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TP53 dysfunction in chronic lymphocytic leukemia: clinical relevance in the era of B-cell receptors and BCL-2 inhibitors

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ABSTRACT

Introduction. Patients with *TP53* dysfunction, assessed by del(17p) or *TP53* mutations, respond poorly to chemo-immunotherapy and fare better with the new therapies (BCR and BCL-2 inhibitors); however, it is unclear whether their response is similar to that of patients without anomalies or whether there is currently an adequate determination of *TP53* dysfunction.

Area covered. A literature search was undertaken on clinical trials and real-world experience data on patients with *TP53* dysfunction treated with different protocols. Moreover, data on the TP53 biological function and on the tests currently employed for its assessment were reviewed.

Expert opinion. Although *TP53* dysfunction has less negative influence on the new biological therapies, patients with these alterations, particularly those with biallelic inactivation of *TP53*, have a worst outcome with these therapies than those without alterations. At present, a determination of *TP53*, particularly with next generation sequencing (NGS) methodologies, may be sufficient for the identifications of the patients unsuitable for chemo-immunotherapy, although integration with del(17p) would be advisable. For the future, more extensive determinations of the *TP53* status, including functional assays, may become part of the current armamentarium for a better patient stratification and treatment with newer protocols.

Keywords: BCR inhibitors, BCL2 inhibitor, Chronic Lymphocytic Leukemia, Clinical outcome, del(17p), Ibrutinib, Idelalisib, Venetoclax, *TP53* mutations.

Article Highlights

- *TP53* dysfunction is operationally defined by the presence of del(17p) and/or *TP53* mutations.
- *TP53* dysfunction is one of the major causes of resistance to chemo-immunotherapy.
- BCR or BCL-2 inhibitors provide an increased likelihood of survival than chemo-immune therapy for patients with *TP53* dysfunction.
- Some exploratory analysis of clinical trials as well as real world evidence, suggest that *TP53* dysfunction, especially in the biallelic inactivation form, continues to have a negative influence on the clinical outcome of patients treated with the new biological therapies.
- New and more stringent laboratory tests to evaluate the residual P53 protein function in patients with *TP53* mutations may plausibly lead to a better risk stratification of patients treated with old and new BCR and BCL-2 inhibitors.

1.0 INTRODUCTION

The strategy of chronic lymphocytic leukemia (CLL) treatment is rapidly changing, since several new biological agents, acting at different levels of leukemic cell metabolism, have been approved or are in advanced experimental phases. These new drugs, with improved efficacy and more favorable toxicity profile, are used alone or are integrated into pre-existing therapeutic protocols [1]. The biological agents currently employed include a glycol-engineered monoclonal anti-CD20 antibody (Obinutuzumab, OB), B-cell receptor (BCR) signaling inhibitors [Ibrutinib (IB) and idelalisib (IDELA)], and the BCL-2 inhibitor venetoclax (Ven). These [2],represent the major subjects of this review.

In the chemotherapy era and even when monoclonal antibodies have been added, it was widely recognized that certain cytogenetic lesions conferred resistance to chemotherapy [3–5]. This was particularly true when a deletion of the short arm of chromosome 17 [del(17p)] was present, suggesting that a *TP53* gene dysfunction was responsible for chemo-immunotherapy resistance, since the site of chromosomal deletion includes the *TP53* locus. Further observations indicated that also *TP53* mutations could confer resistance to chemo-immunotherapy[6] and del(17p) and/or of *TP53* mutations were considered indicative of *TP53* dysfunction. The newer therapies have contributed in part to overcome the poor performance of the chemo-immunotherapy in patients with these alterations, although several issues remain to be clarified. In addition, further studies on *TP53* mutations have indicated the need for refining the current concepts of *TP53* dysfunction. These issues will be the subjects of the present review.

1.0 Chemo-immunotherapy

The addition of the anti-CD20 monoclonal antibody rituximab (R) to fludarabine-cyclophosphamide (FCR) or bendamustine (BR) has led to a remarkable improvement in overall survival (OS) of young and elderly patients, particularly those with a somatically mutated immunoglobulin heavy chain variable region gene (*IGHV*) [7–11], or with an unmutated *IGHV*

gene and a distinctive gene expression profile signature of the leukemic cells [12]. These therapies can induce a minimal residual disease (MRD) negativity[13,14], and a long-term PFS in low-risk CLL patients [1]. The FCR CLL8 clinical trial, demonstrated that patients with del(17p) or *TP53* mutations had a more aggressive clinical course than patients without these abnormalities, with a predicted PFS and OS of roughly 1 and 2-3 years, respectively [4]. A *TP53* dysfunction defined based upon the presence of del(17p) and/or TP53 mutations also was associated with a markedly inferior outcome in BR treated patients [5]. The independent prognostic role of del(17p) and *TP53* mutation has been underlined by the CLL International Prognostic Index (CLL-IPI), which determined that the risk score of the *TP53* status was 3 times higher than that of age and of clinical stage, and two times higher than that of *IGHV* gene unmutated status [15]. Noteworthy, the *TP53* status was considered as a composite factor [i.e. either del(17p) or TP53 mutations] based on the absence of a statistical association between the presence of the sole del(17p) *versus* the sole TP53 mutation or between the presence of a single marker *versus* the presence of both. CLL-IPI has been widely confirmed for patients undergoing chemo-immunotherapy[16–19].

2.0 Targeted new agents

2.1 BCR- inhibitors

Several phase 3 trials have contributed to the switch from chemo-immunotherapy to BCR-inhibitors as summarized in Figure 1. IB proved significantly superior to any comparator drug in terms of PFS and OS, in both treatment naïve[20–25] and relapse/refractory (RR)-CLL patients [26] a finding which changed the treatment paradigm in both clinical settings. Presently, IB continuous use until progression or toxicity is indicated. Besides IB, the current recommendations for RR-CLL case treatment include IDELA in association with R (IDELA-R). A definitive choice between protocols is frequently dictated by comorbidity or expected toxicity profiles. Notably, IDELA-R was superior to R alone [27] commonly used in frail cases unsuitable for chemotherapy (Figure 1).

