Recommended Guidelines for Validation, Quality Control, and Reporting of TP53 Variants in Clinical Practice


Abstract

Accurate assessment of TP53 gene status in sporadic tumors and in the germline of individuals at high risk of cancer due to Li–Fraumeni Syndrome (LFS) has important clinical implications for diagnosis, surveillance, and therapy. Genomic data from more than 20,000 cancer genomes provide a wealth of information on cancer gene alterations and have confirmed TP53 as the most commonly mutated gene in human cancer. Analysis of a database of 70,000 TP53 variants reveals that the two newly discovered exons of the gene, exons 9β and 17β, generated by alternative splicing, are the targets of inactivating mutation events in breast, liver, and head and neck tumors. Furthermore, germline rearrangements in intron 1 of TP53 are associated with LFS and are frequently observed in sporadic osteosarcoma. In this context of constantly growing genomic data, we discuss how screening strategies must be improved when assessing TP53 status in clinical samples. Finally, we discuss how TP53 alterations should be described by using accurate nomenclature to avoid confusion in scientific and clinical reports.

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Introduction

A major goal of cancer research is the identification of tumor-specific vulnerabilities that can be exploited to tailor treatment to the unique genetic and epigenetic tumor profile of individual patients (1). This can be achieved as a result of the enormous progress in cancer genomics and the increasingly detailed knowledge of the genetic landscape of the most common tumor types. Single-nucleotide variants (SNV) as well as small insertions and deletions (indels) targeting cancer genes are among the most common deleterious genetic events that are scattered throughout the entire genome of the tumor (2). In this article, the term “variant” will be used to describe genetic changes (see Box A for more information on terminology).

A unique three-phase pattern of variant description is observed following the discovery of a novel cancer gene:

### Box A: How to avoid confusion: Definitions of genetic variation terminology according to the Human Genome Variation Society

**Recommended standard terms:**

1. **Variant:** every permanent genetic change.
   - **Connotation:** Neutral. Recommended by ACMG and AMP.
   - **Avoid using Mutation** to indicate the variant itself, because of its negative connotation due to frequent use as disease-causing variant instead of the broader concept variant. **Mutation** can be used to describe the process or event generating genetic variation.

2. **Affects function:** HGVS recommended modifier alternative for the term **Pathogenic** used to indicate a disease-causing effect. The term pathogenic is inappropriate for use with traits and creates confusion when used without mentioning specific context (in combination with a similar variant on the same allele) or conditions (when inherited from the father, imprinted) necessary to observe the functional effect causing disease. Germline variants in tumor suppressor genes can only be considered as having functional effects when somatic second hits inactivate the second allele in tumors.

   HGVS recommended five-tier variant classification system: affects function, probably affects function, unknown, probably does not affect function (or probably no functional effect), or does not affect function (no functional effect).

   - The ACMG and AMP guidelines still include the five-tier variant classification system relevant to Mendelian disorders, pathogenic, likely pathogenic, uncertain significance, likely benign, or benign, but recommend providing the context and inheritance pattern to clarify the context in reports.

   - **Discovery** of genetic variation is a three-phase process that usually resembles those used for other cancer biomarkers. During the discovery phase, publications precisely describe novel variants and discuss their potential pathogenicity in relation to the disease. A burst of studies then leads to the identification of novel and generally diverse variants. This phase is commonly associated with parallel reports on the mutation rate and/or clinical novelties, often published in journals with a high impact factor. Transition to the validation phase occurs rapidly when genetic and clinical data start to become redundant. During this phase, sequencing of multiple new clinical specimens mostly reveals variants that have already been described and variant diversity will begin to reach a plateau. The length of this phase is highly dependent on the number of genetic events needed to modify the targeted gene. For oncogenes that require specific events to change their function, this number tends to be limited, because most of them will be missense variants targeting a critical functional region. In contrast, tumor suppressor genes may harbor a large number of genetic events, including nonsense variants, splice variants, as well as indels of varying size scattered throughout the gene. This validation phase is vital, as it adds nuance and validates data from the discovery phase in a wide variety of clinical and/or geographical settings. Consequently, variants are either described in supplementary materials or quoted as unpublished data, leading to a decrease in reported variants. Except for a few very specific cases, the validation phase is accompanied by a decrease in the impact factor of the publishing journals. This decrease in descriptions of variants does not reflect their frequency in the disease or the incidence of their analysis, but rather a lack of interest and lack of novelty, introducing a bias against their publication. If the variants have no clinical significance, the number of studies will decrease rapidly, and then stop.

