The recent development of deep-sequencing approaches for the study of human cancer genomes in individual tumor lesions is already revolutionizing medical oncology and translational medicine (1). These unbiased approaches provide an unprecedented knowledge of the multiplicity of somatic mutations and genetic and epigenetic alterations underlying each human cancer type. This large and growing body of information is now contributing to the elucidation of aberrant molecular mechanisms and signaling circuitries driving tumor progression, hence revealing novel druggable targets for therapeutic intervention to prevent and treat human malignancies. Two studies published in this issue of Cancer Discovery join these efforts (2, 3), exploiting the emerging genomic landscape of head and neck squamous cell carcinoma (HNSCC) to identify actionable cancer drivers and biomarkers predicting favorable therapeutic responses to targeted anticancer agents.

HNSCC, which includes malignant squamous lesions arising in the oral cavity, larynx, and pharynx, is the sixth most common cancer in the world, with approximately 500,000 new cases annually, and results in nearly 11,000 deaths each year in the United States alone (4). The use of tobacco and the excess consumption of alcohol have long been recognized as risk factors for HNSCC oncogenesis (1). These unbiased approaches provide an unprecedented knowledge of the multiplicity of somatic mutations and genetic and epigenetic alterations underlying each human cancer type. This large and growing body of information is now contributing to the elucidation of aberrant molecular mechanisms and signaling circuitries driving tumor progression, hence revealing novel druggable targets for therapeutic intervention to prevent and treat human malignancies.

Two studies published in this issue of Cancer Discovery join these efforts (2, 3), exploiting the emerging genomic landscape of head and neck squamous cell carcinoma (HNSCC) to identify actionable cancer drivers and biomarkers predicting favorable therapeutic responses to targeted anticancer agents. In HNSCC. This makes the search for cancer-driving molecular events daunting, especially regarding the ability to distinguish them from passenger mutations that may have minimal impact on tumor progression and/or clinical response. Nonetheless, the emerging picture from the in-depth analysis of the HNSCC oncognome is that although the specific molecules altered in each individual tumor may be distinct, they all participate in a handful of dysregulated molecular pathways that are likely shared among most HNSCC lesions.

Building on this concept, Pickering and colleagues (2) conducted a detailed integrated multiplatform analysis of the genomic alterations in HNSCC, including genome-wide copy number alterations (CNA), tumor ploidy, gene expression, methylation, and point mutations. This approach revealed many more somatic events than previously reported. While 32% of the HNSCC cases were triploid, 37% were tetraploid or had higher ploidy, and 11 regions of focal chromosomal gain and 33 regions of focal loss were identified (2). Overall, 74% of the tumors exhibited at least 20 CNAs, reflecting the high genomic instability of HNSCC. These include gains in 8q (63%) and 3q (58%), and focal gains in regions containing CCND1 (22%), EGFR (16%), MYC (9%), and TP63 (26%), which represent candidate cancer drivers (2). Also identified were losses of 3p (76%), 18q (58%), and 8p (53%), which harbor multiple tumor suppressor genes, together with focal losses in 9p (32%) that include the CDKN2A locus (2). Gene CNA alterations often correlated with changes in mRNA levels of the encoded genes, but microRNAs were much less affected. Changes in DNA methylation were also observed, particularly in HNSCC lesions from smokers.

Remarkably, hundreds of genetic alterations were also identified, which extend recent published reports (6, 7). However, most of these alterations fell within four major driver biologic processes (Fig. 1): (i) mitogenic signaling (63%), with particular emphasis on aberrant activation of the phosphoinositide 3-kinase (PI3K)/mTOR pathway (including 11% with mutations of PIK3CA, encoding the catalytic subunit of

**Authors’ Affiliation:** Oral and Pharyngeal Cancer Branch, National Institute of Dental Research, NIH, Bethesda, Maryland

**Corresponding Author:** J. Silvio Gutkind, Oral and Pharyngeal Cancer Branch, National Institute of Dental and Craniofacial Research, NIH, 30 Convent Drive, Building 30, Room 320, Bethesda, MD 20892-4330. Phone: 301-496-6259; Fax: 301-402-0823; E-mail: sg39v@nih.gov

doi: 10.1158/2159-8290.CD-13-0239

© 2013 American Association for Cancer Research.
PI3Kα); (ii) defective cell differentiation (including 9% with NOTCH1 gene mutations and 66% with predicted NOTCH signaling pathway alterations); (iii) nearly universal (94%) cell-cycle deregulation due to inactivation of the CDKN2A (p16INK4A) tumor suppressor gene by copy number loss or promoter methylation, together with CCND1 (CYCLIN D1) amplification; and (iv) genomic instability caused by loss of TP53 and other candidate genes, such as those involved in DNA damage recognition and repair. This study also identified two additional key genes likely affecting cell–cell communication and cell death: FAT1 (30%) and CASP8 (10%), respectively. The latter seems to be associated with a cohort of HNSCC harboring activating HRAS mutations, suggesting that these tumors may survive apoptotic stimuli arising from HRAS gene mutations in the tumor microenvironment. These data revealed that together with a widespread loss of function in tumor suppressor genes, the majority (80%) of patients with HNSCC harbor aberrant activity of at least one oncogenic molecular pathway that could be targeted for pharmacologic intervention as part of novel genomically driven therapeutic strategies (2).

