

Activity of Allelic Variants of Pi Class Human Glutathione S-Transferase Toward Chlorambucil

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Clinical efficacy of alkylating anticancer drugs, such as chlorambucil, is often limited by the emergence of drug resistant tumor cells. Increased glutathione (GSH) conjugation (inactivation) of alkylating anticancer drugs or their activated metabolites due to overexpression of the Pi class GSH S-transferase (hGSTP1-1) is believed to be an important mechanism in tumor cell resistance to alkylating agents. Interestingly, the hGSTP1 locus is polymorphic in human populations and involves amino acid residues in positions 104 (isoleucine or valine) and/or 113 (alanine or valine). Here, we report that the allelic variants of hGSTP1-1 significantly differ in their efficiency in catalyzing the GSH conjugation of chlorambucil. Catalytic efficiency of the hGSTP1-1(I104,A113) isoform toward chlorambucil was approximately 2.5-, 7.5- and 15-fold higher compared with I104,V113, V104,A113 and V104,V113 variants of hGSTP1-1, respectively. The results of the present study suggest that hGSTP1-1 polymorphism may be an important factor in GST-mediated tumor cell resistance to some alkylating agents. © 2000 Academic Press

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Alkylating agents, such as chlorambucil, are extensively used in the treatment of neoplastic diseases, but their effectiveness is often limited by the emergence of drug resistant tumor cells. Several different mechanisms have been identified that mediate tumor cell resistance to alkylating agents (1–4). One such mech-

anism involves increased inactivation of the alkylating anticancer drugs or their activated metabolites in drug-resistant tumor cells due to elevation of glutathione (GSH) levels and/or overexpression of GSH S-transferases (GSTs) (3, 4). GSTs are a superfamily of isoenzymes that can catalyze the addition of GSH to a wide variety of electrophilic compounds generally leading to their detoxification (5, 6). It is believed that the GST-catalyzed GSH conjugation of alkylating agents or their activated metabolites reduces their interaction with DNA, which is a critical event in antineoplastic effects of alkylating agents. Other mechanisms that have been suggested to contribute to alkylating agent resistance include reduced drug uptake, reduced bioactivation of the drug, and increased repair of DNA cross-links (1, 2).

Evidence for the involvement of GSH/GST system in cellular resistance to alkylating agents is provided by studies showing (a) increased GSH conjugation of alkylating agents or their activated metabolites in the presence of GSTs *in vitro* (7–10), (b) overexpression of GSTs in alkylating agent resistant tumors cells (3, 4, 11–13), (c) increased sensitization of tumor cells, including drug-resistant cancer cells, to alkylating agents by depleting cellular GSH levels or by inhibiting cellular GST activity (14–16), and (d) reduction in the cytotoxic activity of alkylating agents in cells transfected with GST genes (17–19).

Mammalian GSTs have been grouped into several classes, such as Alpha, Mu, Pi, Theta, etc. (20, 21), and the human GSTs of the above classes are known to exhibit overlapping but distinct substrate affinities (5, 6, 20). For example, while GSH conjugation of the activated metabolite of ifosfamide is solely catalyzed by the Pi class isoenzyme hGSTP1-1 (10), both hGSTA1-1 (an Alpha class isoenzyme) and hGSTP1-1 are equally

