

Impact of Environmental Pollutants in oil sector workers on some Immunological Parameters: A Critical Analysis

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ABSTRACT This study investigated the hematological, inflammatory, and genetic responses in workers in the oil industry who were exposed to long-term and short-term environmental contaminants. There were 300 subjects: 100 long-term exposed, 100 short-term exposed, and 100 controls. Blood was collected after overnight fasting for hematological examination, DNA extraction, malondialdehyde (MDA) analysis, glycemia, and interleukin-6 (IL-6) measurement. The TP53 codon 72 (rs1042522) polymorphism was detected by RFLP-PCR. Results indicated a remarkable decrease in hemoglobin level and remarkable increase in erythrocyte sedimentation rate (ESR) in both exposure groups compared to controls. IL-6 levels were also significantly higher in both exposure groups, Arg/Arg genotype of TP53 codon 72 being greater in the long-term exposure group (52%) than in controls (5%). Arg/Arg genotype employees possessed significantly higher levels of IL-6 than Pro/Pro and Arg/Pro genotypes in both groups. The findings support that TP53 Arg/Arg genotype enhances susceptibility to environmental toxins, highlighting the role of genetic factors in interindividual variability to workplace exposures. This study emphasizes the importance of monitoring and screening according to genetic characteristics among exposed workers.

KEYWORDS TP53 polymorphism, oil sector worker, MDA, pollution

1. INTRODUCTION

Air pollution, with its large toxicological impact on human health and the environment, is an ongoing issue for the past few decades. The sources of pollution vary from minor units of tobacco and natural sources, for example, volcanic eruptions, to substantial amounts of pollutants from motor vehicles and industrial activity [1].

Long-term exposure to environmental pollutants, especially those found in industry, has come to be increasingly identified as a major public health issue. Of these, oil pollution is most noteworthy because of the general prevalence of the problem and the wide array of toxic chemicals it has. Oil industry workers, such as drillers, refiners, and transporters, are frequently exposed to a combination of hydrocarbons, heavy metals, and other chemicals, potentially resulting in a range of negative health outcomes. Earlier research has reported the respiratory, dermatological, and systemic effects of such exposure, but the mechanisms involved and the contribution of genetic susceptibility are not well known [2].

One of the most important areas of research in elucidating the health effects of oil pollution is the contribution of genetic polymorphisms to modifying individual responses to toxic exposure. The TP53 gene, with its pivotal role in cell cycle regulation and apoptosis, has been studied in a number of environmental and occupational health investigations. TP53 polymorphisms can affect susceptibility to cancer and other

long-term diseases in exposed groups. The role of these genetic factors in the adverse health effects of long-term exposure to oil pollution has not yet been explored comprehensively [3].

This research seeks to address this gap by investigating the link between chronic exposure to oil pollution and a variety of health effects, with special emphasis on the role of TP53 gene polymorphisms [4]. We expect that workers with specific TP53 polymorphisms will have increased susceptibility to the toxic effects of oil pollution, as indicated in both clinical symptoms and changes in hematological and biochemical parameters the study was to determine the prevalence of respiratory, dermatological, and systemic health effects among chronically exposed oil pollution workers and to examine the relationship between oil pollution exposure and changes in hematological and biochemical markers and to establish the contribution of TP53 gene polymorphisms to modulating the health effects of chronic oil pollution exposure.

2. MATERIALS AND METHODS

The research had a cohort of 300 employees of the oil industry's occupational service, visited between January 1, 2022, and December 31, 2023. The subjects were divided into three different groups: a long exposure group of 100 workers with direct and prolonged exposure to pollution, a short-term/indirect exposure group of 100 administrative

workers with indirect or short-term exposure to pollution, and a control group of 100 non-exposure workers to pollution. Gas stations were randomly sampled, with priority given to areas that accommodated a greater number of workers likely to be exposed to pollution. The inclusion criteria called for participants who were currently working in the petroleum industry with verified exposure to air pollution, and the exclusion criteria eliminated participants undergoing treatment with antibiotics or antiviral drugs, as well as participants with hyperthyroidism, hypothyroidism, acute renal failure, chronic hepatic diseases, malignant diseases, autoimmune diseases, lung cancer, or chronic obstructive pulmonary disease (COPD).

The protocol of the study was approved by the Scientific and Ethical Committee of the Western Health Area of the College of Medicine, Babylon University. Informed consent was sought from all participants following a clear explanation of the aims of the study. Participants also filled out a specially designed questionnaire.

