Submission - China Tribunal

Maya Mitalipova, PhD
Director of Human Stem Cell Laboratory,
Whitehead Institute for Biomedical Research, MIT
455 Main St, Cambridge, MA 02451
tel: 617-777-4692
email: mitalipo@wi.mit.edu
Fax: 617-258-6505

We know now from credible sources that entire population of Uighurs, Kazakhs and other Muslims in Xinjiang Autonomous Region Of China, had been forcefully health checked and the blood samples were withdrawn since 2016 to date. These procedures were not performed to Han Chinese population of Xinjiang, but only to Muslim population.
The entire Muslim's population blood was used for DNA sequencing.
DNA sequencing is a critical biological technique utilized in laboratories. By using this, we are capable of investigating various diseases and genetic illnesses. Additionally, many mutations are initiated by faulty genetic sequencing. Scientists can gain epidemiological data with multiple genomic candidates. Meaning, genomic sequencing (in clinical trials) can provide convenient information in treatment development. Below are specific advantages of DNA sequencing:

- DNA sequencing has exhibited much importance in disease discovery, novel treatment, forensics, and human understanding. By using genetic sequencing, we are capable of exploring mysteries in many aspects of biology/life.

But, the question remains unanswered: what for Chinese government is using million people's DNA sequenced data? It is very expensive procedure to perform DNA sequencing on such large scale. So, there has to be a very valid pay back outcome.

For successful organ transplantation doctors rely on several important criteria including three main blood tests, cell surface tests and limited DNA tests to determine if a patient and a potential donor are a match.
Now scientists have come up with a comprehensive DNA scoring system using many genes to predict long-term success of transplantation.

Current genetic tests detect differences in DNA sequences at just a few specific locations in the genomes of transplant recipients and their organ donor. The fewer differences, the better the chance of long-term acceptance of the new organ. But scientists reasoned that a much larger scale collection of DNA data for a large number of genes would give a better indication.

Group of researchers study it by taking large samples from 53 pairs of kidney donors and recipients, developed a computational method that assigned a DNA score to each pair based on mismatches in their DNA sequences. They followed the progress of the patients following transplantation surgery over several years and found that the score

significantly predicted the success of the transplanted kidneys. These data showed that there is a need to more future studies to build on this new concept to confirm the initial observations which may lead to using this new concept of DNA sequencing in the clinic to optimise the matching of donor and recipients before transplantation.

The researchers say that any process that improves the success rate of transplants will also take pressure off the shortage of kidneys for transplantation. A major contributor to shortages are patients who have to go back on the waiting list after an organ has failed.

Over the last two decades, more than 300 000 solid organ transplantations have been performed in the United States alone. However, despite improvements in surgical techniques and the development of more effective immunosuppressant therapies, allograft rejection still affects 60% of transplanted individuals and remains one of the major risk factors of graft loss. Up to 40% of graft recipients experience some form of rejection within the first postoperative year, with lung and heart recipients showing the highest rates of rejection, with 55% and 25% of patients, respectively, and kidney and liver the lowest, with 10% and 17% of patients experiencing rejection, respectively. Rejection can occur where genetic disparities exist between donors and recipients, which may lead to presentation of polymorphic peptides that the recipient's immune system recognizes as non-self. Although key HLA loci have traditionally been considered to be the main contributor to the genetic variability of allograft rejection, some degree of rejection still occurs in HLA matched sibling transplantations, which may be the result of non-compatible loci beyond HLA between donor and recipient. Indeed, new findings indicate that non-HLA polymorphisms can impact upon transplantation outcomes since they have the potential of generating histo-incompatibilities influencing allograft rejection, and impacting immunosuppressant responses. Approximately 3.5 million common and rare polymorphisms exist between two unrelated individuals of European ancestry and up to 10 million variants in individuals of African ancestry. However, investigations of non-HLA genetic determinants of clinical outcomes following organ transplantation have yet to be performed in any systematic fashion to date. Recent technological advances in genomics such as genome-wide association studies (GWAS) allow the characterization of hundreds of thousands to several million single nucleotide polymorphisms (SNPs) and copy number variants (CNVs) across the human genome rapidly and efficiently. Furthermore, whole exome and whole genome sequencing, which interrogates the coding regions and the entire human genome, respectively, are quickly becoming commonly used tools within the clinical diagnostic arena. These second-generation sequencing technologies have the ability to extensively characterize genome-wide sources of histo-incompatibility between donors and recipients, potentially unraveling specific genetic risk factors influencing rejection and immunosuppressant responses or severe adverse effects.

In this article I tried to emphasize the current knowledge from existing genetics studies conducted for transplantation outcomes and therapeutic responses to immunosuppression therapies and bring to attention of the court the importance of using large cohort of DNA samples sequencing for the translational components from this genetic knowledge that may be rapidly implemented in organ transplantation field.

There is a huge direct link between DNA sequencing and organ transplantation outcome!

We know that Chinese government favors forced-organ harvesting from prisoners of conscience and this has been practised for a substantial period of time involving a very large number of victims. It is beyond doubt on the evidence presently received that forced harvesting of organs has happened on a large scale by state-supported or approved organisations and individuals. And State approved DNA sequencing of entire Muslim population of Xinjiang without informed consent is another proof of evidence that the knowledge obtain from genomic data analysis will be used to determine if a patient and a potential donor are a better match for a long-term success of transplantation.

Uyghurs detained in secretive "political re-education" camps in China's northwestern Xinjiang region may have their organs harvested for profit by the Chinese Communist Party (CCP), a former medical surgeon who was forced to carry out the procedure in 1995 told The Epoch Times.

Not surprisingly, China has the second-highest transplant rate in the world, with amazingly short transplant wait times of just two-to-three weeks.