   - It has also been observed that the validation phase is associated with an increase in inconsistent studies. An extensive analysis of the various flaws associated with the publication of variants was provided by Kern and Winter in their 2006 review (84). Finally, transition to the clinical practice phase then begins for variants of clinical interest. However, publications fall off, as service laboratories do not consider reporting them in the literature to be an essential part of their work. Descriptions of novel variants then become scarce.

   - **Clinical practice** of gene variant discovery and validation: pathway to clinical practice. The discovery and validation of cancer gene variants follow several phases that resemble those used for other cancer biomarkers. During the discovery phase, publications precisely describe novel variants and discuss their potential pathogenicity in relation to the disease. A burst of studies then leads to the identification of novel and generally diverse variants. This phase is commonly associated with parallel reports on the mutation rate and/or clinical novelties, often published in journals with a high impact factor. Transition to the validation phase occurs rapidly when genetic and clinical data start to become redundant. During this phase, sequencing of multiple new clinical specimens mostly reveals variants that have already been described and variant diversity will begin to reach a plateau. The length of this phase is highly dependent on the number of genetic events needed to modify the targeted gene. For oncogenes that require specific events to change their function, this number tends to be limited, because most of them will be missense variants targeting a critical functional region. In contrast, tumor suppressor genes may harbor a large number of genetic events, including nonsense variants, splice variants, as well as indels of varying size scattered throughout the gene. This validation phase is vital, as it adds nuance and validates data from the discovery phase in a wide variety of clinical and/or geographical settings. Consequently, variants are either described in supplementary materials or quoted as unpublished data, leading to a decrease in reported variants. Except for a few very specific cases, the validation phase is accompanied by a decrease in the impact factor of the publishing journals. This decrease in descriptions of variants does not reflect their frequency in the disease or the incidence of their analysis, but rather a lack of interest and lack of novelty, introducing a bias against their publication. If the variants have no clinical significance, the number of studies will decrease rapidly, and then stop.

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   - discovery, validation, and clinical practice (Fig. 1; ref. 3). The duration of these phases, individually and globally, depends on the scientific “popularity” of the gene, the type of alteration and its clinical relevance (Fig. 1). For several genes, such as **BRAF**, for which the first variants were described in 2002, the three-phase workflow was rapidly completed due to the very limited diversity of the variants. The **BRAF** variant **NM_004333.4:c.1799T>A** (**p.Val600Glu**) is virtually the only
deleterious variant reported in a wide variety of cancers, including melanoma, papillary thyroid cancer, colorectal carcinoma, glioma, and other cancers, and successful targeted therapy has already been developed (4). The three-phase workflow is also well illustrated by the analysis of the TP53 suppressor gene. The discovery phase began in 1989 with the first description of TP53 variants in lung and colorectal cancers (5, 6). Over the following years, there was a steady increase in the number of publications describing novel TP53 alterations in most cancer types, culminating in over 10,000 variants (encompassing about 2,500 distinct mutational events) reported in 300 publications by 2001 (7, 8). More than 85% of the different missense TP53 variants reported in the various TP53 databases were identified during the discovery phase. The decline in the number of published TP53 variants began in 2002, corresponding to the beginning of the second, validation phase. The latest issue of the TP53 variant database was released in 2015 and contains a total of 60,000 variants, encompassing 1,700 different missense and nonsense variants (9). The number of novel single-base variants has not increased significantly for several years now, indicating that a saturation plateau has been reached with the discovery of all potential deleterious TP53 variants.

