

## REVIEW ARTICLE

# Glutathione-S-Transferase M1 and T1: Inconsistency in Association with Severe Diseases

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### ABSTRACT

Development of cancer involves both genetic and environmental factors. Drug or xenobiotic compound metabolizing enzymes (XMEs) like Glutathione-S-Transferase enzyme are capable of converting the active carcinogens or toxic compounds to inactive or non toxic compounds and are crucial for healthy life of an individual. The Glutathione-S-Transferase enzyme family has their role in protection against toxic chemicals including anticancer agents and is involved in the adaptive responses to electrophiles and to oxidative stress. A large number of studies about Glutathione-S-Transferase enzyme have appeared advocating the role of null genotype of Glutathione-S-Transferase M1-T1 resulting in loss of activity of the enzyme and consequently a disease phenotype. Knowledge of the distributions of these genotypes in different populations is important for the investigation of polymorphisms as risk factors in epidemiological studies, related to their geographic and inter-ethnic variation frequency. In this article we discover that the studies on Glutathione-S-Transferase enzyme M1 and T1 are necessary to have a clear picture of the disease association and inconsistency. To find out their genetic variation among populations more studies and data are required to show variable responses to different populations located in same area as well as geographically distinct zones.

**Key Words:** Cancer, XMEs, Glutathione-S-Transferase, Null Genotype, Inconsistency.

Received 03/02/2017

Revised 10/03/2017

Accepted 07/06/2017

### How to cite this article:

Prem Chandra Suthar. Glutathione-S-Transferase M1 and T1: Inconsistency in Association with Severe Diseases. Adv. Biores., Vol 8 [4] July 2017: 232-239.

## INTRODUCTION

Various defense mechanisms have evolved to protect cells against toxic compounds. Such protective mechanisms include drug efflux pumps, drug sequestration, drug metabolism and repair of drug-target sites. Cellular detoxification mechanisms provide protection against diverse and dangerous agents in the environment and thus maintain the health [1]. Alternated activity of proteins or enzymes is involved in drug metabolism and drug transport to resist cytotoxic drugs in the cells [2]. Drug metabolizing enzymes involved in phases I of activation and II of detoxification are the most studied biotransforming enzymes. Xenobiotic compound metabolizing enzymes (XMEs) are essential for a range of disease-free state of an individual. They are capable of converting the active carcinogens or toxic compounds to inactive or non toxic compounds [3]. These compounds include catechol estrogen metabolites [4], activated metabolites of carcinogens, PAHs, Long-term ethanol exposure, diol epoxides [5]. Polycyclic aromatic hydrocarbons (PAHs) are present in incomplete combustion process including vehicles exhaust, chimney emissions, smoked foods, cigarette smoke, and indoor heating and cooking systems [6-8]. Certain natural toxins, including mold aflatoxins, phorbol esters, and pyrrolizidine toxins, are among the most potent carcinogenic and clastogenic compounds known.

### PHASE I AND II METABOLISM

Phase I involves an initial oxidation or metabolic activation of the xenobiotics by cytochrome P450 (CYP) [9-10] supergene family monooxygenases enzymes to their ultimate forms and then bind to DNA, forming

aromatic-DNA adducts that are thought to be an early step in tumorigenesis [11-12]. They activate many environmental procarcinogens by adding or exposing their functional groups [13] followed by phase II metabolism, involving conjugation reactions catalyzed by glutathione-S-transferases [14], N-acetyl transferase, epoxide hydrolase and other xenobiotics metabolizing enzymes (XMEs) [15-17] are involved in the detoxification of all of these products.

