

EXECUTIVE SUMMARY: *(State in layman's terms the application's broad, long-term objectives and specific aims, making reference to the potential public benefits of the project for California.)*

Ovarian cancer is the fifth leading cause of cancer death for women in the United States. Five-year survival rates remain very low (around 30%), in main part due to the absence of symptomatic disease until later, advanced cancer stages. Gene expression profiling of late-stage ovarian tumors and normal ovarian tissue has uncovered many genes whose increased expression is associated with tumors but not normal tissue. It is hoped that understanding the roles these genes play in the progression of ovarian cancer will eventually lead to the development of early screening tests, or even better, targeted therapies that could combat this public health problem. One such tumor-associated gene, MAGP-2, is a secreted protein that can activate an important signaling pathway in other tumor cells and can recruit blood vessels that support tumor growth. It is our aim to determine what role MAGP-2 plays in the progression of ovarian cancer. As a first step, we will determine which cells in normal ovarian tissue express MAGP-2, and whether in ovarian cancer it is the actual tumor cells that overexpress MAGP-2, or whether non-cancerous surrounding cells are producing too much MAGP-2. Understanding both the normal and cancer-associated cellular expression pattern will allow for rational design of further studies in which MAGP-2 expression will be experimentally altered to determine if MAGP-2 plays a causal role in the progression of ovarian cancer. In the long term, understanding the molecular mechanisms that drive ovarian cancer progression may provide the knowledge that will lead to the design of novel therapies.