

Establishment and characterization of novel *PSA-Cre;PtenLoxp/LoxP* mouse prostate cancer models

P.W. van Duijn, A.C.J. Ziel-van der Made, H. Korsten and J. Trapman.

Department of Pathology, JNI, ErasmusMC, Rotterdam, The Netherlands.

Prostate cancer is a heterogeneous disease that once metastasized cannot be cured. The tumor suppressor PTEN is one of the most frequently altered genes in prostate cancer. Establishment and characterization of model systems based on *PTEN* inactivation is therefore highly relevant as a tool to study disease progression.

The previously established *PSA-Cre;PtenLoxp/LoxP* mouse prostate cancer model displays clearly defined stages of hyperplasia and cancer^{1,2}. The mixed 129/FVB genetic background of these mice however complicated biological and molecular characterization of the model. By extensive cross-breeding two novel, genetically homogeneous prostate tumor model systems, based on targeted inactivation of *Pten*, in FVB and C57Bl6/J background have become available.

Initial characterization, based on prostate weights, proliferation rates and histological examination of these novel mouse prostate cancer models showed aberrant prostate tumor development in C57Bl6/J mice as compared to FVB and 129/FVB mice. In addition, quantitative PCRs for cell type specific markers revealed a higher expression level of the basal epithelial cell marker Tp63 in the prostates of C57Bl6/J mice compared to 129/FVB and FVB mice.

From the novel FVB and C57Bl6/J *Pten* knockout models we isolated a series of *in vitro* growing cell lines. Molecular characterization revealed that all cell lines expressed K8, indicative for luminal epithelial progenitor properties. Moreover, all cell lines expressed elevated levels of p-Akt, and its downstream targets Gsk3a/b and PRAS40, as expected for *Pten* knockout models. All cell lines also expressed the androgen receptor. In conclusion, we showed that in the *in vitro* growing cell lines there is a high level of consistency concerning *Pten*/Akt signaling, even among the different genetic backgrounds.

1. Ma et al., (2005) *Cancer Research* 65(13) : 5730-9
2. Korsten et al., (2009) *PLoS One* 4(5) :e5662

The research leading to these results has received support from the Innovative Medicines Initiative Joint Undertaking under grant agreement n° 115188, resources of which are composed of financial contribution from the European Union's 7th Framework Programme (2007-2013) and EFPIA companies' in kind contribution.