REVIEW

Heavy metal‑induced lipogenic gene aberration, lipid dysregulation and obesogenic efect: a review

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Abstract

Lipids are high energy, complex biomolecular compounds essential for cellular and organellar membrane formation. Accumulation of circulatory lipids is however associated with pathophysiological conditions including cardiometabolic disorders, diabetic dyslipidemia and obesity. Epidemiological studies have correlated heavy-metal exposure with dyslipidemias and metabolic syndrome. Here, we review the role of cadmium, lead, mercury and arsenic on inducing dyslipidemias through lipid metabolism dysregulation, with focus on metal efects on lipogenic genes, gut microbiome and endocrine secretion. The main gene transcription factors impaired by heavy metals are CCAAT-enhancer binding protein, peroxisome proliferativeactivated receptor, sterol regulatory element binding protein, carbohydrate responsive element binding protein and liver \times receptor. These factors regulate genes responsible for β-oxidation, *de novo* lipogenesis, and the synthesis and transport of fatty acids, cholesterol, phospholipids and triglycerides. Dysregulated lipid profles in organisms exposed to metals show higher cholesterol and triglycerides, very low-density lipoprotein and non-high density lipoprotein cholesterol levels, with a corresponding low high-density lipoprotein cholesterol. Hormones and gut microbiome are also impaired by heavy-metal exposure.

Keywords Lipid metabolism · Heavy-metals · Dyslipidemia · Lipogenic genes · Diabetes · Obesity

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Introduction

Lipids are hydrophobic molecules that form critical components in organisms, with a functional role of providing both structural and biological support. Lipids are essential for initiating organellar biogenesis and the proliferation of each distinct membrane-bound structures, vesicles and liposomes in the aqueous environment of cells, thus providing a barrier for regulating intracellular exchange of materials among cytoplasmic organelles (Airaodion et al. [2019](#page-26-0); Stefan et al. [2017](#page-31-0)). Aside membrane formation, lipids also insulate neurons, facilitate cell signaling and impulse transmission (Amira et al. [2018](#page-26-1)), exhibit antioxidant and anti-infammation properties (Brites et al. [2017\)](#page-27-0) and may demonstrate cardioprotective functions (Nagao et al. [2018](#page-30-0)). Some forms of lipids are known to act as sensors of cellular stress and thus form important components of signal transduction molecules (Rangholia et al. [2021](#page-31-1)). Despite their many functional roles in cells, an excess accumulation of lipids in blood plasma and tissues, as a result of lipid-metabolism dysregulation, has striking efects on the health of an organism and has

been found to contribute to the initiation and progression of pathophysiological conditions such cancers, cardiovascular deterioration, high blood pressure, kidney damage, hyperlipidemia, obesity and diabetes (Deprince et al. [2020;](#page-27-1) Gai et al. [2019;](#page-28-0) Nickels [2018](#page-30-1)). Although lipid redistribution does not necessarily pose a negative health risk to an individual, the location of its accumulation, however infuences the overall health of a person. Example, accumulation of fat in visceral adipose tissues and organs relative to its accumulation in subcutaneous layers is reported to be associated with an increased risk of metabolic syndromes (Frank et al. [2019](#page-28-1); Małodobra-Mazur et al. [2020](#page-29-0)). The concerted convergence of excess fat and sugar accumulation, hormonal imbalance, alterations in lipid and sugar metabolism genes, gut microbiome perturbation and de novo lipogenesis, resulting from heavy metal exposure, are among the many factors that may contribute to higher risk of lipid-related metabolic syndromes. Multiple reports, as reviewed in this study (Afolabi et al. [2015;](#page-26-2) Chi et al. [2019b;](#page-27-2) Skoczyńska et al. [1993](#page-31-2); Zhou et al. [2016\)](#page-32-0), reveal that acute or chronic exposure to heavy metals in humans or other organisms result in serum lipid profle dysregulation with a signifcant increase in total cholesterol, triglyceride, low-density lipoprotein cholesterol and non-high density lipoprotein cholesterol levels while contemporaneously leading to a decline in high-density lipoprotein cholesterol levels. The disproportionate increase in triglyceride, low-density lipoprotein cholesterol and total cholesterol or a combination thereof, and the corresponding decline in high-density lipoprotein cholesterol in bloodserum defnes the condition of dyslipidemias (Li et al. [2021](#page-29-1)). This comprehensive review therefore explores how heavy metals alter the parameters of serum lipid profles in model organisms (mice, rats, zebrafsh) and in humans, and how these changes afect the quality of life.

