

An update on HLA alleles as pharmacogenetic markers for antiepileptic drug-induced cutaneous adverse reaction

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ABSTRACT: Epilepsy is a common neurological disorder affecting approximately 50 million people worldwide. Antiepileptic drugs (AEDs) are commonly used to treat the disease depending, mainly on the type of seizure. However, the use of AEDs may also lead to cutaneous adverse drug reactions (cADR) such as toxic epidermal necrolysis (TEN), Stevens-Johnson syndrome (SJS), exfoliative dermatitis (ED) and drug-induced hypersensitivity syndrome/drug reaction with eosinophilia and systemic symptoms (DIHS/DRESS), which are unwanted comorbidities in epilepsy. It was first discovered that the HLA-B*15:02 allele was strongly associated with carbamazepine (CBZ)-induced SJS/TEN among Han Chinese and this led to the discovery of other HLA alleles and cytochrome P450 (CYP) genes that were significantly associated with various AED-induced cADRs across various populations. This mini-review is an update on the latest findings of the involvement of various HLA alleles and CYP alleles in cADRs caused by CBZ, phenytoin (PHT), oxcarbazepine (OXC) and lamotrigine (LTG) in different case-control studies around the world. From our review, we found that CBZ- and PHT-induced cADRs were more commonly reported than the other AEDs. Therefore, there were more robust pharmacogenetics studies related to these AEDs. OXC- and LTG-induced cADRs were less commonly reported, and so more studies are needed to validate the reported association of the newer reported HLA alleles with these AEDs. It is also important to consider the allelic frequency within a given population before concluding the use of these alleles as genetic markers to prevent AED-induced cADR. Overall, the current body of research point to a combination of alleles as a better pharmacogenetic marker compared to the use of a single gene as a genetic marker for AED-induced cADR.

Keywords: pharmacogenetic marker; HLA alleles; antiepileptic drugs; AEDs; cutaneous adverse drug reaction; cADR;

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1. INTRODUCTION

The World Health Organisation (WHO) states that epilepsy is the most common chronic neurological disorder, affecting an estimated 50 million people worldwide. Generally, the incidence of epilepsy in developed countries is estimated to be 50 per 100,000 (range 40–70 per 100,000/year) [1] while the epilepsy incidence in resource-poor countries is around 100–190 per 100,000/year [2]; The most recent systematic review provided a better estimate of a pooled incidence rate of epilepsy at 61.44 per 100,000 person-years (95% CI 50.75-74.38) [3]. Epilepsy is defined as recurrent unprovoked seizures, and there are different categories of seizures [4]. A systematic review has shown that focal seizures predominate in the population of most countries compared to generalised seizure [5]. Antiepileptic drugs (AEDs) are drugs used for the management of seizures. Carbamazepine (CBZ), lamotrigine (LTG) and sodium valproate (SVA) are usually used as first-line treatment of focal seizures and generalized tonic-clonic seizures, however SVA is not advisable for girls or women due to its documented teratogenic effects and effects on the developing brain of children born to women taking SVA [6]. LTG is one of the first line AEDs for absence seizures. Phenytoin (PHT) is usually prescribed as a second line drug for focal and generalised seizure. However, it is not helpful for myoclonus or absence seizures [6]. It is not surprising, therefore, that the high usage of CBZ, LTG, PHE and SVA among epilepsy patients could incur a high incidence of cutaneous adverse drug reactions (cADRs). These include severe cutaneous adverse reaction (SCAR) such as toxic epidermal necrolysis (TEN) and Stevens-Johnson syndrome (SJS) and milder forms of adverse reaction such as exfoliative dermatitis (ED) and drug-induced hypersensitivity syndrome/drug reaction with eosinophilia and systemic symptoms (DIHS/DRESS) and and maculopapular eruption (MPE), which are unwanted comorbidities in epilepsy [7].

SJS and TEN are usually considered as one disease entity and the classification is based on the extensiveness of the skin detachment and erosion of the mucous membrane, with 10% or less of epidermis detachment of the body surface area (BSA), 10-30% of BSA for SJS/TEN overlap and more than 30% of skin detachment of the BSA as shown in Figure 1 [8]. The clinical features of SJS and TEN include an initial acute phase characterised by non-specific symptoms such as fever, stinging eyes and discomfort upon swallowing, which precedes the cutaneous manifestation involving the trunk, face, palm and soles. In addition, erythema and erosion of the buccal, genital and/or ocular mucosa occur in 90% of patients. In some cases, the gastrointestinal and respiratory tracts are also affected [9,10]. The second stage of the acute phase involves large areas of epidermal detachment, and the extent of the detachment is a major prognostic factor. In the late stage of TEN, 62.5% of patients suffer from hyper or hypopigmentation, and 37.5% suffer from nail dystrophies and ocular complications [11]. The severity of SJS and TEN can lead to mortality, with a 5% mortality rate for SJS and up to 30% mortality rate for TEN [12]. This is one of the comorbidities that could affect epilepsy patients taking AEDs. A recent analysis of the US Food and Drug Administration (FDA) adverse event reporting showed that the use of AEDs posed a significantly higher risk of SJS/TEN compared to non-AEDs. They reported that AEDs as a class had an odds ratio (OR) of 8.7 (95% CI 7.5-10.2) and a proportional reporting ratio (PRR) of 8.7 (95% CI 7.5-10.2) for SJS/TEN [13]. Another recent study also showed an increased risk of SJS/TEN due to CBZ, PHT and LTG among new users [14,15]. Frey et al. reported substantially increased ORs for CBZ (OR 92.27, 95% CI 16.83 -∞), LTG (OR 49.96, 95% CI 10.13-∞), PHT (OR 26.90, 95% CI 4.88-∞), and SVA (OR 10.51, 95% CI 1.25-∞) [14].