TP53 mutation analysis has now reached the third phase with the development of clinical guidelines for TP53 mutation testing in various settings. Germline TP53 variants have emerged as a significant cause of genetic predisposition to cancer associated with LFS (10). The most recent version of the National Comprehensive Cancer Network (NCCN) guidelines recommends TP53 mutation testing in individuals with onset of breast cancer before 31 years of age, either concurrently with BRCA1/2 testing or as a follow-up test after negative BRCA1/2 testing (NCCN Guidelines Version 1.2017, http://www.nccn.org/professionals/physician_gls/pdf/genetics_screening.pdf). Somatic TP53 mutation analysis is now widely used in clinical trials involving patient stratification based on TP53 status and in trials of novel drugs targeting either wild-type or mutant TP53 in order to activate a TP53 antitumor response. TP53 mutation screening is therefore rapidly becoming an integral part of many therapeutic or prevention strategies in clinical practice.

The TP53 Network

The transcription factor, p53 protein, is at the center of a network that integrates and transmits multiple signals, generated during various stress events to ensure cell and tissue homeostasis (11–13). These pathways include two other members of the p53 family, TP63 and TP73 (14, 15), as well as two negative regulators, MDM2 and MDM4 (previously called MDMX; ref. 16). p53 also has transcription-independent functions via a direct interaction with pro- and antiapoptotic factors in mitochondria, thereby regulating apoptosis (17).

Under normal conditions, p53 protein is maintained at low levels as a result of rapid turnover mediated by Mdm2, its main negative regulator. In response to various forms of stress, p53 becomes activated and elicits a variety of activities including cell growth arrest, apoptosis, or senescence to prevent the propagation of aberrant cells. Although these three cellular responses were originally associated with the tumor suppressor activity of TP53, their importance has recently been challenged in several mouse models (18).

Recent evidence has also linked TP53 function to regulation of metabolism and the redox balance to maintain intracellular homeostasis (19). Whether or not these functions are associated with the tumor suppressor effect of TP53 remains to be elucidated.

A discussion of all aspects of the various signaling pathways regulated by TP53 is beyond the scope of this article and recent reviews on this subject are available (12, 20, 21).

Heterogeneity of TP53 Variants

Among the 14 million new cases of cancer diagnosed in 2012, 7 to 8 million (50 to 60%) tumors harbored a somatic TP53 variant (http://globocan.iarc.fr). With a few exceptions, such as testicular cancer, neuroblastoma, or mesothelioma, TP53 variants can be detected in all types of cancer with a high degree of heterogeneity (ranging from 10% to 90%), making TP53 the most frequently mutated gene in human cancer (2, 22). Apart from variants, TP53 function can also be inactivated via other mechanisms such as amplification of its negative regulators MDM2 and MDM4 or by binding to viral oncoproteins such as E6, expressed by human papillomavirus (23, 24). In acute myeloid leukemia, hyperactivity of histone deacetylase HDAC8 prevents posttranslational acetylation-mediated activation of the p53 protein, which is essential for its tumor suppressor function (25).

Among the 60,000 tumors that harbor TP53 modifications described to date, missense alterations in the coding region of the full-length protein are the most common alterations. Approximately 1,500 different missense TP53 variants have been identified, ranging from several hot spots at positions 175, 248, or 273, reported several thousand times in many different tumors, to infrequent variants detected at very low frequencies (9). On the other hand, more than 4,000 TP53 variants are frameshift events leading to incorrect protein synthesis. This observation raises two important issues that have not been fully resolved. The first issue concerns the pathogenicity of all of these variants. Although there is no longer any doubt about the loss of function of the various hot spot variants, the loss of function of less frequent variants, particularly those that have been described at very low frequencies, remains unclear (26). This is a key issue for genetic counseling, as the use of NGS has led to the discovery of very rare novel germline TP53 variants of unknown significance (VUS) in the normal population (27). Multiple methodologies have been developed to assess the functional effect of TP53 variants, but their specificities and sensitivities remain low for uncommon variants (28–30).

