INTEGRATION OF DATA FROM THE IN VITRO LONG-TERM EXPOSURE STUDY ON HUMAN ENDOTHELIAL CELLS AND THE IN SILICO ANALYSIS: A CASE OF DIBUTYL PHTHALATE-INDUCED VASCULAR DYSFUNCTION



Bojana Stanic, Dunja Kokai, Kristina Pogrmic-Majkic, Dragana Samardzija Nenadov, Biljana Tesic, Svetlana Fa, Nebojsa Andric University of Novi Sad, Faculty of Sciences, Department of Biology and Ecology, Laboratory for Endocrine Disrupters and Signaling (ENDOS), Serbia

INTRODUCTION AND OBJECTIVES

Dibutyl phthalate (DBP)





is a synthetic chemical used in many industrial and consumer products. DBP exhibits its effects mainly on the endocrine and reproductive system, but it can also affect the function of the vasculature, thereby contributing to the incidence of cardiovascular diseases (CVDs) in human population; however, the underlying mechanisms behind the DBP-induced vascular dysfunction are not fully understood. Aside from CVDs, endothelial dysfunction has also been associated with other human diseases such as diabetes, insulin resistance, chronic kidney failure, tumor growth, venous disease, and several viral infection diseases, thus widening the potential target organs affected by DBP and human diseases that DBP can contribute to.

Here, we sought to integrate the experimental data obtained from the long-term exposure of human vascular endothelial cells (ECs) to DBP and the *in silico* analysis to infer the molecular mechanism of DBP's action in vascular ECs and provide a possible association between DBP exposure and human diseases with vascular etiology.

METHODS AND DESIGN



Quantitative RT-PCR \rightarrow mRNA expression analysis **alamarBlue**TM \rightarrow cell viability

Adhesion to gelatin \rightarrow adhesion to extracellular matrix Wound healing ("scratch") assay \rightarrow cell migration **Griess assay** \rightarrow nitrite (NO₂⁻) levels, as a proxy for nitric oxide (NO) production

List of enriched diseases \rightarrow DBP-affected genes entered in the Comparative Toxicogenomic Database's (CTD) Set Analyzer tool **Cytoscape analysis** \rightarrow network visualization

Gene Ontology and KEGG pathway analysis \rightarrow identification of biological processes, molecular functions, and specific signaling pathways for the DBP-affected genes

RESULTS

EA.hy926 \rightarrow human endothelial cell line

4-week-long exposure



. Gene expression during long-term exposure of EA.hy926 cells to DBP. The mRNA expression of the selected (A) integrins, (B) cellular adhesion molecules, (C) MMPs, and (D) NOS3. All results are expressed relative to the vehicle-treated control that was set as 1 (dashed line).

















FIGURE 5. (A) Molecular functions and (B) biological processes for the nine genes affected by the long-term repeated exposure of EA.hy926 cells to DBP.







nebojsa.andric@dbe.uns.ac.rs

 Cardiovascular disease 	MeSH: D002318	1.87E-10	
 Vascular disease 	MeSH: D014652	6.18E-10	
 Myocardial ischemia 	MeSH: D017202	5.67E-06	
 Heart disease 	MeSH: D006331	1.44E-05	
Cardiovascular diseases/Nervous system dise	ases		
 Cerebrovascular disorder 	MeSH: D002561	2.66E-07	
– Stroke	MeSH: D020521	1.56E-06	
 Cerebral hemorrhage 	MeSH: D002543	9.36E-06	
Immune system disease			
– Urticaria	MeSH: D014581	5.79E-06	
 Autoimmune diseases 	MeSH: D001327	2.33E-05	
 Multiple sclerosis 	MeSH: D009103	1.30E-04	

CONCLUSIONS

Our results provide novel information regarding the molecular mechanism of DBP's action in vascular ECs and contribute to the evidence that exposure to DBP may constitute a risk factor for the occurrence of different diseases with vascular etiology. Additional in vivo and in vitro studies are needed to improve the confidence in the chain of molecular events involved in DBP's action in vascular ECs and the association with human vascular diseases.