Project 7.1. Molecular characteristics of the response to neoadjuvant chemotherapy in patients with locally advanced soft tissue sarcomas

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Background:

      Soft tissue sarcomas (STS) are rare solid tumors of mesenchymal cell origin. They represent approximately 1% of all adult malignancies and 15% of pediatric malignancies. These tumors develop from fat, muscle, nerves, blood vessels, and other connective tissues. Multiple histologic subtypes of STS have been identified, with the most common undifferentiated pleomorphic sarcoma (UPS), liposarcoma (LPS), leiomyosarcoma (LMS), or synovial sarcoma (SS). These subtypes are included in our study. Genomic parameters of sarcoma tissue will be analyzed as at treatment initiation (fusions and mutations) and after treatment (mutations). Presence of fusions in sarcoma cells may be used in diagnosis enhancement **(initial diagnostic biomarker)**. When defined and validated, these molecular biomarkers (fusions and mutations) characterizing sarcoma tumor tissue at treatment start may be potentially used in treatment efficacy **(predictive biomarker)** or general overall survival of the patient **(prognostic biomarker)** anticipation. Dynamic tumor feature, changing upon treatment (mutation load), may be also used as biomarker indicating not only treatment efficacy **(final diagnostic)** but also in selecting future (second line) treatment candidates **(predictive biomarker).** **Biomarkers** used as diagnostic and prognostic or predictive and prognostic purposes will be called BINARY.
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Aim:

      The project aims to define novel molecular binary biomarkers of soft tissue sarcoma (STS) multimodal treatment.

Requirements:
- MSc in biology, chemistry, biotechnology, medical biology or related sciences
- Knowledge of molecular oncology and development of biomarkers
- Necessary practical knowledge of laboratory techniques used in molecular biology, including nucleic acid isolation techniques, Western Blot, qPCR and NGS techniques
- Basic skills in working with the RNAseq technique and in analyzing the transcriptome will be an advantage
- Necessary knowledge of practical statistics in in vitro and in vivo tests and dedicated software for analyzes
- Knowledge of the issues of statistical analysis along with the ability to use statistical programs (e.g. SPSS, Statistics, R Studio, Jamovi) will be an additional advantage
- Knowledge of R or Python software would be an advantage
- Ability to document work: creating scientific publications, writing reports
- Motivation for scientific work, supported by previous scientific activity (participation in conferences, internships, publications, membership in scientific societies).
- Authorship or co-authorship in a monograph chapter or a scientific publication in a peer-reviewed journal, confirmed by the presentation of at least 1 scientific work

- Ability to prepare research results for publication and presentation at conferences confirmed by a conference report as a presenter (in English)
- Good English language skills, allowing free communication in speech and writing confirmed by a university degree (that may be verified during interview) or a language certificate at a level not lower than B2
- Ability to work under time pressure

Nice to have:
- Ability to work in a multidisciplinary research team
- Reliability, meticulousness and independence in research work
- Enthusiasm, openness, scientific curiosity
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