Hematologic β-Tubulin VI Isoform Exhibits Genetic Variability That Influences Paclitaxel Toxicity

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Abstract

Cellular microtubules composed of α-β-tubulin heterodimers that are essential for cell shape, division, and intracellular transport are valid targets for anticancer therapy. However, not all the conserved but differentially expressed members of the β-tubulin gene superfamily have been investigated for their role in these settings. In this study, we examined roles for the hematologic isoform β-tubulin VI and functional genetic variants in the gene. β-tubulin VI was highly expressed in blood cells with a substantial interindividual variability (seven-fold variation in mRNA). We characterized DNA missense variations leading to Q43P, T274M, and R307H, and a rare nonsense variant, Y55X. Because variations in the hematologic target of microtubule-binding drugs might alter their myelosuppressive action, we tested their effect in cell lines stably expressing the different β-tubulin VI full-length variants, finding that the T274M change significantly decreased sensitivity to paclitaxel-induced tubulin polymerization. Furthermore, patients treated with paclitaxel and carrying β-tubulin VI T274M exhibited a significantly lower thrombocytopenia than wild-type homozygous patients ($P = 0.031$). Together, our findings define β-tubulin VI as a hematologic isotype with significant genetic variation in humans that may affect the myelosuppressive action of microtubule-binding drugs. A polymorphism found in a tubulin isoform expressed only in hemapoietic cells may contribute to the patient variation in myelosuppression that occurs after treatment with microtubule-binding drugs. Cancer Res; 72(18); 1–9. ©2012 AACR.

Introduction

Microtubules are ubiquitous and highly dynamic polymers of α-β-tubulin heterodimers indispensable for a variety of cellular functions such as structure maintenance, intracellular transport, cell signaling, migration, and mitosis. Several of the most common chemotherapeutic drugs, such as taxanes, vinca-alkaloids, and epothilones, base their mechanism of action on binding to microtubules and altering their dynamics, which leads to mitosis arrest and cell death (1, 2). The therapeutic target of these drugs is β-tubulin, which consists of 8 isotypes encoded by multiple genes that exhibit a tissue-specific expression. In a previous study, we showed that isotypes I, IVb, and V are constitutive, isotypes Ila, Iib, III, and IVa are neuronal, and isoype VI is hematopoietic cell-specific and was detected in platelets, lymphocytes, bone marrow, and spleen (3, 4). The β-tubulin isotypes are highly conserved and have similar sequences, however, the C-terminal region exhibits higher variability and seems to confer differences in microtubule polymerization and stability. The fact that rare mutations in β-tubulin Iib and III lead to a spectrum of severe neuronal disorders suggests specific functions that cannot be compensated by alternative isotypes (5, 6). β-Tubulin VI knockout mice studies proved a specialized role for this protein in platelet synthesis, structure, and function (7, 8).

Because of the crucial role of β-tubulin in cells, genetic variation is not allowed. However, the hematologic isoform VI is an exception, and a common missense polymorphism (Q43P) has been associated with an altered risk of cardiovascular disease by modulating platelet function and structure (9, 10). There is also a report on a rare β-tubulin VI missense variant (R318W) responsible for congenital macrothrombocytopenia (11). Other genetic variations in β-tubulin isotypes correspond to cell lines and lead to acquired resistance to microtubule-binding drugs (12–14). Variations in β-tubulin isoform composition in tumors have also been associated with decreased sensitivity to these drugs (15–18). Thus, polymorphisms in β-tubulin VI, leading to a variant protein or altered expression,
might result in differences in the effect of β-tubulin–binding drugs among patients. Because of the hematologic role of β-tubulin VI, these polymorphisms could affect the action of the drugs in blood cells, leading to interpatient differences in myelosuppression. However, at the moment, the expression of β-tubulin VI has not been well-established, and polymorphisms in this gene have not been investigated.

In this study, we characterized β-tubulin VI expression in hematologic cells and screened for genetic variation by sequencing the coding region of the β-tubulin VI gene (TUBB1). We generated cell lines stably expressing the variant β-tubulin VI proteins detected and conducted functional assays. Furthermore, the clinical implications of these polymorphisms were studied in patients with hematologic malignancies treated with paclitaxel.

