TRANSLATIONAL DERMATO-ONCOLOGY

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SUMMARY & MISSION STATEMENT

Our group applies the latest omics tools to translational research questions in order to identify better predictive biomarkers for precision medicine as well as novel targets in late stage melanoma.

OVERVIEW

We are interested in using functional genomics tools to understand the evolution of heterogeneity in skin cancer progression. In particular, we apply next-generation sequencing approaches to melanoma and other skin cancers. Some of the online tools we have developed are here Link. With access to one of the largest live-cell melanoma biobanks in the world, we have a unique resource in which to study the functional mechanisms of cellular heterogeneity and how these respond to various therapeutic regimens. More information about the biobank can be found here Link.

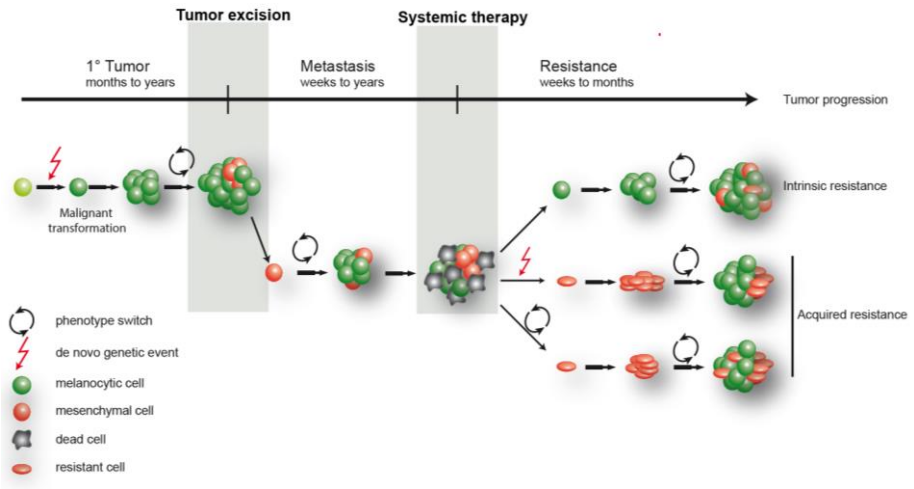
SELECTED CANCER RELATED PUBLICATIONS

Widmer, DS, Hoek, KS, Cheng, PF, Eichoff, OM, Biedermann, T, Raaijmakers, MIG, Hemmi, S, Dummer, R, and Levesque, MP. (2013). Hypoxia contributes to melanoma heterogeneity by triggering HIF1α-dependent phenotype switching. **Journal of Investigative Dermatology** March 8. doi: 10.1038/jid.2013.115).

Das Thakur, M, Salangsang, F, Landman, AS, Sellers, WR, Pryer, NK, Levesque, MP, Dummer, R, McMahon, M, and Stuart, D. (2013). Modeling vemurafenib resistance in melanoma reveals a strategy to forestall drug resistance. **Nature** doi:10.1038/nature11814.

Cheng, PF, Shakhova, O, Widmer, DS, Zing, D, Benedetta, B, Raaijmakers, MMI, Eichoff, OM, Goldinger, SM, Hemmi, S, Hoek, KS, Sommer, L, Dummer, R, Levesque, MP. (2015). Methylation dependent SOX9 expression mediates invasion in human melanoma cells and is a negative prognostic factor in advanced melanoma. **Genome Biology** 16: (1) 42.

Krieg, C, Nowicka, M, Guglietta, S, Schindler, S, Hartmann, FJ, Weber, LM, Dummer, R, Robinson, MD, Levesque, MP*, Becher, B*. (2018). High-dimensional single cell analysis predicts response to anti-PD1 immunotherapy. **Nature Medicine** 24, 144–153 (2018) doi:10.1038/nm.4466 *Shared authors



Phenotype Switching Model of melanoma development. De novo events induce oncogenic and tumor suppressor mutations that convert a benign melanocyte into a melanoma cell. Most of these initial melanoma cells are melanocytic in nature (green), but a phenotype switch as the result of microenvironmental stresses (such as hypoxia, tumor lymphocyte infiltration, etc) or therapeutic intervention can induce mesenchymal features (red). The role of that switch in tumor progression and therapeutic resistance is the main focus of our research.