Exposure and toxicokinetics of heavy metals

Sources and heavy metal toxicokinetics

The ubiquitous nature of heavy metals and their widespread toxicities in plants, animals and humans have been of major concern over the past several decades. Though heavy metals are released into the environment through natural processes such as erosion, spring waters and volcanic eruptions, the increased rate of anthropogenic activities such as fossil fuel combustion, agricultural activities and industrialization have accounted for the recent surge in heavy metal pollution and their overaccumulation on viable agricultural lands, water bodies and air, thus making human exposure inevitable (Brifa et al. [2020;](#page-27-3) Ferrante et al. [2019](#page-28-2); Tchoun-wou et al. [2012](#page-32-1)). Cadmium (Cd^{2+}) , lead (Pb^{2+}) and mercury (Hg^{2+}) are among the most bio-persistent toxic metals

with a high ability to bioaccumulate in cells and tissues, but difficult to excrete once in cells, especially when the victim sufers from iron, calcium or zinc defciency (Moiseenko and Gashkina [2020;](#page-30-2) Schaefer et al. [2020\)](#page-31-3) whereas approximately 70 to 80% of arsenic $(As³⁺)$, a metalloid, can be largely excreted through urine, with hair, nail sweat and feces also contributing to $As³⁺$ removal (Chen et al. [2013](#page-27-4); Roy et al. [2020](#page-31-4)). These heavy metals are ranked highest among the list of priority metals considered to be of great public health concern. Whereas cadmium occupies the seventh position, arsenic, lead and mercury are frst, second and third, respectively, on the basis of their frequency of occurrence, toxicity and potential for human exposure (ATSDR [2020\)](#page-26-3). These heavy metals were selected for this review based on experimental studies demonstrating their toxicities in tissues and cells after exposure (Cartularo et al. [2015](#page-27-5); Elmorsy et al. [2021](#page-28-3); Rosales-Cruz et al. [2018\)](#page-31-5) and in crosssectional studies involving human population with chronic or acute exposure (Ayoub et al. [2021;](#page-26-4) Kang et al. [2021](#page-28-4)), and for the fact that their primary medium of exposure is through inhalation [of polluted air], ingestion [of contaminated food and water], and to some extent, dermal contact, which all constitutes daily human routine (Ferrante et al. [2019](#page-28-2); Kumari et al. [2021;](#page-29-2) Rivas-Santiago et al. [2019](#page-31-6)). With drinking water as the major source of human and animal exposure, the maximum permissible limit has been restricted to 10 μ g/L (As³⁺) (Kumar et al. [2020\)](#page-29-3), 2 μ g/L (Hg²⁺) (Rana et al. [2017\)](#page-31-7), 15 μ g/L (Pb²⁺) (Sui et al. [2020\)](#page-31-8) and 5 μ g/L (Cd^{2+}) (Kubier et al. [2019\)](#page-29-4). In spite of these restrictions, most countries are reported to have metal concentrations in drinking water exceeding this stipulated permissible limit (Alidadi et al. [2019](#page-26-5); Cobbina et al. [2015;](#page-27-6) Shaji et al. [2021;](#page-31-9) Tanvir et al. [2021](#page-31-10)). Moreover, blood, as transport medium for metals, is often used as reliable indicator for recent exposure to quantify toxicity level. The maximum tolerable blood-metal limit is indicated as Cd^{2+} (10 µg/dL) and Pb^{2+} (5 µg/dL) (Xu et al. [2021](#page-32-2)), As (1 µg/L) (Kumar et al. [2020](#page-29-3)) and Hg²⁺ (<20 µg/L) (Ye et al. [2016](#page-32-3)) but these concentrations only refect recent exposures and not necessarily long time exposure since they rapidly disappear from blood and are distributed to tissue storage sites. Due to the high level of toxicity associated with lead (Pb^{2+}) , a net zero permissible limit in drinking water is recommended since even low-levels represent a risk factor for lipid metabolism dysregulation (Xu et al. [2021\)](#page-32-2). Achieving this target however remains a challenge, even in effluent communities, due to the pervasive nature of this metal, with reports indicating that even certifed lead-free plumbing products could leach Pb at a concentration greater than $1 \mu g/L$ as shown in a laboratory study (Parks et al. [2018\)](#page-30-3).

