Wild-type Ras proteins (H-Ras, N-Ras, and K-Ras) function as regulated binary switches that cycle between an inactive GDP-bound and an active GTP-bound state. In normal resting cells, Ras is predominantly GDP bound and inactive. In response to growth factor stimulation and activation of Ras-selective guanine nucleotide exchange factors (RasGEF; e.g., Sos1), Ras rapidly cycles to the GTP-bound state. Activated Ras-GTP then binds and activates downstream effectors that include the Raf serine/threonine kinases and the class I phosphoinositide 3-kinases, leading to the phosphorylation and activation of the extracellular signal-regulated kinase (ERK) and AKT serine/threonine kinases, respectively. The activation state is transient, with Ras-selective GTPase-activating proteins (RasGAP; e.g., neurofibromin) stimulating hydrolysis of the bound GTP, rapidly returning Ras to the inactive GDP-bound state and terminating effector signaling. Current evidence suggests that Ras-GDP is simply an inactive protein. However, whether Ras-GDP preferentially interacts with other proteins and has functions distinct from those of Ras-GTP remains an unresolved issue.

Mutationally activated forms of Ras are found in approximately 30% of human cancers (1). These cancers harbor single amino acid substitutions, most commonly at G12, G13, or Q61, that impair the intrinsic and GAP-stimulated GTP hydrolysis activities and render mutant Ras proteins persistently GTP bound in the absence of extracellular stimuli. Mutant Ras proteins are then persistently bound to their effectors, causing persistent effector signaling. However, persistent Ras signaling may be detrimental to the cancer cell, and mechanisms to dampen ERK activation include upregulated expression of ERK phosphatases (e.g., Dusp6) or ERK phosphorylation of upstream components, also attenuating ERK activation.

Early ectopic expression studies in NIH 3T3 mouse fibroblasts conveyed the perception that the presence of mutational activation of Ras rendered wild-type Ras dispensable for cancer cell growth. This idea was best shown by studies using the dominant-negative Ras S17N mutant, which forms a nonproductive complex with RasGEFs, thus preventing wild-type Ras activation and causing growth inhibition. The actions of Ras S17N could be overcome by concurrent expression of mutational activation of Ras (2). Similarly, introduction of mutations in Ras that impaired RasGEF interactions did not impair mutant Ras-transforming activity (3). These studies suggested that mutant Ras is fully active and functional and independent of RasGEF activity and, consequently, independent of wild-type Ras activity.

In this issue of Cancer Discovery, Young and colleagues (4) addressed the issue of whether the remaining 2 wild-type Ras isoforms contribute to tumor cell growth in the context of mutational activation of Ras. Although this is not a new concept (5), they take a different approach to evaluate this issue. Three tumor cell lines were studied, each with mutant H-Ras, K-Ras, or N-Ras. Conflicting evidence exists for the role of the wild-type counterpart of the mutant Ras isoform, for example, evidence that the wild-type RAS allele can act as a tumor suppressor gene and antagonize the oncogenic properties of its mutational activated counterpart (6), and that human tumor cell lines are often homozygous for mutant RAS (COSMIC). Therefore, to avoid this potential complication, cell lines were chosen that were homozygous for the mutant Ras isoform: KRASG12D-mutant MIA PaCa-2 pancreatic, HRASG12C-mutant T24 bladder, and NRASQ61K-mutant RD rhabdomyosarcoma cell lines.

The key finding is that both mutant and wild-type Ras proteins contribute to tumor cell anchorage-dependent proliferation. Early siRNA silencing of the mutant Ras isoform alone caused a near-complete suppression of proliferation (Fig. 1). In comparison, the combined suppression of the remaining 2 wild-type Ras isoforms caused a less drastic but still significant reduction in tumor cell proliferation. These results suggested that wild-type and mutant Ras may have distinct functions required for tumor cell growth. Because both wild-type Ras isoforms were suppressed, the study did not address whether each wild-type isoform served redundant or distinct functions. In a similar analysis, Lim and colleagues (5) found that stable short hairpin RNA (shRNA) suppression of either

**Summary:** Although the functional interplay between mutant and wild-type Ras in driving tumor initiation and growth has been described, a clear picture of the precise ramifications and mechanisms of this association remains elusive, sometimes with conflicting conclusions. A report in this issue of Cancer Discovery tackles this question, which may have important implications for therapeutic strategies to block mutant Ras for cancer treatment. Cancer Discov; 3(1):24–6. ©2012 AACR.

