Expression of SIP1 protein indicates poor prognosis in pharyngeal cancer

November 14 2014

The expression of SIP1 protein in pharyngeal squamous cell carcinoma tumours often indicates an advanced tumour stage, a high risk of recurrence and a poor prognosis, according to research from the University of Eastern Finland. Based on the results, SIP1 is a potential new prognostic factor for clinical use, helping to single out patients with more aggressive tumour behaviour requiring more intensive therapy and closer follow-up. Ms Anna Jouppila-Mättö, MD, presented the results in her doctoral thesis.

Although pharyngeal squamous cell carcinoma (PSCC) is a rather rare disease, its incidence has been increasing over the past three decades, now accounting for 130,000 new cases and 80,000 cancer deaths worldwide. The prognosis is one of the poorest of all the head and neck squamous cell carcinomas and it has not improved to any significant extent, despite the availability of multimodal therapies. The main risk factors for PSCC are the use of tobacco and alcohol. Recently, the human papilloma virus (HPV) has been shown to be involved in the development and prognosis of oropharyngeal squamous cell carcinoma, and many hospitals routinely test patients for HPV. No other distinct biomarkers for PSCC patient survival have been established thus far.

The first study to assess the role of EMT-related transcription factors in PSCC

Epithelial-mesenchymal transition (EMT) is a complex cellular process

which is not only crucial for embryogenesis, but it is also activated during tumour progression, enabling tumour cells to become invasive and to metastasise. Several transcription factors, like SNAI1, TWIST, SIP1, SLUG, and ZEB1, are fundamental in regulating EMT.

This study was the first to assess the role of EMT-related transcription factors in PSCC. The immunohistochemical expressions of transcription factors SNAI1, TWIST, SIP1, SLUG and ZEB1 were analysed in tumour cells, stromal and endothelial cell nuclei, as well as in cytoplasm of PSCC samples in an effort to evaluate the association of their expressions with clinicopathological variables and patient prognosis.

Tumours with positive epithelial nucleal SIP1 immunostaining were more advanced and had more lymph node metastases. The expression of SIP1 was also linked to poorer disease-specific five-year survival and was an independent prognostic factor in multivariate analysis together with tumour size and general patient status.

SNAI1 expression in endothelial cells predicted reduced survival and increased tumour size, whereas TWIST expression in stromal cells was linked to higher risk of recurrence. The co-expression of SNAI1, TWIST and SIP1 in tumour epithelial cell nuclei predicted poorer prognosis than SIP1 expression alone. The results were originally published in Histology and Histopathology, and *BMC Cancer*.

Provided by University of Eastern Finland