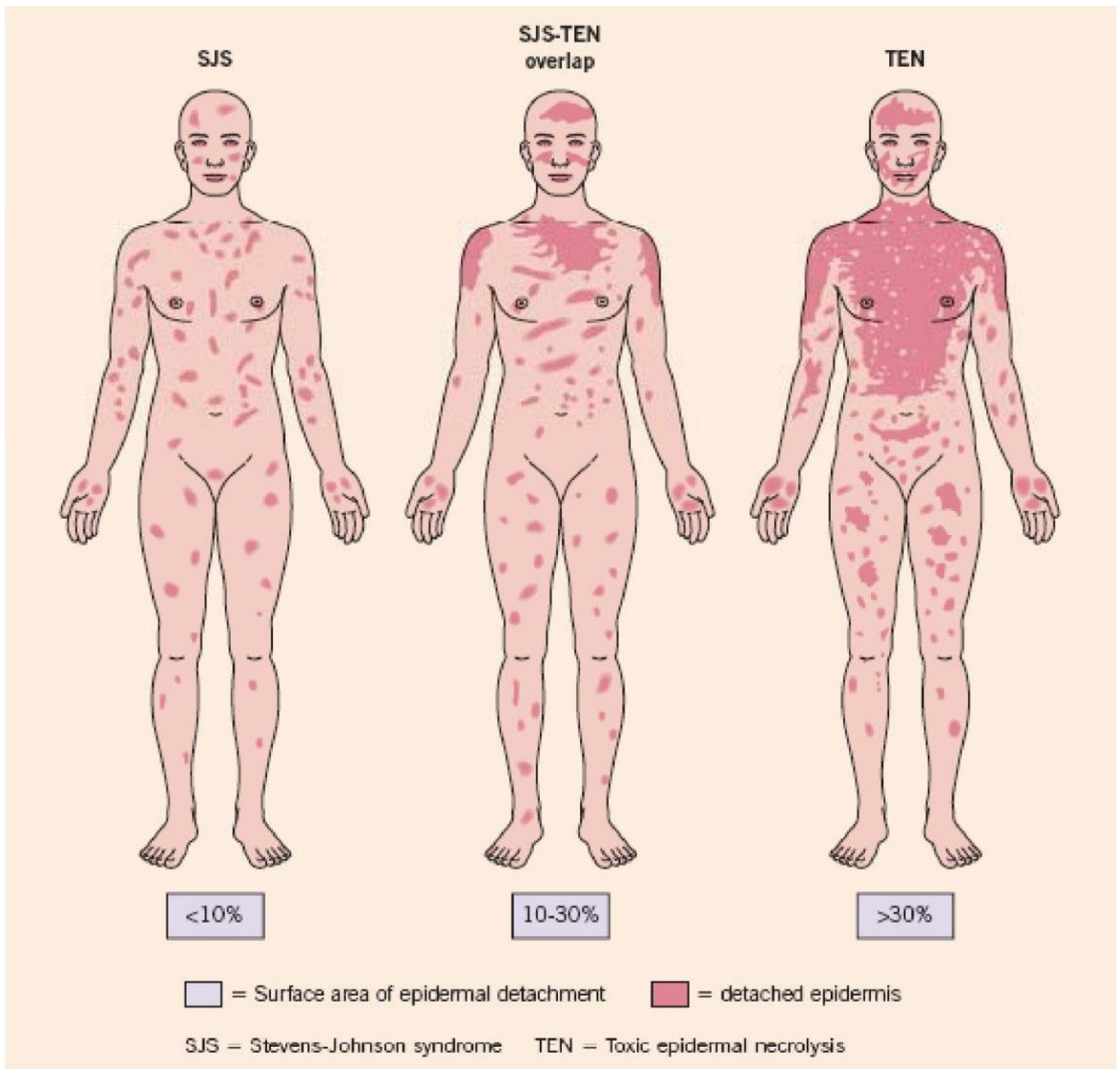


Figure 1: Pictorial representation of the distribution of epidermal detachment for SJS, SJS/TEN and TEN. The figure is reproduced without any modifications from [8] under the terms of the Creative Commons Attribution License (<http://creativecommons.org/licenses/by/2.0>). The figure was originally adapted from [16] by [8].

One of the earliest pharmacogenetic markers for AED-induced cADRs is the strong association of HLA-B*15:02 with a higher risk of CBZ-induced SJS/TEN among the Han Chinese population in Taiwan [17,18]. This was further validated in other Han Chinese populations in Hong Kong [19] and different regions of mainland China [20-22]. Other populations that were also reported to have a similar association of HLA-B*15:02 with CBZ-

induced SJS/TEN include Thailand [23-25], Malaysia [26,27], Singapore [28], Vietnam [29] and northern India [30]. However further investigation in other countries showed that HLA-B*15:02 is not a universal marker for CBZ-induced SJS/TEN for populations with a low allelic frequency of HLA-B*15:02, such as Caucasians [31-33], Japanese [34-36] and South Koreans [37,38]. These population, however, demonstrated that another HLA

allele, HLA-A*31:01 is associated with CBZ-induced SJS/TEN instead of HLA-B*15:02. This review is an update on the current development of genetic markers for AED-induced cADR.

2. THE ASSOCIATION OF HLA-B*15:02 AND OTHER HLA ALLELES WITH CARBAMAZEPINE-INDUCED cADR

Chung et al. (2004) [17] first reported the association of HLA-B*15:02 with CBZ-induced SJS/TEN with an OR of 2504 (95% CI, 125-109) among the Han Chinese population in Taiwan. They were abrupt in confirming this association with a larger cohort of patients (OR of 1357 95% CI, 193.4-8838.3; $P_c=1.6 \times 10^{-41}$) [18]. This was further validated in other Han Chinese populations in Hong Kong with a significant association of the HLA-B*15:02 allele with SJS/TEN induced by CBZ, PHT and LTG (OR of 17.6, 95% CI 2.9-105.2; $P=0.001$), but not with maculopapular exanthema (MPE) ($P=0.32$) [19]. Similar studies in the central [20], southern [21], and southwestern [22] regions of China also confirmed the association of HLA-B*15:02 with CBZ-induced SJS/TEN. In northeastern China, the association of HLA-B*15:02 with CBZ-induced SJS was weaker, at only 22.9% (OR=18.222, 95% CI 3.662-90.662), thus disputing the routine use of HLA-B*15:02 as a general marker for CBZ-induced SJS/TEN among Han Chinese. The authors concluded that due to the low frequency of HLA-B*15:02 among Han Chinese in the northeastern region of China, HLA-B*15:02 is unlikely to be a useful marker for CBZ-induced SJS [39]; their study suggested other HLA alleles as markers as stated in Table 1.