**Materials and Methods**

**Human samples and patients**

cDNAs from 7 different blood fractions were obtained from BD Biosciences (Human Blood Fractions MTC Panel), peripheral blood lymphocytes, platelets, and neutrophils were isolated from healthy volunteers, and CD34⁺ bone marrow cells were isolated from bone marrow aspiration following previously described procedures (19). Frozen samples from peripheral T-cell lymphomas were collected through the Spanish National Cancer Centre (Madrid, Spain) tumor bank network from pathology departments of different hospitals in Spain (20). The main characteristics of this human material and cell lines used for mRNA quantification are shown in Supplementary Table S1. For the estimation of allele and haplotype frequencies, we used DNA isolated from unrelated individuals from different ethnic groups, specifically, 481 Caucasians from Spain, 106 Asians from China, and 71 Africans from Tanzania.

Forty-nine patients with hematologic malignancies planned for autologous transplant (20 with lymphoma, 15 with multiple myeloma, and 14 with acute leukemia), who underwent mobilization of hematopoietic progenitor cells with paclitaxel 170 mg/m² i.v. by continuous infusion for 24 hours followed by 8 μg/kg s.c. recombinant human granulocyte colony-stimulating factor (rhG-CSF) daily, and that had leukapheresis product available, were included in the study (21). In this series, recruited between 1999 to 2008, the time elapsed from the last cytotoxic treatment was at least 3 weeks, to allow recovery of peripheral blood counts before paclitaxel administration. Peripheral blood counts were assessed on days 5, 7, and daily afterward. Maximal hematologic toxicity was retrospectively assessed and recorded according to the National Cancer Institute-Common Toxicity Criteria version 3. The characteristics of the patients, including age at treatment, previous treatments, state of disease at stem cell harvest, weeks from the last treatment, and baseline platelet counts at paclitaxel treatment initiation are provided in Supplementary Table S3.

**RNA isolation and quantitative RT-PCR**

RNA was extracted from blood cells, cell lines, and frozen tumoral tissue using TRI-reagent (Molecular Research Center Inc.) and the concentration quantified by using Nanodrop ND-1000 (Wilmington). One microgram of total RNA was reverse transcribed using Superscript II (Invitrogen) and an oligo dT14 primer following the manufacturer’s instructions. The mRNA content of the different β-tubulin isotypes was quantified by quantitative reverse transcription-PCR (qRT-PCR) with the Sequence Detection System 7900HT (Applied Biosystems) using conditions, primers, and probes previously described (4). Normalization was carried out with the internal standard β-glucuronidase (GUS). Negative controls were present in all qRT series and assays were carried out in triplicates. The ΔΔCt method (22) was used for the calculation of mRNA content.

**DNA isolation, sequencing, and genotyping**

Genomic DNA was isolated from the peripheral blood lymphocytes of the healthy volunteers and from the leukapheresis product of the hematologic patients using FlexiGene DNA Kit (Qiagen), and the DNA concentration was determined using PicoGreen dsDNA quantification reagent (Invitrogen). For TUBB1 sequencing, the exons and proximal promoter region were amplified by PCR using specific primers designed to avoid cross-reactions with other β-tubulin isotype genes/ pseudogenes (Supplementary Table S2). PCR amplification products were purified using the PCR Purification Kit (Qiagen) and run on an ABI PRISM 3700 DNA Analyzer capillary sequencer (Applied Biosystems). Genotyping for the TUBB1 coding polymorphisms was conducted in duplicates with the KASPar SNP Genotyping System (KBioscences) using 15 ng of genomic DNA. All assays included DNA samples with known genotypes and negative controls. The sequence detection system 7900HT (Applied Biosystems) was used for fluorescence detection and allele assignment.

