



The surface marker and gene expression signature linked to plasma-induced toxicity in cancer cells – a comprehensive screening

Sander Bekeschus¹, Jonas Menz^{1,2}, Eric Freund^{1,2}, Kristian Wende¹, Thomas von Woedtke¹,
Anke Schmidt¹

¹ZIK *plasmatis*, Leibniz Institute for Plasma Science and Technology, Greifswald, Germany

²Department of General, Visceral, Thoracic and Vascular Surgery, Greifswald University
Medical Center, Greifswald, Germany

E-mail: sander.bekeschus@inp-greifswald.de

Cancer is still among the greatest medical challenges worldwide. Novel therapeutic avenues are therefore needed to increase efficacy and safety in oncological treatments. Cold physical plasma has received increasing scientific interest as such novel antitumor tool in the past years. Among the greatest challenges in the field of plasma cancer treatment is the identification of molecular determinants that correlate to plasma-induced toxicity. In a recent mRNA screening of 27 redox-related proteins, we have identified HMOX1 as a putative biomarker in eight human plasma-treated cancer cell lines from four tumor entities¹. Since oxidative stress-induced cell death was proposed to be linked with ROS homeostasis, we further examined the role of antioxidant defense and cysteine regulation, and found the cysteine transporter xCT to confer intrinsic resistance to plasma-induced cell death in melanoma cells². To broaden the scope of searching for molecular determinants associated with plasma-induced tumor cells, we have here screened 30 human cancer and non-malignant cell lines and identified their sensitivity to plasma-induced toxicity generated by the atmospheric pressure argon plasma jet kINPen. The IC₂₅ (plasma treatment time needed to inactivate 25% of the cells) was then correlated to the expression of over 30 surface markers quantified via multicolour flow cytometry, including several types of aquaporins, nitric oxide synthase, and NADPH oxidases previously proposed to be associated with plasma-induced toxicity in tumor cells. Importantly, whole genome transcriptome microarray gene expression analysis was performed for all cell lines. Bioinformatics was used to identify gene expression patterns corresponding to the sensitivity as well robustness of tumor cells to plasma-induced toxicity. These results will give the first evidence on the role of several surface markers as well as transcripts in plasma-induced tumor cell toxicity across a large array of different cancer cell lines in the field of plasma cancer treatment and plasma medicine in general.

This work was supported by the German Federal Ministry of Education and Research, grant numbers 03Z22DN11 and 03Z22DN12.

References

1. Bekeschus, S.; Freund, E.; Wende, K.; Gandhirajan, R.K.; Schmidt, A. Hmx1 upregulation is a mutual marker in human tumor cells exposed to physical plasma-derived oxidants. *Antioxidants (Basel)* **2018**, *7*, 10.3390/antiox7110151.
2. Bekeschus, S.; Eisenmann, S.; Sagwal, S.K.; Bodnar, Y.; Moritz, J.; Poschkamp, B.; Stoffels, I.; Emmert, S.; Madesh, M.; Weltmann, K.-D.; von Woedtke, T.; Gandhirajan, R.K. Xct (slc7a11) expression confers intrinsic resistance to physical plasma treatment in tumor cells. *Redox Biology* **2020**, *30*, 10.1016/j.redox.2019.101423.