The association of HLA-B*15:02 with CBZ-induced SJS/TEN is also established in other populations such as Thai, Singaporean, Malaysian, Vietnamese and Northern Indian as shown in Table 1. Interestingly, Man et al. (2007) [19] was amongst the first to discover the association of other AEDs, PHT and LTG with HLA-B*15:02 and this has spurred other studies on the association of these AEDs with HLA-B*15:02, which will be discussed in a later section. In the Javanese and Sundanese population, 66.7% of patients with CBZ-induced SJS/TENs have HLA-B*15:02, interestingly they also found association of HLA-B*15:21 with the disease,

and since both HLA-B*15:02 and HLA-B*15:21 are under the HLA-B75 serotype, they proposed HLA-B75 serotyping instead of screening individual alleles [40].

Lonjou et al. (2006) [31] reported that HLA-B*15:02 is not associated with CBZ-induced SJS/TEN amongst Caucasians, but only in 4 patients with Asian ancestry. Further studies in the UK also confirmed that HLA-B*15:02 is not associated with CBZ-induced SJS/TEN amongst self-reported Caucasian. However, they are unable to decipher what other HLA alleles might be involved in CBZ-induced SJS/TEN amongst Caucasians [32,33]. A large genome-wide association study (GWAS) of patients with European descent was able to uncover the presence of single nucleotide polymorphisms (SNPs) associated with CBZ-cADRs which corresponded to the region of the HLA-B*31:01 allele. Further analysis was able to demonstrate a significant association of HLA-A*31:01 with CBZ-induced SJS/TEN, as well as CBZ-induced hypersensitivity syndrome (HSS) and CBZ-induced MPE [41]. A similar GWAS amongst Japanese patients also demonstrated similar findings, with a high association of SNPs in the region of the HLA-A*31:01 allele, with 60.7% of CBZ-cADR (both DISH and SJS/TEN) patients (OR of 10.8, 95% CI of 5.9-19.6; $P=3.64 \times 10^{-15}$). To validate the GWAS findings, Ozeki et al. (2011) [42] performed a replication study with an independent Japanese case-control cohort and confirmed the association of HLA-A*31:01 with CBZ-cADR (OR of 9.5, 95% CI of 5.6-16.3; $P=1.09 \times 10^{-16}$). A study of the Korean population reported that HLA-A*31:01 was associated with CBZ-induced DIHS while HLA-B*15:11 was associated with CBZ-induced SJS [38]. Another study suggested that HLA-B*15:11 was associated with CBZ-induced SJS/TEN in Japanese patients, although there is a need for a larger study to verify this [43]. The latest study with a larger cohort of CBZ-induced cADRs in Thailand was able to detect a significant association of HLA-B*15:02 and HLA-B*58:01 with CBZ-induced MPE patients, as well as an association of HLA-B*58:01 with CBZ-induced DRESS [43]. This study also confirmed the strong association of HLA-B*15:02 with CBZ-induced SJS as previously reported, as well as

Table 1. Compiled studies of associating alleles with antiepileptic drugs (AEDs)-related cutaneous adverse drug reactions (cADRs) across different populations.

Drug	HLA allele	Phenotype	Frequency	Population	P value	OR (95% CI) [case vs tolerant group]	Sample size	Ref.
CBZ	HLA-B*15:02	SJS	100%	Han Chinese (Taiwan)	3.13×10^{-27} *	2504 (125-109, 522)	CBZ-SJS (n=44); CBZ-tolerant (n=101); population control (n = 93)	[17]
		SJS/TEN	98.3%	Han Chinese (Taiwan)	1.6×10^{-41} *	1357 (193.4-8838.3)	CBZ-SJS/TEN (n=60); CBZ-HSS (n=13);	[18]
	HLA-A*31:01	MPE	33.3%	Han Chinese (Taiwan)	2.2×10^{-3} *	17.5 (4.6-66.5)	CBZ-MPE (n=18); CBZ tolerant (n=144)	
CBZ	HLA-B*15:02	SJS/TEN	100%	Han Chinese (Hong Kong)	1.48×10^{-4} *	71.9 (3.7-1,415.8)	CBZ-SJS/TEN (n=4); PHT-SJS (n=1); LTG-TEN (n=1); PB-HSS (n=1); PHT-HSS (n=1), AED-MPE (n=16), AED-tolerant (n=48)	[19]
LTG *	HLA-B*15:02	SJS/TEN	100%	Han Chinese (Hong Kong)				
PHT *	HLA-B*15:02	SJS/TEN	100%	Han Chinese (Hong Kong)				
CBZ	HLA-B*15:02	SJS/TEN	100%	Han Chinese (central China)	≤ 0.05 *	184 (33.2-1021.0)	CBZ-SJS/TEN (n=8); CBZ-MPE (n=31); CBZ-tolerant (n=50); population control (n=71)	[20]
		SJS/TEN	100%	Han Chinese (southern China)	< 0.001 *	114.826 (6.25-2,111.03)	CBZ-SJS/TEN (n=9); CBZ-MPE (n=39); CBZ-tolerant (n=80); population control (n=62)	[21]
		SJS/TEN	94.11%	Han Chinese (southwestern China)	< 0.0001 *	152 (12 -1,835)	CBZ-SJS/TEN (n=17); CBZ-tolerant (n=21), population control (n=185)	[22]
		SJS/TEN	22.9%	Han Chinese (northeastern China)	0.000 *	18.222 (3.66-90.66)	CBZ-SJS (n=35); CBZ-tolerant (n=125)	[39]
	HLA-A*31:01	SJS/TEN	35%	Han Chinese (northeastern China)	0.000 *	12.923 (3.58-46.59)		
	HLA-B*58:01	SJS/TEN	20%	Han Chinese (northeastern China)	0.013 *	4.958 (1.26-19.49)		
	HLA-C*03:02	SJS/TEN	20%	Han Chinese (northeastern China)	0.013 *	4.958 (1.26-19.49)		
	DQB1*03:03	SJS/TEN	40%	Han Chinese (northeastern China)	0.022 *	3.121 (1.14-8.54)		
	DRB1*07:01	SJS/TEN	35%	Han Chinese (northeastern China)	0.003 *	4.639 (1.57-13.71)		
	HLA-B*15:02	SJS	100%	Thai	0.0005 *	25.5 (2.68-242.61)		[23]

