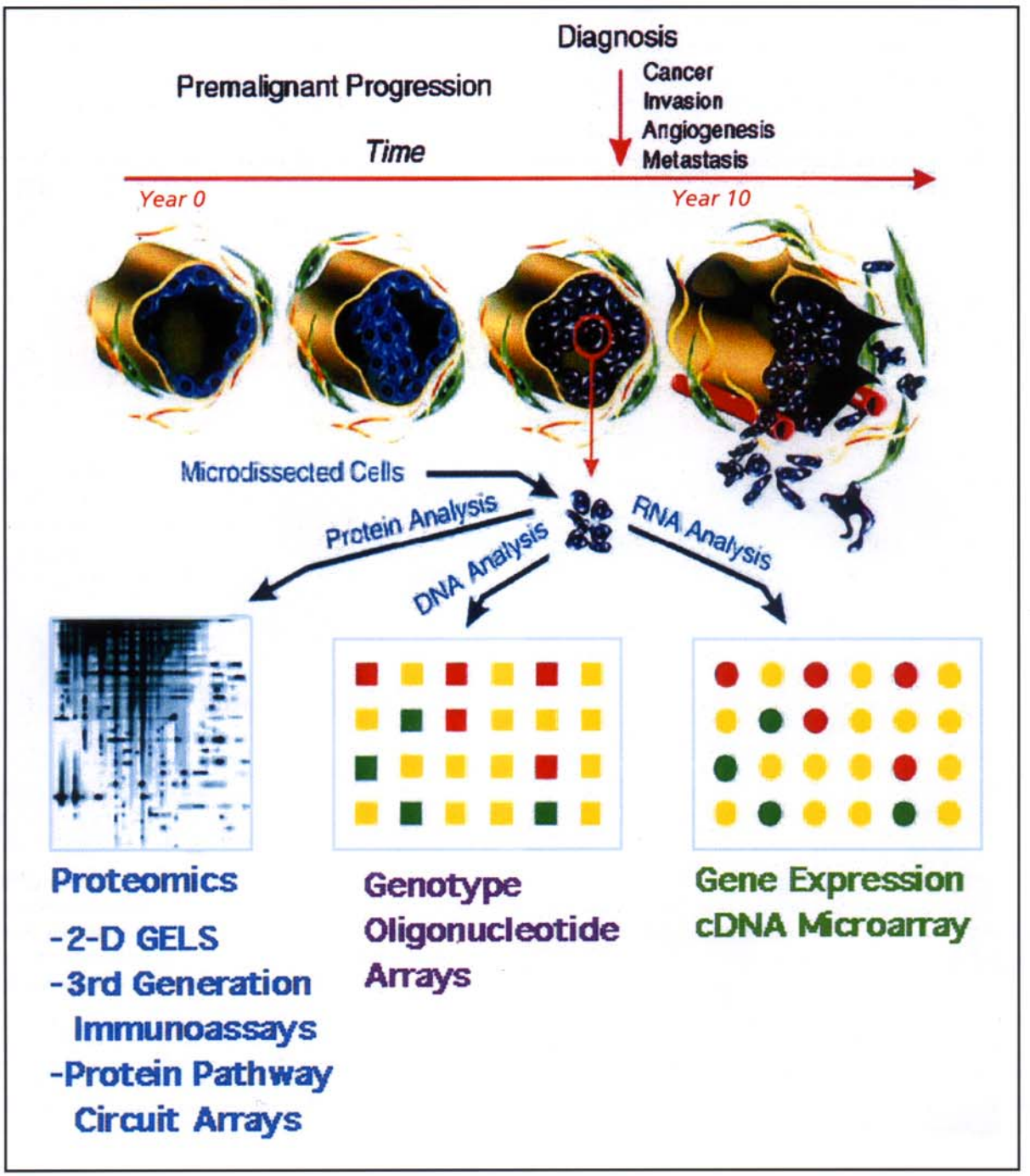

Fig. 3. Application of laser microdissection for studying the molecular events associated with cancer progression. The expression pattern of proteins, the DNA genotype or gene-expression pattern by RNA can be compared with the same tissue of a single patient. In the same tissue section, normal epithelium, stroma, premalignant lesions, invasive cancer foci and host response cells can all be sampled and compared (reprinted with permission of Dr. Michael R. Emmert-Buck from the National Cancer Institute Bethesda).

Microarray usually requires an input of 50–100 μg of total RNA, which can be difficult to obtain from microdissected tissue. A number of techniques have recently been presented for the amplification of small quantities of total RNA from laser-assisted microdissection material (Luo et al., 1999). However, a major challenge in this line of investigation still remains to be the ability to generate a sufficient amount and quality of the desired RNA from biopsied material (Ohyama et al., 2000; Baugh et al., 2001).

The slides used for microdissection are not coverslipped, which makes visualization fuzzy. Routinely stained frozen sections without coverslip as necessary for microdissection show greatly reduced cellular detail, which diminishes the ability to distinguish and isolate specific cell populations from complex lesions