See related article by Young et al., p. 112 (4).
HRAS or NRAS alone reduced the tumorigenic growth of MIA PaCa-2 cells in severe combined immunodeficient mice, suggesting distinct roles for each wild-type Ras isoform.

To determine whether the distinct roles of wild-type and mutant Ras can be explained by differences in effector signaling, the levels of activated phosphorylated ERK (pERK) and AKT (pAKT) were evaluated. Depletion of the mutant Ras isoform caused a partial reduction in basal pERK levels in all 3 tumor lines, but surprisingly, an elevation in pAKT was seen in T24 and RD cells. In contrast, depletion of the wild-type Ras isoforms increased pERK in MIA PaCa-2 and RD cells, suggesting that wild-type Ras may antagonize mutant Ras and ERK signaling. Depletion of wild-type Ras did not cause the same pAKT increase seen with silencing of mutant Ras.

Although these analyses indicate that wild-type and mutant Ras do not regulate effector signaling by the same mechanisms, they also suggest that the requirement for wild-type Ras for proliferation cannot be attributed simply to their regulation of ERK and/or AKT activation.

A second key finding was that depletion of mutant Ras increased signaling (pERK and pAKT) through the EGF receptor (EGFR). Thus, mutant Ras antagonizes EGFR signaling, possibly through ERK-mediated phosphorylation of EGFR at an inhibitory T669 residue. The sensitivity of other receptor tyrosine kinases (RTK) may also be antagonized by mutant Ras. This result suggests that cancer cells may undergo reprogramming when mutant Ras function is blocked, leading to increased EGFR signaling and activation of wild-type Ras, and thus bypassing the block in mutant Ras signaling. This finding additionally suggested that inhibition of EGFR may block this reprogramming mechanism. Consistent with this possibility, the treatment of cells depleted of mutant H-Ras with the EGFR inhibitor erlotinib caused a further reduction in T24 cell proliferation that was associated with enhanced apoptosis. EGFR dependency of T24 cells correlated with AKT activation. This synergy between mutant Ras suppression and EGFR inhibition, however, was not seen with the mutant K-Ras or N-Ras tumor lines, possibly because the increased activities of other RTKs may be associated with loss of mutant Ras function. Alternatively, the different isoforms of mutant Ras or cancers of different tissue origin may not behave identically when mutant Ras activity is blocked.

The mechanism by which RTK signaling causes wild-type Ras activation was not addressed. Whether the mechanisms described in 2 previous studies, in which either endothelial nitric oxide synthase or Sos1 were identified as mechanisms that promoted wild-type Ras activation in cells harboring mutant Ras (5, 7), are relevant for this current report is not clear.

The main implication in this study is that an effective therapeutic strategy to block mutant Ras-driven cancer growth may require concurrent inhibition of mutant as well as wild-type Ras function, and that inhibitors of RTKs may facilitate that strategy. Not surprisingly, with strong evidence for reprogramming signaling mechanisms that overcome protein kinase inhibitors, cancer cells are likely to adapt to the loss of mutant Ras. The recent studies characterizing small-molecule inhibitors of RasGEF interaction with Ras raised the issue of whether this was a worthwhile strategy to target mutant Ras-containing tumors (8, 9). The findings in this report argue that such inhibitors may be effective, but through their inhibition of wild-type rather than mutant Ras function. An issue that remains unclear is whether the effectors that support the requirements for mutant and wild-type Ras in cancer cell proliferation are distinct.

Disclosure of Potential Conflicts of Interest

No potential conflicts of interest were disclosed.

Published online January 14, 2013.

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Mutant and Wild-type Ras: Co-conspirators in Cancer

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