The addition of IB[28] or IDELA[29] to BR was investigated in two phase 3 randomized trials on RR cases. IB and IDELA in combination with BR were superior to BR alone, reducing the risk of both disease progression and death of about 80% and 40% in the IB trial, and of 67% and 38% in the IDELA protocol, respectively (Figure 1). The absence of an additional control arm (i.e. IB or IDELA-R alone) represented an unfortunate limitations in both studiesto indicate the clinical benefit of BR, estimated in previous studies as an 18 month PFS when used as first salvage treatment after FCR, regardless of *TP53* aberrations and/or refractoriness to prior therapy [30] A real-world indirect comparison study showed that BR and IB could be similarly effective in terms of OS when used as first salvage treatment in patients without del(17p) [31]. The retrospective nature of this study suggests caution, however, and this study requires caution and the effectiveness of BR is effective in a RR setting remains to be ascertained.

Despite of the superior performance of the BCR inhibitors in all experimental settings reported in Figure 1, the question of whether such superior results are observed also in high-risk patients defined by the presence of a *TP53* dysfunction (i.e. del(17p) and/or *TP53* mutations) remains open. Explorative analyses of high-risk groups demonstrated better outcomes in both treatment naïve and RR cases (Figure 2). An exploratory analysis of the IB arm of the Resonate trial (median follow-up 65 months) in the RR setting[32] showed a significantly longer median PFS of 75 patients without *TP53* mutations compared with 79 cases with *TP53* mutations (56.9 *versus* 40.7 months) (HR: 1.731; 95% CI: 1.156-2.593). Conversely, an analysis of the IDELA-R arm of Study 165 trial[27] indicated no differences between cases with or without *TP53* dysfunction (HR: 1.03; 95% CI: 0.62-1.72). However, the higher incidence of host- and disease-related risk factors in the IDELA-R trial could have played a major role, as these additional confounding factors may have limited, if not overridden, the prognostic impact of the *TP53* dysfunction. Brown et al. [33] focused on an exploratory subset analysis of 38 patients with loss of *TP53* function defined by the both del(17p) and *TP53* mutation compared with 68 cases with one or neither of these abnormalities. Patients with both abnormalities had an inferior PSF (P=0.0381), while the PFS of the cases with

either del(17p) or *TP53* mutation was not significantly inferior to that of patients without abnormalities (P=0.1306). Further information came from the analysis of RR patients with del(17p) treated with IB in three different studies [34]. The median PFS of cases with del(17p) and complex karyotype (CK) (n=14, 67%) was significantly shorter than that cases with del(17p) without CK (n=7, 33%) (26 *versus* 52 months), indicating that additional abnormalities, besides *TP53* dysfunction may contribute to the outcome following BCR inhibitors treatment.

2.2 BCL-2 inhibitor

Up-regulation of the anti-apoptotic BCL-2 gene, an almost universal feature of CLL clones ([35]) causes overexpression of the BCL-2 protein, which prevents the activation of the intrinsic/mitochondrial apoptotic pathway [35]. This up-regulation is related to several factors, including the constitutive activation status of CLL cells, the numerous activating signals delivered to CLL cells by the micro-environment and epigenetic regulations. In the CLL cases characterized by del (13q14), the loss of the miR15/miR16 locus, located at the deletion site, contributes to BCL-2 up-regulation, given the inhibitory effect of these miRs on BCL-2 expression [36]. Ven binds to the BCL-2 protein and prevents its subsequent binding to a number of pro-apoptotic proteins, such as BAK1, BAX and BOK [37]. Since the latter proteins can cause mitochondrial damage and induce apoptosis, when freed from BCL-2 control, Ven has a strong pro-apoptotic effect on CLL cells [37]. CLL cells with or without *TP53* alterations are equally sensitive to Ven in vitro[38]. In a phase 1, dose-escalation study, Ven proved capable of inducing ORR in 71% of RR patients with del(17p) [(16% of whom reached complete remission (CR)] *versus* 80% of ORR observed in those without this alteration [39]. Notably, cases with del(17p) experienced a median PFS of 16 months (95% CI, 11-25), whereas 71% of patients (95% CI, 57-81) without del(17p) were progression-free at 15 months [39]. In a phase 2 multicentre study, RR-CLL patients with del(17p) were treated with once daily Ven, with the well-known weekly dose ramp-up schedule. The ORR was 79.4% (95% CI 70·5–86.6), with 1-year PFS and OS of 72% and 86.7%, respectively [40]. A more recent extended and updated analysis showed 2-year PFS and OS of 54% and 73%, respectively[41].

Since R increases the cytotoxic capacity of Ven on CLL cells in vitro [42], the VenR combination was used and compared to BR in a RR-CLL setting in the phase 3 Murano trial[43]. The risk of progressing was significantly reduced in the VenR arm (HR, 0.13; 95% CI, 0.05 to 0.29) compared to the BR arm. Interestingly, the clinical benefit of the BCL-2 inhibitor was maintained in the subgroup of patients with del(17p) (PFS at 2-year 81.5% *versus* 27.8%).

Recently, FDA approved Ven for CLL first-line therapy based on the CLL14 study, in which CLL patients with comorbidities were randomized to receive VenOB or CHBL-OB [44]. The estimated 2-year PFS rate was significantly higher in the VenOB group than in the CHLB–OB group (88.2% [95% CI, 83.7% to 92.6%] vs. 64.1% [95% CI, 57.4% to 70.8%]). A superior clinical benefit was also observed in patients with *TP53* dysfunction [44].

