TP53 mutations and Lung Cancer

Not all mutations are created equal

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Summary

Mutations in TP53 are common in non-small cell lung cancer. Apart from the loss of tumor suppressor functions, TP53 mutations may result in gain of function favoring cellular proliferation, inhibition of apoptosis and genomic instability. Some TP53 mutations are more likely to affect the course of the disease than others.
In this issue of *Clinical Cancer Research*, Molina-Vila and colleagues address the prognostic significance of *TP53* mutations in patients with advanced non-small cell lung cancer (NSCLC) keeping the functional impact of specific *TP53* mutations in mind.¹ The complex genomic landscape of lung cancer induced by tobacco smoke is characterized by numerous single nucleotide variations, gene amplifications, deletions and structural variants as outlined recently by The Cancer Genome Atlas Project (TCGA).² Among several novel variants reported, one gene stands out in lung cancer and other cancers—*TP53*.³ Since the initial discovery of this “master regulator” and “guardian of the genome”, over 50 000 papers have been published on *TP53* to date; much has been learned yet there is more to be understood. That wild type *TP53* is a *bona fide* tumor suppressor and mutant *TP53* acquires novel functions facilitating survival of cancer cells against all odds is not in doubt. However, the clinical implications of *TP53* mutations in lung cancer are not so clear. Do the presence of *TP53* mutations portend a poor prognosis? Do all mutations in *TP53* produce the same effect functionally and clinically? Can targeting mutated *TP53* become the Holy Grail of cancer therapy?

*p53* (encoded by the gene *TP53*) is a stress response protein that mediates the transcription of genes in response to genotoxic stress, oncogenic signaling, DNA damage and cellular injury. Like most transcription factors, *p53* has a transactivation domain (TA), DNA binding domain (DBD) and tetramerization and regulatory domain (TD). Expression of *p53* protein is largely controlled through its degradation by the mouse double minute 2 (MDM2) E3 ligase and a related protein
MDM4. Additionally, posttranslational modification of p53 by various kinases/phosphatases and acetylases/deacetylases regulates its activity. The majority of the mutations in TP53 are either missense or nonsense mutations. Mutations in TP53 can result in one of three possible outcomes - mutations that interfere with its tumor suppressor properties (loss-of-function), mutations that confer the protein with a dominant-negative phenotype - where it binds and inactivates co-expressed functional wild type TP53, and conformational mutations that contribute to the emergence of new functions (gain-of-function- GOF). GOF mutations contribute to genomic instability, inhibition of apoptosis, cell migration and drug resistance. GOF mutations usually engage in molecular interactions that either result in the binding and inactivation of TP53 related proteins such as TP63 and TP73, or interactions with other transcriptional factors, resulting in the novel regulation of expression of several genes.

Almost all small cell lung cancers and more than half of NSCLCs harbor alterations in TP53. While TP53 mutations are predominantly G to T transversions and deletions in tobacco smokers, such alterations are infrequent in never-smokers who frequently harbor transitions. Studies that investigated the role of TP53 mutations as a prognostic marker in NSCLC, have reported conflicting results. This may be due to the molecular heterogeneity and differing functional effects specific to various TP53 genotypes, methodological issues related to the assessment of mutation status, and design issues related to small sample size and non-homogeneous groups of patients. Finally, the context in which these mutations
occur, the initiating events and other secondary molecular alterations, may matter as well.

Instead of treating all TP53 mutations the same way to assess their clinical impact, it may be sensible to categorize them in different groups based on the functional effects they induce, that is, loss of tumor suppressor effect versus GOF. Mutations involving TP53 can be classified from a structural viewpoint as “contact mutations” that affect residues directly involved in sequence-specific DNA contacts but do not alter the conformation of the p53 molecule (prototype hotspot mutation: R273H) and “conformational mutations” resulting in partial or complete loss of normal conformation of wild type p53 (prototype hotspot mutation: R175H).11 Conformational changes can interfere with the recognition of DNA binding elements that are normally recognized by wild type TP53 and uncover hitherto hidden interfaces in these DNA binding domains. Another practical way to categorize TP53 mutations is as disruptive or non-disruptive based on the location of the mutation and the predicted amino acid alterations.12 Mutations resulting in the substitution of amino-acids belonging to a different polarity and charge in the L2 and L3 regions of the DNA binding domains, or stop codon are classified as disruptive. All other mutations are categorized as non-disruptive. Importantly, these mutations have already been characterized for their cellular effects using human cell systems and mouse models. Many non-disruptive variants are GOF mutations that mediate oncogenesis through mechanisms already described.
Molina-Vila and colleagues examined retrospectively the impact of \( TP53 \) mutations in 318 patients with stage IIIB-IV NSCLC including 125 patients with epidermal growth factor receptor (\( EGFR \)) mutations. In the group of patients with \( EGFR \) wild type NSCLC, the median overall survival was significantly lower in those with non-disruptive \( TP53 \) mutation than those whose tumor cells had either wild type \( TP53 \) or with a disruptive \( TP53 \) mutation (8.5 month vs. 15.6 months respectively, \( p = 0.003 \)). This difference was seen even in the \( EGFR \) mutant group (17.8 months vs. 28.4 months, \( p = 0.04 \)), underscoring the significant effect of non-disruptive \( TP53 \) mutations independent of \( EGFR \) status. These findings were confirmed in a small independent cohort of patients with \( EGFR \) mutant NSCLC. However, these findings are directly in conflict with the results from Poeta and colleagues who reported worse outcomes in early stage head and neck cancers harboring disruptive \( TP53 \) mutants. It is possible that specific \( TP53 \) mutants may exert unique and seemingly conflicting effects based on the tissue of origin and concomitant genomic alterations. Clearly, more studies need to be done to validate or refute these observations.

Fortunately, ongoing studies by TCGA and other large-scale genomic studies will provide a large body of information on \( TP53 \) mutation status from several thousand patients with NSCLC. Integration of transcriptomic and proteomic studies will enable us to tease out the downstream effects of the various classes of \( TP53 \) mutations in the coming years. Parsing these data carefully using well curated clinical specimens and follow-up functional studies will shed more light on the \textit{in vivo} effects of various mutations involving \( TP53 \).
Disappointingly, therapeutic strategies directed towards \textit{TP53} alterations have largely failed. Many such strategies focused on the reactivation of \textit{TP53} in cancer cells, with the hope of restoring its tumor suppressor properties. Characterizing the downstream pathways activated by \textit{TP53} GOF variants is a critical first step before developing therapies aimed at functionally reestablishing the master regulator that goes awry in so many cancers.
Legend

TP53 mutation profile from cBio portal (http://www.cbioportal.org accessed April 20, 2014) is illustrated here. The data includes tissue samples from 178 patients with squamous cell and 576 adenocarcinoma of the lung.
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Figure 1:

[Diagram showing genetic markers and gene regions with associated data points and labels such as TA, L2, DBD, L3, and TD, with specific coordinates and categories like Frameshift InDels, Inframe InDels, Missense, Nonsense, and Splice site.]
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