Title: The progress of proteomic approaches in searching for cancer biomarkers

Authors: Nina Kočevar, Petra Hudler, Radovan Komel

PII: S1871-6784(12)00868-0
DOI: doi:10.1016/j.nbt.2012.11.011
Reference: NBT 559

To appear in:

Received date: 29-10-2012
Accepted date: 5-11-2012

Please cite this article as: Kočevar, N., The progress of proteomic approaches in searching for cancer biomarkers, *New Biotechnology* (2010), doi:10.1016/j.nbt.2012.11.011

The progress of proteomic approaches in searching for cancer biomarkers

Nina Kočevar, Petra Hudler, Radovan Komel

Medical Centre for Molecular Biology, Institute of Biochemistry, Faculty of Medicine, University of Ljubljana, Vrazov trg 2, SI-1000 Ljubljana, Slovenia. E-mail: nina.kocevar@mf.uni-lj.si, petra.hudler@mf-uni.lj.si, radovan.komel@mf.uni-lj.si

Corresponding author: Radovan Komel, Medical Centre for Molecular Biology, Institute of Biochemistry, Faculty of Medicine, University of Ljubljana, Vrazov trg 2, SI-1000 Ljubljana, Slovenia. Phone: +386 1 543 76 62. Fax: +386 1 543 76 41. E-mail: radovan.komel@mf.uni-lj.si

Abstract

Biomarkers are indicators of a specific biological state. Their detection in pathological conditions, such as cancer, is important for clinical disease management. One of their greatest values could be in early diagnosis and detection of neoplasms when the cancer is more manageable. Protein biomarkers are expected to be reliable predictors of pathological conditions, as they represent the endpoint of biological processes.

The proteomic methodology has rapidly evolved in the past ten years, thus enabling discovery of a vast amount of potential biomarker candidates. However, the majority of novel candidates have not yet reached the integration into clinical environment. To do that, well constructed large population validation studies are necessary as well as development of new algorithms for deciphering complex biological interactions and their involvement in pathological processes.

This review focuses on advances in classical proteomic approaches and emerging high-throughput proteomic technologies for identifying cancer biomarkers.

Keywords: Proteomics, cancer, biomarker