The analysis of the numerous clinical trials reported above may lead to some preliminary conclusions. First, the presence of markers of potential *TP53* dysfunction, such as del(17p) and/or *TP53* mutations, represent negative indicators of response in patients undergoing chemo- or chemo-immuno therapies. Second, BCR or of BCL-2 inhibitors provide an increased likelihood of longer PFS or of OS than chemo-immune therapy for this patient group. Nevertheless, it remains to be determined whether the patients with or without TP53 dysfunction present a similar oucome when treated with the new drugs. Finally, several considerations raise the issue of whether the methodologies so far universally employed to measure *TP53* dysfunction are adequate to provide information on this complex scenario, as it will be discussed below.

2.3 Real-world experience

Given the difficulties in assessing the exact role of *TP53* dysfunction in the outcome of treatments with the new drugs and particularly with BCR inhibitors, we analyzed the "real-world evidence", which is becoming progressively more relevant to confirm or disprove the results of clinical trials [45].

Salles and colleagues investigated the efficacy of IB *versus* other chemo-immunotherapies in treatment-naïve and RR-CLL patients [46] although the issue of the *TP53* dysfunction was not

addressed. The real-world data were compared with those of two randomized registration trials. IB reduced significantly the risk of PFS and OS both in treatment-naïve (adjusted HR for PFS: 0.23, 95% CI: 0.14–0.37; P<0.0001; adjusted HR for OS: 0.40, 95% CI: 0.22–0.76; P=0.0048) and in RR setting (adjusted HR for PFS: 0.21, 95% CI: 0.16–0.27; P<0.0001; adjusted HR for OS: 0.29, 95% CI: 0.21–0.41; P<0.0001) *versus* chemo-immunotherapies regimens.

Results on 428 real-world cases, including roughly 45% with either del(17p) and/or *TP53* mutations from 106 centers throughout France treated with IB were recently reported [47]. IB efficacy and safety was confirmed although no specific data on the group with *TP53* dysfunction were reported.

Dimou and colleagues published efficacy and safety real-world data from IB single drug therapy from a single Greek center [48]. Thirty–seven percent of 11 cases treated in first-line and 22% in $\geq 2^{nd}$ line showed either del(17p) or *TP53* mutation. All cases were still on IB in the 1^{st} line subgroup, while 10% of RR cases progressed.

The Swedish group reported the results of a long-term real-world compassionate IB therapy study on RR-CLL patients [49]. OS was significantly longer in the 42 patients matching the Resonate inclusion criteria (P=0.03) compared with that of the 53 who did not match these criteria. Of interest, in contrast to the early report from the same authors [50], the negative survival impact of del(17p)/TP53 mutation was no longer significant.

Cases with RR-CLL and del(17p) showed a trend toward significance for OS (HR=1.45, 95% CI 0.97-2.18, P=0.07) compared to cases without del(17p) in a real-word series treated with IB [51]. This result was confirmed in a multivariate model in which the four markers constituting the BALL score (β2-microglobulin and lactate dehydrogenase levels, anemia and time from initiation of last therapy <24 months) also were introduced [52].

Patients with del(17p) and/or *TP53* mutation had significantly shorter PFS (HR 2.7, 95% CI 1.08-6.7, P=0.034), but not a shorter OS (HR 1.78, 95% CI .55-5.74, P=0.332) than those without these alterations in a series of 141 Ven treated CLL patients, focusing on outcome following Ven

discontinuation[53]. *TP53* dysfunction remained a significant independent predictor for shorter PFS in a multivariate model including *TP53* dysfunction, CK and prior IB therapy (HR 2.8, 95% CI 1.22-6.4, P=0.03).

The role of *TP53* gene dysfunction in predicting OS was also investigated in an independent real-world cohort of 622 CLL cases treated with IB, IDELA or Ven (Morabito et al., in preparation). CLL patients were stratified into three groups [*TP53*mut/del(17p), *TP53*mut/no-del(17p) and *TP53*wt/del(17p) cases]. OS was significantly shorter in *TP53*mut/del(17p) cases, while the Kaplan-Meier curve of the *TP53*wt/del(17p) group overlapped to that of the *TP53*wt/no-del(17p) group, indicating that only the concomitant presence of the two lesions determined an inferior outcome. In a multivariate model, *TP53*mut/del(17p) status remained independently associated with OS together with increased LDH levels, anemia, lines of preceding therapies and the exposure to other new drugs.

2.4 Therapies with new generation biological agents.

Some CLL trials with next generation drugs are still ongoing. Among those reported in Table 1, only a few have available information of specific results on high-risk patients with *TP53* alterations. Acalabrutinib (Acala), a highly selective inhibitor of Bruton's tyrosine kinase (BTK) with negligible off-target activity, showed an interesting safety and efficacy profile in a phase 1–2 multicenter study in patients with RR-CLL. Among the 18 patients with del(17p), the response rate was 100%[54]. Acala monotherapy was superior to IDELA-R or BR in prolonging PFS in patients with RR-CLL; this improvement was also observed in the group of patients with del(17p) (HR 0.21, 95%CI 0.07-0.68) and *TP53* mutation (HR 0.24, 95% CI 0.11-0.56) [55]. In the Phase 3 ELEVATE-TN study, PFS improvement with Acala-OBI or Acala *versus* CHBL-OBI was consistent across subgroups examined including del(17p) (HR 0.13, 95%CI 0.04-0.46) for Acala-OBI; HR 0.20, 95%CI 0.06-0.64 for Acala monotherapy) [56]. Finally, although Ven is currently the only commercially available BCL-2 inhibitor, research dealing with selective inhibitors of other

molecules of the BCL-2 family members, i.e. BCL-xL and MCL-1, is ongoing. However, no clinical trials have been opened yet.

