Clinical studies of RNA as a prognostic and diagnostic marker for disease

av

Helena Isaksson

Akademisk avhandling

Avhandling för Medicine doktorsexamen i medicinsk vetenskap
med inriktning mot biomedicin,
som kommer att försvaras offentligt
fredag den 15 december 2017 kl. 13.00,
Hörsal C1, Campus USÖ, X-huset, Universitetssjukhuset
Örebro

Opponent: Prof. Ola Hammarsten
Sahlgrenska akademin
Göteborg

Örebro universitet
Institutionen för medicinska vetenskaper
701 82 ÖREBRO

Abstract

Helena Isaksson (2017): Clinical studies of RNA as a prognostic and diagnostic marker for disease. Örebro studies in Medicine 168.

Technologies for RNA detection are evolving rapidly and gives an opportunity for discovery of new markers for early detection of complex diseases. Today in clinical work we rely on signs and symptoms in combination with the measurement of protein levels for diagnosis. The quick turnaround time of mRNA synthesis may provide an earlier diagnostic signal than protein-based biomarkers assays, in acute dramatic conditions such as acute mesenteric ischemia (AMI), for early detection of cancer, as prognostic tool in cancer treatment and as an aid in difficult diagnosis of unknown origin.

The main goals of this thesis was to apply a whole genome approach to study different complex diseases to evaluate the applicability of RNA as a diagnostic or prognostic marker for disease, preferably from an easily accessible source such as peripheral blood. This was investigated in an animal model with induced AMI, a cohort of ovarian cancer patients and in a single-patient study of a girl with a severe inflammatory syndrome.

Through this thesis we have gained insight into how gene expression is regulated in ischemic intestinal tissue.

We found that a peripheral blood test can distinguish between ovarian cancer patients with or without residual tumour mass after surgery with the help of expression analysis of six genes. We also found that gene expressions of three genes can predict overall survival in peripheral whole blood from ovarian cancer patients. And that gene expression profiles indeed can significantly distinguish between two groups of high and low risk ovarian cancer. In the single-patient study, we tried but failed to device a successful treatment before it was too late. Nevertheless, the things we learned and the case studies that were published may serve as a diagnostic tool for clinicians facing similar syndromes.

Keywords: gene expression, ovarian cancer, hypercalprotectinaemia, hyperzincaemia, ischemia, biomarker

Helena Isaksson, School of Health and Medical Sciences, Örebro University, SE-701 82 Örebro, Sweden, helena.isaksson@regionorebrolan.se