PHT	HLA-B*15:02	SJS	100%	Thai	0.005 *	18.5 (1.82-188.40)	CBZ-SJS (n=6); PHT-SJS (n=4); AED-induced MPE (n=21); AED-tolerant (n=50)	
CBZ	HLA-B*15:02	SJS/TEN	88.1%	Thai	2.89×10^{-12} *	54.76 (14.62-205.13)	CBZ-SJS/TEN (n=42); CBZ-tolerant (n=42)	[24]
		SJS/TEN	94.1%	Thai	<0.001 *	75.4 (13.0-718.9)	CBZ-SJS/TEN (n=34), CBZ-tolerant (n=40)	[25]
		SJS/TEN	75%	Thai	4.46×10^{-13} *	70.91 (19.67-255.65)	CBZ-SJS/TEN (n=16); CBZ-MPE (n=17);	[44]
	HLA-B*15:21	SJS/TEN	12.5%	Thai	0.013 *	9.54 (1.61-56.57)	CBZ-DRESS (n=5); CBZ-tolerant (n=271);	
	HLA-B*15:02	MPE	23.52%	Thai	0.002 *	7.27 (2.04-25.97)	population control (n=470)	
	HLA-B*58:01	MPE	29.41%	Thai	0.007 *	4.74 (1.53-14.66)		
		DRESS	40%	Thai	0.032 *	7.55 (1.20-47.58)		
	HLA-B*15:02	SJS/TEN	75%	Malaysians	7.87×10^{-6} #	16.15 (4.57-62.4)	CBZ-SJS/TEN (n=21); population control	[26]
	HLA-A74	SJS/TEN	18.8%	Malaysians		13.62 (2.93-63.2)	(n=300)	
	HLA-B*15:02	SJS/TEN	100%	Malaysians	0.0003 *	N.R.	CBZ-SJS/TEN (n=6); CBZ-rash (n=2); PHT-rash (n=2), AED-tolerant (n=8)	[27]
		SJS/TEN	100%	Singaporeans	N. R.	27.20 (2.67 to ∞)	CBZ-SJS/TEN (n=5); CBZ-HSS (n=6); CBZ-tolerant (n=10)	[28]
		SJS/TEN	89.5%	Vietnamese	<0.0001 *	33.78 (7.55-151.03)	CBZ-SJS/TEN (n=35); CBZ-DRESS (n=3); CBZ-tolerant (n=25)	[29]
		SJS/TEN	66.7%	Indonesians	0.029 *	6.5 (1.2-33.57)	CBZ-SJS/TEN (n=12); CBZ-tolerant (n=17)	[40]
	HLA-B*15:21	SJS/TEN	16.7%	Indonesians	0.55 *	3.2 (0.26-40.05)		
	HLA-B*15:02	SJS/TEN	75%	Indians	0.0014 *	71.40 (0-1698)	CBZ-SJS/TEN (n=8), normal subjects (n=10)	[30]
SJS/TEN		(16.7%-only in patients with Asian ancestry)	United Kingdom (UK)	N. R.	N.R.	CBZ-SJS/TEN (n=12)	[31]	
HLA-A*31:01	SJS/TEN	42%	European	8.0×10^{-5} *	25.93; (4.93 to 116.18)	CBZ-SJS/TEN (n=12); CBZ-HSS (n=26);	[41]	
		HSS	40%	European	0.03 *	12.41 (1.27 to 121.03)	CBZ-MPE (n=43); CBZ-tolerant (n=257);	
	MPE	21.7%	European	8.0×10^{-7} *	8.33 (3.59-19.36)	population control (n=3987)		
	SJS/TEN	83.3%	Japanese	2.35×10^{-4} *	33.9 (3.9-295.6)	CBZ-SJS/TEN (n=6); CBZ-HSS (n=36);	[42]	
	HSS	58.3%	Japanese	2.06×10^{-9} *	9.5 (4.6-19.5)	CBZ-tolerant (n=420)		
HLA-A*15:11	SJS/TEN	14.3%	Japanese	0.0004 #	16.3 (4.76-55.6)	CBZ-SJS/TEN (n=28); normal subjects (n=493)	[43]	
HLA-B*15:11	SJS	42.9%	Korean	0.011 *	18.0 (2.3-141.2)	CBZ-SJS (n=7); CBZ-HSS (n=17); CBZ-	[38]	
HLA-A*31:01	HSS	58.8%	Korean	0.001 *	8.8 (2.5-30.7)	tolerant (n=50)		

