NRG1 Gene Fusions as Markers & Targets for Various Cancers

Invention
Cancer patients frequently bear therapeutically relevant genome alteration. For instance, lung adenocarcinomas of patients that have never smoked carry genome alterations affecting kinases, such as EGFR mutations and translocations affecting ALK, ROS1, and RET genes. These patients can be effectively treated with an ever-growing number of kinase inhibitors. However, despite substantive cancer genome sequencing efforts a majority of tumors still lacks therapeutically tractable alterations.

Scientists of the University of Cologne identified NRG1 gene fusions as ideal diagnostic and prognostic markers and targets for various tumours. The MTSS1-NRG1 fusion event has e.g. been detected in patients with small cell lung cancer and the gene fusion CD74-NRG1 has been shown to occur frequently in never smokers with invasive mucinous lung adenocarcinoma lacking KRAS mutation. The latter has been verified by several other groups.

CD74-NRG1 was found to signal through induction of ERBB2-ERBB3 heterodimers. In light of the multitude of available drugs or drugs in clinical trials targeting ERBB2, ERBB3 and their downstream pathways, the detection of CD74-NRG1 fusions may aid making a decision on the appropriate medical treatment e.g. for invasive mucinous lung adenocarcinomas. Furthermore, the fusion itself represents a promising target for the development of medical interventions. Thus, these findings position MTSS1-NRG1 and CD74-NRG1 as druggable oncogenic fusions.

Commercial Opportunities
On behalf of the University of Cologne, PROvendis offers access to rights for commercial use as well as the opportunity for further co-development.

Current Status
In case of interest we will be pleased to inform you about the patent status.

Further Reading
Gow, Ch. et al. (2014) Multidriver mutation analysis in pulmonary mucinous adenocarcinoma in Taiwan: identification of a rare CD74-NRG1 translocation case. Med Oncol. 31(7):34

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Figure 1: Genomic intron/exon structure of the CD74 (green) and the NRG1 Locus (orange) with the genomic breakpoints marked in red

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