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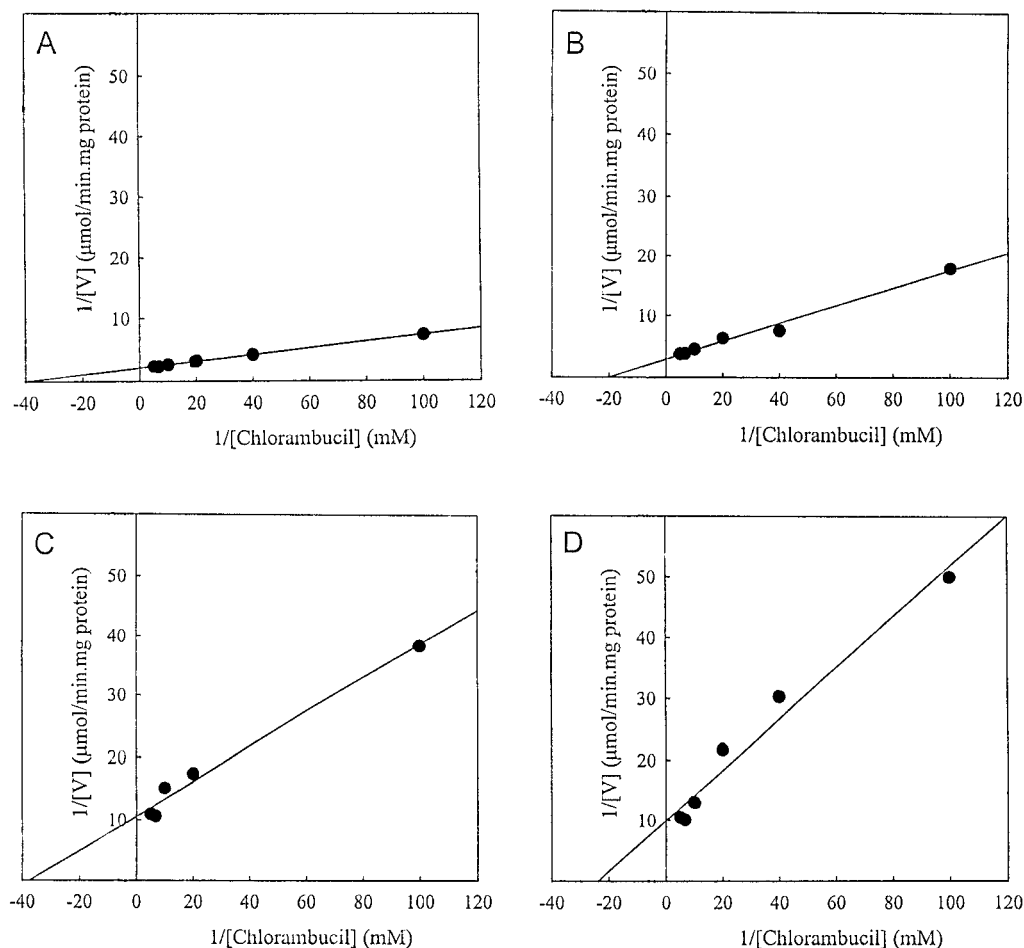


FIG. 1. Lineweaver-Burk plot for hGSTP1-1 variants I104,A113 (A), I104,V113 (B), V104,A113 (C), and V104,V113 (D) in the GSH conjugation of chlorambucil. The concentration of the chlorambucil was varied between 0.01 and 0.2 mM, whereas GSH concentration was kept constant at 2 mM.

effective toward thiotepea (8). Even though Alpha and Mu classes of GSTs can catalyze the addition of GSH to some alkylating agents, GSTP1-1 is likely to play a major role in alkylating agent resistance in humans because (a) the expression of hGSTP1-1 is significantly higher than other classes of GSTs in human cancer cells/tumor tissues, and (b) cellular resistance to alkylating agents in human tumor cells is often associated with the overexpression of hGSTP1-1 rather than other classes of GSTs (3, 4). Interestingly, the *hGSTP1* locus is polymorphic in human populations. The known polymorphisms involve amino acid residues in positions 104 (isoleucine or valine) and/or 113 (alanine or valine) (22–27). However, the physiological significance of hGSTP1-1 polymorphism is not fully understood.

In this communication, we demonstrate that the I104,A113 isoform of hGSTP1-1, which is most frequent in human populations, is significantly more efficient than either V104,A113 or V104,V113 in catalyzing the GSH conjugation of chlorambucil. Our results suggest that hGSTP1-1 polymorphism may be

an important factor in GST-mediated tumor cell resistance to some alkylating agents, and that the hGSTP1-1(I104,A113) isoform expressing tumors are likely to be more resistant to the cytotoxic effects of chlorambucil, and possibly other alkylating agents, than tumors expressing other variants of hGSTP1-1.

