'The Hidden History of the Maltese Genome'
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One of the largest research groups in Malta has recently discovered that certain Maltese families have a mutation. This resulted in a master regulator which could help bone marrow alleviate haemoglobin switching and the blood disorder thalassemia. Another research area the group is looking into is heart disease – the Maltese Acute Myocardial Infraction (MAMI) study – as Malta's morality rate is higher than the European average. Its focus is finding the genetic component behind three key heart-disease related problems.

Tens of Maltese people have already been partially sequenced; the plan being to map the genomes of approximately 1% of the population (4,000 Maltese people). Accomplishment of this would lead to Malta being one of the best genetically documented countries globally. Presently, a public health genomics database, a bio-bank and the current Maltese population's origins have been implemented and become known.

The Malta Human Genome Project (MHGP) consists of the Malta Council for Science and Technology in the Health & Biotechnology sector for funds, the University of Malta for the research consortium lead and Mater Dei Hospital, Erasmus MC, Rotterdam, The Netherlands and Complete Genomics Inc., California, Silicon Valley, USA for partners.

The reading of someone's DNA shows the likeliness of someone developing a disease and their relatedness with others. The reading of a nation's DNA shows why that population is more likely to develop a disease or how that population came to exist.

The Human Genome Project's aim was to decode the sequence of human DNA in order to better understand human biology and evolution. Another result was the development of DNA sequencing technologies; the newest being known as Next Generation Sequencing which allows a small group of scientists to sequence one person's genome in a few weeks for approximately $1000 (the low price encouraging innovation).

99.9% of every human's DNA sequence is the same and only 0.1% is different, accounting for the variations or mutations of a person. As every human is genetically different, so are large groups of populations. When a particular population's genetics are studied, the current data on the human genome does not seem adequate and so many countries are initiating their own genome projects – Malta now being one of them.

The three-year Maltese Genome Project was launched in 2015 and is based on approximately 25 years of human genomic research in Malta. The end result should be an average/representative example of the entire Maltese population which will help the diagnosis of rare diseases and the investigation of new therapies; in particular how gene variants affect the Maltese population.

A human can equate to 200-400 Gb of raw data from the DNA acquired and passed through a sequencing machine, where the DNA fragments are copied and monitored in order to determine the original sequence. This is then aligned to a reference genome to find any gene variants or mutations which are specific to the Maltese population along with information regarding Maltese origins. It is of course important to confirm the results as the machine is not 100% perfect; although errors have been minimised.

Evolutionary genetics studies rely on two genetic markers:

- Mitochondrial DNA – needed to live. It is inherited from one's mother and only passed on by daughters so researchers can trace ancestry through the female lineage due to haplogroups;
- Y chromosome – Human DNA is made up of 46 chromosomes, with each parent contributing half. Gender is determined by the X and Y chromosomes; XX = female and XY = male, the combination depending on the father. It is useful for evolutionary studies on men's origins as it also has haplogroups (specific parts of mitochondrial DNA).

From mitochondrial DNA analysis, humans left East Africa as a small group of males and females. The first Maltese humans are believed to have been Sicilian farmers. Certain revelations about Maltese origins were published in 2004 by the Annals of Human Genetics, situated in Malta, resulting in the fact that contemporary Maltese come from just a few hundred miles north. This resulted from observing Y chromosome haplogroups retrieved from around the Mediterranean and identifying common population groups. The nearly complete mitochondrial DNA data gathered for the Maltese Genome Project seems to point to the same result – that most contemporary Maltese originate from Sicily and southern Italy of about a thousand years ago.

The original Maltese population was visited by many small groups over the centuries and in effect, left behind gene variants and mutations; i.e. Founder Effects. These newly introduced Founder Mutations spread across the population as it expanded and mixed with genomes from faraway countries. The population grew exponentially.

The altering population numbers over historical events created genetic bottlenecks and impacted on genetic diversity in such a way that DNA mutation led to rare diseases; most of the Maltese genetic mutations being shared with Sicily and southern Italy. Some of these DNA mutations which lead to rare diseases are disproportionately high in the Maltese population; some being: gangliosidosis, coeliac disease and blood disorders likes thalassemia.

A 2007 study focused on a mutation in the SPR gene which leads to a rare disorder known as Segawa's Disease (a motor neuron disorder similar to Parkinson's disease). A high proportion of the Maltese population were found to have this single mutation, resulting in diagnosis and treatment at birth to prevent severe disability.

Research and diagnostics will be moving to whole genome sequencing. The Maltese Genome will determine the treatment of diseases widespread locally and help others worldwide. A complete picture of Maltese origins to today will be formed.