For advanced stage high-grade ovarian cancer, the ability to identify biomarkers that can stratify patients to optimal therapy is an important goal. We have carefully evaluated all known prognostic models and developed a new gene expression signature predicting patient survival. While improved, these signatures do not at present affect patient management. In contrast, predictive biomarkers for HRD and debulking status have evolved to be clinically useful. These biomarkers are likely to lead to a more personalized care for ovarian cancer patients.