Peritumoral tissue is a promising source of prognostic biomarkers

Dzenis Koca[1], Joël Lemaoult*[2], and Laurent Guyon†‡[1]

[1]BioSanté, IRIG, CEA/INSERM/UGA – CEA, Institut National de la Santé et de la Recherche Médicale - INSERM, Université Grenoble Alpes, UGA – France
[2]Hemato-Immunology Research Department, Francois Jacob Institute of Biology – CEA – France

Résumé

Traditional medicine often employed a "one treatment fits all" approach, wherein patients were treated based on displayed symptoms. The advent of digital technologies and advancements in data collection, storage, analysis, and comprehension, particularly in cancer science, holds the promise of a more personalized approach to treatment, known as precision medicine. The premise of precision medicine, primarily with regard to cancer, is that treatment should be tailored to more precisely fit the patient. One of the cornerstones of precision medicine lies in accurate risk assessment, mirrored in the correct prognosis of the patient's outcome. The result of correct risk assessment is a treatment that reflects the severity of the disease.
While emerging survival prediction models mostly rely on clinical information (tumor stage, grade,...) supplemented with genomic data from tumors, many of these models struggle to transition to the clinical setting. This limited success may stem from factors such as high intratumoral heterogeneity and the failure of biomarkers to significantly contribute to prognosis based solely on clinical characteristics. Recent studies have revealed the potential of Peritumoral tissue (PTT) as a promising source of prognostic biomarkers. PTT offers complementary information and, in some cases, surpasses the prognostic capacity of tumor tissue-based biomarkers (Huang et al., SciRep 2016; Oh & Lee, Cancer Medicine 2023; Kim et al., Journal of Translational Medicine 2023).

To enhance our understanding of the predictive capacity of peritumoral tissues in clear cell renal cell carcinoma (ccRCC) and discover novel prognostic biomarkers, we applied a systematic approach in order to investigate predictive biomarkers in peritumoral tissue. This process involved re-analyzing molecular data from multiple patient cohorts and various OMIC technologies. Our findings indicate that prognostic models based on PTT exhibit greater transferability between different patient cohorts, and result in more precise survival-prediction and complement models built solely on tumor tissue data. Moreover, we generated a single cell atlas of PTT, carefully merging various public datasets. This new improved single cell dataset further helped the deconvolution of bulk transcriptomes to identify the proportion of cell types to propose a hypothesis for aggressive ccRCC cancers.

Other related reference

*Auteur correspondant:
†Intervenant
‡Auteur correspondant: laurent.guyon@cea.fr

Koca, D., Abedi-Ardekani, B., LeMaoult, J., & Guyon, L. (2024). **Peritumoral tissue (PTT): increasing need for naming convention. British Journal of Cancer**, 131(7), 1111-1115.

Mots-Clés: Kidney cancer, Survival, Peritumoral tissue, Prognostic biomarkers