

Received: 20 May 2019 | Revised: 19 August 2019 | Accepted: 21 August 2019

DOI: 10.1002/gcc.22806

REVIEW ARTICLE

WILEY

Clonal evolution of acute myeloid leukemia from diagnosis to relapse

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Abstract

Based on the individual genetic profile, acute myeloid leukemia (AML) patients are classified into clinically meaningful molecular subtypes. However, the mutational profile within these groups is highly heterogeneous and multiple AML subclones may exist in a single patient in parallel. Distinct alterations of single cells may be key factors in providing the fitness to survive in this highly competitive environment. Although the majority of AML patients initially respond to induction chemotherapy and achieve a complete remission, most patients will eventually relapse. These points toward an evolutionary process transforming treatment-sensitive cells into treatment-resistant cells. Available to the Clinical Decision-Making platform.