

immune response. Neutrophils, basophils, and monocytes produce cytotoxic proteins such as proteases, collagenases, and elastases as well as reactive oxygen radicals, which cause oxidative stress. In turn, this damage promotes the activation of endothelium and

oxidative damage to erythroid cells plays a crucial role in the bone marrow and short survival of red blood cells in circulation. Oxidative stress may be triggered by several switches, including the interaction between sickle red blood cells and the endothelium, nitric

oxide, and chemical stress. These factors provide protection from oxidative and chemical stress. There has been considerable interest in determining the particular allelic variants and those associated with increased risk to investigate whether *GSTP1* and *TLR2* polymorphisms metabolic pathways involved in antioxidant mechanisms or pathogen recognition increase the chances of infectious processes in SCS

Methodology

Casuistry

Eighty patients with sickle cell anemia were recruited from a tertiary care hospital. The study was approved by the Institutional Review Board and all participants gave informed consent.

Ethical Aspects of Research

This study was performed after approval by the Research Ethics Committee. The study was developed fully complying with the ethical principles set out in the Declaration of Helsinki.

Hematologic and Clinical Analysis

Complete blood count, hemoglobin electrophoresis, and genotyping for *GSTP1* and *TLR2* polymorphisms were performed. The analysis was performed using standard laboratory techniques.

were obtained by the analysis of medical records of patients.

Molecular Analysis

Genomic DNA was extracted from peripheral blood leukocytes. The *GSTP1* and *TLR2* genes were amplified by PCR using specific primers. The PCR products were purified and sequenced. The sequences were analyzed using bioinformatics tools. Eight samples were stained with ethidium bromide, where eight samples were analyzed.

In the present study, we analyzed the relationship between *GSTP1* and *TLR2* polymorphisms and clinical outcomes in sickle cell anemia.

The results of the molecular analysis showed that the *GSTP1* polymorphism was associated with increased levels of oxidative stress markers. The *TLR2* polymorphism was associated with increased levels of inflammatory markers. These findings suggest that these polymorphisms may play a role in the pathogenesis of sickle cell anemia.

Statistical Analysis

The data were analyzed using statistical software. The chi-square test was used to compare the distribution of polymorphisms between groups. The p-value was considered significant when less than 0.05.

Results and Discussion

GSTP1 polymorphism analysis

The analysis of the *GSTP1* polymorphism showed that the GG genotype was more frequent in patients with sickle cell anemia.

The distribution of frequency examined showed a higher percentage for the heterozygous variant genotype (Ile/Val) at 46.02%, followed by the wild genotype (Ile/Ile) at 36.23% and the lowest frequency of 17.75% for the homozygous variant (Val/Val). Such findings were similar to those found in two studies also conducted with the Brazilian population by Hatagima et al. [17] and Honma et al [18]. Kiss et al [19] and Ates et al [20] also obtained similar frequencies in studies carried out in Hungary and Turkey, respectively.

We did not find a statistically significant association between the variant genotypes (Ile / Val and Val / Val) and the risk of infection in patients with sickle cell anemia (Table 1). Silva et al found higher levels of glutathione and greater antioxidant capacity in patients with SCA who presented the Val / Val genotype. This was compared to those with the Ile / Ile genotype [21].

In the literature, it has been extensively studied the relationship between *GSTP1* Val genotypes and a variety of diseases. This includes determining the susceptibility to cancer, and responses to metabolism, efficacy, and toxicity of certain drugs [15, 19, 20, 22, 23]. The association not found in this study can be explained by the possibility that these individuals present antioxidant mechanisms to compensate for the deficiency in the activity of isoform GSTP1. It is imperative to note that GST enzymes are part of an integrated defense system, and the combined action of other enzymes such as γ -glutamylcysteine synthase (γ GluCysS) and glutathione synthase guarantees the efficiency of this system. It provides glutathione, as well as carriers to facilitate the removal of GSH conjugates [24].

TLR2 polymorphism analysis

SNPs (Single nucleotide polymorphisms) in TLR2 have been associated with susceptibility to various infectious

and inflammatory diseases such as leprosy [25], increased gram-negative sepsis risk [26], recurrent bacterial infections in children [27] and colorectal and cervical cancer [28, 29]. Also, a study linked variants in the non-coding region of the TLR2 gene with infections in pediatric sickle cell anemia [30].

The polymorphism corresponding to a deletion of 22 base pairs at position -196 to -174 of the TLR2 promoter region has been reported to alter the promoter activity, decreasing responsive promoters [31]. In this study, the wild homozygous genotype (Ins / Ins) was the most frequent in this population (58.27%), followed by the heterozygous variant genotype (Ins / Del, 40.65%) and finally the homozygous variant (Del / Del, 1.8%). The frequency of TLR2 polymorphism alleles investigated correlates well with previously published data on Brazilian, Japanese and German populations [32, 33, 34].

Individuals with the homozygous genotype for the deletion (Del / Del) showed a 95% increased chance of developing an infection compared to wild homozygotes (OR=1.95; CI=0.1 to 38.65) (Table 2). However, despite the central role of TLR2 in the recognition of pathogens and initiation of defense, this result was not statistically significant.

When pairing the analysis of polymorphisms of both genes (*GSTP1* Ile / Val and *TLR2* Ins / Del) for the development of infectious complications, we also did not find a statistically significant (OR=1.27, P= 0.61) (Table 3).