Blood samples were drawn from all participants following overnight fasting. Two milliliters were taken in an EDTA tube for DNA extraction and hematological assays and three milliliters in a gel tube for isolation of serum to do interleukin (IL) and malondialdehyde (MDA) assays. Glycemic indices were analyzed according to standard procedure. Serum human IL-6 was estimated after allowing the samples to clot at room temperature for 10-20 minutes and centrifugation at 2000-3000 RPM for 20 minutes. The enzyme-linked immunosorbent assay (ELISA) kit, pre-coated with a human IL-6 antibody, was used according to the manufacturer's instructions.

Genomic DNA was extracted from blood samples using the G-spin Total DNA extraction kit (Intron) following the manufacturer's protocol. Polymerase Chain Reaction (PCR) was conducted using primers specific to P53 codon72 (rs1042522), designed using Primer-BLAST software and purchased from Bioneer, Korea (Table 1) [5]. 100 pmol/μl stock solutions were made and diluted to working solutions of 10 pmol/μl. PCR conditions such as annealing temperature, amplification cycles, and DNA and primer concentrations were optimized and presented in Tables 2. RFLP-PCR analysis was performed by digesting the PCR products with the BstUI enzyme, and the resulting restriction fragments were separated by electrophoresis on a 2% agarose gel and visualized under UV light. Concordance was maintained by retesting more than 10% of the samples, with a 100% match rate.

Agarose gel electrophoresis was performed by preparing a gel with 1.5 g of agarose dissolved in 100 ml of 1x TBE buffer (pH 8). Ethidium bromide was added to the cast gel, and samples were loaded into wells. Electrophoresis was conducted, and the bands were visualized using a UV transilluminator and documented with a digital camera. Data analysis was conducted using SPSS version 26 (IBM, US). Scale variables were expressed as mean ± standard deviation (SD), while categorical variables were presented as frequencies and percentages. The Student's T-test was employed for comparisons

between two groups, and one-way ANOVA was utilized for comparisons among three or more groups. Odds ratios (OR) with 95% confidence intervals (CI) were calculated to assess treatment response. Bivariate correlation tests were used to evaluate the association between SNP and diabetic variables, with correlation coefficients (R) indicating the strength of the relationship.

3. RESULTS

The study evaluated clinical signs and symptoms in workers exposed to oil pollution. A range of physical symptoms was noted (Figure 1), including sneezing (28.6%), chest pain (25.5%), wheezing (21.1%), and coughing (19.9%). Some workers also exhibited a delay in growth and a bump at the root of the nose (13.9%), potentially related to the accumulation of petroleum derivatives, which may lead to a decline in lung capacity and an increased risk of chronic illnesses. Dermatological symptoms were also prevalent among the exposed workers, with observations of dry skin, a distinctive bronze color, pigmentation on the extremities, severe itching, and visible scars (Figure 2). These findings align with elevated ferritin levels, consistent with previous research. Nail changes were common, with 80% of workers exposed long-term showing hard nails with transparent cracks, and 7% experiencing nail atrophy. Additionally, 40% of long-term exposed workers exhibited eye redness and congested capillaries, with a few showing swelling under the eyeball. Hair characteristics remained mostly unaffected, although 5% of the workers had white hair, possibly due to hyperpigmentation.

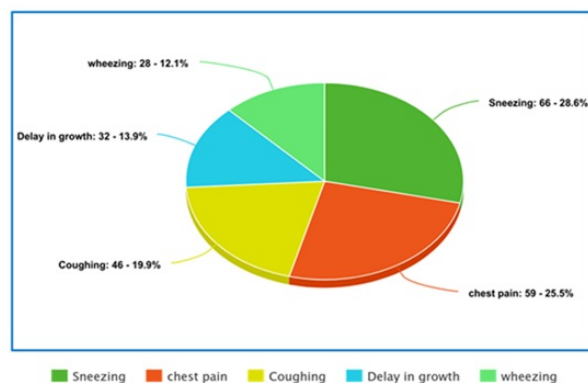


FIGURE 1. Side effects of occupational lung disease exposure to environmental pollution in oil sectors

The population studied included 100 participants each in the long-term exposure, short-term exposure, and control groups, with age ranges from 29 to 59 years (Table 3). Long-term exposure was most prevalent in the 55-59 age group, suggesting an increased risk of complications such as iron and steel foundry overload in older workers. Blood parameter tests revealed no significant differences in blood group distribution between the long-term, short-term, and control groups ($P > 0.05$), with O+ being the most common blood group among exposed workers, though not statistically significant.

