Nature Reviews Clinical Oncology **9**, 6 (2012); published online 6 December 2011; doi:10.1038/nrclinonc.2011.184

SCREENING

Smile, they're taking a SNaPshot of your cancer-causing genes

Personalized cancer treatment is just around the corner, suggests a new study. Using SNaPshot, a "multiplexed, robust, highly sensitive and quick clinical test," Lecia Sequist, Dora Dias-Santagata and colleagues at Massachusetts General Hospital have screened patients with non-small-cell lung cancer (NSCLC) for multiple cancer-causing gene mutations and demonstrated that implementing broad genotyping in routine clinical practice can identify the right type of treatment for the right patients. "Because each tumor harbor[s] a specific set of mutations, [this] test allows us to match individual[s] with the therapies that will most likely be effective in treating their cancer," Dias-Santagata explains.

© Roman Zaremba | Dreamstime.com

The SNaPshot test can identify over 50 mutation sites in 14 key cancer genes within 2–3 weeks. Out of 552 patients with NSCLC who underwent genotyping, 282 (51%) had at least one mutation or genetic rearrangement in the tested gene loci. The most common mutation sites were identified in *KRAS* (24%), *EGFR* (13%), *ALK* (5%), *PIK3CA* (4%), *BRAF* (2%) and *HER2* (1%), for which targeted therapies are either available or forthcoming. In fact, 170 patients with advanced-stage disease, or who recurred during the follow up, had a 'potentially targetable' genotype, and 38% of these enrolled in at least one clinical trial of a targeted therapy.

Patients' survival was also affected by their genotype; mutations in *KRAS* reduced survival, whereas mutations in *EGFR* improved survival compared with wild-type genes. Interestingly, *EGFR* or *KRAS* mutations were associated with adenocarcinoma, whereas *PIK3CA* mutations mostly occurred in squamous cell cancers. Aberrations in *EGFR* and *ALK* were associated with low smoking levels, whereas *KRAS* mutations mostly occurred in heavy smokers.

This group have now expanded SNaPshot genotyping to colorectal, brain and breast cancers. "[We aim] to be on the leading edge of the progress toward expanding the scope and breadth of genotype-specific treatments," Sequist says.

Iley Ozerlat

Original article Sequist, L. V. *et al.* Implementing multiplexed genotyping of non-small-cell lung cancers into routine clinical practice. *Ann. Oncol.* doi:10.1093/annonc/mdr489