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Review

Epigenetic alterations induced by genotoxic occupational and environmental human chemical carcinogens: A systematic literature review



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ABSTRACT

Accumulating evidence suggests that epigenetic alterations play an important role in chemically-induced carcinogenesis. Although the epigenome and genome may be equally important in carcinogenicity, the genotoxicity of chemical agents and exposure-related transcriptomic responses have been more thoroughly studied and characterized. To better understand the evidence for epigenetic alterations of human carcinogens, and the potential association with genotoxic endpoints, we conducted a systematic review of published studies of genotoxic carcinogens that reported epigenetic endpoints. Specifically, we searched for publications reporting epigenetic effects for the 28 agents and occupations included in Monograph Volume 100F of the International Agency for the Research on Cancer (IARC) that were classified as "carcinogenic to humans" (Group 1) with strong evidence of genotoxic mechanisms of carcinogenesis. We identified a total of 158 studies that evaluated epigenetic alterations for 12 of these 28 carcinogenic agents and occupations (1,3-butadiene, 4-aminobiphenyl, aflatoxins, benzene, benzidine, benzo[a]pyrene, coke production, formaldehyde, occupational exposure as a painter, sulfur mustard, and vinyl chloride). Aberrant DNA methylation was most commonly studied, followed by altered expression of non-coding RNAs and histone changes (totaling 85, 59 and 25 studies, respectively). For 3 carcinogens (aflatoxins, benzene and benzo[a]pyrene), 10 or more studies reported epigenetic effects. However, epigenetic studies were sparse for the remaining 9 carcinogens; for 4 agents, only 1 or 2 published reports were identified. While further research is needed to better identify carcinogenesisassociated epigenetic perturbations for many potential carcinogens, published reports on specific epigenetic endpoints can be systematically identified and increasingly incorporated in cancer hazard assessments.

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Contents

	Introduction Methodology		
3.	Categories of epigenetic alterations induced by chemicals and associated occupations included in the systematic review		
	3.1. DNA methylation	. 31	
	3.2. Histone modifications	. 31	
	3.3. Non-coding RNAs	. 32	
4.	Epigenetic effects associated with carcinogenic chemicals and associated occupations	. 34	
	4.1. Benzo[a]pyrene	. 34	
	4.1.1. Routes of exposure, associated cancers, and genotoxicity	. 34	
	4.1.2. DNA methylation	. 34	

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	4.1.3.	Histone modifications	. 34
	4.1.4.	Non-coding RNA	35
4.2.	Aflatoxii	ns (naturally occurring mixtures)	35
	4.2.1.	Routes of exposure, associated cancers, and genotoxicity	
	4.2.2.	DNA methylation	
	4.2.3.	Histone modifications	
	4.2.4.	Non-coding RNA	
4.3.	Benzene	2	
	4.3.1.	Routes of exposure, associated cancers, and genotoxicity	36
	4.3.2.	DNA methylation	36
	4.3.3.	Histone modifications	
	4.3.4.	Non-coding RNA	
4.4			
4.4.		lehyde	
	4.4.1.	Routes of exposure, associated cancers, and genotoxicity	
	4.4.2.	DNA methylation	. 37
	4.4.3.	Histone modifications	. 37
	4.4.4.	Non-coding RNA	. 37
4.5.	Coke pro	oduction, occupational exposures	
1.5.	4.5.1.	Routes of exposure, associated cancers, and genotoxicity	
	4.5.2.	Routes of exposure, associated cancers, and genotoxicity	20
		DNA methylation	
	4.5.3.	Non-coding RNA	
4.6.	1,3-buta	dienediene	
	4.6.1.	Routes of exposure, associated cancers, and genotoxicity	38
	4.6.2.	DNA methylation	
	4.6.3.	Histone modifications	
4.7.		nustard	
4.7.			
	4.7.1.	Routes of exposure, associated cancers, and genotoxicity	
	4.7.2.	DNA methylation	
	4.7.3.	Non-coding RNA	. 39
4.8.	Vinyl ch	lloride	39
	4.8.1.	Routes of exposure, associated cancers, and genotoxicity	39
	4.8.2.	DNA methylation	
4.9.		biphenyl	
4.5.		Routes of exposure, associated cancers, and genotoxicity	
	4.9.1.		
	4.9.2.	Histone modifications	
	4.9.3.	Non-coding RNA	. 39
4.10.	Benzidir	ne	
	4.10.1.	Routes of exposure, associated cancers, and genotoxicity	39
	4.10.2.	DNA methylation	
4.11.		thylenebis(2-chlorobenzenamine)	
7.11.	4.11.1.		
		Routes of exposure, associated cancers, and genotoxicity	
	4.11.2.	Histone modifications	
4.12.	Occupat	ional exposure as a painter	40
	4.12.1.	Routes of exposure, associated cancers, and genotoxicity	40
	4.12.2.	DNA methylation	40
Summ	arv		
		needs	
		liceus	
		est	
Ackno	wledgeme	ents	41
Refere	nces		41

1. Introduction

6.

Epigenetic alterations represent non-genotoxic mechanisms of carcinogenesis that may occur independently or concomitantly with genotoxic aberrations. Further, the epigenomic landscape may directly influence the genotoxic potential of a chemical; for example, several studies have indicated preferential binding of reactive chemicals to regions of DNA that harbor specific histone modification marks and/or DNA methylation patterns [1–6].

There are several major types of epigenetic and epigenomic alterations: DNA methylation, histones/chromatin structure, nucleosome positioning, and expression of non-coding RNAs, all of which can alter gene activity without change to the DNA sequence. A wealth of data demonstrates that changes in these epigenetic marks may occur as a consequence of exposure to environmental

chemicals [7,8], and may play a role in the etiology of various human diseases, including cancer [9]. It has been demonstrated that chemically-induced epigenetic alterations occur early during exposure and may also have significance as biomarkers of carcinogen exposure.

To enable incorporation of epigenetic endpoints in chemical safety assessments, further characterization of the role of epigenetic alterations induced by chemical exposure is necessary [10]. Specifically, additional studies are needed to characterize the relationship between epigenetic alterations and toxicity phenotypes, and the epigenetic-specific dose-response [11]. Several recent publications [9,12] reviewed the current state of knowledge of epigenetics and cancer, and the application of epigenetic endpoints in cancer hazard assessments, including for chemical carcinogens. Despite the fact that the utilization of epigenetic

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