### **Glutathione-S-Transferase (GSTs)**

The glutathione S-transferases (GSTs) characterize a key group of isoenzymes which detoxify both endogenous compounds and extraneous chemicals such as environmental contaminants, pharmaceuticals and providing protection against electrophiles and of oxidative stress products. GSTs exhibit remarkably wide substrate specificity as well as possess the ability to sequester nonsubstrate drugs and hormones. These multifunctional dimeric proteins catalyze many reactions between glutathione (GSH) and lipophilic compounds with electrophilic centers [15]. These enzymes are involved in the antioxidant systems and conjugation reactions in phase II metabolism of wide range of xenobiotics including environmental carcinogens, chemotherapeutic agents, and reactive oxygen species [18], catalyzing conjugation of reduced glutathione (GSH) with products of oxidative stress, DNA-reactive intermediates and a variety of electrophilic compounds including Polycyclic Aromatic Hydrocarbon (PAHs) [19-21]. Due to the detoxifying action, it has been suggested that these enzymes play an important role in cancer susceptibility [22-24]. Variation in drug metabolism capacity may be attributable to genetic variation in the population, or they may be due to other factors, such as enzyme induction, affected by diet or drugs, environment-gene interaction. Genetically determined susceptibility to cancer and other detoxification pathway related defects may depend on the metabolic balance between phase I and phase II enzymes which are either polymorphic within the population or inducible, or both. [1, 25-30].

### **Diseases under GSTs association studies**

Although the etiologies of most commonly occurring cancers, recurrent miscarriages (RM) and infertility, liver defects, heart diseases, diabetes, kidney diseases cannot be explained by allelic variability at a single locus, the major burden of these body defects in the general population probably results from the complex interactions of multiple genetic and environmental factors over time. An understanding of the interplay of xenobiotic exposures, endogenous physiology, and genetic variability of GSTs will facilitate our knowledge about these etiologies and the identification of individuals who are at increased risk for developing such abnormalities.

#### **Cancer**

Most cancers are caused by exposure to environmental carcinogens and not by the inheritance of specific susceptibility genes. Studies have shown that both GSTT1 and GSTM1 enzymes protect cells from the toxic products of phase I detoxification reactions [31-32]. Individuals having the null genotype of GSTM1 and GSTT1 has a decreased capability in detoxifying some carcinogens are at increased risk of major types of cancers, including Lung cancer [33-47] Colorectal cancer [48-57], Urinary bladder cancer [58-65], Breast Cancer [66-70], Oral cancer [72-74], Multiple skin cancer [75-76], Bronchogenic carcinoma [34, 39,77], Head and neck cancer [78-80], Adenocarcinoma [77, 81], Gastric cancer [42,48,82], Acute myeloid leukemia [83], Laryngeal cancer [61], Colon cancer [52], Esophageal cancer [84], Cervical cancer [85], Chronic Myeloid leukemia [86], Prostate cancer [87], Thyroid cancer [88].

#### **Liver cirrhosis**

It has been reported that genetic polymorphism of the GSTT1 locus may be important in the inherited susceptibility to liver cirrhosis [89] because of its patho-biological association with alcohol-induced liver damage.

#### **Endometriosis and Recurrent Miscarriages (RM)**

Association between the GSTM1 null mutation and endometriosis has been reported in one study [90]. In another study twenty six (26.8%) women with endometriosis and 15 (14.7%) of the controls had the GSTM1 null genotype, which showed significant association ( $P=0.03$ ) with endometriosis indicating that GSTM1 null polymorphism might have an increased susceptibility of endometriosis [91]. Allelic variants of the detoxification genes that have impaired biotransformation functions may increase susceptibility to reproductive toxicity leading to endometriosis, recurrent miscarriage (RM) or poor pregnancy outcome. Significant protective effects of phase I wild-type genotypes and association of the GSTT1 null genotype with RM has been reported and through combined analyses the importance of the balance of phase I/phase II detoxification systems has been highlighted in the etiology of RM [92].

#### **Infertility**

The possible role of GSTM1 and GSTT1 gene variants in male infertility has been already suggested with inconsistent data [93-94]. One study investigated the association between the GSTM1 and GSTT1 gene

deletion and MTHFR C677T mutation and male infertility encompassing 52 infertile and 56 fertile males they found that the carriers of double GSTM1/GSTT1 deletion and the MTHFR 677CC genotype are at higher risk of infertility [95]. Sperms are susceptible to oxidative damage and excessive reactive oxygen species (ROS) generation may lead to subfertility or infertility. A literature-based meta-analysis of 6934 individuals case-control study showed the GSTM1 null genotype was significantly associated with idiopathic oligozoospermia, while the null genotype of GSTT1 was significantly associated with normozoospermia and azoospermia [96].

