The role of nucleotide excision system’s recognition proces in head and neck carcinogenesis

14-17.05.2025, SMM, Poznań

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Update:

- Article publication

  Impact of soft tissue homogenization methods on RNA quality

  Molecular Biology Reports, IF 2.6, Springer Nature

  Julia Ostapowicz, Bartosz Maćkowiak, Kamila Ostrowska, Barbara Kaczmarek, Natalia Pietras, Dawid Frąckowiak, Magdalena Fundowicz, Katarzyna Kulcenty, Wojciech Golusiński, Wiktoria Suchorska

article's QR code

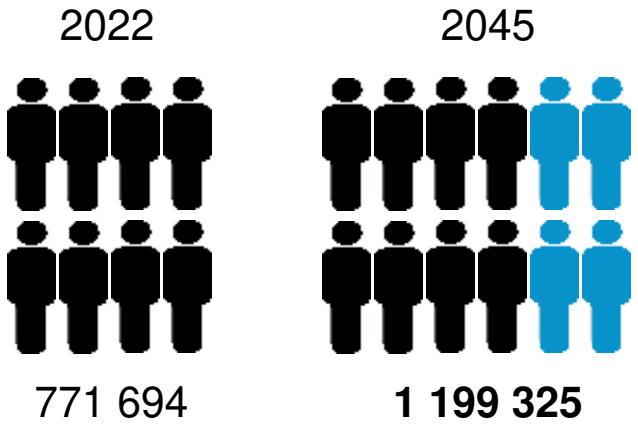
- XVI International Conference of Contemporary Oncology

