Topical Genomics and the Many Opportunities it Produces

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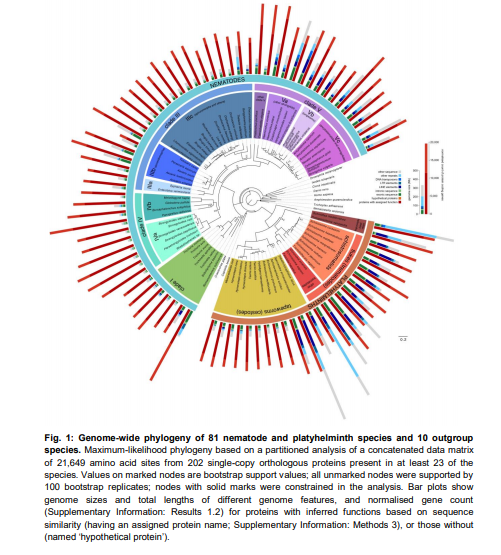
Topical genomics applies the techniques of genetics and molecular biology by using whole genomes of selected organisms and multiple sequencing options (Genomics, 2018). Schools, companies, and federal agencies are taking advantage of the sequencing abilities of topical genomics. Topical genomics can apply to any field and any biology issue. With the use of whole genomes researchers are finding new vaccines, immunology options, and even conservation options. Disease control and conservation acts for animals is the main interest for this paper. Topical genomics in theory goes hand in hand with both the human and animal genomes and because of this topical genomics can open new doors to help alleviate new or worsening issues.

The first example of using and comparing both human and animal genomes starts with worms. Researchers from the University of Edinburgh and Washington University found a way to sequence and compare the genomes of parasitic worms to find new vaccines and drugs. They used 81 species to conduct their experiment; the researchers sequenced 45 worm species’ genomes from scratch and used published data for the other 36 species. After the sequencing, an analysis of the sequence data was performed, and it revealed nearly a million novel genes and new gene families. The researchers cross-referenced the gene database with a current database of available drugs. The cross-reference identified 40 drug targets in the worm genomes and hundreds of existing drugs that could have the potential to hit those targets. The team’s approach could repurpose existing drugs for the use of deworming (Taylor, 2018). A second study on worms was performed on parasitic nematodes and plathelminths to identify new drug targets. A broad comparative study of 81 genomes of parasitic and non-parasitic worms was conducted, and a genome wide phylogeny was constructed to help compare the genomes (Fig. 1). The genomes of 36 species were sequenced at WSI, genomes of 6 species were sequenced at MGI, and the genomes of three species were sequenced by BaNG. After sequencing, repeat libraries were built for each species using RepeatModeler, TransposonPSI, and LTRharvest. The three libraries were merged, and the merged library was used to find repeats in the species’ genome. A tree was constructed, and the database information was used to identify gene families, orthologs, and paralogs. Once all of the information was put together, the researchers found targets in the genomes to compare to drugs that were already made. This study had a very similar ending as the first but showed different whole genome sequencing pathways that can be utilized to discover new things (Berriman, 2017). A third study was conducted on hookworms which infect over 400 million people. Researchers determined an *A. ceylanicum* genome sequence with transcriptomic data throughout infection. It was 313 Mb and showed expression of 30,738 genes. Genomic sequencing and RNA-seq were carried out, and assemblies and maps were created. The researchers approximated that 900 genes were upregulated during early infection in vivo. A downregulation of genes during early infection was observed in both parasitic and free-living nematodes. A previously undescribed protein family was encoded when C-lectin genes were upregulated. After thorough analysis and comparisons, the researchers knew that with further research their findings could provide new drug and vaccine targets to illuminate hookworms (Schwarz, 2015). Thus, all three studies have created a whole new outlook on genome sequencing. Through simply sequencing genomes, new drugs and current drugs can be directed towards eradicating parasitic worms and other organisms.

A second example of using and comparing both human and animal genomes along with conservation acts starts with tigers. Dr. Shu-Jin Luo of the University of Peking and his colleagues proposed in 2004 that there were six total subspecies of tigers. Shu-Jin Luo and his colleagues recently proved that their finding was correct by using whole-genome sequencing. To determine the number of existing subspecies, Luo and his colleagues preformed whole-genome sequencing on 32 tigers. It was found that all the genomes fell into six distinct clusters. Each cluster showed evidence of unique evolutionary history in the tigers. An example was given for a gene that affects body size and it was suggested that the tigers genomic change depending on their unique pressures. One of the six subspecies, South China tiger, is already extinct in the wild, but there are only 150 individuals in captivity. With the information the researchers have gained, they can further analyze the genomes of the tigers, and hopefully create more conservation efforts to save the tigers. Shu-Jin Luo told the *Times* that in order to preserve the genomic signatures, they have to preserve the evolutionary uniqueness that the tigers have gained over the thousands or years (Taylor, 2018). A second study on tiger populations and genomics was done by Meghana Natesh and colleagues in India. They collected samples from 38 wild tigers in seventeen protected areas. They used genome-wide SNPs to infer genetic connectivity. With this they genotyped 10,184 SNPs and identified three genetically distinct clusters. In the northwest cluster, the tiger’s genome was isolated with low variation and high relatedness. The central cluster had the highest variation in the genome (meaning it had a larger genome diversity). The southern cluster didn’t have stated results, but with this information the researchers were able to conclude that the northwest population needs specific conservation attention due to low variation (Natesh, 2017). A third study was conducted by Anuradha P Reddy and colleagues to distinguish how the Bengal tiger adapts to different habitats. They used a total of 345 Gb (144X coverage of the genome) from 1,149,381,669 raw read pairs from the Bengal tiger, and cut it down to 990,060,793 clean read pairs. The Amur tiger genome was then compared to the raw data of the Bengal tiger. Once compared they created the first high coverage genome sequence of the Bengal tiger and an overview of its genomic variants. With this report they can discover single nucleotide and large structural variants within the two genomes (Reddy, 2018). This can help conservationists understand why certain tigers are surviving. Thus, using the genomes of tigers is just the start. Using tiger’s genomes to help conservationists is just a small part of the genomic world. This research can open the doors to studying the genomes of different subspecies and possibly slowing down the processes of extinction.

Therefore, human and animal genomes can be directly compared together and because of this topical genomics can open new doors to help alleviate new or worsening issues. Worms may not seem to be a large threat or issue, but they are parasitic and cause infectious or communicable disease which is an illness caused by another living agent (Jonathan, 2015) . These studies show a direct correlation of the comparison of human and animal genomes. Studies have previously sequenced human genomes to find drugs to eradicate or alleviate issues. By sequencing the worm genomes researchers can compare humans to the worms. If researchers continue to compare both genomes, topical genomics can help find new ways to resolve issues with disease and immunology. The second set of studies done on the tigers can be a stretch, but does show a significant discovery for both the genomes. By sequencing the tigers’ genomes, the researchers were able to find evolutionary genes that kept certain species alive. When new diseases arise, and outbreaks occur scientists try to find people who are not affected by the disease. Studies are done on the individuals that are immune in order to try and find a cure. If we can sequence their genomes to find an evolutionary gene or trait we can try to quickly find faster ways to prevent the disease. All in all, topical genomics can help scientists with multiple issues. From diseases to conservation acts, topical genomics is wide spread and a gift sent from above. New technologies are always arising, but don’t necessarily help with multiple and different issues and topical genomics does. New doors and opportunities are happening now thanks to topical genomics, and it helps me believe that one day disease and conservation issues will no longer be a threat to us.

Figure:



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