

MOLECULAR PREDICTION OF RESPONSE TO CHEMOTHERAPY

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This contribution is focused on the application of molecular diagnostic techniques to enable individualization of malignant tumors therapy. Molecular diagnostics may lead to a therapeutically relevant molecular tumor classification and highlight prognostic aspects, shed light onto tumor predisposition, etc. The highest and clinically most relevant goal along this line, however, is the individualization of tumor treatment, both, for the detection of new therapeutic targets/development of specific drugs (Gleevec, Herceptin, etc.) and the prediction of response to “classical” (poly-) chemotherapy. Currently, the routine detection of individual therapeutic targets is restricted to few tumor entities but its number of applications is growing rapidly. The prediction of response to single “classical” chemotherapeutic drug or complex chemotherapeutic regimens in malig-

nant tumors is still in its infancy and would be of a major clinical relevance. One approach to accomplish this high set goal is to study pretherapeutic tumor biopsies and perform analysis on DNA-, RNA and protein level. Several technical aspects and technologies including CGH-, LOH-, SNIP-analysis ect, RNA expression arrays, quantitative RT-PCR technologies and proteomics approaches can be applied and will be discussed on different examples of solid tumors in different locations. Furthermore, problems associated with these approaches will be stressed and problem solving ideas will be presented. Heterogeneity of tissue, genetic heterogeneity of tumors, study design, particularly availability of representative patient cohorts and interpretation of results, including statistical analysis are among the problems discussed.