TABLE 1. Primer sequences of P53codon72 " rs1042522"

P53codon72" rs1042522"	F	Forward primer "5 GCTCTTTTCACCCATCTACAG -3"	279 bp
	R	Reverse primer "5 TGAAGTCTCATGGAAGCCAGC -3"	

TABLE 2. Mix reaction for genotyping of P53codon72 " rs1042522" in Polymerase chain

Component	Volume (µl)
Forward primer	Volume (µl)
Reverse primer	1.25
DNA template	1.25
Deionized water	5
Premix	12.5

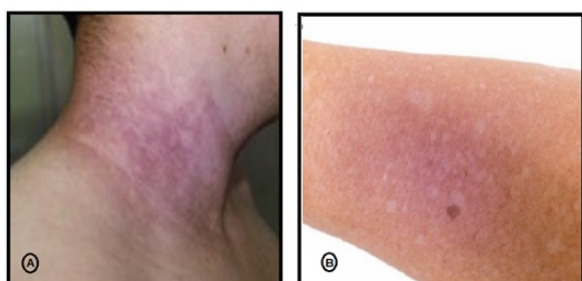


FIGURE 2. Showed Skin pigmentation is a common condition that can be triggered in workers oil sectors A/ represented hyperpigmentation in neck and B/ represented pigmentation of skin in arm

TABLE 3. Distribution of oil sector workers according to age

Age (Years)	Oil sector workers		Control
	Long exposure pollution	Short exposure pollution	
25-29	27	17	25
35-39	19	25	8
45-49	22	19	40
55-59	32	39	27
Total	100	100	100

There was a significant decrease in hemoglobin concentration in both exposed groups compared to the control group ($P = 0.0135$). The long-term exposure group had a mean hemoglobin concentration of 20.77 ± 2.4 g/dL, while the short-term exposure group had 17.777 ± 3.5 g/dL, and the control group had 13.207 ± 3.4 g/dL. Erythrocyte sedimentation rate (ESR) showed a significant increase in both exposed groups compared to the control group ($P = 0.042$), with the long-term exposure group recording 50.7 ± 3.8 mm/hr, the short-term group 43.9 ± 4.6 mm/hr, and the control group 13.5 ± 4.3 mm/hr. Additionally, a significant increase in the total white blood cell (WBC) count was observed among the exposed groups compared to the control group ($P = 0.0023$). The long-term exposure group had a WBC count of $8.72 \pm 1.2 \times 10^3$ /mL, the short-term exposure group $7.373 \pm 1.6 \times 10^3$ /mL, and the control group $5.49 \pm 0.85 \times 10^3$ /mL. Significant differences were also observed in other hematological parameters, including lymphocytes, neutrophils, MID, MCV, MCH, MCHC, and PLT between the exposed and control groups (Table 4).

TABLE 4. Blood counts and related hematological parameters measurements against long and short term exposure pollution with control health

N.	The test	Means± SD			P-value
		Control	Short exposure	Long exposure	
1	WBC (103 /mL)	5.59	7.373	8.72	0.00023
2	LYM (103/ mL)	32.687	47.453	53.029	0.0387
3	NEUT (103/ mL)	40.86	66.867	69.836	0.019
4	MID (103/ mL)	7.047	9.057	10.881	0.066
5	MCV (fL)	86.194	95.176	125.755	0.039
6	MCH (pg)	27.219	27.787	38.646	0.0301
7	MCHC (g/dL)	31.401	32.401	44.745	0.0054
8	PLT (103 /mL)	140.203	148.073	201.385	0.0128

Biochemical parameters showed that Interleukin 6 (IL-6) levels were significantly elevated in both exposure groups compared to the control group ($P < 0.05$). The long-term exposure group had a mean IL-6 concentration of 203.5 ± 15.98 ng/mL, the short-term exposure group 88.06 ± 15.31 ng/mL, and the control group 49.52 ± 9.35 ng/mL (Figure 3). Malondialdehyde (MDA) concentrations were also significantly higher in the exposed groups ($P < 0.05$), with the long-term exposure group recording 366.4 ± 20.03 pg/mL, the short-term exposure group 189.55 ± 12.16 pg/mL, and the control group 58.52 ± 7.36 pg/mL (Figure 4).

