Head and neck cancer: Identifying markers to facilitate better treatment in the future

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Credit: AI-generated image (disclaimer)

Malignant tumors in the head and neck region are very heterogeneous and therefore difficult to treat. In addition, the lack of prognostic markers is a significant impediment to personalized treatment. A joint study by MedUni Vienna and the Christian Doppler Laboratory for Applied Metabolomics focused on the development and identification of

specific markers to improve risk assessment for patients. The study was published in the *European Journal of Nuclear Medicine and Molecular Imaging*.

So far, only limited research has been done on the genetic characteristics of the extremely diverse tumors in the head and neck region. There are also no suitable parameters for risk assessment in high-risk patients. This is the context for the recent study conducted by the research team led by Lukas Kenner from MedUni Vienna's Clinical Institute of Pathology and Alexander Haug from MedUni Vienna's Department of Radiology and Nuclear Medicine in cooperation with the Christian Doppler Laboratory for Metabolomics and its corporate partner Siemens Healtheneers.

Based on DNA sequencing of 127 tissue samples from affected patients, the researchers analyzed the cellular characteristics of the tumors using artificial intelligence (AI) and positron emission tomography (PET) as an imaging method. The aim of the retrospective study (lead author Clemens Spielvogel) was to calculate specific numbers that can be used as markers for risk assessment in patients by combining the data from the genetic analysis and imaging.

Calculated on the basis of genetics and imaging

First, the DNA from the tissue sections was sequenced, the three-dimensional PET images of the patients were evaluated, and specific image patterns extracted. The research team then merged the data using machine learning algorithms to identify genetic networks with different patterns of disruption in the tumors that trigger cellular senescence. Cellular senescence means that the cells neither divide nor secrete inflammatory messenger substances, but still do not die. The problem here is that these cells can release molecules into neighboring tissues that contribute to further tumor development.

The results of the study show that cellular senescence in combination with the specific patterns that were extracted in the course of the analysis are associated with high risk for head and neck cancer patients. In conclusion, the computationally identified markers from genetic and image-based data are a more effective means of capturing the heterogeneity of the tumors. This makes it possible to develop and apply more targeted treatment options swiftly and to monitor high-risk patients more closely.

830,000 new cases per year

The term head and neck tumors covers various types of cancer that occur in these parts of the body, including carcinomas of the oral cavity, pharynx, larynx and nose and sinuses. Most of the malignant tumors are squamous-cell carcinomas, i.e. tumors that originate from surface cells. Other, less common, tumors are adenocarcinomas, which originate from glandular tissue, and sarcomas from soft tissue.

According to estimates from the international database Global Cancer Studies, more than 830,000 people worldwide are diagnosed with head and neck cancer every year. According to Statistics Austria, 1,184 men and 404 women were diagnosed with ENT cancer in Austria in 2019. Smoking and alcohol consumption, but also human papilloma viruses are risk factors for head and neck cancer.

More information: Clemens P. Spielvogel et al, Radiogenomic markers enable risk stratification and inference of mutational pathway states in head and neck cancer, *European Journal of Nuclear Medicine and Molecular Imaging* (2022). DOI: 10.1007/s00259-022-05973-9

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