6-TIMP is converted successively into 6-thioinosine diphosphate (6-TIDP) and triphosphate (6-TITP) to form 6-TIMP once again by the action of the enzyme inosine triphosphatase (ITPA) [4]. TGs incorporate into DNA causing further DNA damage by single-strand breaking, inter-strand crosslinking and DNA-protein crosslinking [5]. Despite this knowledge, the pharmacokinetic profile of 6-MP remains partially understood. A better understanding of the disposition of 6-TGs and 6-MMPs would be of extreme value towards an improved design of 6-MP dose regimens, diminishing drug toxicity [2]. In this context, the application of pharmacogenetics that relies on studying sequence variations in candidate genes that probably affect drug response could serve for patient monitoring and stratification [6].

In this study, the pharmacokinetic profile of 6-MP was investigated in patients with different types of leukemia and lymphoma under 6-MP maintenance chemotherapy. Also, the TPMT polymorphisms and gene methylation were examined, both retrospectively and prospectively. Understanding the metabolism of 6-MP along with the detection of TPMT variants in patients with different types of leukemia and lymphoma will contribute to the improvement of the 6-MP therapeutic regimen, eliminating the associated toxicity.

Materials and Methods

Patients

Nineteen patients with different types of leukemia and lymphoma (Table 1) upon 6-MP treatment were enrolled for this study. The majority of patients (18) were hospitalized at the University Hospital of Patras, Greece, and 1 patient was hospitalized at the University Hospital of Ioannina, Greece. Samples were collected according to the ethics rules and upon patients’ approval. Eleven subjects have completed their therapy before this study and 8 subjects were on treatment. Peripheral blood samples (1.5 ml) were collected in ethylene-diaminetetraacetic acid (EDTA) tubes at the appropriate
time point’s pre and post (1h, 1.3h, 1.45h, 5h, 8h, and 24h) 6-MP administration and centrifuged at 1000 g for 10 min to separate plasma from red blood cells (RBCs). The RBCs were washed twice with a Hank’s balanced salt solution (HBBS) and then suspended at a density of 8x10^8 RBCs per 200ml and kept frozen at -20°C until required for further processing. An extra peripheral blood sample (1 ml) from all patients was collected in an EDTA tube and kept at-20°C without centrifugation for TPMT genotyping.

**Reagents and chemicals**

HPLC-grade acetonitrile (CH3CN) and methanol (CH3OH) (Honeywell Burdick & Jackson, Seelze, Germany), mono-potassium phosphate (KH2PO4), phosphoric acid (H3PO4) and potassium hydroxide (KOH) (Merck KgaA, Darmstadt, Germany) and ultra-pure water from a MilliQ® instrument (Millipore, Billerica-USA) were used.

**Bench-top stability and freeze and thaw studies of 6-MP, TG and 6-MMP**

The bench-top stability of the analytes of interest (6-MP and its major metabolites) in human RBCs was evaluated at room temperature. Two concentrations per analyte were tested (low and high) at t=1h and t=24h. A freeze and thaw experiment was also performed for the evaluation of the analytes’ stability in RBCs at the same concentrations.

**Preparation of standards and calibration curve for the detection of 6-MP and its metabolites**

Stock solutions of 6-MP (1.6 mg/ml), 6-TG (1 mg/ml) and 6-MMP (2.5 mg/ml) were prepared in 0.1 NaOH. Two sets of standard solutions were then prepared for the analysis in the RBCs of patients. The standard solutions prepared were in the concentration range of 8.5-170 ng/ml, 0.025-1.25 μg/ml and 0.20-20 μg/ml for 6-MP, 6-TG and 6-MMP, respectively. Concentrations were chosen as such in order to exhibit clinical relevance. A different set of solutions at three different concentrations (low, medium and high) were prepared depending on the analyte tested, serving as quality control (QC) samples. Calibration curves and QC samples were prepared daily in RBCs.

**HPLC analysis**

HPLC was performed with an Ultimate 3000 Pump system (Dionex Corporation, Sunnyvale, CA, USA), sharing an infusion valve 8125 (Rheodyne, Rohnert Park, CA, USA) with a 20 μL loop and an Ultimate 3000 Photodiode Array Detector (Diode Array Detector, DAD). The Chromeleonv.6.80 software was employed for the sample and data analysis. Resolution was achieved using a reverse phase analytical column, C18 (250 x 4.6 mm, i.d. 5 μm, Xterra) at a flow rate of 0, 9 mL/min. The mobile phase consisted of solvents A: KH2PO4 (pH=2.25) 0.02M, B: acetonitrile (HPLC grade), and C: methanol (HPLC grade). A 16 min-isocratic run was developed (A:B:C, 96:3:1). Typical injection volume was 20 μl. A stable temperature of 25°C was used towards peak shape optimization. Three absorption UV-V wavelengths were selected, being specific and optimum for each analyte; 322 nm (6-MP), 303 nm (6-MMP) and 342 nm (TG).