3.0 TP53 gene, mutational status and P53 protein function.

The definition of *TP53* dysfunction, provided by del(p17) or *TP53* gene mutations may leave some imprecision. Moreover, not all mutations may be equal since different mutations may impact differently on the *TP53* protein function and certain *TP53* gene mutations may also cause impairment of the function of the unmutated allele. Therefore, we have deemed necessary to analyze a number of these aspects in the paragraphs below since they may be relevant for the interpretations of the existing data on clinical trials and for the design of new ones.

3.1 TP53 gene

TP53 is an evolutionary highly conserved tumor suppressor gene [57], located at the telomeric portion of the short arm of chromosome 17 (17p13.1), encoding a protein of 393 amino-acid long with transcription factor activity. Consistent with its tumor suppressor activity is the presence of *TP53* mutations as a hallmark of the hereditary cancer predisposition disorder Li-Fraumeni syndrome [58].

The P53 protein consist of two N-terminal transactivation domains, a proline-rich domain, a central sequence specific DNA-binding domain (DBD), an oligomerization (or tetramerization) domain , and an unstructured C-terminal domain that regulates the binding to the DNA (Figure 3A). *TP53* acts mainly as an inducible TF, which regulates a plethora of target genes involved in cancer suppression [59]. P53 protein is generally undetectable in normal cells, although it can accumulate upon different stress conditions (e.g. DNA damage, oncogenic stress and hypoxia) which also cause P53 activation. Upon detection of DNA lesions by specific sensors, and through the activation of certain signal transduction pathways such as those involving the ATM-kinase, P53 is modified post-translationally, for example by undergoing phosphorylation on Ser15. This specific modification causes P53 release from the ubiquitin-ligase MDM2, which normally leads to P53 degradation

through the proteasome. The undegraded P53 protein then accumulates into the nucleus binds as a tetramer to TP53 response elements (p53-REs) in the promoter regions of effector genes, thus activating their transcription. Hundreds of *TP53* effector genes are involved in regulation of different processes, including cell cycle arrest, DNA repair, apoptosis, senescence, metastasis, autophagy and metabolism.

How *TP53* coordinates the activation of down-stream effector genes is not fully understood. In principle, a promoter-specific activation can depend on i) the intensity of the stress (low/constitutive *vs* high/acute) [60], ii) the cell type and the cell physiological status which allows the recruitment of specific co-factors iii) the specific features of the p53-RE [61], since REs of different effector genes have variable sequences for which the wt p53 protein has distinct binding affinities.

3.2 Functional effects of TP53 mutations in CLL.

In human cancers, *TP53* is mostly altered by missense mutations (i.e. a mutation causing a single amino-acid substitution) affecting more frequently six residues (known as hotspot codons, i.e. R175, G245, R248, R249, R273 and R282) within the DBD domain [62]. However, the spectrum of *TP53* missense mutations is extremely broad with more than 2,000 different amino-acid changes collectively reported [62], with specific differences in the various tumor types. The *TP53* mutations from CLL studies reported by The Cancer Genome Atlas consortium (TCGA, http://www.cbioportal.org/) [63,64] are presented in Figure 3 (Panel A). Mutations affecting codons 175, 179, 220, 248, 273 and 281 represent the majority of identified TP53 alterations (34%); in addition, the codon 209 was reported as frequently mutated by Zenz et al [65]. Mutant P53 proteins are categorized into DNA contact- or structural- mutants, according to the effect that the amino-acid substitution may have on the direct interaction with DNA (e.g. p.R273H) or on the p53 protein structure structure (e.g. p.R175H), respectively [66]. However, not all TP53 mutations equally affect the P53 functions, potentially generating a wide range of phenotypic diversity [67]. Over the last 25 years, many data on the functional impact of missense mutations on P53 have been

generated and are publicly available (p53.free.fr/); indeed, functional assays have been performed in yeast and in human cells to measure the properties of single mutant P53 proteins including (i) transactivation potential, (ii) dominant negative effect over the wild-type protein, i.e. the capacity of the mutant protein to inhibit the activity of the wild type counterpart in heterozygous state, and (iii) gain-of-function, a condition indicating that a mutation confers to P53 protein the property of facilitating clonal expansion by acquisition of new properties [62,68]. The emerging picture is that mutant P53 proteins constitute a functional rainbow capable of conferring heterogeneous properties to the cells (Figure 3A)[69,70]. Analyses of genotype/phenotype correlations in germline TP53-associated disorders demonstrated that severely deficient P53 proteins were associated with more severe cancer proneness syndromes (e.g. Li-Fraumeni syndrome), while partial deficient mutant P53s were more frequently found in less severe cancer proneness conditions (e.g. family history)[71]. Consistently, Trbusek et al, [72] found that CLL patients with TP53 missense mutations located in DNA-binding motifs (DBMs), structurally well-defined and essential parts of the P53 DBD, manifested a shorter median survival and TTFT compared with CLL patients having missense mutations outside these DBMs. These results suggested a that TP53 DBMs mutations induced a gain-of-function phenotype, which can determine the expression of genes promoting CLL cell survival, such as the mitogen-activated protein kinase kinase 3 (MAP2K3) [73] and an altered expression of microRNAs [74].

3.3 Dysfunction of the P53 pathway in CLL.

In the last decade assays have been developed to evaluate the function of the whole P53 pathways in purified CLL cells [75]. These are based on the quantification of P53 and P53 target coding or non-coding genes at the RNA level (e.g. p21, bax, puma, fas and mir-34a) by RT-PCR or at the protein level (e.g. P21) by FACS (Fluorescent activated Cell Sorting) and Western Blotting.