In a pathway-specific effort, Lui and colleagues (3) studied targetable mitogenic signaling routes genomically altered in HNSCC, including the MAPK, JAK/STAT, and PI3K pathways. Among these, the PI3K pathway harbored the highest percentage of mutations (30.5%), whereas the MAPK and JAK/STAT pathways were mutated in less than 10% of the cases, further emphasizing that PI3K is the most altered

---

**Figure 1.** The HNSCC oncogenome. Despite the remarkable complexity of genomic alterations found in HNSCC, most of them fall within few major driver-signaling pathways. Alterations found in each key gene are shown. Copy loss refers to homozygous and heterozygous gene deletion. Data were extracted from the publicly available Cancer Genome Atlas consortium (http://cancergenome.nih.gov/) HNSCC provisional dataset containing CNA, mutational, and gene expression data from 295 HNSCC samples.
30% of tumors have genomic alterations in the PI3K pathway, more than 80% to 90% of HNSCC lesions present activation of the PI3K–AKT–mTOR axis, including those cases associated with HPV infection (10). This suggests that although genomic alterations in the PI3K pathway might be excellent predictors of a response to its inhibitors, this genomic analysis alone may miss a substantial number of patients that have PI3K/mTOR pathway activation arising from other factors and hence could benefit from the same pharmacologic intervention. For example, STK11 (also known as LKB1), REDD1, SESTRIN1, and SESTRIN2 all converge to inhibit the mTOR pathway downstream of PI3K. STK11 links mTOR inhibition to cell metabolic and energy sensing and is mutated in 1% and downregulated in more than 10% of the HNSCC cases (Fig. 1). Of specific relevance to HNSCC, REDD1, SESTRIN1, and SESTRIN2 are all downstream targets of TP53, and hence their mTOR inhibiting activity is disabled in HNSCC lesions harboring TP53 mutations or expressing high-risk HPV onco-genes, thereby resulting in mTOR activation in the absence of obvious PI3K pathway genomic alterations (Fig. 1).

Clearly, a comprehensive genetic and biochemical approach to evaluate the status of activation of the PI3K/mTOR network will likely yield valuable information predicting a clinical response to PI3K/mTOR pathway inhibitors. Newly developed PI3K/mTOR inhibitors are also excellent candidates for combination therapies with currently available treatment options for HNSCC, such as chemotherapy and chemoradiation, or biologic or small-molecule inhibitors of EGFR, which acts upstream of PI3K/mTOR. One can envision that, building on similar integrated studies, it will soon be possible to harness the power of modern genomics and functional proteomics analytic strategies to study cancer-associated signaling circuitries, and to identify molecular pathways that each specific cancer and its tumor-initiating cells are addicted to. This will help identify the patients who may benefit the most from a growing repertoire of signal transduction-based anticancer therapies, either as single agents or as part of rational combinations that may bypass intrinsic and acquired resistant mechanisms.

Disclosure of Potential Conflicts of Interest
No potential conflicts of interest were disclosed.

Acknowledgments
The authors thank Drs. Molinolo and Doci for insightful suggestions and apologize to all of their colleagues for not citing some of their original studies due to strict space limitations.

Grant Support
This work was supported by the Intramural Research Program of the NIH, National Institute of Dental and Craniofacial Research, and by the Human Frontier Science Program Grant #RGP0041-2011.

Published online July 11, 2013.

REFERENCES
Exploiting the Head and Neck Cancer Oncogenome: Widespread PI3K-mTOR Pathway Alterations and Novel Molecular Targets

Ramiro Iglesias-Bartolome, Daniel Martin and J. Silvio Gutkind


Updated version
Access the most recent version of this article at:
http://cancerdiscovery.aacrjournals.org/content/3/7/722

Cited articles
This article cites 12 articles, 8 of which you can access for free at:
http://cancerdiscovery.aacrjournals.org/content/3/7/722.full.html#ref-list-1

Citing articles
This article has been cited by 9 HighWire-hosted articles. Access the articles at:
/content/3/7/722.full.html#related-urls

E-mail alerts
Sign up to receive free email-alerts related to this article or journal.

Reprints and Subscriptions
To order reprints of this article or to subscribe to the journal, contact the AACR Publications Department at pubs@aacr.org.

Permissions
To request permission to re-use all or part of this article, contact the AACR Publications Department at permissions@aacr.org.