



SFB 1027 - Seminar

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Melanoma preclinical studies: how to use models to improve discovery

The landscape for personalized therapy in melanoma is expanding with an increasing number of inhibitors available, a rising number of combination strategies being investigated, and a growing spectrum of genetically distinct lesions being unraveled. Additionally, the contribution of the tumor microenvironment in modulating malignant biology and treatment response can no longer be ignored. Thus, we must integrate knowledge gained from multiple disease models in order to make significant and patient-relevant discoveries. Our laboratory routinely uses a pipeline of increasingly complex melanoma models to conduct biological and preclinical studies. This approach allows us to prioritize inhibitors for further study and to identify compounds that could be most effective in more physiological environments. Such is the case for PI3K pathway inhibitors that are more effective against melanoma cells grown as 3D spheroids than adherent cultures. In vivo studies confirm the anti-melanoma benefits of PI3K inhibitors, and our studies now focus on further understanding the role of PI3K in melanoma pathobiology. Our pipeline also involves studies in patient-derived xenograft models where we identified novel targets for combination therapies and observed that BRAF and MEK inhibitor combinations are not always the most effective strategy in resistant BRAF mutant melanomas. We also used models of co-cultures or hypoxia in order to monitor cell heterogeneity, dynamics, and stem-like behavior and showed that melanoma cells grown in the presence of tumor-associated B cells express higher levels of stem cell-associated markers. Finally, we suggest that more complex models of melanoma are necessary to fully understand the disease and to develop effective treatment strategies.

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Campus Homburg, Geb. 60, HS

Der Gast wird betreut von Dr. Ivan Bogeski

Alle Interessenten sind herzlich eingeladen,

Der Sprecher des SFB
Heiko Rieger

**SFB 1027 Physikalische Modellierung von Nicht-Gleichgewichtsprozessen
in biologischen Systemen**