Proteome-based fingerprinting of skin cancer cells after physical plasma treatment and oxidative stress

Maximilian Schwarzmann[1], Kristian Wende[1], Debora Singer[1,2], *Sander Bekeschus[1,2], Andrea Rau[3]

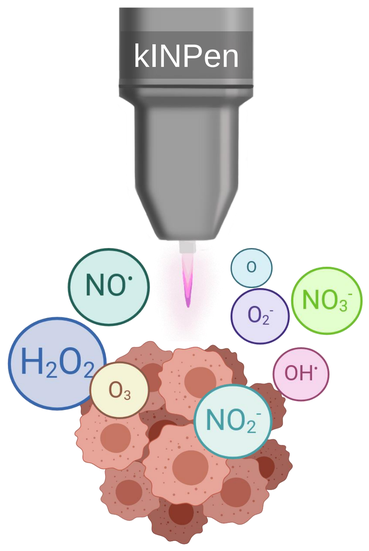
[1] ZIK *plasmatis*, Leibniz Institute for Plasma Science and Technology (INP), Greifswald, Germany
[2] Department of Dermatology and Venerology, Rostock University Medical Center, Rostock, Germany
[3] Department of Oral and Maxillofacial Surgery / Plastic Surgery, Greifswald Medical Center, Greifswald, Germany
* correspondence: sander.bekeschus@inp-greifswald.de

MOTIVATION

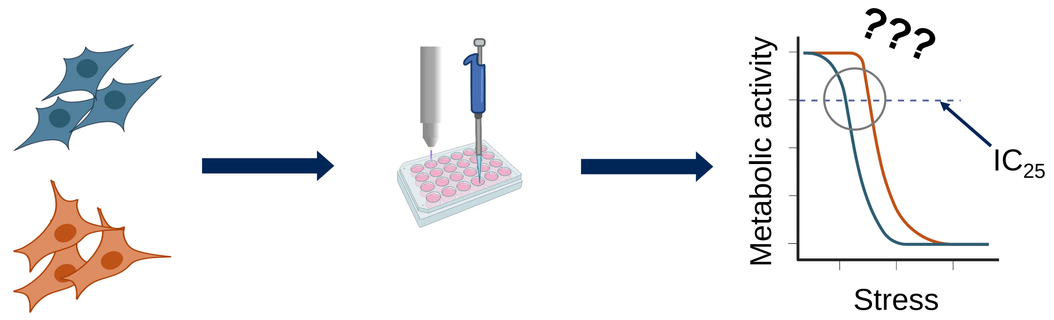
Skin cancer can be treated with cold physical plasma generated with the atmospheric pressure argon plasma jet kINPen [1].

Gas plasma effects are throught to be mediated via reactive oxygen species (ROS) [1].

Different cell lines show varying sensitivities to physical plasma, H_2O_2, and HOCl treatments [2,3,4].



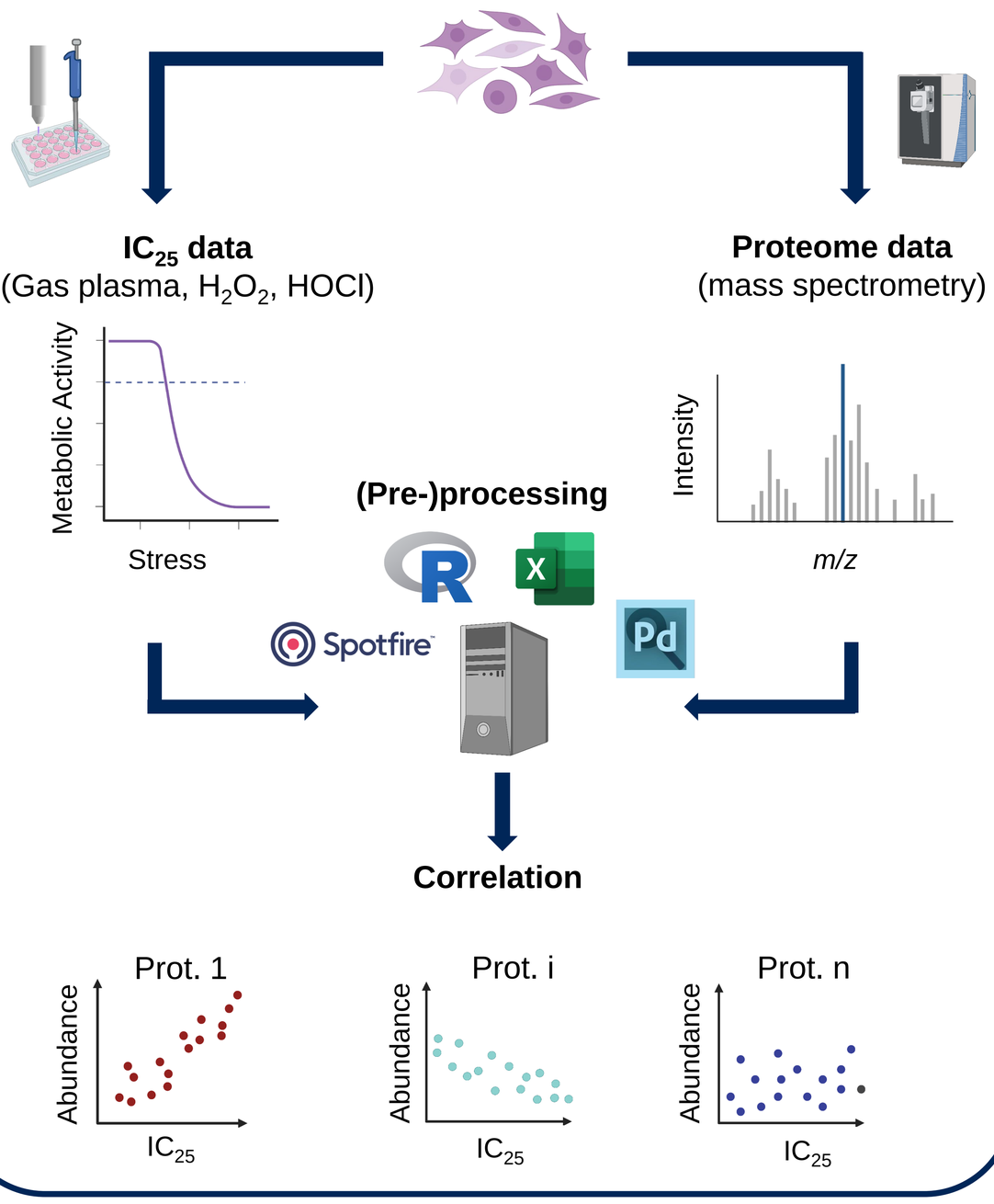
Cell lines → **ROS stress** → **Cell sensitivity to ROS**