Woehrle et al. 2008 [35], studying 325 patients with septic shock, observed that in patients with sepsis caused by gram-positive bacteria, the variant profile TLR2 did not alter the pattern of cytokines produced, so, had no involvement in the immune response. TAHARA et al. 2008 [36] in Japan also studied polymorphisms -196 to -174 of the TLR2 gene, relating them to the risk of gastroduodenal disease induced by

Table 1: Association between *GSTP1* variant genotype and the risk of infections in 278 patients with sickle cell disease

<i>GSTP1</i> Genotype	With infection	Without infection	Chi-square	Odds Ratio	CI* of 95%	P value
Ile/Val	98	29	0.14	1.13	(0.60 - 2.08)	0.7
Val/Val	34	15	0.52	0.75	(0.35 - 1.16)	0.47
Ile/Val or Val/Val	132	44	0.01	1	(0.57 - 1.76)	1
Ile/Ile	75	25		1(reference)		

* Confidence interval

Table 2: Association between TLR2 variant genotype and the risk of infection in 278 patients with sickle cell disease

Variant Genotype TLR2	With infection	Without infection	Chi-square	Odds Ratio	CI*of 95%	P value
Ins/Del	78	35	3.08	0.61	(0.35 - 1.06)	0.08
Del/Del	3	0	0.04	1.95	(0.1 - 38.65)	0.85
Ins/Del or Del/Del	81	35	2.63	0.63	(0.37 - 1.1)	0.1
Ins/Ins	127	35		1(reference)		

* Confidence interval

Citation: Géssyca Jerônimo Silva, Romério Alencar de Oliveira Filho, Igor de Farias Domingos, Rodrigo Marcionilo de Santana, Thais Helena Chaves Batista, Aderson da Silva Araújo, Marcos André Cavalcanti Bezerra, José Luiz de Lima Filho, Danyelly Bruneka Gondim Martins, Rosângela Ferreira Frade de Araújo. Relationship between Glutathione S Transferase P1 and Toll like Receptor 2 Polymorphisms and Infections in Sickle Cell Anemia. Archives of Clinical and Biomedical Research. 8 (2024): 53-58.

Table 3: Association between GSTP1 and TLR2 variant genotypes and the risk of infections in 278 patients with sickle cell disease

GSTP1 and TLR2 Genotypes	With infection	Without infection	Chi-square	Odds Ratio	CI* of 95%	P value
GSTP1(Ile / Val) and TLR2(Ins / Del)	43	17	0.95	0.67	(0.3 – 1.5)	0.33
GSTP1(Ile / Ile) and TLR2(Ins / Ins)	53	14		1(reference)		
GSTP1(Ile / Val) and TLR2(Ins / Del)	43	17	0.25	1.27	(0.5 – 3.16)	0.61
GSTP1(Ile / Ile) and TLR2(Ins / Ins)	22	11		1(reference)		
GSTP1(Ile / Val) and TLR2(Ins / Del)	43	17	1.71	0.57	(0.25 – 1.3)	0.19
GSTP1(Ile / Val) and TLR2(Ins / Ins)	53	12		1(reference)		
GSTP1(Val / Val) and TLR2(Ins / Del)	14	6	0.72	0.62	(0.2 – 1.89)	0.39
GSTP1(Ile / Ile) and TLR2(Ins / Ins)	53	14		1(reference)		
GSTP1(Val / Val) and TLR2(Ins / Del)	14	6	0.01	1.05	(0.3 – 3.6)	0.93
GSTP1(Val / Val) and TLR2(Ins / Ins)	20	9		1(reference)		
GSTP1(Val / Val) and TLR2(Ins / Del)	14	6	0.06	1.17	(0.35 – 3.9)	0.8
GSTP1(Ile / Ile) and TLR2(Ins / Del)	22	11		1(reference)		

* **Confidence interval**

Helicobacter pylori in 309 patients, and no found association of this polymorphism with the risk of ulcer gastric, duodenal ulcers and gastritis. Taken together, our data suggest that deletion -196 to -174 of the promoter of the TLR2 gene region was not enough to establish a correlation of polymorphism as a risk factor for infections that affect individuals with sickle cell disease. Possibly it is explained by numerous genetic variations in the pathogens recognition system, responsible for specific differences [37], and also because of the wide range of functionally relevant genetic alterations of the innate immune system [38].

It is necessary to search simultaneously for other candidate genes such as those encoding receptors that interact directly in the formation of heterodimers with TLR2 (TLR1, TLR6, and CD14) and protein signaling pathways, to characterize the profile of severe infections. For example, the presence of CD14 enhances the efficiency of recognition of TLR2-specific ligands [39].

Conclusions

The genotypes Ile/Val and Ins/Ins related to GSTP1 and

TLR2, respectively, were the most frequent in this study. No association was found between GSTP1 (Ile/Val) and TLR2 (Del/Del) variant genotypes and increased risk of infections in sickle cell anemia.

Declaration of interest

None

Author contributions

Géssyca Jerônimo Silva: Formal analysis, investigation; *Romério Alencar de Oliveira Filho:* Formal analysis, investigation; *Igor de Farias Domingos:* Formal analysis, investigation; *Rodrigo Marcionilo de Santana:* Writing - review & editing; *Thais Helena Chaves Batista:* Writing - review & editing; *Aderson da Silva Araújo:* Conceptualization, Funding acquisition; *Marcos André Cavalcanti Bezerra:* Methodology, Supervision; *José Luiz de Lima Filho:* Funding acquisition; *Danyelly Brunaska Gondim Martins:* Methodology, Supervision; *Rosângela Ferreira Frade de Araújo:* Methodology, Project administration, Roles/Writing - original draft.

Funding

This work was supported by Conselho Nacional de Desenvolvimento Científico e Tecnológico/CNPq and Fundação de Amparo à Ciência e Tecnologia do Estado de Pernambuco/FACEPE.

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