Researchers highlight genomics' potential in cancer research

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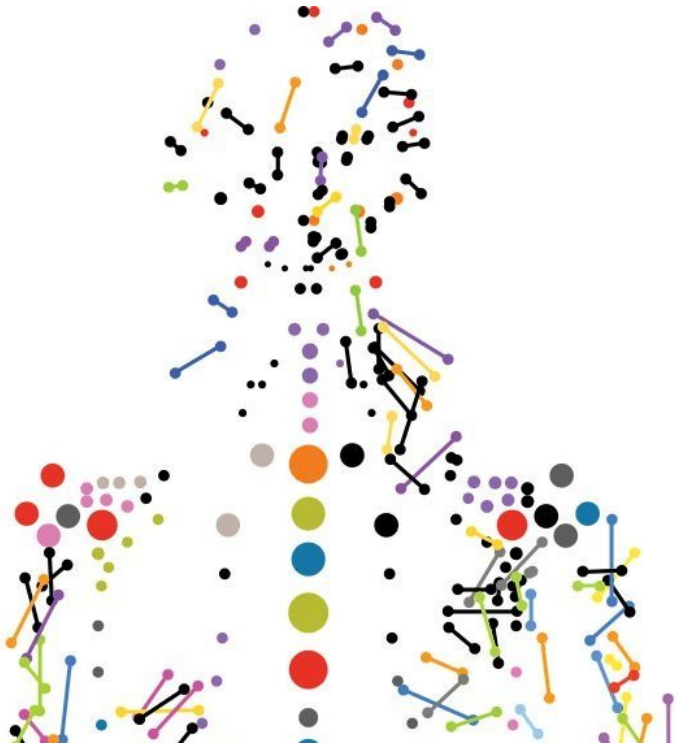

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A new editorial paper titled "Genomics has more to reveal" has been published in *Oncotarget*.

In this new editorial, researchers Laurène Fenwarth and Nicolas Duployez from the University of Lille and CHU Lille discuss molecular

and cytogenetic analyses that are now used to identify mutations and structural variants defining distinct subtypes of acute myeloid leukemias (AML) and myelodysplastic syndromes (MDS). These genetic considerations have become essential for risk stratification and the selection of appropriate treatments, including the use of allogeneic hematopoietic stem cell transplantation.

"Despite over 15 years of genomic research since the first publication of the AML genome and large studies like The Cancer Genome Atlas (TCGA), around 15% of AML cases remained genetically unclassifiable with current knowledge," write the researchers.

Notably, several studies in both adults and children identified a subset of AML without known initiating events but particularly enriched in FLT3-ITD and WT1 mutations, and normal karyotypes with an overall unfavorable prognosis. In 2021–2022, notably thanks to advancements in bioinformatic approaches and tools, recurrent somatic tandem duplications (TD) of a portion of the UBTF gene were identified in high-risk pediatric AML cases.

"With increased screenings of retrospective cohorts, the characteristics associated with this molecular alteration have since been confirmed. UBTF-TD are considered initiating events in leukemogenesis and define a distinct entity of myeloid malignancies," the researchers add.

More information: Laurène Fenwarth et al, Genomics has more to reveal, *Oncotarget* (2024). DOI: 10.18632/oncotarget.28596

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