Cadmium, mercury, lead and arsenic are all potent hepatotoxic heavy metals/metalloid which are easily incorporated into the food chain through absorption by plants and animals, and subsequent biotransformation especially in aquatic organisms (Zhang et al. [2019\)](#page-32-4). These metals are mostly present in their divalent forms and thus compete with essential metal ions for binding sites to be transported into cells and tissues. Once transported into cells, they bind strongly to proteins and nucleic acids, induce oxidative stress through reactive oxygen species generation which destroys macromolecular structures and disrupt their cellular function (Brifa et al. [2020;](#page-27-3) Engwa et al. [2019](#page-28-5)), alter lipid metabolism profle in the liver and induce epigenetic changes in the expression and function of lipid metabolism genes (Cartularo et al. [2015;](#page-27-5) Cheng et al. [2011;](#page-27-7) Lacerda Leocádio et al. [2020](#page-29-5)). Mercury, often converted to its toxic methylmercury form by bacteria in soil or water, enters the food chain and bioaccumulates in plants and fshes (Chang et al. [2020;](#page-27-8) Donadt et al. [2021;](#page-27-9) Vieira et al. [2021\)](#page-32-5), has been associated with decreasing the antioxidant status of glutathione, increases oxidative stress and infammation, alters lipid profle and infuence the development of dyslipidemias, cardiovascular diseases, obesity and hypertension (Park and Seo [2017](#page-30-4)). Similarly, though arsenic (a metalloid) is toxic in all its oxidation states and forms, the inorganic trivalent arsenic (arsenite, As^{3+}) is known to be highly toxic compared to its oxidized pentavalent arsenic (arsenate, $As⁵⁺$) (Kumari et al. [2021\)](#page-29-2), and these modifcations into diferent states are facilitated through bacterial metabolism and by the environment where As is exposed (Ferrante et al. [2019](#page-28-2); Kumari et al. [2017](#page-29-2); Rivas-Santiago et al. [2019\)](#page-31-6).

Reports from in vivo, in vitro and epidemiological studies show a close association between chronic or acute heavy metal exposure and dyslipidemias as manifested by the upregulation in triglyceride, low-density lipoprotein cholesterol and total cholesterol levels with a corresponding decrease in high-density lipoprotein cholesterol levels (Cheng et al. [2011;](#page-27-7) Cho et al. [2020](#page-27-10); Go et al. [2015;](#page-28-6) Olisekodiaka et al. [2012](#page-30-5); Park and Seo [2017](#page-30-4)). The changes in these lipid profle markers are clinically used to determine one's susceptibility to developing metabolic syndromes such as diabetes, hypertension, obesity, stroke and heart diseases. Therefore, the ability for heavy metals to alter serum lipid profle through DNA damage, epigenetic modifcation via DNA methylation, lipid peroxidation induction and the dysregulation of several metabolic pathways, pose a signifcant health risk to individuals and could serve as a precursor for the initiation and progression of clinical conditions (Rivas-Santiago et al. [2019\)](#page-31-6).