**Platelet activation and aggregation assays**

The effect of β-tubulin VI R307H polymorphism in platelet function was investigated by conducting aggregation assays in 6 healthy volunteers of known genotype (3 women homozygous for the wild-type allele and 2 women and 1 man homozygous for the variant allele). Platelet aggregation was measured in nonadjusted-citrated platelet-rich plasma obtained by centrifuging blood at 140 x g for 12 minutes. Platelets were stimulated with 6-mer thrombin receptor agonist at 0.78 to 25 μmol/L (Sigma-Aldrich), collagen at 0.125 to 2 μg/mL (Menarini Diagnostics), ADP at 0.16 to 0.5 μmol/L (Menarini Diagnostics), arachidonic acid at 0.4 to 1.6 mmol/L (Bio-Rad), and ristocetin at 0.75 to 1.25 mg/mL (Sigma-Aldrich). Changes in light transmission of platelet-rich plasma over baseline were recorded for 5 minutes using an Aggrecorder II aggregometer (Menarini Diagnostics).

**Generation of cell lines expressing β-tubulin VI wild-type and variant proteins**

We amplified the full coding sequence of TUBB1 using specific primers that introduced NheI and NotI cleavage sites (Supplementary Table S2) and cDNA from peripheral blood lymphocytes that carried in homozygosity the wild-type TUBB1 coding region. The PCR product was cloned into pIRESpuro2 vector (Clontech) to generate pIRESpuro2_TUBB1 wild-type.
plasmid. By means of the GeneTailor Site-Directed Mutagenesis System (Invitrogen) and following the manufacturer’s indications and adequate primer pairs (Supplementary Table S2), the pIRESpuro2-TUBB1 wild-type construct was used to generate plasmids that contained TUBB1 sequence with variants encoding for the following protein changes: Q43P, Y55X, T274M, R307H, and T274M/R307H. Correct TUBB1 sequence and lack of artifacts was confirmed by sequencing.

MCF7 breast cancer cells were provided by Dr M. Esteller (IDIBELL, Barcelona, Spain). MCF7 cells were chosen for heterologous expression of β-tubulin VI based on their lack of endogenous expression of this protein and sensitivity to microtubule-binding drugs. MCF7 cells were transiently transfected with the different TUBB1 constructs and the empty vector by using Lipofectamine-2000 (Invitrogen) following the manufacturer’s instructions. To generate stable cell lines, the different TUBB1 constructs and the empty vector were electroporated using the Gene Pulser XCell Electroporation System (Bio-Rad) into cells and 24 hours later, 0.5 μg/mL of puromycin (Sigma-Aldrich) was added for selection. Puromycin-resistant clones were analyzed for β-tubulin VI expression by Western blot analysis. Control cells were also selected with puromycin, all resistant empty vector clones pooled together. Stable transfectants were maintained in Dulbecco’s Modified Eagle’s Medium supplemented with 10% FBS, penicillin, streptomycin, and puromycin at a concentration of 0.4 μg/mL.

β-Tubulin VI protein detection

For Western blotting, total cell extracts from cell lines were separated by using the Criterion XT Gels Bis-Tris 10% and the Criterion electrophoresis cell (Bio-Rad) and transferred to 1.5 mL Eppendorf tubes, rinsed with 100 μL of hypotonic buffer (20 mmol/L Tris-HCl pH 6.8, 1 mmol/L MgCl2, 2 mmol/L EGTA, and 0.5% Nonidet P40) containing protease inhibitors (Protease Cocktail inhibitor tablets; Roche). The lysates were transferred to 1.5 mL Eppendorf tubes, rinsed with 100 μL of hypotonic buffer, mixed by vortexing, and centrifuged at 14,000 rpm for 10 minutes at room temperature. The 200 μL supernatants containing soluble (cytosolic) tubulin were transferred to another tube, and pellets containing polymerized (cytoskeletal) tubulin were resuspended in 200 μL of hypotonic buffer. The cytosolic and cytoskeletal fractions were each mixed with electrophoresis sample buffer, sonicated, boiled, and analyzed by immunoblotting. The percentage of polymerized tubulin was determined by dividing the densitometry value of polymerized tubulin by the total tubulin content (the sum of the densitometry values of soluble and polymerized tubulin) in at least 3 independent experiments.