Since both the *TP53* and *ATM* genes are integral to the DNA damage response (DDR) pathway, activated by double-stranded DNA breaks, the function of the P53 pathway is evaluated after induction of DDR with appropriate stimuli (e.g. IR, fludarabine/doxorubicin) [76]. If the P53

pathway is functioning, the P53 protein itself, and other known P53 effector gene products, are expected to be induced, while in the absence of such a response a dysfunction is inferred. Interestingly, Cerna et al., [77] identified mir-34a as a positive regulator in the cross-talk between P53 functionality and the B-cell receptor in CLL; in fact, mir-34a is the most prominently up-regulated mir during DDR in CLL cells *in vitro* and *in vivo* following FCR therapy (fludarabine, cyclophosphamide, rituximab), causing the down-regulation of the transcription factor FOXP1 to limit the pro-survival/pro-proliferative signals from BCR.

A specific functional assay using etoposide plus Nutlin-3a, a molecule that releases the P53 protein from the deadly embrace of MDM2, was also developed to detect and distinguish the presence of *ATM* or *TP53* mutations in CLL [78]. Notably, in these assays, the size of the subclone with *TP53* alteration (s) and also the purification of the leukemic cells can influence the results.

4.0 Discussion

The notion of *TP53* dysfunction was introduced long ago to indicate lesions of the *TP53* gene demonstrated by del(17p), detected by FISH, and/or *TP53* mutations, detected by DNA sequencing. This definition raises the issue of whether determination of del(17p) and/or of *TP53* mutations may not represent an oversimplification of the conditions leading to an impaired *TP53* function, both in terms of quality and quantity.The effect of del(17p) may be different in the various cases depending upon the proportion of the cells carrying the deletion, a consideration which also relates to FISH sensitivity. Moreover, the outcome of patients with equivalent proportions of cells with the deletion, can vary depending upon the type of therapy In addition, del(17p) will have different consequences when accompanied by mutations of the other *TP53* allele. Finally, chemo-immunotherapy is likely to necessitate of a more efficient apoptotic apparatus than BCR and for BCL-2 inhibitors.

The issue becomes even more complex for TP53 mutations. First, the sensitivity of the sequencing technique is becoming even more relevant. This article is not intended to provide many methodological details, for which we refer to recent ad hoc publications [79–81], nevertheless

clinicians should be aware that the Sanger methodology currently employed has a threshold of detection of variant allelic frequency (VAF) of 10% at best, and that its sensitivity is influenced by the degree of purification of the leukemic cells (which may be in turn influeced by the peipheral lymphocyte count) and by the choice of including or excluding *TP53* exons 2 and 11 in the analysis, in addition to the mandatory exons 4-10. The issue of the sensitivity of the methodoly is not trivial. TP53 mutations are detected in approximately 6% of patients in the early stages (and often confined to minor CLL subclones) and increase with disease progression reaching about 40% among the refrctory cases [82,83]. Moreover, patients who fail to respond or respond for a short time to chemo-immunotherapy may have minor subclone(s) carrying TP53 mutations. These suclone(s) can subsequently expand under the selective pressure of chemotherapy to become the major disease component in later periods [83–85]. It remains to be clarified whether such selection also occurs with the new biological therapies and what are the mechanisms involved. As already mentioned, a dysfunction of the p53 pathway causes a diminished response of the BCR to stimulation [77], although clonal expansion could still be facilitated by signals delivered through the JAK/STAT pathway, as it occurs for IL23 stimulation of CLL cells, which is BCR-independent [86]. BCR inhibitors can be less effective in these conditions and the expansion of subclones with TP53 dysfunction could be favoured.

To overcome the problems of sensitivity of the Sanger sequence, many laboratories haveswitched to next generation sequencing (NGS) methodologies, which offer higher sensitivity, although require a careful calibration to prevent false positivity. Moreover, the data of NGS too are influenced by the purification of the leukemic cells and by the choice of the *TP53* gene segments to be analyzed. Finally, and, more important to the clinicians, although NGS allows a higher sensitivity, the optimal threshold of mutation detection has still to be determined based upon evidence- based criteria.

The mutations of the *TP53* gene have a different impact if they are present alone or concomitantly with del(17p), since the presence of the two allelic lesions is likely to have a greater

impact on function. Finally, not all mutations may have a similar effect on P53 protein function. Although both missense and non missense mutations have a negative prognostic impact, the former mutations appear to impact more on the disease course [72]. Moreover, the mutations which affect the *TP53* DNA binding motifs are also those which confer a worst prognosis [72]. Finally, the presence of a mutation in one allele may have a different impact on the function of the remaining allele, depending on the nature of the mutation itself, as discussed above.

Particular conditions have to be considered before drawing possible conclusions on therapy strategies. Patients with CK, identified by chromosome banding, and defined by the presence of >-3 chromosomal alterations may have a dire clinical course [87,88]. In a recent European Research Initiative on CLL (ERIC) collaborative study, involving 5290 cases [89], it was determined that CK occurs in approximately 15% of patients. Among these, the group with the highest cytogenetic complexity, with >- 5 chromosomal alterations, had a particular dismal prognosis. In contrast, patients with a lower number of chromosomal alterations had an adverse clinical course only if there was a concomitant evidence for a *TP53* disfunction. Notably, patients with CK including trisomy 12 and trisomy 19 presented a remarkably indolent course and generally were characterized by the absence of other negative prognostic factors. This group, however, represented approximately 10% of the whole patients with CK. Therefore, an unsatisfactory response to chemo-immunotherapy and also to the newer biological therapies may find an explanation in a CK, irrespective of, or in addition to, other adverse prognostic factors.

A number of patients treated with BCR or BCL-2 inhibitors may respond for a short time and subsequently present a rapid downhill course. This is particularly true for those cases that are characterized by NOTCH mutations and by trisomy 12, in addition to *TP53* dysfunction. These patients most likely developed a Richter transformation (RT), wich is defined by the onset of a very aggressive lymphoma in a CLL backgroud [90,91]. Lymph-node biopsy, which may also reveal MYC hyperexpression by malignant cells, a characterizing feature of RT [92], and PET could

confirm the diagnostic hypothesisis and the patients may be switched to a suitable therapy for aggressive lymphomas.