For the construction of calibration curves with spiked samples the method of constant addition was used. The calibration curves of peak areas (in mAU x min—peak areas of blank samples were subtracted from those of the spiked samples) versus concentration (ng/mL) were linear in the concentration range studied. Blank samples were analyzed with each calibration curve. Then a random sample of RBCs

---

**Table 1: The demographic data of the patients treated with 6-MP that were included in the current study.**

<table>
<thead>
<tr>
<th>No</th>
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<th>Therapy status</th>
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<tr>
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<td>F</td>
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</tr>
<tr>
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<td>M</td>
<td>20</td>
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<tr>
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was analyze during HPLC (data not shown). In order to verify the
detection capacity of the method, standard concentrations of 6-MP,
6-TG and 6-MMP were added into a healthy volunteer’s RBCs, as
described in “Materials and Methods” section. An HPLC analysis
was performed and an indicate chromatograph is demonstrated in
Figure 1A. The performance of analysis for the standard solutions was
followed by the analysis of samples from patients treated with 6-MP.

Detection of VNTR promoter polymorphisms and
methylation pattern in the TPMT gene

All subjects were genotyped in the TPMT gene promoter VNTR
and coding regions, as described previously [7]. Genomic DNA was
isolated from blood specimens using QIAamp® DNA Blood Mini
Kit (Qiagen GmbH, Hilden, Germany). The number and type of
tandem repeats were determined by PCR amplification followed by
direct re-sequencing, as previously described [7], using the Big Dye®
Terminator Version 3.1 Ready Reaction Kit (Applied Biosystems, CA,
USA) and by capillary electrophoresis using an automatic sequencer
(3130 Genetic Analyzer, Applied Biosystems) according to the
manufacturer’s instructions. The sequences of the primers employed
were; TPMT_VNTR_F: AGGACTAGGGATGGGTAGGG and
TPMT_VNTR_R: ACCTCGCTTACAGCTGGTG. To investigate
TPMT methylation, we focused on V4/V7, V5/V5, V5/V7, V6/V6
and V6/V8. A pyrosequencing-based methylation assay was used,
according to the Pyromark Q24 software quick start guide and
Pyromark Q24 Vaccum workstation quick start guide. Ten samples
were analyzed.

Results

HPLC analysis of patients’ samples undergoing
therapy, to detect 6-MP and its metabolites

The patients that were on treatment with 6-MP during this study
and the patients that have completed their treatment are shown in
Table 1. Samples were collected at the indicated time points as
described in the “Material and Methods” section. The sample of patient
4 was subjected to haemolysis and therefore, further analysis was not
performed. Table 2 shows the 6-MP levels in the RBCs’ of patients (13,
16, 17, 18 and 19) prior and post their standard treatment at various
time points. In all cases, except patient 18, the inactive form of 6-MP
was not detected prior drug administration. In patients 13 and 16, the
levels of inactive 6-MP were decreased in a time dependent manner,
as expected. Patients 17 and 19 exhibited a similar pharmacokinetic
profile as 6-MP was detected only 1h after drug administration
and its levels decreased gradually with time resulting in no 6-MP
detection. The major metabolites of 6-MP, namely 6-TG and 6-MMP
were also analyzed (Table 2). In patients 13 and 16, the levels of both
metabolites increased in a time dependent manner, as expected.
Interestingly, only 6-MMP was detected in patient 17 within 1h after
6-MP treatment. On the contrary, in patients 18 and 19, only 6-TG
was detected prior and 1h post treatment. At this point, it should be
noted that patients 17, 18 and 19 demonstrated a very steep drug
elimination profile. Representative chromatographs for 6-MP, 6-TG
and 6-MMP of patient 13 are depicted in Figure 1B.

Analysis of the TPMT gene promoter VNTR
polymorphism and gene methylation

The patients enrolled in this study were either upon 6-MP

![Figure 1: An HPLC analysis of A) an indicative chromatograph of a 6-MP, 6-TG, 6-MMP mixture in the RBCs of a healthy volunteer. The analysis was conducted at 342 nm, the optimum wavelength for the 6-TG. B) A representative chromatograph of sample No 13, 1.45h post 6-MP treatment, the peaks indicate the levels of 6-MP, 6-TG and 6-MMP, 6-MP: 6-mercaptopurine, 6-TG: 6-thioguanine, 6-MMP: 6-methyl-mercaptopurine.](image-url)
treatment or treatment completion. The genotyping of the VNTR promoter of the TPMT gene was conducted on samples of all patients enrolled. The results of the VNTR analysis are summarized in Table 3. All patients were found to be wild-type (wt), except patient 18 where the TPMT*3C polymorphism was detected. No methylation was obtained (data not shown).