MATERIALS AND METHODS

Expression and purification of hGSTP1-1 variants. The hGSTP1-1 variants were expressed as described by us previously (28). The hGSTP1-1 variants were purified by GSH affinity chromatography according to the method of Simons and Vander Jagt (29) with some modifications described by us previously (30). Protein content was determined by the method of Bradford (31).

Determination of GST activity toward chlorambucil. The activity of hGSTP1-1 variants toward chlorambucil was determined by the method described by us previously (32). GST activity was measured as a function of varying chlorambucil concentration (0.01–0.2 mM) at a fixed concentration of GSH (2 mM) to determine the kinetic parameters. The K_m and V_{max} values were determined by nonlinear regression analysis of the experimental data points using the Michaelis-Menten (hyperbolic) equation. For calculation of the cat-

TABLE I

Kinetic Constants for hGSTP1-1 Variants in the GSH Conjugation of Chlorambucil

Isoform of hGSTP1-1	V_{\max} (nmol · min ⁻¹ · mg ⁻¹)	K_m (μM)	Catalytic efficiency (mM ⁻¹ · s ⁻¹)
I104,A113	478 ± 10	26 ± 2	15 ± 1.0
I104,V113	319 ± 34*	43 ± 14	6 ± 1.5
V104,A113	110 ± 13*	43 ± 16	2 ± 0.6*
V104,V113	147 ± 25*	91 ± 35	1 ± 0.3*

Note. Activity of the hGSTP1-1 variants was determined at constant GSH (2 mM) and varying (0.01–0.2 mM) chlorambucil concentrations. V_{\max} and K_m values were estimated by nonlinear regression fitting of a hyperbola (Michaelis–Menten equation) to the experimental points. Catalytic efficiency was determined by direct fitting of a reparametrized Michaelis–Menten equation (as described under Materials and Methods) rather than by division of the individual kinetic constants. All values are shown ± asymptotic error of the mean obtained from nonlinear regression. *Significantly different from hGSTP1-1(I104,A113), $P < 0.005$.

alytic efficiency, the Michaelis–Menten equation, $v = V_{\max} \cdot [S]/(K_m + [S])$, was rearranged to yield $v = K_m \cdot Q \cdot [S]/(K_m + [S])$, where $Q = V_{\max}/K_m$. The Q is equivalent to the catalytic efficiency (after appropriate change of units for V_{\max}).

RESULTS AND DISCUSSION

As shown in Fig. 1, all four variants of hGSTP1-1 (I104,A113), (I104,V113), (V104,A113) and (V104,V113)] obeyed Michaelis–Menten equation when GST activity was measured as a function of varying chlorambucil concentration and at a fixed saturating concentration of GSH. Kinetic constants for hGSTP1-1 variants in the GSH conjugation of chlorambucil are summarized in Table I. The hGSTP1-1(I104,A113) variant, which is most frequent in human populations (25–27), was found to be most efficient in catalyzing the GSH conjugation of chlorambucil. The catalytic efficiency of the hGSTP1-1(I104,A113) isoform was about 2.5-fold higher compared with hGSTP1-1(I104,V113) variant. This was mainly due to an approximate 1.7-fold higher K_m and 33% lower V_{\max} for the hGSTP1-1(I104,V113) isoform compared with hGSTP1-1 (I104,A113) variant. These results indicate that alanine-to-valine substitution at position 113 in the presence of isoleucine 104 causes a marked decrease in the activity of hGSTP1-1 toward chlorambucil. Interestingly, the isoleucine-to-valine substitution at position 104 results in a much more pronounced decrease in the activity of hGSTP1-1 toward chlorambucil. The catalytic efficiencies of the hGSTP1-1 variants with valine in position 104 were approximately 87–93% lower than that of the hGSTP1-1 (104,A113) isoform.

