

MicroRNA Expression Signature to Predict Cervical Cancer Outcome
Xiaowei Wang PhD

Project Summary:

Estimates are that in 2009, about 11,000 women in the US will be diagnosed with cervical cancer, and about 4,000 of them will die from this deadly disease. This is a significant public health problem, and is also a leading cause of life years lost. Most cervical cancer patients receive standard radiotherapy and chemotherapy; however, clinical outcomes vary significantly and are difficult to predict. Thus, a method for more accurately predicting treatment outcomes would help oncologists and patients decide when (and when not) to be aggressive. However, traditional clinicopathologic features, such as tumor grade and stage have limited prognostic value.

In our study, we have performed expression profiling analysis on microRNAs for the identification of cervical cancer biomarkers. MicroRNAs (miRNAs) are a newly discovered family of small non-coding RNA molecules that control the expression of their protein-coding gene targets. MicroRNAs are extensively involved in tumorigenesis and they have deregulated expression in human cancers. We have identified two miRNAs that are predictive of cervical cancer outcome. These prognostic miRNAs were used to build a computational outcome prediction model for cervical cancer, and the outcome prediction model has been validated experimentally with independent cervical tumor tissues. The reliable prediction of patient outcome would make it possible to provide individualized cervical cancer therapy to improve overall patient survival.

Publication: Hu X, Schwarz JK, Lewis JS., Huettner PC, Rader JS, Deasy JO, Grigsby PW, Wang X (2010) A microRNA expression signature for cervical cancer prognosis. *Cancer Research* 70(4):1441-1448.