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The oncopig cancer model: An innovative large animal translational platform for addressing unmet clinical needs

Despite an improved understanding of cancer molecular biology, immune landscapes, and advancements in cytotoxic, biologic, and immunologic anti-cancer therapeutics, cancer still remains a leading cause of death worldwide. The development and investigation of new diagnostic modalities and innovative therapeutic tools is critical for reducing the global cancer burden. Towards this end, transitional animal models serve a crucial role in bridging the gap between fundamental diagnostic and therapeutic discoveries and human clinical trials. Such animal models offer insights into all aspects of the basic science-clinical translational cancer research continuum (screening, detection, oncogenesis, tumor biology, immunogenicity, therapeutics, and outcomes). To date, however, cancer research progress has been markedly hampered by lack of a genotypically, anatomically, and physiologically relevant large animal model. Our group developed a transgenic porcine model - the oncopig cancer model (OCM) - as a next generation large animal platform for addressing unmet clinical needs. The OCM recapitulates transcriptional hallmarks of human disease while also exhibiting clinically relevant histologic and genotypic tumor phenotypes. Moreover, as the global population becomes increasingly unhealthy, cancer patients commonly present clinically with multiple comorbid conditions. Due to the effects of these comorbidities on patient management, therapeutic strategies, and clinical outcomes, an ideal animal model should develop cancer on the background of representative comorbid conditions (tumor macro and microenvironments). The OCM has the capacity to develop tumors in combination with such relevant comorbidities. Furthermore, studies on the tumor microenvironment demonstrate similarities between OCM and human cancer genomic landscapes.

Biography

Kyle Schachtschneider, PhD, graduated with a Bachelor's in Animal Sciences from the University of Illinois at Urbana-Champaign in 2008, and received his PhD in Animal Sciences from the same institution in 2013. Following the completion of his Doctoral training, he worked as a Post-doctoral Researcher at the Animal Breeding and Genomics Centre at Wageningen University, the Netherlands performing next generation sequencing analysis to investigate genomic, epigenomic, and transcriptomic variation associated with healthy and disease states in porcine biomedical models. Following his time overseas, he joined the Department of Radiology at the University of Illinois at Chicago to develop epigenetic and bioinformatics-based projects to compliment the clinically focused research efforts of the department. He is currently utilizing multi-omics datasets to elucidate the mechanisms underlying tumor biology and the impact of the tumor microenvironment on clinically relevant phenotypes in both preclinical and clinical settings.

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