The results of the present study reveal that the I104,A113 variant of hGSTP1-1 is statistically significantly more efficient (approx. 7.5- to 15-fold) than either V104,A113 or V104,V114 in catalyzing the GSH conjugation of chlorambucil. Since the reaction rate of an enzyme

at low substrate concentrations (substrate concentrations $\ll K_m$) is determined by its catalytic efficiency, our results suggest that, at low pharmacologically relevant chlorambucil concentrations, the GSH conjugation of this anticancer drug would be significantly higher in subjects homozygous for the *hGSTP1-1(I104,A113)* allele compared with heterozygotes or *hGSTP1-1(V104,A113)* and *hGSTP1-1(V104,V113)* homozygotes. In a previous study, we have demonstrated that the I104,A113 isoform of hGSTP1-1 is also significantly more efficient than either V104,A113 or V104,V113 in catalyzing the GSH conjugation of thiopeta (33), which is another clinically relevant anticancer agent. However, it is important to point out that the difference in catalytic efficiency between I104,A113 and V104,A113 or V104,V113 is much less pronounced toward thiopeta (1.9- to 2.6-fold) than for chlorambucil (33, present study). Taken together, our results suggest that hGSTP1-1 polymorphism may be an important factor in differential response of individuals to the antineoplastic effects of alkylating agents, and that subjects with the *I104,A113* genotype may be at a greater risk for developing GST-mediated resistance to chlorambucil and thiopeta, and possibly other alkylating agents, than those having *V104,A113* or *V104,V113* allele.

The physiological significance of hGSTP1-1 polymorphism may not be limited to alkylating agent resistance. We have shown previously that the allelic variants of hGSTP1-1 significantly differ in their ability to catalyze the GSH conjugation, and hence detoxification of the ultimate carcinogenic metabolites (diol epoxides) of polycyclic aromatic hydrocarbons (28, 34–36), which are widespread in the environment and suspected human carcinogens. For example, the hGSTP1-1 variants with valine in position 104 (V104,A113 and V104,V113) are about 1.3- to 4.7-fold more efficient than I104,A113 isoform in catalyzing the GSH conjugation of (+)-*anti*-7,8-dihydroxy-9,10-epoxy-7,8,9,10-tetrahydrobenzo[α]pyrene [(+)-*anti*-BPDE] (28), which is the activated form of widely spread environmental pollutant benzo[α]pyrene (37). Thus hGSTP1-1 polymorphism may also be an important factor in differential susceptibility of individuals to cancers where polycyclic aromatic hydrocarbons are etiological factors.

The hGSTP1-1 variants are the result of conservative amino acid substitutions; isoleucine versus valine in position 104, and more divergent but still apolar alanine versus valine in position 113. The pronounced effects of these amino acid replacements on catalytic activity of the hGSTP1-1 protein is somewhat surprising. Recently, we have solved the crystal structures of the hGSTP1-1(I104,A113) and hGSTP1-1(V104,A113) variants in complex with GSH conjugate of (+)-*anti*-BPDE (GSBpd) at 2.1 and 2.0 Å resolution, respectively (38). Our studies reveal that the binding mode of the GSBpd is significantly different in hGSTP1-1(I104,A113) compared with hGSTP1-1(V104,A113). For example, the distance between the hydroxyl group

of Y7 and the sulfur atom of the GSBpd is markedly higher in hGSTP1-1(I104,A113) · GSBpd complex (5.9 Å) than in hGSTP1-1(V104,A113) · GSBpd structure (3.2 Å). Second, one of the hydroxyl groups of GSBpd forms a direct hydrogen bond with R13 in hGSTP1-1(V104,A113) · GSBpd complex; in contrast, this hydrogen bond is not observed in the I104 complex (38). In addition, two of the five water molecules in the hydrophilic portion of the H-site are displaced by the GSBpd in V104,A113 complex (38). Even though it is possible that some or all of these interactions may contribute to catalytic differences between hGSTP1-1(I104,A113) and hGSTP1-1(V104,A113) toward chlorambucil and thiotepa, actual crystal structures of allelic variants of hGSTP1-1 in complex with GSH conjugates of chlorambucil and thiotepa are needed to validate this assumption. Furthermore, structural studies with hGSTP1-1(I104,V113) and hGSTP1-1(V104,V113) are also needed to determine the role of residue 113 in the activity of hGSTP1-1 toward alkylating agents.

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