"Study Of Secondary Cancers In Patients With Hereditary Retinoblastoma; Design Of A Strategy Based On Liquid Biopsy For An Early Diagnosis And Adequate Follow-Up (RET-LB Project)"

EURbG Meeting

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The problem we would like to face: secondary malignancies

- Improvements in the treatment and follow-up of **hereditary retinoblastoma** children have resulted in a growing population of adult **survivors**.
- However, hereditary retinoblastoma survivors have a significantly increased risk of **secondary malignancies**. This is a major concern for patients and families.
- Their onset follows a somehow ordered temporal logic, conditioned by the type of therapy received previously for retinoblastomas.
- Some of these tumors are: leukemias, Ewing sarcoma, osteosarcomas, leiomyosarcomas and other soft-tissue sarcomas, melanoma, and epithelioid tumors.





What we propose to do: NGS-based test in liquid biopsy for early detection

Generate a genomic and epigenomic radiography of the most frequent secondary neoplasia appearing in the context of hereditary retinoblastoma.

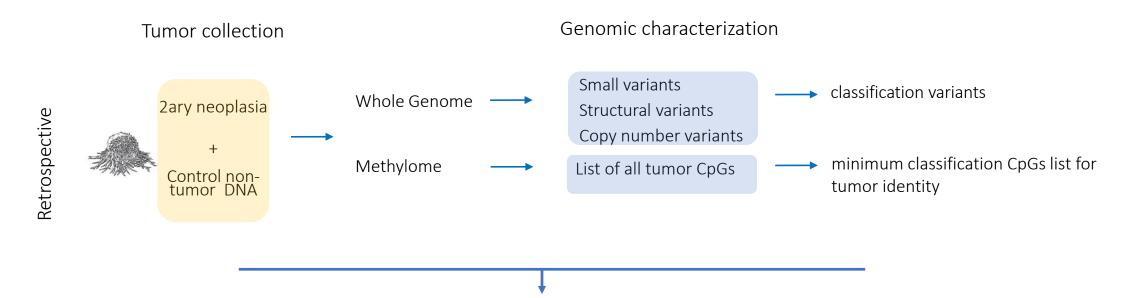
 Develop a combined genomic and epigenetic test using nanopore NGS sequencing for a differential diagnosis.

 Perform a proof of concept analysis using DNA mixtures resembling real proportions of tumor DNA in plasma.

Analyze real liquid biopsies from patients with hereditary retinoblastoma.







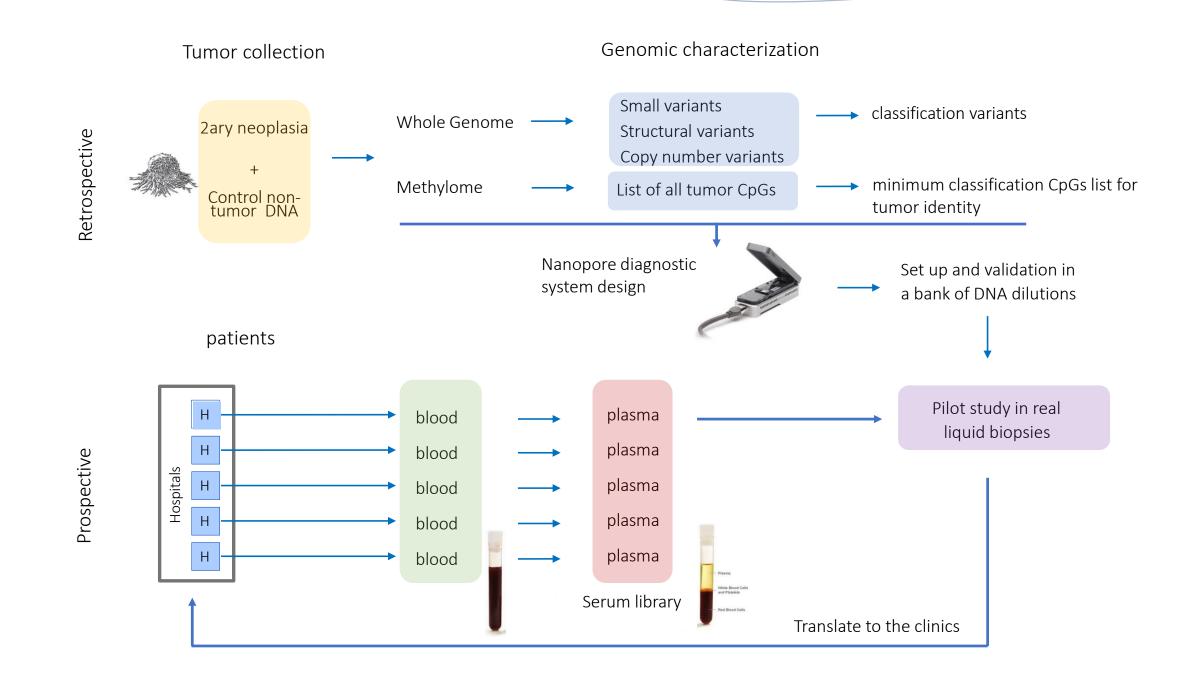
- Obtain a list of genomic regions and a list of CpGs to set up the test
- This information must allow the identification of all secondary neoplasia characterized
- This information must allow the differential diagnostic among them.

Nanopore diagnostic system design









Current teams involved





















Open to collaborate/participate

In the retrospective part:

Share genomic data on secondary neoplasia Provide samples, either DNA or tissue

In the prospective part:

Share your experience in liquid biopsy

Share your experience in liquid biopsy sequencing

Provide liquid biopsy samples

- In any other way you like
- We can offer:

Open to incorporate new teams into the project Open to share genomic data produced Provide genomic analysis of new samples





Contact

Research issues

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Organization issues

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