Cancer genome sequencing advancing personalized treatment

As the cost of DNA sequencing plummets, the possibility of testing all cancer patients' tumor genomes is becoming a reality. For just $1,000 or so, a doctor might submit most any malignant specimen for a complete genetic work-up.

The sample might be a core needle biopsy taken from a breast, a blood sample from a person with leukemia, or a snippet of a sarcoma removed in an operating room. In principle, checking a tumor for genetic changes should be straightforward, do-able.

But most cancer patients undergo surgery and other treatment long before their doctors consider sending a biopsy for full molecular evaluation. A recent published survey among oncologists at two prestigious Boston teaching hospitals suggests that a significant proportion of specialists have a low level of confidence about their knowledge of cancer genomics. Aside from some kinds of lymphoma and leukemia, some lung cancers and a few other malignancies, examining cancer cells for genetic mutations is not routine in oncology practice.

Carolyn Hutter, an epidemiologist and co-leader of The Cancer Genome Atlas (TCGA), has been working on tumor genomics for some time. The TCGA project, a collaborative work by NIH's Cancer and Human Genome Research Institutes, aims to characterize over 10,000 human tumors at the molecular level. Sequencing genes in tumor cells – and seeing how those differ from a person's germline, or inherited DNA segments – helps us to better understand the biological causes of cancer, she said in a phone interview. "It's also useful because it can point to new targeted therapies."

Read the full, original story: Cancer genome sequencing will mean more targeted therapies