The first discriminatory step illustrating the ***PPPM***-oriented survey is estimating of the correlation strength between ***genetic polymorphism*** and ***risks of the disease***, and subsequent construction of the groups at risks. Those goals can be solved by using of ***BioChip*** methodology (each disease has individual ***fingerprints***). As a result, a patient becomes a ***data carrier,*** *i.e.,* he/she knows about possible risks of a disease, and the physician can reasonably select of ***preventive*** protocol, proceeding from the assays made. Individuals, selected at the first stage, undergo ***the second phase*** of the survey, which uses a panel of phenotypic ***biopredictors***.

Two examples to illustrate the topic: **T1D** and **MS** models.

T1D is an chronic autoimmune disease resulting in a destruction of pancreatic *beta*-cells capable alone of producing insulin, by two autoreactive tools, *i.e.,* cytotoxic T lymphocytes and anti-islet autoAbs. For T1D, about half of the total risk is genetic and about half of that genetic risk is in the HLA region on the chromosome 6 to be used for gene-based ***predictive*** testing! Other genes are associated with T1D as well, but their contribution to risks is small.

Subclinical stages are also determined by identification of highly-specific proteomic-related *biopredictors, i.e.,* different anti-islet autoAbs whose presence would determine risks for initiating *subclinical* abnormalities and then result in clinical manifestations of T1D.

MS is an autoimmune disorder of the central nervous system resulting in a destruction of neuro-myelin compartment including demyelination, axon loss and development of disability. Most of the studies confirmed the supreme role of the variations within HLA genes, particularly HLA-II DR region as MS gene-related risk factors!

The crucial step in the MS evolution is a primary myelin damage which is mediated by cytotoxic anti-myelin autoAbs! A portion of those are autoAbs against myelin-basic protein/MBP endowing with MBP-targeted proteolytic activity (so-called, ***Ab-proteases***). Screening for those could become the next step to secure ***subclinical*** diagnosis of MS and ***to predict*** the clinical course.

The activity of Ab-proteases established markedly differs: *(i)* between MS patients and healthy controls; *(ii)* among different disease courses; and would correlate with EDSS scales of demyelination and thus the disability of the patients.

The ***sequence-specificity*** of Ab-proteases would illustrate a common but specific pattern revealing ***six*** sites of preferential proteolysis. Some of those sites are located within the **immunodominant** and ***encephalitogenic*** regions of MBP that are responsible for the induction of severe and aggressive forms of MS or for getting the disease run in a similar way. The other sites are less immunogenic to be responsible for either the induction moderate courses of MS or for maintaining clinically moderate courses.

The Ab-proteases were initially registered at the ***subclinical*** stages of MS, presumably, presumably demonstrating their defined sequence specificity with low immunogenicity.

Meanwhile, apart from MS patients, about 24% of the direct relatives were also seropositive for Ab-proteases but to reveal much lower activity as compared with the patients. Half of those seropositive relatives being monitored for 2 years have been demonstrating stable growth of the activity of Ab-proteases which reached their mid-level indices at a time point when had coincided with the initial occurrence of the primary clinical and MRI manifestations.

A unique value of Ab-proteases for monitoring MS at different stages of the disease whilst providing a fantastic tool for ***predicting*** demyelination is becoming evident and thus a reality. Moreover, Ab-proteases can be programmed and re-programmed to directly affect the remodeling of tissues (for instance, myelin). Such functionally valuable tools may thus be designed for the newer drug catalysts to act as ***preventive*** therapeutic tools!

Just comments and reference to malignant neoplasms: the initiation and progression of tumors depend on the stepwise acquisition of specific functions by cancer cells at both the ***primary*** and ***metastatic*** sites.

Tumor initiation (at ***subclinical*** stages) is provided by ***oncogenic*** mutations and ***inactivation of tumor-suppressor genes*** to be identified by genomic tailoring approach!

The initiation of metastasis would have to be ***predicted*** by a combination of genomic and proteomic approaches! And newer ***algorithms*** to suit the need of making the ***subclinical*** diagnosis of tumor are already in progress!

It would be extremely useful to integrate data harvesting from different databanks for applications such as ***prediction*** and ***personalization*** of further treatment. Medical practitioners will be able to thus provide more tailored *prevention* and *treatment* programs for their patients resulting in improved patient outcomes, reduced adverse events, and more cost effective

Contd...