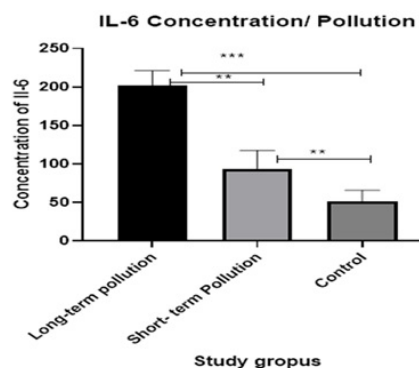


FIGURE 3. Concentration of IL-6 in long and short term exposure pollution and control groups

Analysis of the TP53 gene polymorphism at codon 72 (rs1042522) revealed three genotypes: Pro/Pro, Arg/Arg, and Arg/Pro. Significant differences in genotype distribution were found between the exposed and control groups. The Arg/Arg genotype was more prevalent among the long-term exposure group (52%) compared to controls (5%), with an odds ratio (OR) of 0.204 (95% CI 0.114–0.337, $P < 0.0001$). A similar pattern was observed in the short-term exposure group, where the Arg/Arg genotype was present in 36% of workers compared to 5% in the control group (OR = 4.21, 95% CI 2.71-6.43, $P < 0.01$) Table 5 and 6.

TABLE 5. Genotype and Allele Frequencies of the Polymorphism rs1042522 gene TP53 among occupational long exposure of pollution

TP53 (rs1042522)	Healthy (n = 100) No (%)	Pollution (n = 100) No (%)	Odds ratio (95% CI)	P-value
CC (Pro/Pro)	62 (62%)	25 (25%)	1	-
CG (Pro/Arg)	33 (33%)	23 (23%)	0.57 (0.28–1.137)	0.128
GG (Arg/Arg)	5 (5%)	52 (52%)	0.038 (0.009–0.098)	<0.0001*
CG (Pro/Arg) + GG (Arg/Arg)	38 (38%)	75 (75%)	0.204 (0.114–0.337)	<0.0001*
TP53 alleles				
C	157 (78.5%)	73 (36.5%)	-	
G	43 (21.5%)	127 (63.5%)	0.157 (0.101-0.245)	<0.0001*

TABLE 6. Genotype and Allele Frequencies of the Polymorphism rs1042522 gene TP53 among occupational short exposure of pollution

TP53 (rs1042522)	Healthy (n = 100) No (%)	Pollution (n = 100) No (%)	Odds ratio (95% CI)	P-value
CC (Pro/Pro)	62 (62%)	29 (29%)	1	-
CG (Pro/Arg)	33 (33%)	35 (35%)	2.26 (1.18–4.33)	0.128
GG (Arg/Arg)	5 (5%)	36 (36%)	15.3 (5.44–43.3)	<0.01*
CG (Pro/Arg) + GG (Arg/Arg)	38 (38%)	71 (71%)	3.99 (2.21-7.215)	<0.0001*
TP53 alleles				
C	157 (78.5%)	93 (46.5%)	-	
G	43 (21.5%)	107 (53.5%)	4.21 (2.71-6.43)	<0.0001*

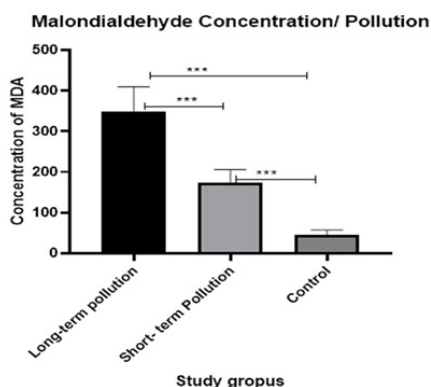


FIGURE 4. Malondialdehyde (MDA) concentration in studies groups

Moreover, IL-6 concentrations were significantly higher in workers with the Arg/Arg genotype compared to those with the Pro/Pro or Arg/Pro genotypes in both long-term and short-term exposure groups ($P < 0.05$) (Table 7). On the other hand, there was no significant association found between IL-6 levels and TP53 polymorphism in the control group. MDA concentrations also showed significant differences with TP53 polymorphism, with higher levels observed in the Arg/Arg genotype (Table 8).