The second issue concerns the heterogeneity of TP53 variants. Missense mutant proteins exhibit severely impaired transcriptional activity as well as a gain of oncogenic activities that promote tumorigenesis, leading to the notion that tumors are addicted to mutant p53 (22, 31, 32). Furthermore, a wealth of in vitro data as well as data from animal models indicate that the oncogenic activities of TP53 variants are heterogeneous and can vary according to the tissue type and the genetic background of the cells (33–36). In breast carcinoma, the spectrum of TP53 variants is subtype specific, each one with a different prognostic relevance (37). Classifying TP53 status as either “wild-type” or “mutant” is therefore an oversimplification, as TP53-null tumors due to loss of p53 expression have a different phenotype compared to tumors overexpressing an oncogenic TP53 variant.
Clinical Relevance of TP53 Mutation

Somatic TP53 mutation in human tumors

The predictive and prognostic value of TP53 status in various types of cancer has been the subject of several thousand studies with conflicting findings and limited clinical application, and a review of this literature is beyond the scope of this article (38–40). These discordant results are due to multiple causes, such as the methodology and strategy used to assess TP53 status, the heterogeneity of tumor types, the genetic background of the tumor, and the large number of different TP53 variants.

To circumvent some of these problems, TP53 variants have been tentatively divided into different categories according to their localization on the protein, the type of variant (missense versus indel) or the evolutionary conservation of the mutated residue. Although some of these classifications have improved the clinical value of TP53 status for head and neck cancer (30), breast carcinoma (41), or diffuse large B-cell lymphoma (42), no clear rationale to definitively score TP53 variants has yet been defined.

One of the best examples of the clinical value of TP53 status is chronic lymphocytic leukemia. Although the frequency of TP53 variants is very low in asymptomatic patients, the presence of TP53 variants is usually associated with poor prognosis characterized by advanced clinical stage, rapid disease progression, chemoresistance, and shorter overall survival (43). The recent CLL8 trial identified TP53 variants as one of the strongest prognostic markers in patients receiving standard-of-care first-line therapy (44). An European consortium (European Research Initiative on CLL, ERIC) has developed and standardized the TP53 mutation analysis in CLL to allow better patient stratification (45).

The development of liquid biopsies and analysis of circulating cell-free tumor DNA (ctDNA) as a surrogate for tumor genotyping has raised renewed interest in TP53 variants, as the high gene mutation rate makes TP53 an attractive biomarker (46). ctDNA analysis during therapy can provide early information about treatment resistance related to the emergence of TP53 variants in response to the selective pressure of therapies. In many tumor types, such as lung, gastric, high-grade serous ovarian, or breast carcinoma, TP53 variants are an early event that can be detected in ctDNA from patients with early-stage disease (47, 48). The possible role of detection of TP53 variants in ctDNA from individuals at high risk of cancer, allowing early clinical diagnosis and resulting in a higher cure rate, constitutes an exciting challenge for the future.

Because of the extremely high frequency of missense variants, the oncogenic gain of function of many variants and the fact that cancer cells overexpress the mutant protein, TP53 is a promising target for the development of therapies designed to induce inhibition or restoration of p53 function by small molecules (49). This prospect is supported by recent studies showing that reconstitution of p53 activity leads to the suppression of established tumors in mouse models (50, 51). Molecules targeting mutant p53 have been developed and are currently at the stage of clinical trials (52). Components of the various pathways leading to accumulation of mutant p53, such as hsp90 (53), or gain of function, such as TP73, can also be targeted (54). More than 150 clinical trials related to TP53 pathways are currently under way, including the use of novel molecules that specifically target mutant p53 (55).