Statistical analysis

The myelotoxicity of the patients was analyzed taking into account gender, age at paclitaxel treatment, type of disease, previous treatments, state of disease at stem cell harvest, weeks from last treatment, and baseline platelet counts at the initiation of paclitaxel and genotypes. For the analysis, quantitative variables were dichotomized according to the median. To include previous chemotherapy as a covariable, we used a bone marrow toxicity scoring system, which takes into account drugs and number of chemotherapy cycles used (24). This chemotherapy score correlates with damage to the stem cell pool caused by previous chemotherapy and with the ability to mobilize hematopoietic cells (25, 26). Acute leukemias were excluded from this analysis because, although treatments only include low/medium myelotoxic drugs and they have low chemotherapy score, the intense dosages in these protocols cause prolonged aplasias (Supplementary Table S3). The χ2 test and Fisher exact test were used to compare the hematologic toxicity grade of patients with clinical variables and genotype. To correct for the possible effect of previous treatments on the thrombocytopenia, the Mantel–Haenszel test was used. Nominal 2-sided P values < 0.05 were considered statistically significant. All statistical analyses were carried out using SPSS software package version 17.0 (SPSS).

Results

β-Tubulin isotype VI has a broad and variable expression in blood cells

We previously showed that β-tubulin VI expression was exclusively found in hematopoietic lineage cells, specifically, in...
platelets, lymphocytes, bone marrow, and spleen; however, a detailed characterization of β-tubulin VI expression has not been conducted. Here, we show that β-tubulin VI mRNA was detected in all blood samples tested with the highest expression corresponding to erythrocytes, platelets, and monocytes (cells of myeloid origin; Fig. 1A). To further investigate the expression of β-tubulin VI, we also determined β-tubulin VI mRNA content in hematologic malignancies by studying tumoral cell lines and samples. Again, cells of myeloid origin showed higher expression than those of lymphoid origin, with the megakaryocytic MC-3 and CHRF288-11 cell lines showing the highest expression levels (Fig. 1B).

To confirm the relevance of β-tubulin VI in blood cells, we studied its expression in peripheral blood lymphocytes from 100 healthy volunteers. Figure 2A shows that isotype VI was the major β-tubulin component of lymphocyte microtubules, followed by β-tubulins IVb and I, accounting for 82, 10, and 7.5% of the total β-tubulin content, respectively. Interestingly, β-tubulin VI mRNA content was subjected to a substantial interindividual variability (7.2-fold variation in expression; Fig. 2B). To substantiate this variability, we also measured the expression of the ubiquitous and highly conserved β-tubulins IVb and I in the same samples, finding a 2.5- and 2.2-fold variation in mRNA content, respectively (data not shown).

**TUBB1 gene has common missense polymorphisms**

To determine whether TUBB1 gene could differentiate from the other β-tubulin isotypes and be subjected to common genetic variability, we sequenced the 4 exons and part of the 5′ and 3′ untranslated region of TUBB1 in genomic DNA from 20 unrelated Caucasians. In addition to the already studied missense polymorphisms, rs463312 (Q43P) and rs415064 (Q43H), we found 2 other nucleotide changes leading to amino acid changes, rs35565630 (T274M) and rs6070697 (R307H), and one resulting in a premature stop codon (c.585G>A; Y55X). To determine the allelic frequency of these genetic variations, we conducted genotyping in a series of unrelated Caucasians, Asians, and Africans (Table 1). The nucleotide change leading to an early stop codon was only detected in the initial case used for sequencing. Regarding the other variants, the polymorphism leading to R307H was the most frequent, followed by those corresponding to Q43P, Q43H, and T274M, this latter not detected in Asians. When we established the haplotypes formed by these missense variants (Table 1), we found that, as previously observed, rs463312 and rs415064 were in total linkage disequilibrium resulting exclusively in Q43P. rs35565630 was found only in the presence of rs6070697, thus, encoding a protein with 2 amino acid changes (T274M and R307H), whereas a relatively high number of cases carried only rs6070697 (R307H).