Discussion

The efficacy and safety of 6-MP therapy rely on the concentration of the cytotoxic TGs metabolites, which in turn depends on the metabolism of 6-MP by TPMT [8,9]. Herein, the pharmacokinetic analysis of 6-MP confirms the heterogeneity that accompanies the metabolism of this drug. In particular, 6-MP as well as its major metabolites (6-TG and 6-MMP) were detected in patients 13 και 16, while only 6-MP and 6-TG were detected in patients 18 and 19 and 6-MMP was only detected inpatient 17. 6-MP detection at several time points after drug administration- especially in the case of patient 13 – should be noted. The slow rate of drug elimination might be correlated with methotrexate that was also included in patient treatment along with 6-MP. Methotrexate is a potent inhibitor of dihydrofolate reductase (DHFR), a key enzyme for intracellular folate metabolism, and functions to regenerate tetrahydrofolate from dihydrofolate, a product of thymidylate synthase. As a consequence of DHFR inhibition, intracellular levels of tetrahydrofolate coenzymes are decreased, resulting in the inhibition of thymidylate and consequently DNA biosynthesis, as well as purine biosynthesis [10].

Previous in vitro and in vivo studies have shown that the simultaneous treatment with 6-MP and methotrexate affects 6-MP metabolism. De novo inhibition of purine biosynthesis by methotrexate causes increased intracellular levels of phosphoribosyl pyrophosphate which is a cofactor of HPRT enzyme in 6-MP metabolism [11-13]. It has been found that the combination of 6-MP with methotrexate leads in a synergistic conversion of 6-MP to 6-TG. Furthermore, XO is inhibited and the levels of 6-MP increased in plasma. In addition, data showed that increased accumulation of polyglutamate derivatives of methotrexate in red blood cells is correlated with increased 6-TG levels during all maintenance therapy using low dose methotrexate (40 mg/m²) and daily treatment with 6-MP (75 mg/m²). However, when high dose of methotrexate (1g/m²) are used, 6-TG accumulation is disrupted after treatment with 6-MP (1g/m²) during induction phase [11,14]. Indeed, patients 13, 16, 17, 18 and 19 participated in the current study were also treated with methotrexate (Table 1) and this might contributed to 6-MP metabolites’ accumulation in red blood cells resulting in increased toxicity.

Table 2: The demographic data of the patients treated with 6-MP that were included in the current study.

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<th>1,45h</th>
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Herein, the highest levels of 6-TG were only observed in patient 18. This might be correlated with the polymorphism TPMT*3C (A/G heterozygous) that was revealed after the analysis of the TPMT gene promoter. The TPMT gene promoter VNTR polymorphisms are known to affect the activity of the enzyme. A recent study also shows that the number and the type of the repeats affect gene transcription levels [7]. Interestingly, no gene methylation was observed.

Besides the genetic factors that affect TPMT activity, nongenetic factors might be implicated, too. In fact, nationality seems to be an important factor [15,16]. TPMT is an enzyme with great interest because of its implication in drug metabolism. Many studies show a worldwide attempt for mapping the TPMT polymorphisms [17-25] that affect its activation and hence, determine drug dosage in the clinic. Previous data demonstrated that the frequency of TPMT polymorphisms is 1 to 300 cases or 1 to 200 cases [26]. These studies refer to Caucasians and non-Caucasians or describe nations. Furthermore, there is a detailed study in South India that considers people migration from other countries [19]. Genetic analyses show that the frequency of TPMT polymorphisms is higher in Caucasians compared to North Asians. Also, their frequency is similar between black and white Americans [26]. Differences in TPMT variants across different populations are increasingly being recognized and a more detailed TPMT screen should be conducted to better define the clinical implications of TPMT heterogeneity with respect to thiopurine treatment. However, the genotyping of TPMT is not adequate for determining the activity of TPMT. In the UK, there were some cases of low TPMT activity that were detected independently of TPMT genotyping [27]. Besides the frequency of TPMT polymorphisms, the type of the polymorphism is important, too. TPMT*3A και *3C are detected in Caucasians [28] at a percentage of 95%, while type *2 is less frequent. The same pattern is observed in European people, with the exception of TPMT*3B that is also detected, yet less frequently in Swedish people [30]. In Italy, the most frequent variant is the TPMT*3A, although the TPMT*3B and *3C variants are equally detected [29]. This difference might be correlated with the influence of other populations like Sardinians [30] that have been affected by several invaders in their history. Greece is another typical example that has been influenced by many invaders in its history. In the current project, noteworthy, the only polymorphism that was detected was TPMT*3C, although the number of patients was small and more samples should be analyzed for a robust outcome.

We believe that the understanding of the pharmacokinetic profile of 6-MP along with the detection of the TPMT gene promoter VNTR polymorphisms in patients with different types of leukemia and lymphoma will result in an improved therapeutic strategy and patient stratification.

Statement of human rights/ Informed consent

The studies have been approved by the appropriate institutional research ethics committee and have been performed in accordance with the ethical standards as laid down in the 1964 Declaration of Helsinki and its later amendments or comparable ethical standards. Informed consent was obtained from all individual participants included in the study.
References


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