Germline TP53 variants in hereditary cancer predisposition syndromes

Germline TP53 variants were first identified in individuals from families with LFS (36). LFS is a rare autosomal dominant syndrome, in which patients are predisposed to a wide variety of cancer types, with a young age at onset of malignancies, and the potential for multiple primary cancer sites during the affected individual’s lifetime (57). A Li–Fraumeni-like (LFL) syndrome with less stringent criteria than LFS was subsequently described. The frequency of TP53 variants in LFS and LFL is 70% and 20% to 40%, respectively. LFS and LFL present a similar spectrum of germline and somatic TP53 variants with missense and indel variants scattered throughout the gene. The frequency of de novo TP53 mutation (creating variants in the germ cells of one of the parents or in the fertilized egg) has been estimated to be as high as 30%, which is very high compared with the frequency of other tumor suppressor genes such as BRCA1/2 (less than 5%; ref. 58). Identification of TP53 germline variants in LFS and LFL could potentially be beneficial for individual patients by allowing initiation of surveillance, early cancer detection, and/or prevention (59).

A specific pathogenic germline variant arising from a founder event (c.1010G>C, p.(Arg337His)) has been identified in Brazilian children with adrenal cortical carcinomas (ACC; ref. 60). The prevalence of this variant is particularly high in Southern Brazil, where it can as high as 0.3% in the general population (61) and is also common in patients with LFS and LFL from this geographical region (62).

Recent studies have detected germline TP53 variants in various cohorts of BRCA1/2-negative patients with early onset of breast cancer, indicating that the TP53 gene should be added to the cancer gene panel used for screening in these patients (63–66).

Assessing TP53 Status in Human Cancer

TP53 mutation analysis has now reached the clinical practice phase, as cancer patients are likely to benefit from this information. Somatic TP53 variants were initially reported to cluster within DNA sequences encompassing exons 5 through 8, encoding the core DNA-binding domain of the protein (6, 67). The majority of subsequent studies therefore exclusively focused on these regions, introducing a major bias with underrepresentation of variants that may occur in other regions of the gene. Over the last decade, most sequencing centers encompass the entire coding region of the gene, and this expanded coverage, together with the recent use of next-generation sequencing (NGS) that covers all TP53 exons, has revealed that up to 10% of TP53 variants are localized in exons 2 to 4 and exons 9 to 11 (9). Of note, the spectrum of these variants differs from that of variants occurring in exons 5 to 8, as they mostly consist of indels that usually lead to a TP53-null phenotype (9). The discovery and validation phases have clearly demonstrated the pathogenicity of these variants as well as their clinical utility; screening exons 2 to 11 is now highly recommended (Fig. 2).

For a long time, the TP53 gene was considered to be expressed as a single protein of uniform size (mRNA derived from exons 2–11, encoding 393 amino acids). However, the more complex architecture and expression pattern of the TP53 gene has only been recognized in recent years (Fig. 3 and Supplementary Fig. S1). TP53 mobilizes various mechanisms to transcribe at least eight different mRNA isoforms, which are generated by alternative splicing or alternative promoter usage (68, 69). Collectively, these
mRNAs have the potential to give rise to up to 12 different proteins, although the exact expression level, tissue distribution, and biological function of each of these protein variants are poorly understood. This complex expression pattern implies that sequences located in TP53 introns and involved in the production of alternative forms of the protein may have a critical impact on overall biological functions of p53 and may therefore be important target regions for somatic or germline variants. Mouse models have shown that constitutive expression of a short p53 isoform lacking the transactivation domain (A122p53) leads to chronic inflammation and a different and more aggressive tumor spectrum compared with TP53-null mice, suggesting that this isoform could act as a dominant oncogene (70).

Intron 9 of TP53 is a typical example of this type of situation, as it has now been clearly established that intron 9 contains two novel alternative exons, each one encoding a different carboxy-terminus for the p53 protein (Fig. 2; ref. 71). The biological functions of these novel p53 protein isoforms, p53β and p53γ, have not yet been elucidated. Both proteins lack part of the oligomerization domain and have different transcriptional activities compared with full-length p53 (72).

