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Dear LLFS Family:

Happy Holidays! The Long Life Family Study is well into its 7th year. We greatly appreciate your willingness to talk to us every year on the phone to update us on your health status.

Our research investigators are very busy examining the extensive data that you have provided to us during your participation in either a home or telephone visit a few years ago. New this year is the genetic data that we have been waiting for. Using the latest genome scanning technology, approximately 2 million genotypes were classified for each and every LLFS family member. Remember that genotypes are similar to blood group types, such as A, B, AB, and O. Furthermore, we used these data to statistically generate information on an additional 7 million additional genotypes for every LLFS member! So, now we have estimates for 9 million additional genotypes on each person, in addition to information on cholesterol levels, blood pressure, et cetera. On one hand, this is a lot of information, but on the other hand, everyone has a total of 3.4 billion genotypes, so we are only marking about 1 in 500 genotypes or less than two tenths of 1 percent of all of the genetic information. However, with these new data, we are now performing sophisticated statistical tests to determine if specific traits, such as blood cholesterol levels and blood pressure are correlated with specific genotypes – both within families and across the entire LLFS group. As a simple example of what we are doing, suppose there are three types at a specific gene: AA, AB, and BB. Furthermore, suppose that the average systolic blood pressure of individuals with type “AA” is 130, with type “AB” is 120, and with type “BB” is 110. This result may indicate that the “B” genotype may lower blood pressure. This is a very simple example of the type of analysis we will do to identify regions of the DNA molecule that may contain specific genetic variants that contribute to a healthy, long life.

Last year we determined that a trait correlated to exceptional survival, the Healthy Aging Index (HAI) was heritable. This means that we can see that it runs in the LLFS families. This year we have identified two DNA regions on chromosomes 8 and 19 that influence HAI. We also determined that another trait related to exceptional survival, the Scale of Aging Vigor in Epidemiology (SAVE), was heritable. Thus, we can now target these region of the DNA to find novel genes that had not previously been known to influence exceptional survival. These findings were presented at The Gerontological Society of America and the American Society of Human Genetics annual meetings a few weeks ago. We are very excited by these results and are currently trying to verify them. We also look forward to sharing more of our results as they are published. Stay tuned!

Thank you again for your continued participation in this important research program. We greatly appreciate the time and effort you put forth to make this study a success. Best wishes for a wonderful 2013.

Sincerely,

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