

Leukemia Research Project Update #2

December 3, 2009

- 24 patient samples of DNA have been selected for the Leukemia Research Project. 1 sample is Jacquie's which had been saved. The analysis, genes, chromosomes, micro RNA, statistics, correlation, and gene sequence in both young and old patients (most of which succumbed to the disease) will be valuable information gained through this research.
- Details of the individuals, their ages, old vs. young, and an indepth look at their cancers will help determine where and what in their gene sequence went wrong. Were genes 10 times higher, 10 times lower, etc.? A collaborative effort with the University of Chigao will assist with analysis and correlation of the data. Specifically: What is unique to each individual or unique to other patient samples? Gene levels, protein levels, and what occurred between younger or older patients will be examined. How does this result in a cancer diagnosis or a specific cancer? Does this happen to ALL patients? Does this happen to AML patients? The genes will be looked at and data summarized to see what went wrong. In addition, why is leukemia so aggressive? Why does it resist chemotherapy? Why, after transplantation, does it come back?
- First, will be the initial diagnosis of the patient samples, then, why Jacquie's leukemia returned after bone marrow transplantation.
- It is our understanding the gene class can be broken down to show what makes it into leukemia. What makes it grown faster, what makes it grow slower, what makes it resistant to chemotherapy?

"This is the patient's cancer. How it happened and what went wrong is based on the genes. We are looking at new things with new technology. I want to look at the genes and have them tell me what went wrong." - Dr. Eunice Wang