

Genomics and COVID-19

Wishing all the readers of Polymorphism a happy new year. The journal is now three years old and taking baby steps. We thank the readers, authors and reviewers for unconditionally supporting us and take the journal forward. We continue seeking this backing in the years to come.

The year that went by was exceptional in many aspects. The world was grappled with a virus having a ~30Kb genome that took lives of millions and created a medical emergency. While the world came to a near standstill, medical science progressed at extraordinary speed to wage a war against the coronavirus SARS-CoV-2. The field of genomics provided us several weapons which were effectively used in the last 365 days and we are now at a point of tipping the outcome of the war in our favor. The year 2020 opened with the availability of the genome sequence of SARS-CoV-2 within 8 weeks of the first published case of COVID-19. This speed was unthinkable even in the last decade. Using this information, even before COVID-19 was declared as a pandemic, many countries could be equipped with molecular assays for detection of SARS-CoV-2. This became our first line of armor in this combat. The original design of the armor underwent a very rapid evolution in its design making it quick, ultrasensitive and accurate. In the beginning of 2020, we had assays which took hours to detect the virus, and by the end of 2020 we are equipped with assays which can do molecular detection of SARS-CoV-2 in minutes (<https://pubmed.ncbi.nlm.nih.gov/33025503/>, <https://pubmed.ncbi.nlm.nih.gov/33244462/>, <https://pubmed.ncbi.nlm.nih.gov/33181329/>).

The genome sequence of the virus also

allowed cloning and expression of individual viral proteins, which fueled the development of rapid antigen/antibody tests for point of care screening for SARS-CoV-2 (<https://pubmed.ncbi.nlm.nih.gov/32621814/>). Both these resulted in a massive wave in the biotech business. In 2020, the global COVID-19 diagnostics market size was valued at USD 19.8 billion. By 2027, this is expected to grow at a compound annual growth rate (CAGR) of 3-5% and projected to reach USD 4.63 billion. The readiness of smart testing solutions for COVID-19 alone is expected to boost market growth in the immediate future. As of today, the vast sums of capital needed to support the biotech industry are in place and several brilliant scientists are coming forward to translate their ideas into clinical application. Indeed, we are seeing a revolution in the way genomic diagnostics is transforming our lives in real time.

As the pandemic spread from one country to another, the genomic identity of SARS-CoV-2 was getting documented and made publicly available in a near real time fashion. This information became useful in tracking natural course of the virus and provided a quick yet accurate estimate of its genetic evolution in humans. The parallel documentation of the SARS-CoV-2 genome from all the parts of the world allowed epidemiologists to accurately pinpoint geographical hotspots and take emergency measures to flatten the rising curves and save lives (<https://pubmed.ncbi.nlm.nih.gov/33316947/>, <https://pubmed.ncbi.nlm.nih.gov/33189939/>).

Armed with the genome information, the cloning and expression of all the SARS-CoV-2 proteins aided to probe the host pathogen interactions

(<https://science.sciencemag.org/content/370/6521/eabe9403>). This not only fueled us with the road maps of disease pathogenesis, but also led to the identification of novel drug targets and repurpose existing drugs to defeat the virus. Computational and structural biologists used this information to predict the structures of viral proteins and identify several drugs, some of which were even sued in clinical trials in early days of the pandemic (<https://pubmed.ncbi.nlm.nih.gov/33371846/>).

It is historical that the vaccine is launched and made available for public use in less than a year of the discovery of the virus. Thanks to the genome technologies which equipped the immunologists with effective tools and made the DNA and RNA based vaccines available for public use in a very short span of time. The near real time information on the genetic diversity of SARS-CoV-2 is also helping the pharmaceutical industry to ensure that vaccine remains effective at the global scale. It is also aiding the policy makers to develop strategies on how the vaccines must be administered at the population scale.

Parallel to the information on viral genome, the readily available human transcriptome data (mainly single cell transcriptomes) allowed researchers to predict viral tropism at the cellular level, tissue level (<https://pubmed.ncbi.nlm.nih.gov/32578263/>, <https://pubmed.ncbi.nlm.nih.gov/32413319/>) and even organismal level (<https://pubmed.ncbi.nlm.nih.gov/32946807/>, <https://pubmed.ncbi.nlm.nih.gov/33125439/>). Thanks to the researchers that had made the tissue-wide cell type specific transcriptome data of almost all human tissues publically available. Using this data, researchers identified the tissues which express the primary receptors and necessary factors involved in SARS-CoV-2 infection. Should the virus cross the lungs, we can accurately judge the extra-pulmonary

tissues that could act as reservoirs for SARS CoV-2

(<https://pubmed.ncbi.nlm.nih.gov/32861070/>).

This data provided an explanation for multi-organ involvement seen in patients with SARS-CoV-2 infection and clinicians can use this information to develop effective treatment and management modalities of this disease. This data also helped us to predict if the virus can also be transmitted from the mother to child congenitally

(<https://pubmed.ncbi.nlm.nih.gov/32974340/>).

You would agree that reaching this stage would not have been possible had we not capitalized in genomics. The investments in high-throughput technologies and computational tools along with a broad knowledgebase in genomics have paid their dividends in 2020. We are emerging victorious against the notoriously dangerous 30 Kb genome. With our past experience on the natural course of other respiratory viruses, in the absence of genome technologies, it would have been impossible to defeat SARS-CoV-2 in such a short span of time. We all owe a gratitude to the thousands of known and unknown scientists who contributed to the discovery of nucleic acids and technologies to probe them. We must continue sharpening our genomics tools to keep prepared to tackle unknown genomes in an even more rapid and effective way than how we handled SARS-CoV-2.

We, on behalf of the editorial board of Polymorphism, once again wish you a happy, rewarding and technology rich 2021.

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Associated editors

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