  10-12.04.25, Poznań

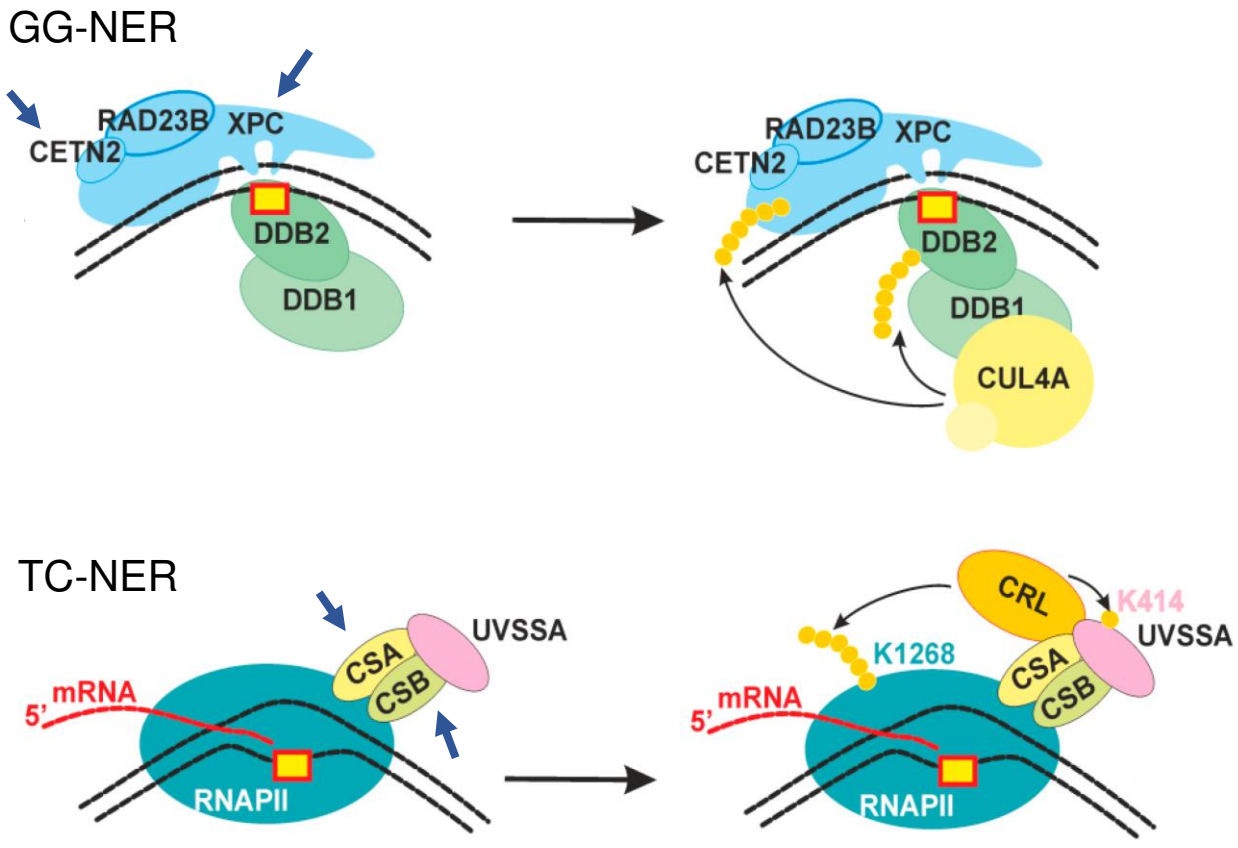
Background

Cancer site	Incidence	Mortality
Lip, oral cavity	5,6	2,6
Larynx	4,3	2,3
Pharynx	4,3	2,5

Age-Standardized Rate (Poland) per 100 000, both sexes, in 2022, IARC WHO



Estimated numer of new cases, both sexes, head and neck cancer, IARC WHO



An overview of recognition proces of NER figure from publication: doi.org/10.3390/ijms22126220

Hypotesis: **The impaired nucleotide excision repair system plays a vital role in head and neck carcinogenesis.**

Aims:

- To determine the expression of both TC- and GG-NER system-related genes in tumor, histopathologically unchanged patients' tissues from free margin and cell lines, then to select the most differentially expressed genes in initial DNA damage recognition system of both TC- and GG-NER.
- To describe selected genes' functional role in tumorigenesis by knock-down *in vitro* experiment.
- Broaden the knowledge of DNA damage recognition process in cancer cells response to chemo- and radiotherapy.

Study cohort characteristics

Anatomical site	n	%
Oral	46	53%
Larynx	40	47%
Sex		
Male	74	85%
Female	13	15%
G status		
G1	5	6%
G2	56	71%
G3	18	23%

TNM stage	n	%
T1&2	4+17	27%
T3	19	24%
T4	39	49%
N0	32	44%
N1	18	25%
N2	23	31%
M0	79	100%
M1	0	-

Head and neck squamous carcinoma tissues were collected from **87 patients** who underwent surgical tumor resection in the Department of Head and Neck Surgery, The Greater Poland Cancer Centre as part of cooperation with prof. Wojciech Golusiński.

The **inclusion** criteria involved diagnosed squamous cancer of oral cavity or larynx.

The **exclusion** criteria involved a distant metastasis, a second primary tumor, and HPV infection.