4. DISCUSSION

The findings from this study highlight the severe health impacts of long-term exposure to oil pollution, emphasizing the multifaceted nature of these risks and the urgent need for improved protective measures within the industry. The high prevalence of respiratory symptoms, including sneezing, chest pain, wheezing, and persistent coughing among exposed workers, is particularly concerning. These symptoms suggest significant respiratory distress due to airborne exposure to volatile organic compounds and particulate matter associated

with oil pollution. This is consistent with existing literature linking chronic exposure to petroleum-derived pollutants with adverse respiratory outcomes, such as an increased incidence of chronic obstructive pulmonary disease (COPD), asthma, and other chronic respiratory conditions [6], [7].

TABLE 7. Relationship between three groups of il-6 concentration with Polymorphism rs1042522 gene TP53

Genotype	No. of genotype Frequency rs1042522	Concentration of IL-6 Pg/ml Mean \pm SD
Long exposure of pollution Groups	CC (Pro/Pro)	84.2 \pm 5.2
	CG (Pro/Arg)	123.6 \pm 8.3
	GG (Arg/Arg)	197.5 \pm 19.5
P value		0.001
Short exposure of pollution Groups	CC (Pro/Pro)	27.6 \pm 3.2
	CG (Pro/Arg)	62.9 \pm 3.28
	GG (Arg/Arg)	98.6 \pm 11.3
P value		0.035
Healthy Groups	CC (Pro/Pro)	48.6 \pm 5.7
	CG (Pro/Arg)	41.39 \pm 6.2
	GG (Arg/Arg)	39.8 \pm 5.1
P value		0.48

TABLE 8. Relationship between three groups of MDA concentration with Polymorphism rs1042522 gene TP53

Genotype	No. of genotype Frequency rs1042522	Concentration of MDA Pg/ml Mean \pm SD
Long exposure of pollution Groups	CC (Pro/Pro)	102.4 \pm 16.5
	CG (Pro/Arg)	289.5 \pm 17.7
	GG (Arg/Arg)	374.6 \pm 18.3
P value		0.001
Short exposure of pollution Groups	CC (Pro/Pro)	44.15 \pm 11.5
	CG (Pro/Arg)	97.4 \pm 15.7
	GG (Arg/Arg)	184.8 \pm 10.5
P value		0.035
Healthy Groups	CC (Pro/Pro)	49.7 \pm 8.9
	CG (Pro/Arg)	48.05 \pm 15.5
	GG (Arg/Arg)	59.4 \pm 10.4
P value		0.69

Globally, air pollution has been associated with various health effects, including lung diseases (such as asthma, res-

piratory infections, COPD, and cancer), cardiovascular, and neurological disorders [8], [9]. Particulate matter (PM), especially PM_{2.5}, is frequently investigated due to its ability to penetrate alveoli and induce systemic effects [10]. Furthermore, air pollution exposures are related to immune-mediated diseases like asthma and allergy [6], [11] and autoimmune diseases such as systemic lupus erythematosus [12] and rheumatoid arthritis [8]. The biological mechanisms underlying these associations include oxidative stress, inflammatory responses, tissue damage, vascular alteration, and DNA damage [11], [13].

The dermatological symptoms observed in the exposed groups—such as dry skin, hyperpigmentation, and severe itching—support the hypothesis of systemic absorption of toxic substances from oil pollution. Skin contact with oil and its derivatives has been documented to cause dermatological issues, indicative of deeper systemic involvement. The systemic absorption of these toxicants likely contributes to the observed hematological and biochemical changes, suggesting widespread physiological stress and potential damage beyond the respiratory and dermal systems [14].

There was a significant reductions in hemoglobin levels in both long-term and short-term exposure groups indicate potential bone marrow suppression or direct hemolytic effects due to chronic exposure to oil pollutants. This decline, coupled with elevated erythrocyte sedimentation rate (ESR) and white blood cell (WBC) counts, points to a sustained inflammatory state, a recognized risk factor for chronic diseases, including cardiovascular and metabolic disorders [15]. The elevated WBC counts suggest an ongoing immune response to prolonged exposure to harmful substances, including volatile organic compounds and polycyclic aromatic hydrocarbons, contributing to increased ESR and systemic inflammation, which may predispose individuals to chronic health conditions beyond immediate symptoms [16], [17].

