Characterization of clonal heterogeneity in Chronic Lymphocytic Leukemia

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Résumé

Chronic lymphocytic leukemia (CLL) is the most common adult leukemia in adult and results from the abnormal proliferation of mature B cells that accumulate in the blood, bone marrow and secondary lymphoid organs.
Recently, **next-generation sequencing (NGS)** has shown that some patients exhibit **clonal heterogeneity** when the **VDJ genes** encoding the variable region of the B-cell receptor are analysed. This heterogeneity is characterised by the presence of major and minor clones in the global leukemic mass but not considered in treatment, which targets only major clones, leaving a selective advantage to minor clones, which may be more aggressive and lethal to patients.
The aim of our study is to better characterise the clonal heterogeneity in the global CLL leukemic mass, by using a new **bio-informatics** approach to obtain the full-length VDJ sequence in order to analyse the clone's abundance and the mutational profile.

Mots-Clés: CLL, Heterogeneity, Immune repertoire, Bioinformatics, VDJ sequences

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