Concerning the putative effect of the TUBB1 coding variants, previous results have shown that Q43P affects cardiovascular risk through an alteration of platelet aggregation. To determine whether the newly described missense polymorphisms could also alter platelets function, we isolated DNA from 100 healthy volunteers and identified individuals carrying the variants in homozygosity. For T274M, we could not find homozygous variant individuals, thus, we conducted platelet activation and aggregation assays only for rs6070697 (R307H) and wild type homozygous individuals; however, we did not detect significant differences (data not shown).
whether the missense polymorphisms could be associated with an altered $TUBB1$ mRNA content and thus explain the interindividual variation found in the expression of this gene (Fig. 2B); however, none of the polymorphisms was significantly associated with an altered mRNA content (data not shown). Sequencing of $TUBB1$ proximal promoter region in individuals with maximal and minimal mRNA content did not identify polymorphisms associated with the expression of the gene.

$\beta$-Tubulin VI T274M alters paclitaxel effect on tubulin polymerization and is associated with decreased thrombocytopenia in patients treated with paclitaxel

To test the effect of the $TUBB1$ missense polymorphisms, we carried out transient transfections using appropriated expression vectors in MCF7 cells. These cells are derived from a solid tumor and do not express $\beta$-tubulin VI protein. As shown in Fig. 3A and B, the exogenously expressed $\beta$-tubulin VI proteins were correctly produced and colocalized with $\alpha$-tubulin, indicating a correct incorporation into the cytoskeleton of the transfected cells. Cells stably expressing the different $\beta$-tubulin VI proteins were used to study tubulin polymerization after treatment with increasing amounts of paclitaxel. We found that in control cells, transfected with the empty vector, most of the cellular $\beta$-tubulin shifted to a polymerized form at 100 nmol/L paclitaxel. This same effect was also appreciated in cells expressing wild-type, Q43P, and R307H $\beta$-tubulin VI proteins. However, cells expressing T274M and T274M/R307H variant proteins had significantly higher amounts of soluble

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Table 1. Genetic variants in $TUBB1$ coding region and common haplotypes

<table>
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<tr>
<th>Variants in coding region</th>
<th>Amino acid change</th>
<th>Caucasians ($N = 481$) Frequency $^a$</th>
<th>Frequency $^b$</th>
<th>Asians ($n = 106$) Frequency</th>
<th>Frequency</th>
<th>Africans ($n = 71$) Frequency</th>
<th>Frequency</th>
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<td>rs463312</td>
<td>Q43P</td>
<td>0.042</td>
<td>130</td>
<td>0.086</td>
<td>105</td>
<td>0.029</td>
<td>68</td>
</tr>
<tr>
<td>rs415064</td>
<td>Q43H</td>
<td>0.042</td>
<td>130</td>
<td>0.086</td>
<td>105</td>
<td>0.029</td>
<td>68</td>
</tr>
<tr>
<td>rs35565630</td>
<td>T274M</td>
<td>0.036</td>
<td>481</td>
<td>0.000</td>
<td>100</td>
<td>0.000</td>
<td>71</td>
</tr>
<tr>
<td>rs6070697</td>
<td>R307H</td>
<td>0.192</td>
<td>453</td>
<td>0.107</td>
<td>98</td>
<td>0.123</td>
<td>69</td>
</tr>
</tbody>
</table>

Haplotypes $^c$

| Hap_AGCCG                 | None              | 0.791                                  | 0.823          | 0.846                       | 0.110     |
| Hap_AGCCA                 | R307H             | 0.146                                  | 0.107          | 0.110                       | 0.110     |
| Hap_CCCCG                 | Q43P              | 0.037                                  | 0.069          | 0.029                       | 0.029     |
| Hap_AGCTA                 | T274M/R307H       | 0.023                                  | 0.000          | 0.013                       | 0.013     |

$^a$Frequency for the different alleles and haplotypes.

$^b$Number of individuals used in each determination.

$^c$Haplotypes estimated with frequencies $>1\%$. The nucleotides correspond to rs463312, rs415064, the nucleotide change leading to Y55X, rs35565630, and rs6070697.
β-tubulin at 100 nmol/L paclitaxel ($P = 0.011$; see Fig. 3C and D). These results suggest that β-tubulin VI T274M variant protein is less sensitive to the polymerization effect of paclitaxel.

