

Centenarians With Healthy Lifestyles and Environments

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EDITORIAL NOTE

The idea to look for the reasons for longevity in centenarians was exciting and promising but figuring out how to design and conduct the study was complicated. How could we study a population that had no living control group? And what should we be looking for? When we started the longevity genes project we had three different hypotheses about what made centenarians so special genetically. One was that the centenarians had a perfect genome, one without any variants or other errors or imperfections in the sequence of the genetic code of DNA, allowing them to grow and age in the most optimal way. The second hypothesis was that centenarians had very healthy lifestyles and environments. Our third hypothesis was that centenarians had all an equivalent variants in their DNA because the remainder of us but were being shielded from their negative effects by other variants within the sequence of their DNA, If that was the case, though how could we discover those protective variants? As strong data suggests that exceptional longevity runs in families people with a centenarian parent are about ten to twenty times likelier to become a centenarian parents. For that reason, it made sense for us to review exceptional longevity genetically. Because its rare, its easier to find genetic differences in a group of centenarians than in a group of people with common illnesses like diabetes or hypertension. The human genome was sequenced, we searched for common variant differences between people with diseases and other people without diseases, but are disappointed by the

how little we found. Despite the great expense of the technology at the time, the genetic information we got usually explained less than 5% of the contribution that these common variants made to each of the common diseases. This happened because most of the DNA we have is not coding for the genes that make up the less than 30000 proteins that make up our biology. So about 90 percent of the variants are overrepresented in noncoding areas and underrepresented in the regions that code the exact sequence of a protein. In other words, there are more variants near the genes, between the genes, and between the coding sequences of the genes than in the coming sequences of the genes themselves. Curious about how many centenarians were living close by the records at voter registration. At that time, the population of the Bronx was just over six hundred thousand, so estimated that 100 centenarians in borough.

The narrative aging, centering on decay, decline, burden and costs is becoming increasingly less true. But it's not yet been replaced by a story that reflects present reality. Confirmation bias comes in here we see that we expect to see and disregard new facts and realities. Even though many older adults, people we all know enjoy active lives, their stories barely dent the decay narrative. Indeed, we all change over time but we'd like to challenge the notion that change is usually decay. Just as important, our cognitive abilities will not fail most of us very late in life. Seniors do better later in life than any generation before them.

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