PHT	CYP2C9*3	cADR (not specified)	30%	Korean	0.007 *	167 (N.R.)	PHT-cADR (n=10); PHT-tolerant (n=40); population control (n=58)	[45]
	HLA-B*15:02	SJS/TEN	30.8%	Han Chinese (Taiwan)	0.0041 *	5.1 (1.8-15.1)	PHT-SJS/TEN (n=26); LTG-SJS/TEN (n=6);	[46]
	HLA-B*13:01	SJS/TEN	34.6%	Han Chinese (Taiwan)	0.0154 *	5.1 (1.8-15.1)	OXC-SJS (n=3); PHT-tolerant (n=113);	
	Cw*0801	SJS/TEN	34.6%	Han Chinese (Taiwan)	0.0281 *	3.0 (1.1-7.8)	LTG-tolerant (n=67); population control	
	DRB1*1602	SJS/TEN	26.9%	Han Chinese (Taiwan)	0.0128 *	4.3 (1.4-12.8)	(n=93)	
OXC	HLA-B*15:02	SJS/TEN	100%	Han Chinese (Taiwan)	8.4×10 ⁻⁴ #	80.7 (3.8-1714.4)		
LTG	HLA-B*15:02	SJS/TEN	33%	Han Chinese (Taiwan)	0.1266 *	5.1 (0.8-33.8)		
PHT	HLA-A*33:03	SJS/TEN	30.77%	Thai	0.0495 *	2.70 (1.10-6.63)	PHT-SJS/TEN (n=39); PHT-DRESS (n=21);	[47]
	HLA-B*38:02	SJS/TEN	20.51%	Thai	0.0281 *	3.70 (1.19-11.51)	PHT-tolerant (n=92)	
	HLA-B*51:01	SJS/TEN	17.95%	Thai	0.0163 *	4.81 (1.32-17.54)		
		DRESS	19.05%	Thai	0.0381 *	5.18 (1.18-22.74)		
	HLA-B*56:02	SJS/TEN	10.26%	Thai	0.0274 *	10.40 (1.12-96.31)		
	HLA-B*58:01	SJS/TEN	23.08%	Thai	0.0431 *	3.15 (1.11-8.91)		
	HLA-C*14:02	SJS/TEN	17.95%	Thai	0.0077 *	6.49 (1.59-26.62)		
	CYP2C9*3	SJS/TEN	23.08%	Thai	0.0133 *	4.30 (1.41-13.09)		
		SJS/TEN	20.0%	Thai	0.0251 *	5.70 (1.39-23.36)	PHT-SJS/TEN (n=15); PHT-tolerant	[48]
	HLA-B*13:01	DRESS	52.4%	Thai	0.0003 *	6.76 (2.42-18.85)	(n=100); population control for HLA	
	HLA-B*56:02/04	DRESS	14.3%	Thai	0.0046 *	38.03 (1.88-767.19)	alleles (n=758); population controls for	
							CYP alleles (n=250)	
	CYP2C19*3	DRESS	19.0%	Thai	0.0478 *	4.47 (1.09-18.36)		
	HLA-B*15:02	DRESS	18.0 % (tolerant group)	Thai	0.0402 *	0.10 (0.01-1.79)		
	CYP2C9*3	SJS/TEN	41.70%	Han Chinese (Taiwan)	1.2×10 ⁻¹⁰ *	30.0 (8.4-109)	PHT-SJS/TEN (n=48); PHT-DRESS (n=42);	[49]
	HLA-B*15:02	SJS/TEN	27.1%	Han Chinese (Taiwan)	7.0×10 ⁻⁴ *	5.0 (2.0-13)	PHT-MPE (n=78) PHT-tolerant (n=130);	
	CYP2C9*3	DRESS	31.0%	Han Chinese (Taiwan)	7.0×10 ⁻⁷ *	19.0 (5.1-71)	population control (n=41)	
		MPE	11.5%	Han Chinese (Taiwan)	0.011 *	5.5 (1.5-21)		
		SJS/TEN	22.0%	Japanese	1.2×10 ⁻³ #	10.0 (3.4-32)	PHT-SJS/TEN (n=9); population control	
							(n=2869)	
		SCAR	17.0%	Malaysians	0.048 #	6.9 (1.4-34)	PHT-SJS/TEN (n=4); population control	
							(n=374)	
PHT	HLA-B*15:02	SJS/TEN	31.0%	Han Chinese (Taiwan)	1.73×10 ⁻⁷ *	6.52 (3.34-12.73)	PHT-SJS/TEN (n=65); PHT-DRESS (63);	[50]
	HLA-B*.13:01	DRESS	29.0%	Han Chinese (Taiwan)	3.38×10 ⁻⁴ *	3.46 (1.82-6.55)	PHT-MPE (n=107); PHT-tolerant	
		SCAR+MPE	21.0%	Han Chinese (Taiwan)	5.35×10 ⁻⁴ *	2.28 (1.44-3.59)	(n=367);	
	HLA-B*51:01	SCAR+MPE	16.0%	Han Chinese (Taiwan)	6.40×10 ⁻⁴ *	3.62 (2.03-6.46)		
	CYP2C9*3	SJS/TEN	34.0%	Han Chinese (Taiwan)	1.22×10 ⁻¹³ *	20.86 (9.03-48.20)		

