Genomics Paper

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Topic’s title :

The diagnosis of the genome of CLL (chronic lymphocytic leukaemia) using the nanopore sequencing.

Abstract :

The considerable clinical and biological heterogeneity had characterised the CLL genome with some genomic alterations, like for example the TP53 mutations, IgHV mutational status and the deletion of chromosome 17P, and it has an impact on the response to chemo-immunotherapy and targeted agents. That makes the diagnostic for these biomarkers a priority in the clinical guidelines (both national and international).
The current methods for this diagnostic screening is not the best thing in case of the cost, speed and sensitivity. Even the second-generation sequencing methods have some technical limits due to the short-read lengths and bioinformatics analysis.
The oxford Nanopore technologies execute around (1-100kbp) read-length in a very short time and a low cost which makes it a great way to diagnose this genome.
In this paper I will summarize the original article where they presented the reading of a Nonpore sequencing for a single patient in a one sequencing run. They sequenced about 11 CLL patients and were able to diagnose the full dataset for all of them.
They concluded at the end that using the Nanopore sequencing has an accurate execution in the chronic lymphocytic leukemia genome case with low cost and short period of time, which could be applied to other cancer types.

Introduction :

The chronic lymphocytic leukemia (CLL) is characterised by clinical and biological heterogeneity. Specifically, the percentage of igHV caused by AID activity in the secondary lymphoid organs. Besides, there is a strong connection between chemo-immunotherapy resistance and the disruption of TP53, either through the deletions of 17P chromosomes or from clonal or sub-clonal mutations in the TP53 DNA-binding domain.
Finally, there is an increment in the evidence that acquired GC (genomic complexity), they are associated with poor response to targeted agents such as BCR and BCL2.
These predictive biomarkers have been a priority in both national and international guidelines.
Anyway, the current diagnostic methods such as FISH for the deletion of 17P case, or sanger sequencing for the TP53 and the IgHV genes, and the karyotyping of lymphocytes have a lot of drawbacks in the overall cost,speed,sensitivity and quality.
The short-read next-generation sequencing has a great role to determine genomic changes in cancer. However, there are some technical challenges when it comes to these short-read next-generation sequencing.
That’s why single-molecule/ third-generation sequencing, such as the MinION platform offered by Oxford Nanopore Technologies enables the sequencing of native DNA with the length of (1-100kbp). This will make an ideal result with low cost, rapid sequencing and maintenance.
This is what I will summarize about in this current study, the way they developed Nanopore testing for patients with chronic lymphocytic leukemia, giving a full diagnostic for a whole genome dataset.