We propose the following project for a master student:

**Involvement of long non coding RNA (LncRNA) in tumor microenvironment of breast cancer**

Breast cancer constitutes the most prominent forms of cancer in women. The aggressiveness of these cancers is mostly due to the arising of metastases, which will lead to the death of the patients. Both in the primary tumor and in the metastatic site, it appears that the role of tumor microenvironment and in particular of inflammation is essential.

In particular, the dialog between tumor cells and cells of tumor microenvironment such as cancer associated fibroblasts (CAFs), endothelial cells and immune cells will dictate the fate of the tumor and its ability to metastasize.

The goal of the project is to study the involvement of long non coding RNA (LncRNA) in the context of breast tumor microenvironment. LncRNAs represent the largest and most diverse class of non-coding transcripts in the cell. Current studies suggest the presence of up to 60,000 lncRNA genes in the human genome. LncRNAs are defined by length (>200 nt) and can be capped, spliced and polyadenylated, but lack a significant open reading frame. LncRNAs have been implicated as regulatory molecules in a variety of cellular functions, including epigenetic gene regulation, splicing, mRNA stability and translation. Our aim is to identify LncRNA in the most aggressive subtypes of breast cancer and determine to which extent, they contribute to their properties in terms of proliferation, invasion, and metastasis, by in vitro and in vivo assays. In parallel, the relevance of the identified LncRNA will be determined on tumor samples from patients and their impact on the outcome of the patients will be evaluated. This will offer the possibility to propose novel strategies to target breast cancer.

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