Heavy metal toxicology and metabolism dysregulation

Experimental and epidemiologic evidence indicate that acute and chronic exposure to heavy metals is associated with the development of clinical and metabolic symptoms relating to immunotoxicity, hepatotoxicity, cardiovascular disorders, cognitive defciencies, nephrotoxicity, hypertensions, dyslipidemia and diabetes mellitus (He et al. [2015;](#page-28-7) Lamas et al. [2016;](#page-29-6) Nie et al. [2016](#page-30-6)). These toxicities elicited by heavy metals have been studied, and the mechanisms and pathways involved illustrated to some extent to aid the development and discovery of therapeutic agents. By altering the cellular and biochemical pathways of glucose, lipids and proteins metabolism and facilitating the induction of membrane phospholipid abnormalities through oxidative damage, toxic metals evoke lethal efect to cells by inducing apoptosis and a subsequent cell death in the process (Rivas-Santiago et al. [2019;](#page-31-6) Tinkov et al. [2021](#page-32-6)). Studies in recent years have tightly linked glucose and lipid metabolism dysregulation to the presence and accumulation of heavy metals within tissues and organs (Bambino et al. [2018](#page-27-11); Wang et al. [2018a](#page-32-7)). It is widely reported that these toxic metals directly disrupts lipid and glucose metabolism by altering both glucose and lipogenic gene expressions (Adebayo et al. [2015](#page-26-6); Sun et al. [2017;](#page-31-11) Zhang et al. [2018\)](#page-32-8), disrupting endocrinal cell function and the release of hormones (Rana [2014;](#page-30-7) Sabir et al. [2019](#page-31-12)), altering the functioning of cell surface receptors and the uptake of glucose and lipids (Ficková et al. [2003\)](#page-28-8), and infuencing de novo lipogenesis (Adebayo et al. [2015\)](#page-26-6), thus inducing lipid dysregulation and redistribution resulting in fat accumulation, weight gain and obesity (Fig. [1](#page-3-0)).

Heavy metals are also known to inhibit insulin signaling and have been suggested to be responsible for indirectly promoting de novo lipogenesis as a result of surge in circulating glucose among hyperglycemic patients (Leff et al. 2018). Cd²⁺, Pb^{2+} , As³⁺ and Hg²⁺ are reported to influence the redistribution of cholesterol, fatty acids and triglycerides into various tissues and cells. Whereas multiple studies indict these heavy metals for their association with lipid metabolism disorders (Cheng et al. [2011;](#page-27-7) Feng et al. [2015;](#page-28-9) Go et al. [2015](#page-28-6); Lacerda Leocádio et al. [2020\)](#page-29-5), an assessment study by Rotter et al. [\(2015\)](#page-31-13) and Padilla et al. ([2010](#page-30-8)) showed a negative correlation to that efect which prompts the need for further investigation to confrm their specifc role in lipid metabolism. It should however be noted that in contrast to these two reports, a substantial amount of experimental evidence associates heavy metals with lipid metabolism disorders and obesity (Attia et al. [2021\)](#page-26-7) but a review on how they afect lipid metabolism genes and lipid regulatory factors is yet to be examined, hence this study seeks to partially fll this knowledge gap by evaluating available data through the years.

Lipoprotein and heavy metal interaction

Lipid transport and lipoprotein formation

The liver is the central organ for regulating systemic glucose and lipid metabolic fuxes (Mu et al. [2019\)](#page-30-9). The principal

Fig. 1 Exposure of heavy metals to cells and tissues induces serum lipid profle dysregulation which results in the initiation and progression of several metabolic syndromes

sources of these systemic lipids are from dietary absorption and de novo lipogenesis. Absorbed lipid molecules from digestion, modifed by the endoplasmic reticulum, are transported to the liver in association with hydrophilic protein molecules by forming a lipid-protein complex known as lipoprotein, due to the water insoluble nature of the absorbed lipid products (Wang et al. [2013\)](#page-32-9).