Because of the bias toward screening for somatic variants exclusively in exons 5 to 8, these alternative exons have been excluded from most studies that used Sanger sequencing to assess variants. The increasing use of NGS strategies that address a wider range of sequences within the TP53 locus demonstrates that significant variants may occur within these alternative exons. The latest version of the UMD TP53 database containing 78,000 TP53 variants derived from 4,200 curated and annotated publications including recent whole-genome sequencing studies was released in December 2016. Analysis of this database identified several somatic nonsynonymous variants in the coding region of exon 9β and five nonsynonymous variants in the coding region of exon 9γ (Fig. 3 and Table 1). Furthermore, two variants in the untranslated region of exon 9β and four variants in a splice site common to both alternative mRNA isoforms were also identified (Fig. 3 and Table 1). Analysis of the latest issue of dbSNP (build 148, https://www.ncbi.nlm.nih.gov/projects/SNP/snp_summary.cgi) also showed that numerous synonymous and nonsynonymous germline variants are localized in introns 9β and γ (Table 1). The clinical significance of these variants is unknown at the present time, but their discovery warrants further analysis to validate whether or not screening of this region could be important to determine TP53 status.

Another example of the importance of including TP53 intronic sequences in mutation screening strategies is the identification of a hotspot region for rearrangements occurring in intron 1. More than 20 years ago, recurrent rearrangements in TP53 intron 1 (~10 kb) were identified by Southern blot, but at the time this information was not included in guidelines for mutation screening (73, 74). A recent study of intron 1 rearrangements found cosegregation with cancer risk in four generations of a family with LFS features, suggesting this genetic alteration may predispose to a wide range of cancers (75). However, intron 1 rearrangements have been observed in only one type of sporadic cancer, osteosarcoma, where they occur in about 50% of cases (75, 76). Of
**Figure 3.**

TP53 variants detected in exon 9β and exon 9γ. Alternative splicing events in TP53 intron 9 lead to the expression of β and γ isoforms. Exons 9β and 9γ have different splice acceptor sites, but share the same donor site (blue AG and GT sequence, respectively). Due to the marked overlap between the two exons, it is possible that substitutions localized in the translated region of exon 9β impair exon 9γ splicing. The main splicing event occurs between exon 9 and 10. Somatic variants detected in human cancer are shown in red, whereas germline variants from dbSNP are shown in green. See Table 1 for more information. The intron 9 splice donor site contains three single-nucleotide substitutions and one insertion in three different tumors. The NC_000017.10:g.7576522_7576523insCTT probably has a deleterious effect on splicing. The substitution at the stop codon (NM_000546.5:c.993+1T>G) is predicted to add 17 novel amino acid residues to the 10 residues encoded by exon 9β. All these variations are concentrated within a narrow 150-bp region of intron 9, which is 2,800 nucleotides long. A total of 22 germline variants, shown in green, have been identified and are associated with an increased risk of cancer. Overall, these data indicate that TP53 exon 9β and exon 9γ are targeted by substitutions in human cancer and contain numerous germline variants. Due to the importance of TP53 status in the evaluation of patients with multiple primary cancers or a strong family history of cancer, analysis of exons 9β and 9γ is now warranted to more clearly determine the clinical significance of germline variants in this region.

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Note, osteosarcoma has long been considered to be a type of cancer in which missense TP53 variants were relatively rare, and it has been proposed that amplification of MDM2, rather than TP53 variants, was a key mechanism for inactivation of the p53 protein in these cancers (77). The detection of intronic rearrangements in a large subset of human osteosarcoma suggests that this cancer should also be considered to have a high rate of somatic TP53 aberrations. In most cases analyzed to date, rearrangements in intron 1 led to balanced translocations involving different chromosomes, apparently without preference for a specific translocation product. The sites of breakpoints for rearrangements in intron 1 currently remain unclear. Ribi and colleagues have documented seven rearrangements that all occurred within a defined region of 1.7 kb (75). In contrast, in another study, Chen and colleagues (76) identified breakpoints occurring across the entire sequence of intron 1.

