



## In Love with Genetics

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I've been in the biotechnology industry for more than 20 years and believe that now is the time for genetics to realize its full potential in the identification of disease genes and their translation into novel therapeutics.

I have been privileged to have had the opportunity to work with some very influential people, key leaders, and top intellects in field of genetics, and to learn from them as much as possible. Much of my enthusiasm for science derives from the mentors that I have had. I fell in love with genetics during the first genetics course I ever took, at Tufts University where I did my undergraduate education, and decided at that time that's where I wanted to make a contribution to science.

I received my Ph.D. at Harvard, where I worked with one of the preeminent population geneticists in the field, Richard Lewontin, and continued my postdoctoral studies with him. There were not many women at Harvard in the sciences when I began there, but by the time I completed my Ph.D. and postdoctoral fellowship, this was starting to change. I decided to transition from a pure academic focus into industry, where I could work on more practical applications. This took me from strict population genetics research using model organisms to human genetics with a real focus on human health.

In 1986, I joined Collaborative Research, one of the first biotechnology organizations focused on developing the tools to make genetics a force in the future. A key mentor at Collaborative Research was Helen Donis-Keller, who was lead author on a 1987 *Cell* paper titled "A genetic linkage map of the human genome." I was very fortunate to be in the right place at the right time, during an exciting period of rapid progress in human genetics, which solidified my commitment to this field.

Over the past 20 years, Collaborative Research became Genome Therapeutics, and then Oscient Pharmaceuticals. During my tenure there, we forged several alliances with pharmaceutical companies to translate our disease gene discoveries into novel therapeutics. These programs were

quite successful but somewhat limited in scope, because the tools needed to perform a comprehensive analysis of the genome in complex disorders were not available until very recently.

As a continuation of my focus on identifying susceptibility genes for common diseases, I was enthusiastic to join Genizon BioSciences 2 years ago as their Chief Scientific Officer. Genizon utilizes a unique resource in its discovery efforts, the Quebec founder population, which descended from a few thousand French immigrants who arrived in Quebec between the early 1600s and the mid-1700s. Importantly, the population grew very rapidly in the next 300 years, but remained very homogeneous due to little intermarriage with the other residents of Quebec. As a result, this population is excellent for genetic studies, especially for complex diseases.

Genizon is performing discovery research in more than 20 disease areas and has more than 36,000 DNA samples in its biobank. We've recently conducted genome-wide association studies in seven of our disease programs. Key to the success of these studies has been the unique resource of the Quebec founder population. I believe that we were the first company to complete a genome-wide association study for a complex disease and have partnered the results of this study on Crohn's disease with Genentech, which will be translating our studies into the development of novel therapeutics and companion diagnostics.

While there were a lot of promises delivered by researchers in human genetics 5 to 10 years ago regarding the identification of disease genes to improve therapeutics and much progress was made, the scope of what we were able to do was quite limited. I am very enthusiastic about where the field is today. The completion of the human genome sequence and the HapMap project has facilitated the development of dense linkage disequilibrium-based genetic maps. These, combined with high-throughput low cost genotyping technology, have enabled cost-effective and comprehensive genome-wide studies to identify susceptibility genes for complex human diseases. There are still challenges to face in managing and analyzing vast amounts of data and selecting the best targets for therapeutic development, but we now have the tools and expertise to be successful.

-As told to Lynne Lederman, a medical writer based in Mamaroneck, NY.