	DRESS	27.0%	Han Chinese (Taiwan)	8.83×10^{-11} *	16.95 (6.93-41.47)		
	MPE	9.0%	Han Chinese (Taiwan)	0.003 *	4.20 (1.66-10.63)		
	SCAR+MPE	21.0%	Han Chinese (Taiwan)	4.66×10^{-14} *	10.74 (5.16-22.34)		
CYP2C9*3/HLA-B*13:01/HLA-B*15:02/HLA-B*51:01	SJS/TEN	72%	Han Chinese (Taiwan)	1.77×10^{-15} *	9.82 (5.36-17.96)		
	DRESS	70%	Han Chinese (Taiwan)	3.83×10^{-13} *	8.05 (4.46-14.53)		
	MPE	45.0%	Han Chinese (Taiwan)	8.27×10^{-6} *	2.83 (1.80-4.44)		
	SCAR+MPE	60.0%	Han Chinese (Taiwan)	2.70×10^{-20} *	5.12 (3.59-7.31)		
PHT	HLA-B*15:02	SJS/TEN	61.5%	Malaysians (Malay)	0.016 *	5.71 (1.41-23.10)	PHT-SJS/TEN (n=13); PHT-DRESS (n=3)
	HLA-B*15:13	SJS/TEN	53.8%	Malaysians (Malay)	0.003 *	11.28 (2.25-59.6)	PHT-tolerant (n=32); population control (n=300)
		DRESS	100%	Malaysians (Malay)	0.003 *	59.0 (2.49-1395.74)	
	HLA-A*02:01/HLA-Cw*15:02	SJS/TEN	16.7%	Spanish	0.009 #	14.75 (1.54-167.0)	PHT-SJS/TEN (n=9); LTG-SJS/TEN (n=3); CBZ-SJS/TEN (n=2); PHT-DRESS (n=5);
PHT-LTG	HLA-B*38:01	SJS/TEN	41.7%	Spanish	0.012 *	12.86 (1.66-123.82)	LTG-DRESS (n=3); CBZ-DRESS (n=4); PHT-tolerant (n=28); LTG-tolerant (n=10);
LTG	HLA-B*24:02	DRESS	75.0%	Spanish	0.003 *	22.56 (2.19-559.39)	PHT-LTG-tolerant (n=38); CBZ-tolerant (n=28); AED-tolerant (n=61)
LTG	HLA-B*38:01	SJS/TEN	100%	Spanish	0.001 *	147 (1.88-483)	
	HLA-B*24:02	DRESS	100%	Spanish	0.015 *	49.0 (1.25-46.13x10 ⁶)	
OXC	HLA-B*15:02	MPE	44.4%	Han Chinese (southwestern China)	0.011 #	8.8 (1.853-41.790)	OXC-MPE (n=9); OXC-tolerant (n=9); population control (n=72)
	HLA-B*13:02	MPE	14.3%	Han Chinese (southern)	0.001 #	7.83 (2.32-26.41)	OXC-MPE (n=14); OXC-tolerant (n=35); population control-southern Han Chinese (n=264); population control-Hong Kong Chinese population (n=569); population control-Guangzhou Han Chinese population (n=106)
	HLA-B*40:02	MPE	25%	Koreans	0.018 *	4.33 (1.36-13.79)	OXC-MPE (n=40); OXC-tolerant (n=70);
	DRB1*04:03	MPE	17.5%	Koreans	0.003 *	14.64 (1.73-123.90)	Population control (n=485)
	HLA-B*15:02	MPE	22.9%	Koreans	0.016 *	0.18 (0.04-0.82)	
			(tolerant group)				
	HLA-B*15:02	SJS/TEN	70.6%	Han Chinese (Taiwan)	1.87×10^{-10} *	27.90 (7.84-99.23)	OXC-SJS (n=20); OXC-DRESS (n=6); OXC-MPE (n=21); OXC-tolerant (n=101)
	HLA-B*15:02	MPE		Thai	2.65×10^{-3} *	49.00 (2.39-1006.00)	OXC-SJS (n=3); OXC-MPE (n=1); population control (n=99)
LTG	HLA-A*02:02/HLA-B*35:01/HLA-C*04:01	MPE	25.0%	Mexican Mestizo	0.0009 *	18.33 (1.99-169.08)	LTG-SJS/TEN (n=4); LGT-MPE (n=10); CBZ-MPE (n=5); PHT-MPE (n=2); LTG-tolerant (n=28); CBZ-tolerant (n=18);
CBZ	HLA-A*01:01	MPE	30%	Mexican Mestizo	0.028 *	7.29 (1.02-52.01)	

	HLA-A*31:01	MPE	20%	Mexican Mestizo	0.04 #	4.64 (0.93-23.11)	PHT-tolerant (n=5); population control (n=225)
PHT	HLA-C*08:02	MPE	75%	Mexican Mestizo	0.002 #	48.92 (4.92-486.80)	
LTG	HLA-A*24:02	MPE	71.4%	Korean	0.025 *	4.09 (1.22-13.69)	LTG-MPE (n=21); LTG-tolerant (n=29) [58]
	HLA-A*24:02/Cw*01:02	MPE	47.6%	Korean	0.007 *	7.88 (1.81-34.28)	
	HLA-Cw*07:02	MPE	33.3%	Korean	0.034 #	2.82 (1.10-7.23)	
	HLA-A*33:03	MPE	28.9 % (population control)	Korean	0.012 #	0.12 (0.02-0.93)	
	HLA-A*02:07	MPE	70%	Thai	0.005 *	8.27 (1.83-37.41)	

Keys: The AEDs included in the table are carbamazepine (CBZ), phenytoin (PHT), oxcarbazepine (OXC), lamotrigine (LTG), with the associating severe cutaneous adverse reactions (SCARs): Steven-Johnson syndrome (SJS), toxic epidermal necrolysis (TEN) and less severe reactions: drug-induced hypersensitivity syndrome/ hypersensitivity syndrome (DIHS/HSS), drug reaction with eosinophilia and systemic symptoms (DRESS) and maculopapular eruption (MPE).

* case vs AED-tolerant group (significant when compared with AED-tolerant group and population)

case vs population control (only significant when compared with population control)

another allele, HLA-B*15:21 with CBZ-induced SJS/TEN [44]. The latest update on HLA typing that is significantly associated with CBZ-induced cADRs has painted a complex interplay of various HLA alleles in the disease as detailed in Table 1 besides HLA-B*15:02.