Several N-terminally truncated p53 isoforms are encoded by transcripts generated by a promoter localized in intron 4 of the TP53 gene (Supplementary Fig. S1). It is conceivable that variants localized in this region would impair the synthesis of several p53 isoforms. This question has yet to be resolved, and a discovery phase will be necessary to investigate further.

**The Importance of Rigorous Description of Genetic Variants and Their Effects**

Most researchers and clinicians like to describe genetic variants in a tangible way in terms of the protein. Amino acid

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(Continued on the following page)
Box B: Describing TP53 variants unambiguously

1. Use the official HGNC gene symbol: TP53
2. Specify the genomic reference sequence. For next-generation sequencing, use the chromosomal accession and version number NC_000017.10 for genome build GRCh37.p13 or NC_000017.11 for genome build GRCh38.p2. Do not replace by chr 17!

For diagnostic purposes, preferably use the stable Locus Reference Genomic Sequence LRG_321 (http://ftp.ebi.ac.uk/pub/databases/lrgex/LRG_321.xml). See Dalgleish and colleagues (http://www.genomemedicine.com/content/pdf/gm145.pdf; ref. 87) and Supplementary Fig. 2A and B.

3. Use HGVS nomenclature (http://varnomen.hgvs.org/) to describe genetic variants at all different levels
4. All variants must be reported at the genomic DNA (g.) and coding DNA level (c.). The genomic reference sequence must cover the entire gene, including the promoter and the 3' and 5' untranslated regions.

Example: genomic description LRG_321t1:g.18749G>A, coding DNA: LRG_321t1:c.818G>A

Alternative: the accession and version number of the corresponding RefSeq Gene NC_017013.2. Note: the annotation of this reference sequence may change without version update.

5. All variants should be reported at the RNA level (r.). Example: LRG_321t1:r.818G>A (cDNA sequenced) or LRG_321t1:r.818G>A (cDNA not sequenced)

6. All variants should be reported using HGVS nomenclature at the protein level (p.). Example: LRG_321p1:p.Arg273His (cDNA sequenced) or LRG_321p1:p.Arg273His (tDNA not sequenced)

7. Predicted effects at the RNA and protein level should be indicated in parentheses.

8. A dbsNP entry (rs number) is insufficient to unambiguously describe the genetic variant found in an individual, because the alleles are not specified.

9. Somatic variant: Variant generated by a somatic mutation event. Variants should only be labeled as somatic when normal tissue from the same individual tested negative. When normal tissue from the same individual tested positive, the test has revealed a germline variant. When normal tissue from the same individual was unavailable and the variant has not been transmitted by one of the parents, the variant should be labeled as detected in tumor (tissue).

names are more distinct and the numbers of amino acids in reference sequences is less than the number of nucleotides in the corresponding reference sequences. Due to the complexity of the human genome and the existence of genes with multiple transcripts and protein isoforms, description of the numerous variants associated with genetic diseases has become complicated and can lead to erroneous descriptions and growing confusion in the genetics community. For more than 15 years, the Human Genome Variation Society (HGVS) has provided guidelines for variant terminology and nomenclature (Box A to D; ref. 78). The consistent use of a uniform
nomenclature in the management of DNA sequence variations is critical for concise communication of diagnostic testing and genetic risk assessment. The importance of nomenclature has been recognized in the standards and guidelines for the interpretation of sequence variants recently published by the American College of Medical Genetics and Genomics (ACMG) and the Association for Molecular Pathology (AMP; ref. 79). These guidelines are partly based on the HGVS guidelines for variant interpretation (83).

To what degree does TP53 loss of function induced by targeting certain upstream or downstream components, such as MDM2 or MDM4 amplification or microRNA dysregulation, resemble that induced by TP53 variants?