Biochemical analyses reveal significantly elevated levels of Interleukin 6 (IL-6) and malondialdehyde (MDA) in the exposed groups. IL-6, a key pro-inflammatory cytokine, is central to the immune response and often elevated in chronic inflammatory conditions. The increased IL-6 levels among exposed workers suggest that oil pollution induces a broader inflammatory response with potential long-term health implications [18], [19]. Elevated MDA levels further indicate increased oxidative stress, reflecting the depletion of antioxidant defenses due to continuous exposure to toxic substances. Oxidative stress leads to cellular damage, lipid peroxidation, and DNA damage, which are implicated in chronic diseases, including cancer and cardiovascular disorders [20], [21].

The particular interest is the significant association found between the TP53 gene polymorphism at codon 72 and exposure to oil pollution. The increased prevalence of the Arg/Arg genotype among workers in the long-term exposure group is especially noteworthy, as it suggests a potential genetic predisposition to the harmful effects of oil pollutants. The TP53 gene, known for its role as a tumor suppressor, plays a crucial role in regulating the cell cycle and preventing

the proliferation of damaged cells. The Arg/Arg genotype has been associated with a higher susceptibility to cancer and other inflammatory diseases, as it may alter the tumor suppressor function of the TP53 protein, reducing its ability to respond effectively to DNA damage [22]–[24].

The elevated IL-6 levels observed in workers with the Arg/Arg genotype further suggest that this genetic variant may exacerbate the inflammatory response to environmental toxins, potentially increasing the risk of developing chronic diseases, including cancer. These findings align with a growing body of evidence that suggests genetic polymorphisms can modulate an individual's response to environmental exposures, leading to differential health outcomes.

The implications of these findings are profound. First, they underscore the critical importance of genetic screening in occupational health settings, particularly for workers exposed to high levels of environmental pollutants. Identifying individuals with high-risk genotypes, such as the TP53 Arg/Arg variant, could enable targeted interventions aimed at mitigating the adverse health effects of long-term exposure. For instance, workers identified as being at higher genetic risk could be provided with enhanced protective measures, more frequent health screenings, and early interventions to reduce their exposure and monitor for the development of chronic diseases. Additionally, the observed hematological and biochemical changes suggest that routine monitoring of these parameters could serve as early indicators of health deterioration in exposed workers, allowing for timely medical intervention before more severe health outcomes develop [23].

5. CONCLUSION

In conclusion, this study provides compelling evidence of the significant health risks associated with long-term exposure to oil pollution, particularly in relation to respiratory health, systemic inflammation, and genetic susceptibility. The findings highlight the need for stringent occupational health regulations, including the implementation of protective measures, regular health screenings, and targeted interventions for workers identified as being at higher genetic risk. Future research should focus on the long-term health outcomes of workers with high-risk genotypes and investigate potential interventions to mitigate the effects of chronic exposure to oil pollutants. Moreover, there is a need for further studies to explore the molecular mechanisms underlying the observed associations, which could lead to the development of novel therapeutic strategies to protect and improve the health of workers in this industry. These efforts are crucial not only for protecting the health of current workers but also for informing policy and regulatory decisions that could prevent future generations from experiencing the same risks.

REFERENCES

- [1] Doiron, Dany, et al. "Air pollution, lung function and COPD: results from the population-based UK Biobank study." *European Respiratory Journal* 54.1 (2019): 1802140.