3. THE ASSOCIATION OF CYP2C9*3 AND HLA ALLELES WITH PHENYTOIN-INDUCED cADR

PHT is another AED that is commonly prescribed to epileptic patients and may cause cADR. PHT-induced cADR was first reported in 2004 to be significantly associated with the cytochrome P450 allele, CYP2C9*3 [45] as 90% of the drug is metabolised by the CYP2C9 enzyme in the liver [60]. Depondt et al. (2011) [61] also reported a similar association of CYP2C9*2 and CYP2C9*3 alleles with PHT-induced cADR ($P_c=0.008$). Both of these studies did not specify the type of cADR in their analysis. Association of HLA-B*15:02 with PHT-induced SJS/TEN was first reported alongside CBZ-induced SJS/TEN in Han Chinese from Hong Kong (1/1) [19], followed by Taiwan (8/26) [46] and Thai (4/4) [23]. Besides HLA-B*15:02, Hung et al. (2010) [46] also reported other HLA alleles that have a significant association with PHT-induced SJS/TEN, such as HLA-B*13:01, Cw*08:01 and DRB1*16:01. However, due to the small sample sizes, these studies needed replication. In a case-control study of 39 SJS/TEN, 21 DRESS and 92 phenytoin-tolerant patients, Tassaneeyakul et. al (2016) [47] reported that 6 HLA alleles including HLA-A*33:03, HLA-B*38:02, HLA-B*51:01, HLA-B*56:02, HLA-B*58:01, and HLA-C*14:02 were significantly associated with phenytoin-related SJS/TEN, whereas only the HLA-B*51:01 was significantly associated with phenytoin-related DRESS. The ORs of phenytoin-related SJS/TEN in the patients who carried one of these alleles ranged from 4-10 folds (refer to Table 1). CYP2C9*3 was reported to be significantly associated with PHT-induced SJS/TEN, with an OR of 4.30 (95% CI 1.41-13.09; $P<0.05$). For this study, interestingly there was no significant association of HLA-B*15:02 with PHT-induced SJS/TEN or PHT-induced DRESS as the frequencies of patients who carried the HLA-B*15:02 in the SJS/TEN (12.82%) or the DRESS (9.52%) groups were

not significantly different from that of the PHT-tolerant controls (14.13%) [47]. Another Thai study looked at different HLA alleles and CYP alleles in PHT-associated cADR cases. Their multiple logistic regression analysis found that HLA-B*13:01, HLA-B*56:02/04, CYP2c19*3 and co-medication with omeprazole were strong risk factors for PHT-induced DRESS/DHS (adjusted OR of 13.29, $P=0.0001$; adjusted OR of 56.23, $P=0.0007$; adjusted OR of 6.75, $P=0.0414$; adjusted OR of 9.21, $P=0.0020$ respectively). As for PHT-induced SJS/TEN, the CYP2C9*3 allele and having Chinese ancestry were significant risk factors (adjusted OR of 10.41, $P=0.0042$ and adjusted OR of 5.40, $P=0.0097$, respectively). For this study, the carrier rate for HLA-B*15:02 was found to be higher in SJS cases compared to the tolerant group and population control, but was not statistically significant. Interestingly, HLA-B*15:02 was found to be a protective factor in PHT-induced DRESS with OR of 0.10 (95% CI 0.01-1.79; $P=0.0402$) [48].

Using GWAS, Chung et al. in 2014 [49] was able to demonstrate a strong association of both CYP2C9*3 and HLA-B*15:02 with PHT-induced SJS/TEN amongst Taiwanese Han Chinese patients. CYP2C9*3 has a strong association with PHT-induced SJS/TEN and PHT-induced DRESS and a moderate association with PHT-induced MPE (refer to Table 1). The CYP2C9*3 allele is also shown to be a risk carrier gene for PHT-induced SJS/TEN in Malaysian and Japanese cohorts. The meta-analysis of the three cohorts showed a pooled OR of 12 (95% CI, 6.4-22; $z=7.82$; $P<.00001$) for a CYP2C9*3 association with phenytoin-related SJS-TEN, a pooled OR of 9.2 (95% CI, 4.3-20; $z=5.70$; $P<.00001$) for a CYP2C9*3 association with phenytoin-related DRESS, and an overall OR of 11 (95% CI, 6.2-18; $z=8.58$; $P<.00001$) for a CYP2C9*3 association with phenytoin-related sADR in these three populations. However, the frequency of HLA-B*15:02 is not as obvious, at 27.1% in PHT-induced SJS/TEN patients (OR of 5.0, 95% CI of 2.0-13; $P_c=0.025$) [49]. A recent study of ethnic Malays in Malaysia confirmed the association of HLA-B*15:02 with PHT-induced SJS/TEN, being positive in 61.5% of SJS/TEN cases (8/13) compared to 21.9% in controls (7/32); with

OR of 5.71, ($P=0.016$) compared with PHT-tolerant controls. The study also reported another novel HLA allele, the HLA-B*15:13 that was significantly associated with PHT-induced SJS/TEN, being positive in 53.8% of the SJS/TEN cases (7/13) with an OR of 11.28 ($P=0.003$) and all 3 patients with PHT-DRESS with an OR of 59.00 ($P=0.003$) when compared with PHT-tolerant controls, with only 9.4% (3/32) positive cases [51]. Among the Caucasian population, a Spanish study showed that concomitant HLA-A*02:01/Cw15:02 alleles were significantly associated with PHT-SJS/TEN, with OR of 14.75, ($P=0.009$) compared to the AED-tolerant control group in a Caucasian population [52]. Table 1 shows a detailed description of the studies mentioned earlier. Each of these predisposing alleles for phenytoin-cADR accounts for up to only 30% of cases. Therefore, the currently available data suggest that the association of HLA alleles with the incidence of PHT-related cADR is only moderate and considerably weaker compared to HLA-B*15:02 and HLA-A*31:01 in CBZ-induced SJS/TEN. This led to the latest combined study of Han Chinese, Japanese and Thai patients by Su et al. [50]. They demonstrated that concurrent testing of CYP2C*3/ HLA-B*13:01/ HLA-B*15:02/ HLA-B*51:01 increased the sensitivity of the pharmacogenetic testing from 16.41% up to 71.88% with an OR of 8.88 (95% CI of 5.63-14.01; $P=2.12 \times 10^{-23}$) in the Taiwanese Han Chinese cohort. The meta-analysis of the three population groups showed that the four combined risk alleles have significant associations with PHT-cADR with an overall OR 4.55 (95% CI 1.44-14.41; $z=2.58$; $P=0.01$) [50]. With regards to PHT-associated cADR, current knowledge gleaned thus far points to the use of multiple predisposing alleles to improve the usefulness of predictive genetic testing before the prescription.