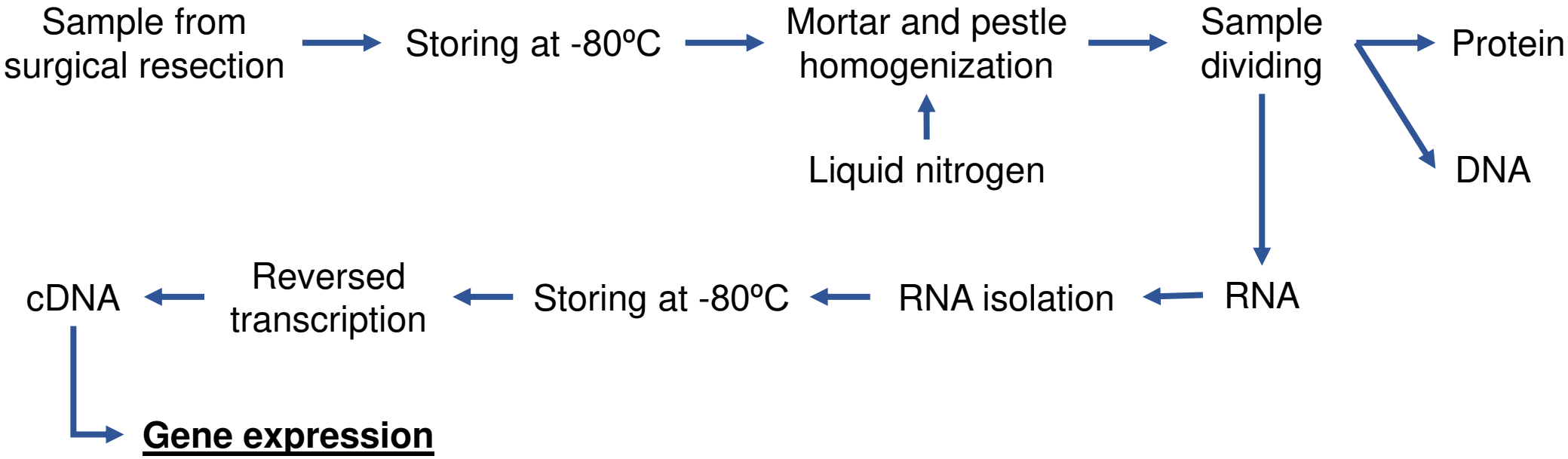
Cell lines

Cell line	Correspondance location
FaDu	Hypopharyngeal cancer
H103	SCC tongue
Detorit 562	Pharyngeal cancer
SCC9	SCC tongue HPV neg.
SCC25	SCC tongue HPV neg
SCC152	Hypopharyngeal cancer HPV pos.
SCC154	SCC tongue HPV pos.

SCC – squamous cel carcinoma

All cell lines were harvested in triplicates after 48h culture.

Sample library preparation



All of the patients' samples were prepared according to this graph.
The procedures were approved by the Local Ethical Committee of Poznan University of Medical Sciences (Consent no. 121/23)

Real Time qPCR optimalization

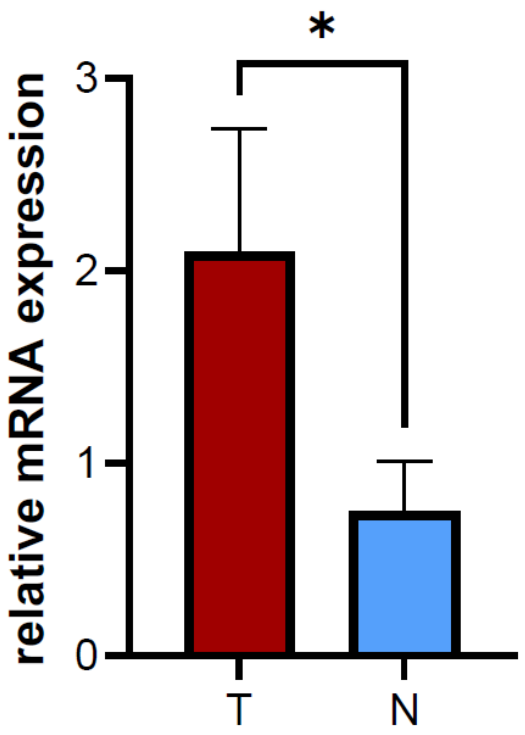
Gene	Forward sequence	Reverse sequence	R^2	T_m [°C]
B2M	GTCTCGCTCCGTGGCCTTA	TGGAGTACGCTGGATAGCCTC	0,9782	60,0
XPC	ACTGATGGATACATCGTCTG	TTCTCCTTCTCCTTCCTTTC	0,9927	58,2
CETN2	ATGATGATGAAACTGGGAAG	AGACACTGATCTTAATAGAGGC	0,9368	58,7
ERCC6	CAAGACCATCCAGATAATTGC	AACCTGTAATTTGAACCACG	0,9691	60,8
ERCC8	TTATAGTGGTAGCAGAGACTG	TCTCATCATCATCAGGAACTG	0,9412	57,8

Data was obtained by preparing concentration series of studied samples, temperature gradient, analyzing standard curve and R^2.

