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Institution: Wake Forest University School of Medicine
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Project Status: Closed

**Update 2 (02-2014)**

The expression patterns of certain tumor genes have been found to contribute important prognostic information that can be used clinically to improve therapeutic decisions for patients. This is particularly true of breast cancer, with similar success stories currently emerging in prostate and colon cancer. Few, if any, meaningful biomarkers predictive of PMP outcomes are currently available. Using DNA microarray technology to study the gene expression profiles of virtually all human genes in a small panel (n=24) of appendiceal (PMP) tumors, we previously identified a group of genes that had statistical associations with patient outcomes (Levine, et. al., J Am Coll Surg, 2013). In the first aim of our NORD-funded research, we have now verified the reproducible statistical significance of these genes, and discovered more genes that also appear to contribution to patient outcome prediction (manuscript in preparation). These data suggest the existence of different molecular subtypes of PMP with more (subtype 1) or less (subtype 2) clinically aggressive characteristics. Moving forward in aim 2, we will develop a "fixed statistical model" to predict these subtypes and rigorously test its performance in a much larger population (n>100) of appendiceal cancer patients. By clearly defining high risk patients who are unlikely to benefit from HIPEC, we can substantially reduce unnecessary patient morbidity and identify PMP patients most in need of, and most suitable for the testing of, next-generation therapies or investigational drugs currently under study in clinical trials.