What is the contribution of TP53 variant heterogeneity to the phenotype of the tumor? (missense versus indel variants, hot spot versus non-hot spot variants)

What is the contribution of TP53 isoforms to tumor phenotype?

What is the contribution of germline TP53 mutations in familial cancer unrelated to LFS and LFL?

Is there any tumor or cell type specificity for loss and/or gain of function of TP53 variants?

Which drugs would be the most effective on tumors with functional and nonfunctional p53 pathways?

What is the impact of synonymous variants in TP53 and codon usage on p53 protein expression and function?

Box C: Eliminating sources of confusion when reporting assay results in the literature

 Specification of transcripts and protein isoforms.

TP53 transcripts should be specified using LRG_321 followed by the t1 to t8 suffixes (http://ftp.ebi.ac.uk/pub/databases/lrgex/LRG_321.xml). p53 protein isoforms should be specified using LRG_321 followed by the p1 to p13 suffixes. See Soussi and colleagues for examples (83).

Variants in the TP53 gene may affect its 8 transcripts and 12 protein isoforms in different ways. Researchers should be aware of this variation when analyzing TP53 functional effects using different assays at the RNA and protein level. If possible, the transcripts and protein isoforms analyzed by the assays should be specified when describing their results to avoid confusion. Validation of the ability of common p53 assays to detect various transcripts and protein isoforms could help to resolve existing discrepancies and seemingly contradictory data in the literature and databases.

Box D: TP53 variants in human cancer: Unresolved questions

Which cancer types and/or subtypes will benefit the most from determination of TP53 status?

To what degree does TP53 loss of function induced by targeting certain upstream or downstream components, such as MDM2 or MDM4 amplification or microRNA dysregulation, resemble that induced by TP53 variants?

What is the contribution of TP53 variant heterogeneity to the phenotype of the tumor? (missense versus indel variants, hot spot versus non-hot spot variants)

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What is the contribution of germline TP53 mutations in familial cancer unrelated to LFS and LFL?

Is there any tumor or cell type specificity for loss and/or gain of function of TP53 variants?

Which drugs would be the most effective on tumors with functional and nonfunctional p53 pathways?

What is the impact of synonymous variants in TP53 and codon usage on p53 protein expression and function?

Conclusions

Accurate assessment of TP53 status is essential for optimal patient care, but several major questions remain unresolved (Box D). The recent discovery of TP53 variants within regions outside the sequences encoding the canonical form of the p53 protein calls for reconsideration of the guidelines for TP53 mutation screening in cancer patients. The use of NGS readily allows increased coverage of TP53 sequences with no significant increase in cost or analysis time. However, implementing TP53 intrinsic and alternative exonic sequences in NGS depends on the selection of appropriate regions by probes deduced from databases derived from the Consensus Coding Sequence Project (CCDS) or other similar databases. Only the recent versions of these databases include full information on alternative TP53 exons, but it remains unclear whether this information is taken into account by the manufacturers of the various commercial products used for exome sequencing. Moreover, many standard bioinformatic pipelines used for the identification of somatic variants are tailored to exclude intrinsic TP53 variants because they were not thought to have any functional significance. Therefore, large-scale studies on the precise clinical significance of TP53 variants in introns and alternative exons are now required to improve our understanding of the significance of these regions (Box D). In the meantime, a pragmatic recommendation would be to consider the entire sequence of the TP53 gene for mutation screening strategies using NGS in sporadic cancers as well as in the germline of subjects who meet the criteria for TP53 mutation testing (80–82).

Disclosure of Potential Conflicts of Interest

T. Zenz reports receiving speakers bureau honoraria from Gilead and is a consultant/advisory board member for Abbvie. No potential conflicts of interest were disclosed by the other authors.

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References

76. van Duren JT, Antonarakis SE. Mutation nomenclature extensions and suggestions to describe complex mutations: a discussion. Hum Mutat 2000;15:7–12.
Recommended Guidelines for Validation, Quality Control, and Reporting of TP53 Variants in Clinical Practice


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