

Gene expression to distinguish metastasizing from non-metastasizing head and neck cancers

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The validation of a test, based on gene expression and predicting the tumours that will metastasize in lymph nodes of head & neck cancers, was presented today at the 3rd International Conference on innovative approaches in Head and Neck Oncology (ICHNO), in Barcelona.

Dr Robert Takes, from the Radboud University Nijmegen Medical Centre, the Netherlands, reported results of a study involving 222 cases of oral or oropharyngeal [cancer](#). The study was jointly led by scientists from Nijmegen and the University Medical Center Utrecht, and involved all eight head and neck oncological centres of the Netherlands.

"Today, it is impossible with current diagnostic tools to detect small lymph node metastasis in patients with head and neck squamous cell carcinoma and therefore it is common practice to operate on the neck even if no metastases have been detected," said Dr Takes. "The majority of these operations is unnecessary because, in most cases, no metastases are present."

If the chance of metastasis could be predicted more accurately, the number of operations could be reduced. "In our study, determining [gene expression](#) changes in the primary tumour improved the distinction between tumours that do metastasize from those that don't," continued Dr Takes.

With an array containing a set of 825 relevant genes, identified in a prior study and suitable for clinical application, distinction between metastasizing and non-metastasizing tumours was possible. The test correctly predicted the absence of metastasis in 89% of the cases.

"This is the first biological test that was able to obtain a high level of accuracy and has been validated in multiple centres on a large cohort of patients," said Dr Takes.

"The possible reduction of unnecessary neck treatments in case of a negative test may result in decreased morbidity without deterioration of oncological outcomes. Also, in the remaining cases that still develop metastasis in the neck, salvage treatment is still possible," added Dr Takes.

This signature is an additional method to already existing means to assess the neck, like imaging techniques and sentinel node procedures. "One important message arising from the study is that the combination of biological (gene signature) and clinical factors did better than either alone," commented Prof Adrian Begg from the Netherlands Cancer Institute (NKI). "It thus appears that this signature is a useful addition which can help the decision on treatment policy."

"Treatment is usually mainly selected based on the anatomical extent of the primary tumour and its metastasis. Additional biological information on the behaviour of each individual tumour could result in a more tailored treatment resulting in better survival," said Dr Takes.

"Takes and colleagues have carried out an important and essential step in all studies on gene signatures," concluded Prof Begg, "namely to move on from the initial finding of potential prognostic or predictive significance to validation in an independent clinical series."

"We look forward to further validation and refinement of this approach which opens promising developments. In such studies it would still be useful to look at genome-wide expression, which would provide the opportunity to not only validate the present signature but also to look for even better ones."

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