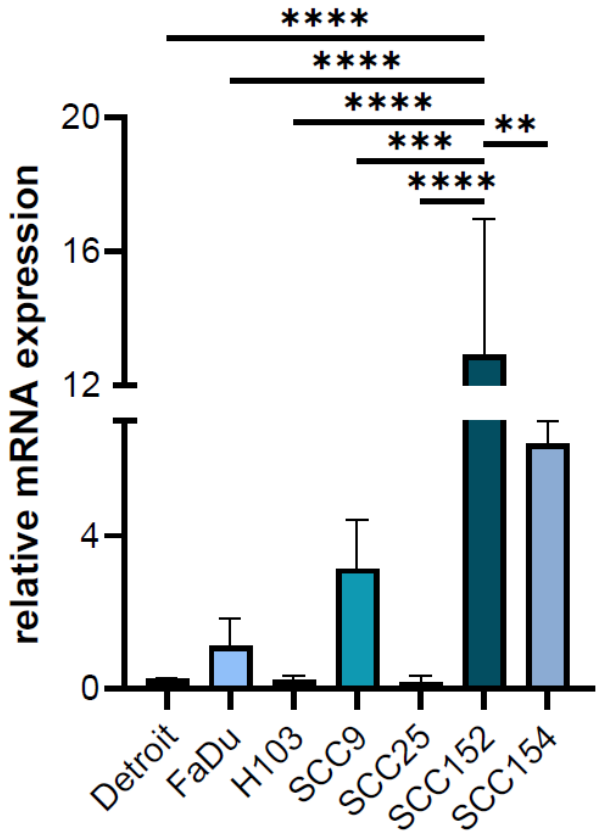
Results – XPC gene

Calculated using Pfaffl method, *p=0,0136*, n=81 Mann-Whitney test

A. XPC gene expression at mRNA level in patients



B. XPC gene expression at mRNA level in cell lines

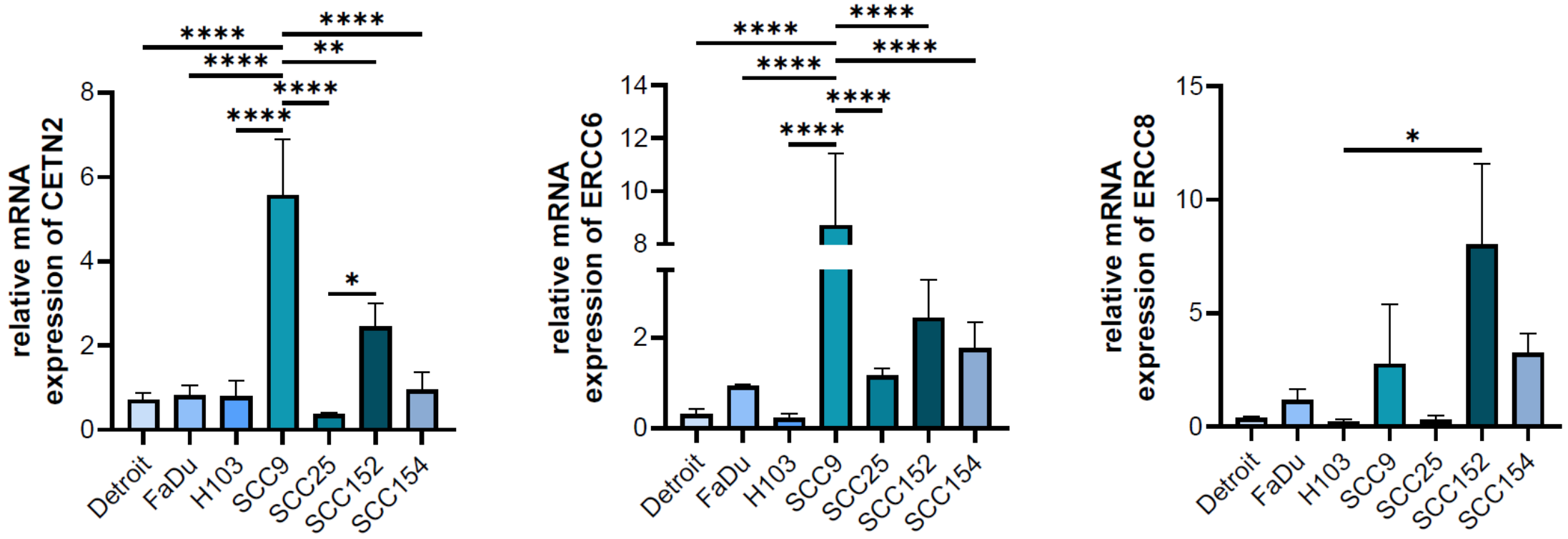


Calculated using Pfaffl method, one-way ANOVA

**p<0,05*
***p<0,01*
****p<0,005*
*****p<0,001*

Results – gene expression amongst cell lines

C. Gene expression at mRNA level in cell lines



Calculated using Pfaffl method, one-way ANOVA

Next steps

- Waiting for expanded Bioethical Comitee consent
- qPCR analysis of other genes
- Selecting the patients' samples for Sanger sequencing, based on most differently expressed genes between cancerous and unchanged tissue
- Applying for Preludium grant, NCN

Gene	subpath of NER	ClinVar database variations number
XPC	GG	1089
CETN2	GG	207
ERCC6	TC	1932
ERCC8	TC	596

SNPs mutations amount in NER genes based ClinVar database

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