#### ***Chronic kidney disease (CKD)***

It has been found that the patients with GSTM1 or GSTT1 null genotypes are more vulnerable to oxidative stress compared with those who possess normal gene expression in chronic kidney disease [97]. There is significant association between the genetic risk factors of GSTT1 and GSTM1 genes in the end stage renal disease (ESRD), and low level of GST enzyme in the ESRD patients so the GSTM1 and GSTT1 (null) genotypes were suggested independent risk factors for ESRD [98].

#### ***Coronary artery disease (CAD)***

A Meta analysis to assess the association between polymorphism of GSTM1 null genotype and coronary artery disease risk found a significantly increased myocardial infarction risk [99].

#### ***Type2 diabetes***

Significant association was seen in GSTM1 null and GSTP1 (I/V) and multiple association in GSTM1 null, T1 present and P1 (I/I), in a representative cohort of Indian patients with T2DM. The research revealed that these polymorphisms can be screened in the population to determine the diabetic risk [100].

#### ***Inconsistency about the association***

Several polymorphic genes encoding the XMEs involved are currently being investigated as a possible basis for inter-individual variability in disease susceptibility. But studies provide inconsistent associations among ethnically/regionally different populations [43,101-103]. Both positive and negative results have been reported for associations between GSTM1 and GSTT1 null genotype and disease risk. The effect of the GSTM1 deletion and lung cancer among Caucasians and African Americans in Southern California suggests that, in these populations the association of the GSTM1-null deletion and breast cancer is not strong and yielded inconsistent results [51, 104-106]. Another study found that there was no increased risk associated with the GSTM1 null allele in postmenopausal breast cancer risk study in either smokers or nonsmokers [107]. No consistent associations between GSTM1 or GSTT1 genotype and colorectal cancer have been observed by other studies [42, 50, 52, 54]. In Japanese population, there is no association of endometriosis with the GSTM1 and GSTT1 null mutations [108] which is consistent with the previous reports the OXEGENE collaborative group [109]. There was also no significant relation in GSTT1 genotypes among histopathology types of lung cancers in Turkish population [46]. No association for GSTM1 null genotype in pre or postmenopausal women has been reported [110]. In Korean population also association of endometriosis with the GSTM1 mutations was not found significant [111-113]. Results suggest that the four genetic polymorphisms studied in the CYP1A1, GSTM1, GSTT1 and GSTP1 metabolic genes are not associated with lung cancer risk in total population of Caucasians from Northern Spain [114]. A Meta-analysis aimed to examine the associations GSTM1, GSTT1, and GSTP1 genetic polymorphisms with thyroid cancer risk found no significant associations for subgroup analyses performed by ethnicity and histological type concluded that these three polymorphisms are unlikely to be major determinants of susceptibility to thyroid cancer [115]. No significant association was found between lung cancer and GSTT1 deletion either overall or in Caucasians but among Asians, a positive association was found in the meta-analysis, whereas the association was not confirmed in the pooled analysis. GSTM1, GSTT1, and GSTP1 gene polymorphisms are not associated with susceptibility of developing diabetic neuropathy in T2DM Romanian patient [116]. The research on GSTs polymorphism has become challenging to draw any inference about disease risk. Thus additional research in a directed way is required.

#### **CONCLUSIONS**

Cancer has been the main target for research studies involving the Glutathione-S-Transferase polymorphism all over the world. Pregnancy loss is another problem major among Indian women and it has also been given weightage for research along with other diseases. While investigating such diseases interrelated to detoxification pathways significant results for disease association are expected because detoxification mechanism is the basic which keeps an individual healthy by means of eliminating the toxicity of the body and failing of which they can't even survive. Positive as well as negative finding have been reported in preceding years but the explanation to the inconsistency in the association with diseases

is still awaited. The main reasons for the inconsistent findings seem to be derived from the gene environment interactions and/or gene-gene interactions as hypothesized by Hamajima et al. [117]. The discrepancies can be partially explained as the result of interpopulational differences in genetic backgrounds of susceptibility and/or of geographical differences in environmental exposure to carcinogens. Though huge reviews and research articles are available on worldwide research a handful of information is available on Indian populations with reference to GSTM1 and T1 null genotype as very few studies have been conducted in this context. Therefore, extensive population-specific studies on GSTs including other polymorphic loci are needed to have an explored view of such polymorphism and their significance for particular diseases.

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