Which proteins relate to the oxidative stress sensitivity and resistance in skin cancer cell lines?

METHODS

8 untreated melanoma cell lines



OXIDATIVE STRESS-CORRELATING PROTEINS

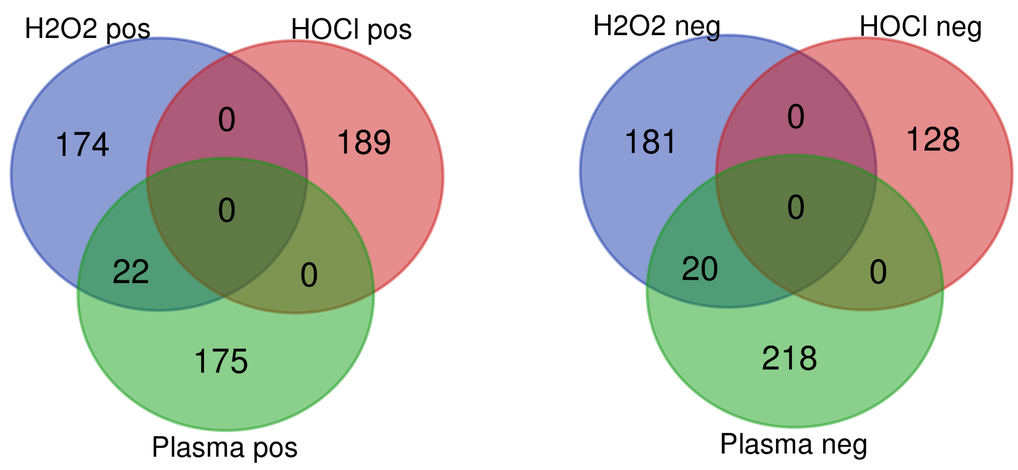


Fig. 1. Venn diagram of all significantly correlating proteins for gas plasma, H_2O_2, and HOCl treatment.
a) Positive correlation
b) Negative correlation

Protein	Rank R	p-value	
GRAMD2B	0.95	2.60E-004	
FHL3	0.91	2.01E-003	
SKA1	0.91	2.01E-003	→ Chromosome alignment
S100A7	0.91	2.01E-003	
MTFMT	0.91	2.01E-003	
DDX19B	0.91	2.01E-003	
FNBP1L	0.88	3.85E-003	→ Endocytosis
RAD23B	0.88	3.85E-003	
DOCK6	0.88	3.85E-003	→ Intracellular signaling
PARD6G	0.88	3.85E-003	

Fig. 2. Top 10 positively correlating proteins (gas plasma).

Protein	Rank R	p-value	
STOM	-0.95	2.60E-004	→ Ion channel activity
ZYG11B	-0.95	2.60E-004	
ITM2B	-0.95	2.60E-004	
UBA3	-0.95	2.60E-004	→ Cell cycle progression
TMEM11	-0.95	2.60E-004	
TSPAN14	-0.93	8.63E-004	
COQ10B	-0.93	8.63E-004	→ Respiratory chain
PRR15L	-0.93	8.63E-004	
SACM1L	-0.91	2.01E-003	
OTULINL	-0.91	2.01E-003	

Fig. 3. Top 10 negatively correlating proteins (gas plasma).

NEXT STEPS

1. Identify target proteins, networks, and pathways from analyzed data
2. Focus on four melanoma cell lines and gas plasma treatment
3. Gather mass spectrometry data before and after treatment
4. Analyze changes in proteome with respect to targets
5. Use inhibitors to confirm pathway involvement

References:

[1] Privat-Maldonado, Schmidt, Lin, Weltmann, Wende, Bogaerts, Bekeschus (2019), Oxidative Medicine and Cellular Longevity
[2] Bekeschus, Liebelt, Menz, Berner, Sagwal, Wende, Weltmann, Boeckmann, von Woedtke, Metelmann, Emmert, Schmidt (2021), Free Radical Biology and Medicine
[3] Bekeschus, Liebelt, Menz, Singer, Wende, Schmidt (2022), Redox Biology
[4] Singer, Schmidt, Bekeschus (2024), Advances in Redox Research

Some of the images were created with a commercial license of biorender.

GERHARD DOMAGK Nachwuchsförderprogramm
plasmatis Plasma plus Cell
GEFÖRDERT VOM Bundesministerium für Bildung und Forschung
Leibniz Association