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PREDICTIVE MEDICINE BY CYTOMICS: CHALLENGES AND POTENTIAL G.Valet, Max-Planck-Institut für Biochemie, Martinsried, Germany

Diseases are caused by molecular changes in cellular systems or organs. They are induced by exposure to external influences like microorganisms, allergens, toxic substance a.o. or alternatively by genetic disposition or genetic aberrations. *Disease course predictions* (>95% correct) for individual patients are usually considered impossible in the majority of diseases. Exceptions concern e.g. genotypic aberrations detected during amniocentesis or preimplantation diagnostics (PID). The substantial *clinical interest* in predicting the future disease development in individual patients prompts for the search of relevant information at the cellular level. Considering *genomics* or *proteomics* for genome and proteome analysis, the high multiparametric complexity and the usual preanalytic content mixing of different cell populations in cell or tissue extracts constitute substantial drawbacks for predictive conclusions in common diseases. *Cytomics*, in contrast, as multiparameter cytometric analysis of the cellular heterogenity in *cytomes* (cellular systems/organs), access a maximum of information of the *molecular cell phenotype* resulting from *genotype* and *exposure*. The cell phenotypes in the naturally existing cellular and cell population heterogeneity contain the information on the future development (*prediction*) as well as on the present status (*diagnosis*) of a disease. This permits to formulate a *general concept* for *predictive medicine* by cytomics: **1.** multiparametric cytometric measurements of disease associated cells according to functions or constituents, **2.** exhaustive numeric analysis of all measured cell populations for >95% of the collected cells, **3.** data pattern classification (http://www.biochem.mpg.de/valet/classif1.html) of the entire cellular information against the future disease course of patients during the learning phase. **4.** subsequent classification of an embedded test set of patient data, measured under the same conditions as the learning set but unknown to the learning process. The generation of robust classifiers which classify unknown prospective test samples similarly as samples of the learning set is assured in this way. Such classifiers are standardized and laboratory independent (http://www.biochem.mpg.de/valet/cellclas.html). The potential of predictive medicine for high-grade non-Hodgkin lymphomas (HG-NHL) as well as for stem cell transplantation (SCT) patients is described in a separate abstract.