

Genome Decoders

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Overview

The Genome Decoders project is looking at breaking down and analysing the genetic make-up of the Human Whipworm (*Trichuriasis trichiura*). The Human Whipworm is a parasite that is a carrier for the neglected tropical disease, Trichuriasis. By analysing the genome of the Whipworm, we can look at a way to stop the spread of this disease and break the cycle of poverty that it chains people to. We have been analysing genes within a chromosome to help complete the full genetic profile of the Whipworm. The genes that we have analysed are then sent to research scientists at the Sanger Institute who verify our results.

Aims

- To fully annotate chromosome 2 of the Whipworm.

Background information

A Neglected Tropical Disease (NTD) called Trichuriasis is caused by a parasitic worm known as the whipworm (*Trichuris trichiura*). Children can become seriously infected with these worms when living with conditions of poor sanitation, and the infection causes diarrhoea, abdominal pain, malnutrition and developmental problems. This disease can have chronic social and economic impact on these communities, creating a relentless cycle of poverty.

Studying the whipworm can help scientists to find new ways of treating and preventing trichuriasis. Scientists at the Wellcome Trust Sanger Institute have sequenced the genome of the human whipworm. This is the complete set of DNA instructions that makes up the whipworm. But we need to make sense of all these instructions to understand the biology of the worm and to find new ways to fight the disease.

Methodology

The whole genome has been sequenced by scientists, however there are around 15,000 genes to annotate. Along with students and schools from all around the country, we will be going through each potential gene to see if there were any mistakes by the computer while it was analyzing of the data. We will correct any mistakes by setting the stop and start

all areas match up correctly with all available data. By using the online program called Apollo, we are able to see exactly what data is available and annotate the genes. This is accessible by scientists at the Wellcome Genome Campus who can then check our results.

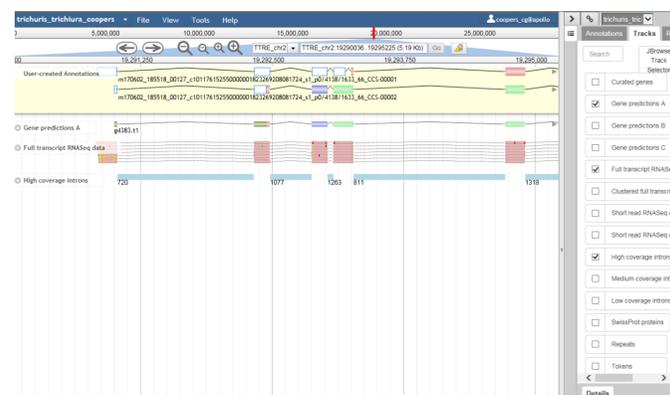


Fig.1 View of Apollo

Results

We are a long way from finishing this project as there are 15,000 genes to be annotated and checked. However, once this has been completed, we can compare the results against a similar genome for the mouse whipworm and compare the differences. This should highlight areas which can be used to stop the poverty cycle.

Conclusion

We are still in the early stages of the project currently, however the project is groundbreaking and has the potential to be used for other disease vector genomes.

Evaluation

We are planning to continue working our way through the project, with greater collaboration with other schools. We will also use this project as a springboard towards engaging pupils in other research science projects.