



A Porcine Model of T-cell Lymphoma

KN Kuzmuk¹, LA Rund¹, SJ Adam⁴, JF Zachary², CM Counter³ and LB Schook^{1,2,3}

¹Department of Animal Sciences, ²Pathobiology, and the ³Institute for Genomic Biology, University of Illinois, Urbana

⁴Department of Pharmacology and Molecular Cancer Biology, Duke University, Durham, NC

<http://www.swinegenomics.com>



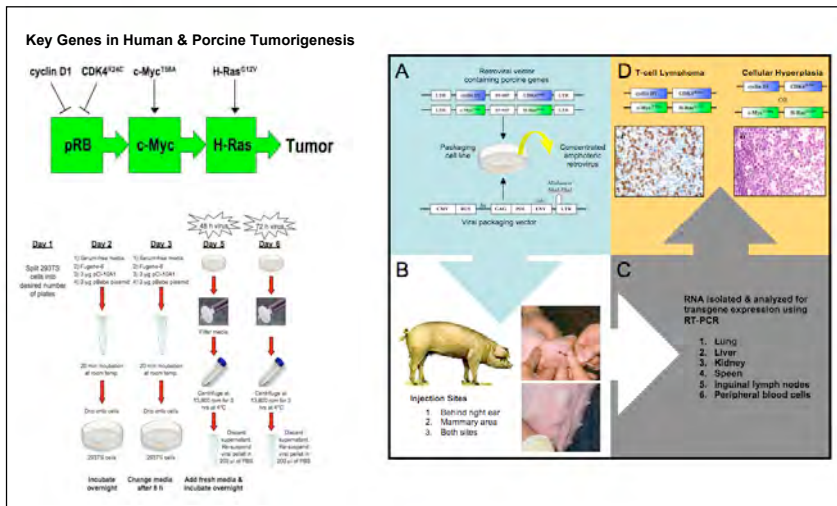
ABSTRACT

Non-Hodgkin's lymphoma (NHL) is a disease of increasingly serious proportions. The highest incidence rate in the world is seen in the United States and Canada, with forty to fifty thousand new cases per year in the U.S. NHL is the sixth most common cancer and the sixth most common cause of cancer death, accounting for 4% of all cancers and 4% of cancer-related deaths. There is a clear need for relevant animal models of lymphoma that provide preclinical tools. Our objective is to create a porcine model of lymphoma analogous to the human disease. Genetically engineered porcine tumors may prove to be invaluable for: (1) determining the efficacy of anti-cancer drugs; (2) studying the process of tumorigenesis; and (3) producing cancer in a genetically compliant animal model that is physiologically more similar to humans than rodents. We have previously shown that solid tumors could be readily induced in immunosuppressed pigs via the expression of proteins disrupting the p53 tumor suppressor pathway, and activating c-Myc and Ras pathways, all of which are commonly corrupted in human cancers. In an attempt to induce a less immunogenic tumor with a defined phenotype retroviral vectors encoding four genes (Cyclin d1, CDK 4, c-Myc, and H-Ras) were constructed and injected SC into the mammary area and/or behind an ear, or IV via the ear vein. Both challenge routes induced T-cell lymphoma in the absence of immunosuppression. The effects of vector dose responses are currently being evaluated and future studies will attempt to induce tumors in cloned animals, thus producing tumors that can be transferred to any number of identical animals to study the process of tumorigenesis and cancer

INTRODUCTION

- Current limitations in cancer biology have delayed the transition from basic science to patient benefit.
- Mouse models are the predominant choice currently for cancer studies. However, the differences between murine and human tumorigenesis and pharmacodynamics prevent adequate comparisons to human cancers.
- Achieving an understanding of the pathogenesis of lymphoma in a model similar to humans is key to developing successful treatments.
- Previous research demonstrates that solid tumors can be readily induced in immunosuppressed pigs via the expression of proteins disrupting the p53 tumor suppressor pathway, and activating the c-Myc and Ras pathways, all of which are commonly corrupted in human cancers.

MATERIALS AND METHODS



REFERENCES

- Adam SJ, Rund LA, Kuzmuk KN, Zachary JF, Schook LB, and Counter CM. (2006) Genetic induction of tumorigenesis in swine. *Oncogene*. In press.
- Rangarajan A and Weinberg RA. (2003) Comparative biology of mouse versus human cells: modeling human cancer in mice. *Nat Rev Cancer* 3(12):952-959.
- Kamb A. (2005) What's wrong with our cancer models? *Nat Rev Drug Discov* 4(2):161-165.



Acknowledgements: This work was supported in part by grants from the USDA (USDA/NRI-CSREES AG2001-35205-11698, USDA-ARS AG58-5438-2-313), Elsa U Pardee Foundation, Duke Comprehensive Cancer Center, and NIH (CA94184).

RESULTS



Table 1. Mortality rate for pigs injected with retroviruses encoding cyclin D1, CDK4^{R24C}, c-Myc^{T58A}, and H-Ras^{G12V}. Two of 16 pigs demonstrated visible signs of disease development and were found dead or euthanized prior to the endpoint of the study. Necropsies showed pigs had developed aggressive T-cell lymphoma. Remaining pigs euthanized two months after injection were also diagnosed with T-cell lymphoma, albeit a less aggressive form.

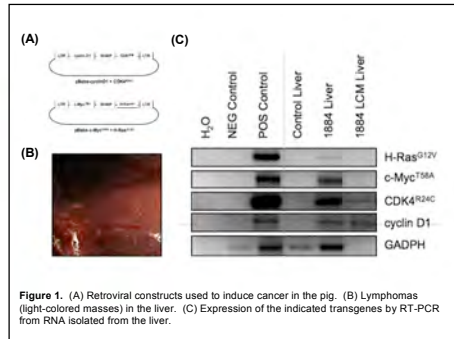


Figure 1. (A) Retroviral constructs used to induce cancer in the pig. **(B)** Lymphomas (light-colored masses) in the liver. **(C)** Expression of the indicated transgenes by RT-PCR from RNA isolated from the liver.

OBJECTIVES

- Develop methods to induce genetically defined tumor formation by altering pathways commonly disrupted in human cancers.
- Develop a porcine model of lymphoma analogous to the human disease.

CONCLUSIONS

- A porcine model of T-cell lymphoma was successfully created by genetically modifying pathways commonly disrupted in human cancers.
- This genetically compliant animal model is physiologically more similar to humans than rodents and supports adjunct therapies.
- The ability to manipulate gene expression *in vivo* and rapidly generate pathologically accurate tumors makes this model an ideal preclinical system for the generation of novel therapeutics and testing new drugs for the treatment of lymphoma and other types of diseases.
- The rapid development of novel technologies for manipulating the pig genome has allowed and will allow, in the next few years, to recreate in the pig virtually any pathological condition whose molecular basis has been elucidated in humans.

FUTURE DIRECTIONS

- Expand methods to support a preclinical model for testing of novel therapeutics, experimental therapies and imaging.
- Develop cell-based solid tumor models from known tissue of origin and with designated clinical outcomes in the absence of immunosuppression.
- Establish a porcine model for breast cancer using retroviral injection methods.
- Generate a transgenic pig model that will be used to induce tissue-specific, conditionally expressed solid tumors.
- Induce tumors in cloned animals, thus producing tumors that can be transferred to any number of identical animals to study the process of tumorigenesis and cancer phenotypes.