A final note concerns a consideration for relapsing patients, in whom the success of any therapy is often conditioned by the number of previous therapy lines (both chemotherapies and biological therapies) irrespective of or in addition to the presence of adverse prognostic factors [52].

5.0 Conclusions

The analysis of clinical trials and of real-life experience demonstrates that *TP53* dysfunction determines the outcome of therapy in CLL. Moreover, the proportion of leukemic cells carrying such dysfunction and the type of *TP53* gene lesion also influences the subsequent fate of patients. Although it is well established that the new biological agents are far superior to chemo-immunotherapy in patients with *TP53* dysfunction, there are a number of issues to be clarified including that of whether the new therapies are equally effective in patients with and without *TP53* dysfunction and whether there are differences for the different agents. Several considerations strongly support a widespread search for *TP53* dysfunction in the patient work-up and possibly suggest the future extension to functional studies. Testing for *TP53* dysfunction should be completed by other investigations aimed at assessing the overall aggressiveness of the disease (e.g. *IGHV* gene mutational status and CK, as well as RT predisposition).

6.0 Expert Opinion

At present, for a patient who is a candidate for a first line therapy, there is the choice for two treatment groups, i.e. chemo-immuno or biological therapies. As already discussed, there is still room for chemo-immunotherapy, which can induce long lasting remissions [13,14]. This result can be achieved only with a careful consideration of the patient risk factors, which primarily include the assessment of the of *TP53* dysfunctions. The ERIC group recommends *TP53* mutational screening as a first step in the algorithm leading to therapeutic decision [79]. This approach appears to be safe and capable of identifying most patients who are not eligible for chemo-immunotherapy. In the near

future, additional advantages will be brought about by the increased use of NGS methodologies with a reasonably high coverage. The choice of the sole determination of *TP53* mutations is based upon considerations that there is a large overlap between patients with *TP53* mutations and those carrying del(17p). Therefore, the two alterations are concomitant in most of leukemic clones and the choice of determining only the *TP53* mutational status will provide an indication of the *TP53* function in most patient except those charactrized by the presence of del(17p) only. Although there are variations in the proportions of these patients depending on the different cohorts studied and the disease stage in which the tests were performed, it is possible that these *TP53*-unmutated, del(17p)-positive cases represent 5-10% of patients with *TP53* dysfunction [72,84,93] (Monti et al., under revision). These patients (most likely not eligible for chemo-immunotherapy) will escape detection in the ERIC suggested approach. *TP53* mutations alone, in the absence of del(17p), have a significant impact on chemo-immunotherapy as documented by the clinical trials. Hence all patients with *TP53* mutations should be excluded from chemo-immunotherapy. This exclusion is justified even considering the differences in the biological impact of the various mutations and also the biological consequences of the single mutations on the remaining *TP53* allele (see for example, mutations causing haplo-insufficiency *versus* those determining haplo-sufficiency). Nevertheless, functional analyses of *TP53* mutations are indicated for experimental research only and are so far excluded from the current practice.

The determination of del(17p) and of the *IGHV* gene mutation status, deserves a different consideration, since are feasible in a clinical setting. They ate important to detect the few del(17p)-positive *TP53* mutation-negative cases and for an overall evaluation of disease aggressiveness[94], respectively. Notably, the presence of *IGHV* somatic mutations in *TP53*-mutated CLL clones characterize patients that do not have a negative prognosis [95]. Financial rather than medical considerations may eventually suggest or prevent the use of these tests, which in our opinion should be strongly recommended. Likewise, additional laboratory tests, like the determination of NOTCH mutations, of trisomy 12 and of CK would be desiderable in the everyday clinical practice, given

their importance for predicting particular clinical conditions such as predisposition to RT or to a dismal outcome. Unfortunately, the utilization of a wide array of molecular and chromosomal diagnostic tests remains a prerogative for a relative minority of patients in the current practice [96].

The next question is whether the above recommendations are applied at least in part in the current practice. In this regards, it comes somehow to a surprise to see the low proportion of cases tested for del(p17) and for *TP53* mutations documented by the inform CLL registry [97]. This information is perhaps even more striking considering that cases with *TP53* mutations (26%) or del(17p) were eventually treated with chemotherapy only. This attitude, although difficult to understand, given the importance of assessing *TP53* dysfunctions in the patient workup and in any further strategy decision, may relate to communication problems and to a certain conservatism of the medical community, which should hopefully change in the near future.

Patients for whom it is intended to use a biological first line therapy or are in a RR following chemo-immunotherapy are all likely to equally respond to biologival therapies? Specifically, does the quality of the response to these agents depend upon the presence/absence of *TP53* dysfunction? This is an old question which goes back to time of the alentuzumab use as an alternative agent for chemotherapy resistant cases, with a likely *TP53* dysfunction [98]. The answer to this question may also determine whether or not the assessment of *TP53* mutations is a mandatory requirement before therapeutic decisions are made, although we would strongly support an extensive diagnostic work-up as stated. Unfortunately, the analysis of relevant trials does not provide unequivocal response as we have already outlined [53]. Clearly the issue deserves exploration in future clinical trials, where new and more stringent laboratory tests to evaluate the residual *TP53* function in patients with *TP53* mutations are possibly employed. This approach may conceivably lead to a new scenario in which patients are stratified in different risk groups based upon residual *TP53* function within the leukemic clone. For most of the groups so classified, it is plausible that the current and maybe the newer biological therapies have a great chance of a durable effect, whereas for other groups, that likely involve a minority of patients, these therapies may

prove ineffective and hence there will be indications for alternative approaches represented by Car-T cell therapies [99] or even by allogeneic bone marrow transplantation [100].

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Legends to Figures

Figure 1.

Forest plots showing the benefit of BCR inhibitors, either alone or in combination, compared with chemotherapy or chemo-immunotherapies assessed by the risk of progressing (PFS) or dying (OS) in several clinical trials.