Because β-tubulin VI is a hematologic isotype, we investigated whether β-tubulin VI T274M patients could be less sensitive to the myelosuppressive effect of paclitaxel. To determine this, we genotyped a series of 49 patients with nonsolid tumors scheduled for autologous transplant treated for mobilization of hematopoietic progenitor cells with paclitaxel 170 mg/m² i.v. by continuous infusion for 24 hours, followed by 8 μg/kg s.c. rhG-CSF daily. With this highly myelosuppressive protocol, grades III and IV leukocytopenia and thrombocytopenia occurred in 55% and 43% of patients, respectively. We did not find a statistically significant association between clinical variables (e.g., type of disease, previous treatments, state of disease at stem cell harvest, weeks from last treatment, and platelet counts at baseline before the initiation of treatment with paclitaxel) and the hematologic toxicity of the patients; however, we found a statistically significant effect for T274M polymorphism. Heterozygous T274M patients showed significantly lower thrombocytopenia than homozygous wild-type subjects. The 2 T274M patients exhibited grade I toxicity, whereas 85% of homozygous wild-type patients developed higher thrombocytopenia grades (II, III, or IV; $P = 0.031$; Fig. 4). The association was also significant (Mantel–Haenszel test, $P = 0.028$) when the previous chemotherapy treatments were taken into account. No significant association was found between T274M and neutropenia. We also genotyped the patients for Q43P and R307H variants and, as expected, no differences in thrombocytopenia and neutropenia were found (data not shown).

Discussion

In this study, we show that β-tubulin VI is a hematologic-specific isotype subjected to a substantial genetic difference that is likely contributing to the interindividual variability observed in the myelosuppressive effect of paclitaxel. A thorough characterization of β-tubulin VI expression in cells of hematopoietic lineage revealed a high β-tubulin VI expression not only in lymphocytes and platelets, as previously described (3, 4), but also in most blood cells and several hematologic malignancies (Fig. 1). These data and the lack of β-tubulin VI in nonhematopoietic tissues (4) indicate that this is a hematology-specific isotype, and hence a major target mediating the hematologic toxicity of the β-tubulin–binding drugs. In contrast, the low expression of this isotype in hematologic malignancies of lymphoid origin does not support a major role of the β-tubulin VI in the physiopathology of these diseases. Furthermore, we found substantial interindividual variability in...
β-tubulin VI mRNA content and common amino acid changes affecting TUBB1 gene (Fig. 2 and Table 1).

So far, β-tubulin isotype genes have been considered highly conserved (27); however, here we prove that β-tubulin VI differentiates in this respect from the rest of isotypes and exhibits common variation in the coding region. β-tubulin VI Q43P was previously described and associated with a reduced risk of arterial thrombosis and an increased risk of intracerebral hemorrhage by modulating the platelet function and structure (9, 10). In addition, a rare β-tubulin VI variant, R318W, was described in a case of congenital macrothrombocytopenia (11). In this study, a nonsense variant (Y55X) was detected in heterozygosity; however, no deviations from normal ranges were found in the hemograms of this individual. So far, all the β-tubulin pathogenic variants are missense mutations (5, 6, 11), suggesting that early truncated proteins, that do not integrate into microtubules, might not be as damaging as variant proteins that lead to altered dynamic instability of microtubules (5, 6). This is in agreement with the lack of Y55X phenotype. The R307H polymorphism is located in a conserved region encoding β-tubulin VI M-loop; however, computational algorithms (PolyPhen and SIFT) predicted a benign variant and we found no significant effects on platelet activation and aggregation. T274M change also affects a conserved amino acid in the M-loop and was predicted as probably damaging by PolyPhen and SIFT; however, we detect this variant in the general population, suggesting it will not substantially alter its function. In regard to the microtubule-targeted drugs, residue 274 is located near the taxanes binding site (28).

