

Functional Genomics

CANCER RESEARCH WITH MICE AND FLIES



COMBINE

From flies to humans combining whole genome screens and tissue specific gene targeting to identify novel pathways involved in cancer and metastases

Programm: 7. EU-Rahmenprogramm für Forschung, technologische Entwicklung und Demonstration

Förderlinie: ERC

Projekttyp: Einzelprojekt

Projektkosten: 2,5 Mio. Euro, davon 2,5 Mio. Euro EU-Förderung

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Projektkoordinator: IMBA Institut für Molekulare Biotechnologie der Österreichischen Akademie der Wissenschaften

Cancer care will be revolutionized over the next decade by the introduction of novel therapeutics that target the underlying molecular mechanisms of the disease. The primary goal of the project is to use functional genomics in *Drosophila* and mice to understand cell transformation, invasion, and cancer metastases of epithelial tumors.

With the advent of human genetics, a plethora of genes have been correlated with human diseases such as cancer the SNP maps. Since the sequences are now available, the next big challenge is to determine the function of these genes in the context of the entire organism. Genetic animal models have proven to be extremely valuable to elucidate the essential functions of genes in normal physiology and the pathogenesis of disease. Using gene-targeted mice we have previously identified RANKL as a master gene of bone loss in arthritis, osteoporosis, and cancer cell migration and metastases and genes

that control heart and kidney function; wound healing; diabetes; or lung injury. Our primary goal is to use functional genomics in *Drosophila* and mice to understand cell transformation, invasion, and cancer metastases of epithelial tumors.

The following projects are proposed:

- Role of the key osteoclast differentiation factors RANKL-RANK and its downstream signalling cascade in the development of breast and prostate cancer.
- Requirement of osteoclasts for bone metastases and stem cell niches using a new RANK^{flox} allele; function of RANKL-RANK in local tumor cell invasion.
- Role of RANKL-RANK in the central fever response to understand potential implications of future RANKL-RANK directed therapies.
- Integration of gene targeting in mice with state-of-the art technologies in fly genetics; use of whole genome tissue-specific in vivo RNAi *Drosophila* libraries to identify essential and novel pathways for cancer pathogenesis using whole genome screens.

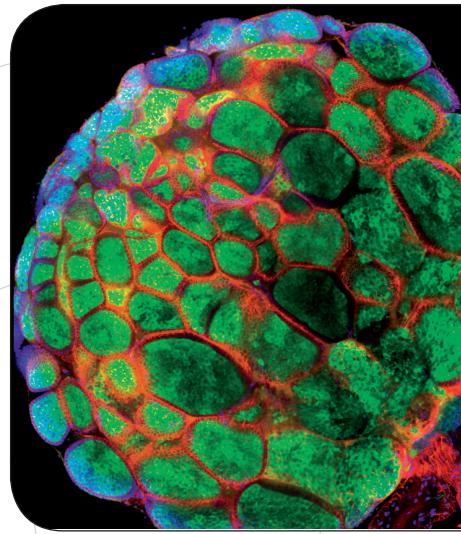
SERVICE

Ihr **Wegweiser** durch die Europäischen und Internationalen Programme:
Information, Beratung, Coaching von der Projektidee bis zum Projektabschluss
bieten Ihnen die ExpertInnen der FFG.

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Projektkoordinator
Josef Penninger



Fotos: IMBA

- Role of TSPAN6, as a candidate lung metastasis gene. Identification of new cancer disease genes will allow us to design novel strategies for

cancer treatment and will have ultimately impact on the basic understanding of cancer, metastases, and human health