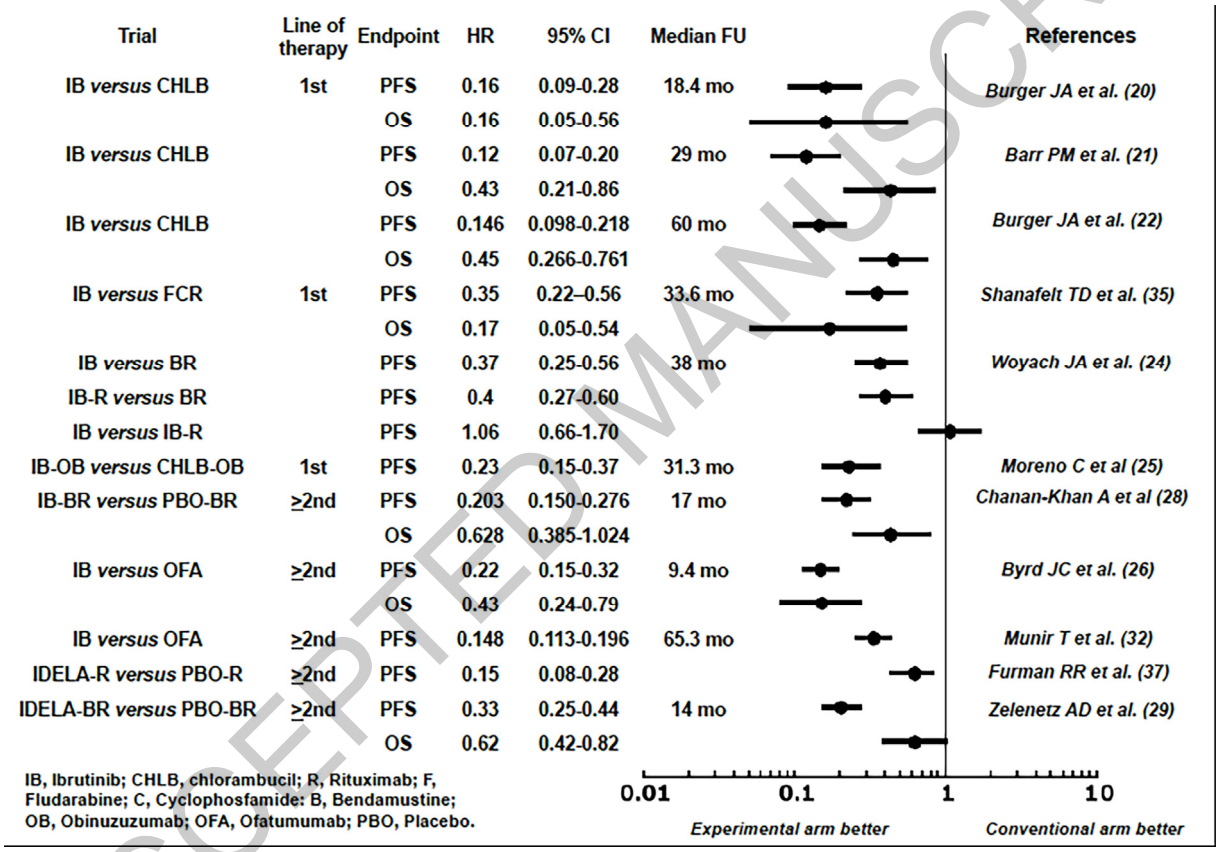

Figure 2.

Forest plots showing the benefit of BCR inhibitors in higher-risk groups in both treatment naïve- and RR-CLL settings, irrespective of the comparator arm, assessed by the risk of progressing (PFS) in several clinical trials.