We found that cells stably expressing β-tubulin VI 274M variant, alone or in combination with 307H, were less sensitive to the polymerizing effect of paclitaxel compared with control cells transfected with the empty vector and those expressing β-tubulin VI wild-type, 43P, and 307H variant proteins (Fig. 3). Human β-tubulin isotypes are essentially invariant within paclitaxel-binding site and, specifically, residue 274 is evolutionarily conserved in all vertebrate β-tubulins and all known β-tubulin isotypes in these organisms (29). Interestingly, residue 274 clusters in a space that has been identified as essential for interaction of paclitaxel with tubulin and an acquired mutation in residue 274 of β-tubulin 1 (T274I) renders cell lines resistant to paclitaxel and epothilone A (28, 30). These data suggest that variants affecting threonine 274 can lead to impaired drug binding and, thus, patients carrying the T274M variant could be resistant to the myelosuppressive effects of these microtubule-binding drugs. To investigate the impact of this polymorphism in patients and its potential as a marker of hematologic toxicity, we worked with a series of patients treated with paclitaxel. Because paclitaxel hematologic toxicity greatly depends on the time used for drug infusion (31), we decided to work with an outstanding set of 49 patients treated with a highly myelosuppressive protocol used for mobilization of hematopoietic progenitor cells. Although only 2 patients were T274M carriers, they showed a statistically significant lower grade of thrombocytopenia (P = 0.031; Fig. 4), suggesting that TUBB1 T274M conferred protection against this paclitaxel toxicity. It is important to highlight that the T274M carriers had similar characteristics than the noncarriers in terms of age, disease state, base line platelets, and chemotherapy score (Supplementary Table S3). With respect to the type of disease, both were patients with myeloma with treatments that have an important effect on platelet production. Concerning the interval from last chemotherapy, the two carriers were among the patients with shorter times. No significant associations were found for leukocytopenia, but the results are inconclusive, because patients were treated with granulocyte colony-stimulating factor (G-CSF) to stimulate the production of neutrophils, and this is an important confounding factor. The effect found for T274M in thrombocytopenia risk is supported by the critical role that β-tubulin VI plays in platelets, showed both in knockout mice (7) and in patients carrying a mutation in this gene (11). Although in these previous studies, no pathogenic phenotypes were reported in neutrophils, we detected high contents of β-tubulin VI in these cells (Fig. 1A). This, together with the fact that the microtubule-binding agent 2-methoxyestradiol does not have an effect on β-tubulin VI (3) and does not result in any type of myelosuppression (32), supports a function of this isotype also in neutrophils and consequently in drug induced neutropenia. The similar structure of paclitaxel and docetaxel, which share the binding domain with epothilones, and the fact that cell lines expressing β-tubulin I T274I are resistant to all of these agents (28), warrants further studies to investigate the role of T274M in the hematologic toxicity of these drugs. It can be estimated that approximately 7% of Caucasians carry T274M and might show differences in myelosuppression.

In summary, this is the first study showing that β-tubulin VI is a hematology-specific isotype that differentiates from other β-tubulin genes by relevant genetic and expression variability. In addition, we show that β-tubulin VI T274M decreases the effect of paclitaxel on tubulin polymerization and, although
validation in independent patient series is required, we provide data supporting that it might constitute a marker of hematologic toxicity induced by paclitaxel.

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

Authors’ Contributions
Conception and design: I.J. Leandro-Garcia, S. Leskela, C. Rodriguez-Antona
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Analysis and interpretation of data (e.g., statistical analysis, biostatistics, computational analysis): I.J. Leandro-Garcia, S. Leskela, I. Ingładza-Perez, J. Rivera, M.L. Lozano, C. Rodriguez-Antona
Writing, review, and/or revision of the manuscript: I.J. Leandro-Garcia, S. Leskela, I. Ingładza-Perez, J.C. Ramírez, S. Alvarez, J. Rivera, C. Martínez, M.L. Lozano, A. Cascon, M. Robledo, C. Rodriguez-Antona
Administrative, technical, or material support (i.e., reporting or organizing data, constructing databases): I.J. Leandro-Garcia, S. Leskela, S. Alvarez, M. Robledo

References

Study supervision: I.J. Leandro-Garcia, I. Ingładza-Perez, M. Robledo, C. Rodriguez-Antona

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