- [2] Gómez Gallego, Diana Maryory, Juan C. Hernández, and José Alberto Mendivil-de la Ossa. "Adverse effects of prenatal exposure to airborne particulate matter on the fetus and newborn." *Iatreia* 35.3 (2022): 278-296.
- [3] Xing, Yu-Fei, et al. "The impact of PM2. 5 on the human respiratory system." *Journal of Thoracic Disease* 8.1 (2016): E69.
- [4] Xu, Min-Xuan, et al. "Prolonged PM2. 5 exposure elevates risk of oxidative stress-driven nonalcoholic fatty liver disease by triggering increase of dyslipidemia." *Free Radical Biology and Medicine* 130 (2019): 542-556.
- [5] Bowatte, Gayan, et al. "The influence of childhood traffic-related air pollution exposure on asthma, allergy and sensitization: a systematic review and a meta-analysis of birth cohort studies." *Allergy* 70.3 (2015): 245-256.
- [6] Khreis, Haneen, and Mark J. Nieuwenhuijsen. "Traffic-related air pollution and childhood asthma: recent advances and remaining gaps in the exposure assessment methods." *International Journal of Environmental Research and Public Health* 14.3 (2017): 312.
- [7] Alves, Andressa Guariento Ferreira, et al. "Influence of air pollution on airway inflammation and disease activity in childhood-systemic lupus erythematosus." *Clinical Rheumatology* 37.3 (2018): 683-690.
- [8] Parks, Christine G., et al. "Rheumatoid arthritis in agricultural health study spouses: associations with pesticides and other farm exposures." *Environmental Health Perspectives* 124.11 (2016): 1728-1734.
- [9] Cevallos, Victoria M., Valeria Diaz, and Cherilyn M. Sirois. "Particulate matter air pollution from the city of Quito, Ecuador, activates inflammatory signaling pathways in vitro." *Innate immunity* 23.4 (2017): 392-400.
- [10] Valderrama, Andrés, et al. "Systematic review of preclinical studies on the neutrophil-mediated immune response to air pollutants, 1980–2020." *Heliyon* 8.1 (2022): e08778.
- [11] Chan, Yik Lung, et al. "Pulmonary inflammation induced by low-dose particulate matter exposure in mice." *American Journal of Physiology-Lung Cellular and Molecular Physiology* 317.3 (2019): L424-L430.
- [12] Jakasa, Ivone, Sanja Kezic, and Peter J. Boogaard. "Dermal uptake of petroleum substances." *Toxicology Letters* 235.2 (2015): 123-139.
- [13] Kezic, S., et al. "Review of dermal effects and uptake of petroleum hydrocarbons." *Concawe Report* 5.10 (2010).
- [14] Li, Daochuan, et al. "Multiple organ injury in male C57BL/6J mice exposed to ambient particulate matter in a real-ambient PM exposure system in Shijiazhuang, China." *Environmental Pollution* 248 (2019): 874-887.
- [15] Li, Yaqi, et al. "Reactive oxygen species induced by personal exposure to fine particulate matter emitted from solid fuel combustion in rural Guanzhong Basin, northwestern China." *Air Quality, Atmosphere & Health* 12 (2019): 1323-1333.
- [16] Xu, Fanfan, et al. "Investigation of the chemical components of ambient fine particulate matter (PM2. 5) associated with in vitro cellular responses to oxidative stress and inflammation." *Environment International* 136 (2020): 105475.
- [17] Molfino, N. A., et al. "Effect of low concentrations of ozone on inhaled allergen responses in asthmatic subjects." *The Lancet* 338.8761 (1991): 199-203.
- [18] Audi, Christelle, et al. "Serum cytokine levels related to exposure to volatile organic compounds and PM2. 5 in dwellings and workplaces in French farmers—a mechanism to explain nonsmoking COPD." *International Journal of Chronic Obstructive Pulmonary Disease* (2017): 1363-1374.
- [19] Marín-Palma, Damariz, et al. "PM10 promotes an inflammatory cytokine response that may impact SARS-CoV-2 replication in vitro." *Frontiers in Immunology* 14 (2023): 1161135.
- [20] Longhin, Eleonora, et al. "Cell cycle alterations induced by urban PM2. 5 in bronchial epithelial cells: characterization of the process and possible mechanisms involved." *Particle and Fibre Toxicology* 10 (2013): 1-19.
- [21] Gałuszka-Bulaga, Adrianna, et al. "Transcriptional response of blood mononuclear cells from patients with inflammatory and autoimmune disorders exposed to "Krakow smog"." *Cells* 11.16 (2022): 2586.
- [22] Volodko, Natalia, et al. "TP53 codon 72 Arg/Arg polymorphism is associated with a higher risk for inflammatory bowel disease development." *World Journal of Gastroenterology* 21.36 (2015): 10358.
- [23] Bulgakova, O., A. Kussainova, and R. Bersimbaev. "The cell cycle regulatory gene polymorphisms TP53 (rs1042522) and MDM2 (rs2279744) in lung cancer: a meta-analysis." *Vavilov Journal of Genetics and Breeding* 24.7 (2020): 777-784.
- [24] Ahmed, Shaza, et al. "Prevalence of TP53 gene Pro72Arg (rs1042522) single nucleotide polymorphism among Egyptian breast cancer patients." *Egyptian Journal of Medical Human Genetics* 24.1 (2023): 24.