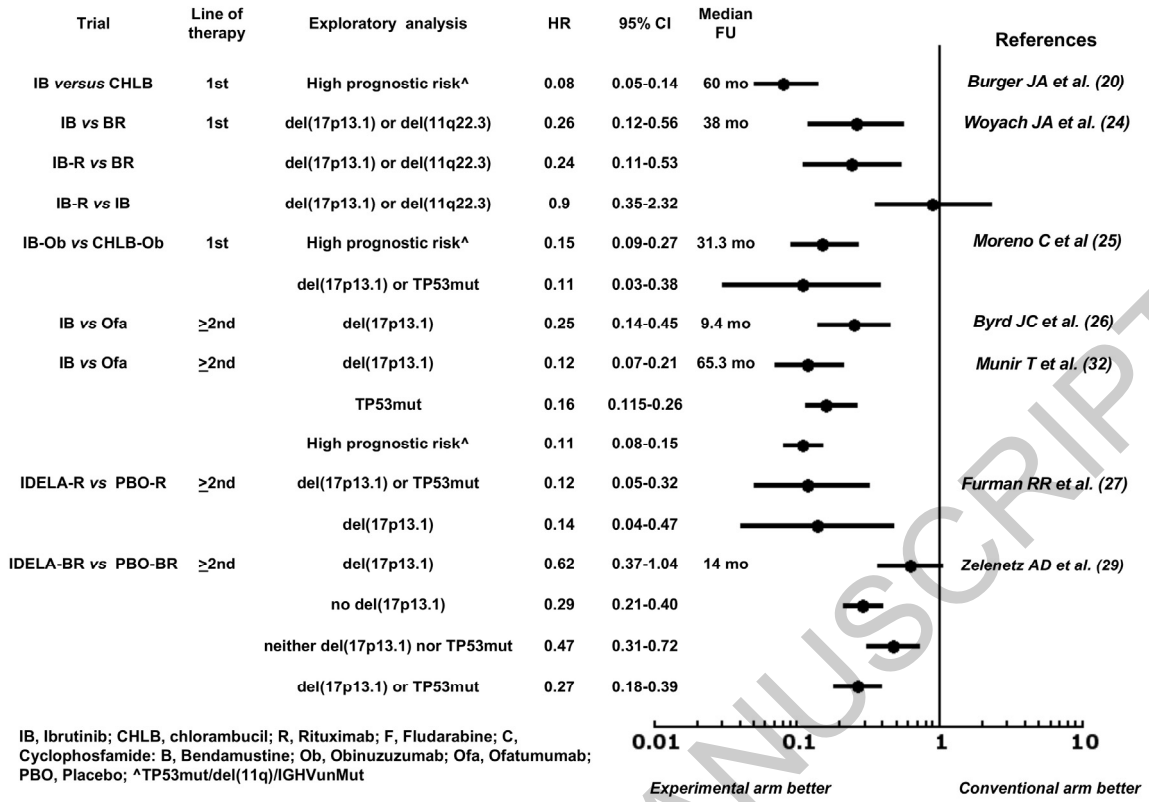

Figure 3.

Panel A). CLL TP53 mutations (missense, truncating and other mutations) from the cBioPortal online tool (The Cancer Genome Atlas consortium, TCGA, http://www.cbioportal.org/) are shown according to the frequency (Y axis) and the position of the amino acid hit (X axis). P53 functional domains are indicated as colored boxes. Panel B). Functional heterogeneity of mutants P53 may have variable consequences on CLL clinical phenotypes. Upon the detection of different kind of stress by specific sensors and the activation of signal transduction pathways, such those involving tjhe ATM-kinase, P53 is post-translationally modified. In case of Wild-Type (WT) P53, this modification releases P53 from its negative regulator MDM2 and allows the transcription of P53 target genes responsible for the control of cell proliferation, apoptosis, DNA damage response, autophagy and gene regulation. In case of mutant P53 (MUT), the negative feedback loop with MDM2 is no longer active and mutant P53 proteins will accumulate in the cells regardless any modifications or activation. Moreover, TP53 mutations potentially generate a rainbow of mutant

P53 proteins that can differ for transactivation ability, dominant negative potential and gain of function (e.g. ability to interfere with other TFs including P53 family members). This may lead to a wide range of phenotypic diversity that could impact on important CLL clinical variables, such as tumor aggressiveness, chemo-resistance, and metastatic potential.

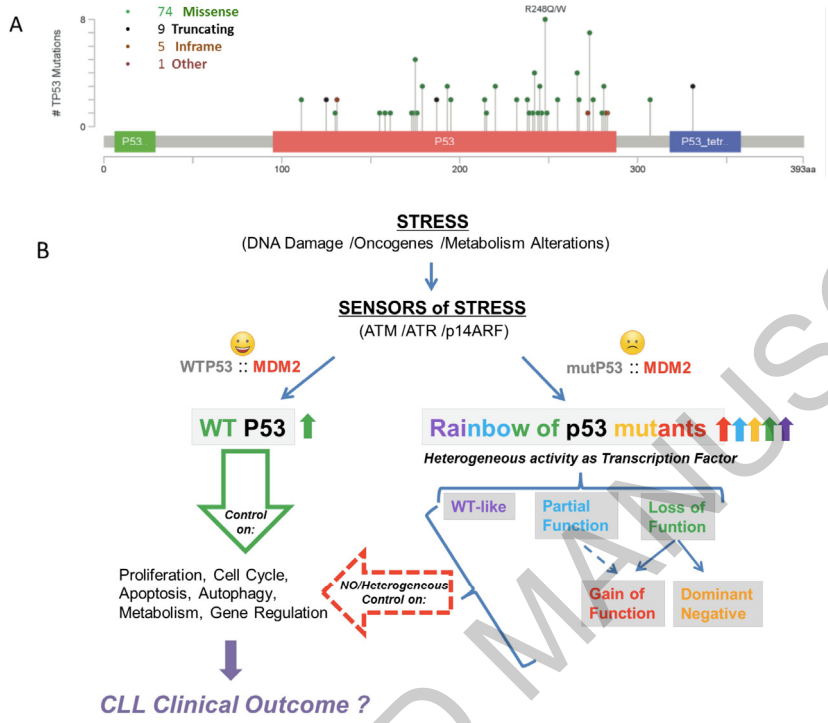

Table 1. Main clinical trials on single novel targeted drugs or drug combinations in CLL patients harboring del(17p) or *TP53* mutation.

Drug	Trial	Treatment setting	Del(17p)	TP53 mutation	ORR	Median PFS in patients with TP53 dysfunction
Acalabrutinib	NCT02029443 Phase 1-2	RR	30% (59)	NR	100%	NR
	ASCEND Phase 3	RR	18% (155)	NR	NR	88% at 1year
	ELEVATE-TN Phase 3	TN	8.9% (179)	10.6% (179)	NR	NR
Zanubrutinib	NCT02343120 Phase 1	TN/RR	19.1% (94)	NR	100%	NR
	SEQUOIA Phase 3	TN	100% (109)	NR	92.2%	NR
Tirabrutinib	NCT01659255 Phase 1	RR	NR	46.4% (28)	100%	NR
Nivolumab + Ibrutinib	NCT02329847 Phase 1-2	RR	100%[1] (36)	NR	61%	NR
Pembrolizumab	NCT02332980 Phase 2	RR	38% (16)	NR	0%	NR
Duvelisib	DUO Phase 3	RR	21% (160)	20% (160)	NR	13.8 months
Umbralisib	NCT01767766 Phase 1	RR	NR	NR	NR	NR
Ublituximab + Ibrutinib	GENUINE Phase 3	RR	About 50% (59) 100% high risk	NR	78%	NR
Otlertuzumab + Bendamustine	NCT01188681 Phase 2	RR	5.7% (32)	5.7% (32)	50%	NR
Entospletinib	NCT01799889 Phase 2	RR	24.4% (41)	NR	33.3%	NR