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A new integrative procedure to identify and explore new RNA in myeloid leukemia: From software development to biological markers validation

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The comprehensive analysis of expression profiles based on RNA-seq provides unprecedented sensitivity for exploring transcriptome in all its complexity. The difficulty lies in the ability to detect and extract rigorously this type of information before biological validations. To this end, we have developed a new program called Crac, more efficient than the tools currently used in the field and which is based on an innovative algorithm and on double indexing the human genome and RNA-Seq data (crac.gforge.inria.fr/: Philippe et al, 2013). It allows extracting with high specificity and sensitivity, all the biological transcriptional events irrespective of annotation (substitutions, indels, splice junctions, potential chimeric RNAs…). The strong point of our approach is the ability to use our own program Crac for categorizing transcripts variants specifically new splice junctions and chimeric RNAs which could have a role in the establishment of tumor mechanisms, and to use a new integrated transcriptome analysis procedure for the characterization and the discovery of new non-coding RNAs (ncRNA) combining data from both RNA-seq and Digital gene expression (DGE) in order to identify transcriptional abnormalities, not only in assessing changes in gene expression, but by analyzing the complete repertoire of transcription. Applications in the study of myeloid leukemia are currently done. Investigating the biological features of novel chimeric RNA and ncRNA candidates with such combinatorial approach is an interesting and challenging goal to achieve as it can pave the way for identifying the new potential prognostic and diagnostic biomarkers.

Biography

After 2 years of researcher position in the anticancer centre in Montpellier, Commes Therese was recruited as Assistant Professor (1992-2007) and as Professor in 2007 at the University Montpellier 2. Head of the group "Transcriptomics, bioinformatics and myeloid leukemias" at INSERM U1040-Montpellier, he is involved in interdisciplinary projects since 2005. Since 2012, he is involved in the advisory board of the "Computational Biology Institut (IBC)" (Director: O Gascuel) and in the management of the program "Methods for high-throughput sequencing analysis" with E Rivals (http://www.ibc-montpellier.fr/wp/wp1), Advisory board of the Montpellier-Genomic platform (MGX) and the Bioinformatics platform (ATGC, LIRMM, ReNaBi), member of the FRANCE GENOMIQUE Bioinformatics network (WP"RNA-seq"). Contribution to the creation and consultant of the Skud-tech company.

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