4. ASSOCIATION OF HLA ALLELES WITH OXCARBAZEPINE-INDUCED cADR

Oxcarbazepine (OXC) was developed as a second-generation AED. It is a 10-keto analogue of CBZ, with similar clinical efficacy as CBZ but with less severe adverse effects, as it is metabolised differently compared to CBZ [62]. Although the incidence of

SJS/TEN induced by OXC is lower compared to CBZ, there have been reports of OXC-induced cADR [63]. OXC-induced SJS/TEN was first observed to have a strong association with HLA-B*15:02 in Han Chinese [46], being positive in all three cases of OXC-induced SJS/TEN. Another study in central China also reported an association of HLA-B*15:02 with OXC-induced SJS/TEN for three patients [64]. Hu et al. (2011) [53] reported that OXC-induced MPE from southwest China was also associated with HLA-B*15:02, although only among 44.4% of the 9 patients, but the association was significant with an OR of 8.8; 95% CI of 1.853-41.790; $P=0.011$ (refer to Table 1). However, this study did not report the HLA genotype of the OXC-induced MPE that were negative for HLA-B*15:02 [53]. On the other hand, a slightly bigger study from southern China, however, reported that there was a statistically significant association between HLA-B*15:02 and OXC-induced MPE compared to the OXC-tolerant group. However another allele HLA-B*13:02 has shown significant association with OXC-induced MPE compared with the general population with OR of 7.83, 95% CI 2.32-26.41; $P=0.001$ [54]. Lv et al. also reported the lack of association of HLA-B*15:02 with OXC-induced MPE in patients of northern China, but the OXC-induced MPE was associated with HLA-B*38:02 [65]. Moreover, some case reports also reported that the genotyping of patients with OXC-induced SJS/TEN revealed its association with HLA-B*15:18 [66,67]. The latest study by Chen et al. (2017) [56] included the largest cohort to date, which addressed the role of HLA alleles in OXC-induced cADR. This study confirmed the strong association of HLA-B*15:02 with OXC-SJS/TEN in both Han Chinese and Thai patients (OR of 27.90; 95% CI 7.84-99.2; $P=1.87 \times 10^{-10}$) but did not find a significant association of HLA-A*31:01 with OXC-cADR [56]. A Korean study looked at OXC-induced MPE and found an association with HLA-B*40:02 (OR 14.64, 95% CI 1.73-123.90; $P=0.003$) and DRB1*04:03 (OR 0.18, 95% CI 0.04-0.82; $P=0.016$). Interestingly, this study also found that HLA-B*15:01 was a protective allele (OR of 0.18, 95% CI 0.04-0.82; $P=0.016$) [55]. From the studies done thus far, HLA-B*15:02 is strongly associated with both

OXC-induced SJS/TEN and OXC-induced MPE in populations with a high frequency of this allele. However, more studies are needed to establish the links of other HLA alleles with OXC-MPE in populations that have a low allelic frequency of HLA-B*15:02.

5. ASSOCIATION OF HLA ALLELES WITH LAMOTRIGINE-INDUCED cADR

LTG-induced SJS/TEN was also first reported to be associated with HLA-B*15:02 in Han Chinese patients [19,46]. However, another study reported the lack of association of HLA-B*15:02 with LTG-induced SCAR and MPE amongst Han Chinese population in the southern region of China [68]. A Thai study reported these HLA alleles that have a significant association with LTG-induced MPE: HLA-B*15:02, HLA-B*33:03, HLA-B*35:08 and HLA-B*44:03 with the ORs reported in table 1 [59]. There were a few studies in Korea looking at the association of HLA alleles with LTG-induced cADR. Park et al. (2015) [69] reported that in their cohort of patients, the HLA-B*44:03 is present in three out of five patients with LTG-induced SJS/TEN. However, their sample size was too small to draw any conclusions. They did a follow-up study with larger sample size and confirmed that HLA-B*44:02 may have an association with LTG-induced SJS/ TEN with an OR of 12.75 (95% CI 1.03-157.14; $P=0.053$) [70]. Another study that looked at the association of HLA genes with LTG-induced MPE reported a significant association of HLA-A*24:02, HLA-Cw*01:02 and HLA-Cw*07:02 with the disease (refer to Table 1). They also found that concomitant A*24:02 and Cw*01:02 alleles were significantly more frequent in the LTG-MPE group than in the LTG-tolerant group (OR of 7.88, 95% CI 1.81-34.28; $P=0.007$). HLA-A*33:03 was reported as a protective allele against LTG-induced MPE with an OR of 0.12 (95% CI 0.02-0.93; $P=0.012$) [58]. As regards the Caucasian population, McCormack et al.

(2012) were not able to find a significant association of HLA-A*31:01 with LTG-induced cADR in their GWAS [71]. Meanwhile, Fricke-Galindo et al. (2014) [57] reported that the haplotype that included the alleles, HLA-A*02:01/ HLA-B*35:01/ HLA-C*04:01:01 was significantly associated with LTG-induced MPE in Mexican Mestizo patients, with an OR of 18.33; 95% CI 1.99-169.08, $P=0.0009$. As the incidence of LTG-induced cADR is lower compared to other AEDs, there is a need for a larger multicentre study to observe the effect of HLA alleles in LTG-induced cADR cases.

6. CONCLUSION

Established data pertaining to the association of HLA alleles with AED-induced cADR still need further refinement as this appears to depend on the frequencies of the alleles in question in a given population. Further research is needed to confirm the validity of newer HLA alleles reported in the literature. Screening of these susceptible HLA alleles prior to drug prescription, either as a single or multiplex gene detection is important to prevent the unwanted side effects of AEDs.

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