

CLINICAL PROTEOMICS EXPERIENCES IN JAPAN ON LUNG CANCER TREATMENTS WITH EGFR-TKI – IRESSA

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Pulmonary Diseases such as Lung Cancer and Chronic Obstructive Pulmonary Disease (COPD) are currently the major leading cause of death and its prevalence is increasing. The leading cause of COPD is smoking and an estimated 600 million patients suffer from the disease. We collected blood plasma from gefitinib-treated NSCLC patients in Japan in a pharmacoepidemiologic cohort study. Today, we are able to optimise lung retention and correlate drug Pharmacokinetics in lung with effect and toxicity when only total concentration of drug in lung tissue homogenate can be measured [1].

Examples will be given from large clinical studies where we have developed dedicated protein Biomarker diagnosis technologies in order to discover proteomic markers associated with development of acute ILD events, and drug efficacy. In addition, targeted Multiple Reaction Monitoring (MRM) multiplex quantitation assay developments will be outlined and presented. These current MRM methods were applied to biofluid and tissue applications from patients, as well as Biobanking archives. The MRM assays platforms as such are generic and can be developed and applied in principle to any set of key regulating target proteins within disease [2].

[1] Marko-Varga G, Ogiwara A, Nishimura T, Kawamura T, Fujii K, Kawakami T, Kyono Y, Tu HK, Anyoji H, Kanazawa M, Akimoto S, Hirano T, Tsuboi M, Nishio K, Hada S, Jiang H, Fukuoka M, Nakata K, Nishiwaki Y, Kunito H, Peers IS, Harbron CG, South MC, Higebottom T, Nyberg F, Kudoh S, Kato H., *J Proteome Res.* 6 (2007) 2925-2935, “*Personalized Medicine and Proteomics: Lessons from Non-Small Cell Lung Cancer*”

[2] Vegvari A. and Marko-Varga G., *Chemical Reviews*, 2010, 110, 3278-3298, “*Clinical Protein Science and Bioanalytical Mass Spectrometry with an Emphasis on Lung Cancer*”