Lipoproteins are macromolecular complexes consisting of a mixture of proteins and lipids with a cholesterol esters and triglyceride central core, surrounded by free cholesterol, phospholipids, and apolipoproteins which facilitates the formation and function of the lipoprotein. Apolipoproteins which binds to the surface of the lipoprotein structure are essential for lipoprotein stabilization, activation of lipophilic enzymes and facilitates the binding of low density lipoproteins to lipoprotein receptors on cell surface to aid their uptake (Gursky [2015](#page-28-10)). Plasma lipoproteins are classifed into six groups based on size variations, lipid composition and apolipoproteins, and these include chylomicrons, chylomicron remnants, very low-density lipoprotein, intermediate density lipoprotein, low-density lipoprotein and high-density lipoprotein.

Lipoprotein metabolism and the efect of heavy metals

Lipoprotein metabolism occurs via two main pathways, exogenous and endogenous, depending on whether its origin is of dietary or hepatic source (Fig. [2\)](#page-4-0). In exogenous pathway, dietary lipids are incorporated into chylomicrons in the intestines and absorbed into blood. During circulation, lipoprotein lipase found on the surface of endothelial cells cleaves the triglycerides from the chylomicrons which further hydrolyzes the triglycerides into fatty acids, diglycerides and monoglycerides (Zhyvotovska et al. [2019](#page-32-10)). These lipid components then difuse into cells to be oxidized for the release of energy or become incorporated into adipose tissues to be re-synthesized into triglycerides and stored as fat (Ory [2007;](#page-30-10) Tao et al. [2020\)](#page-32-11). In endogenous lipoprotein pathway, triglycerides synthesized in the liver are packaged into very low-density lipoprotein. The triglycerides carried in very low-density lipoprotein are stripped and hydrolyzed by the action of lipoprotein lipase, which then difuses into muscle and adipose tissues to be metabolized or re-synthesized into storage fat. Very low-density lipoprotein after releasing its triglyceride is converted into intermediate density lipoprotein which is further metabolized to low-density lipoprotein (Behl et al. [2020](#page-27-12); Feingold and Grunfeld [2018](#page-28-11)).

Heavy metals are a major disruptor to the homeostatic regulation of circulating lipids and the expression of lipid receptors. Afolabi et al. and Liu et al. observed an increase in total plasma cholesterol levels in rats after exposure to Cd^{2+} and reported that the reduced efflux of very low-density lipoprotein cholesterol was as a result of low-density lipoprotein activity loss or a decrease in low-density lipoprotein receptor function, leading to a decrease in low-density lipoprotein catabolism (Afolabi et al. [2012;](#page-26-8) Liu et al. [2020](#page-29-8)). Jolibois et al. [\(1999](#page-28-12)) also observed a decrease in the mRNA expression of low-density lipoprotein receptor (*LDLR*) in human placental cells after exposure to Cd^{2+} . Similarly, Chi et al.

Fig. 2 Exogenous lipoprotein pathway is characterized by dietary lipid absorption, metabolism and transport to liver, cells and adipose tissue. Endogenous lipoprotein pathway involves the formation of

[\(2019a\)](#page-27-13) observed that expression of the cholesterol transporter genes low-density lipoprotein receptors (*LDLR*) and scavenger receptor class B type 1 (*SCARB1*) were signifcantly lower in mice exposed to arsenic compared to the control, suggesting that this efect might have been responsible for the high serum cholesterol levels. These fndings together indicate that exposure to toxic metals can infuence the levels of plasma cholesterol and low-density lipoprotein lipids by downregulating the expression and function of *LDLR*, lipoprotein lipase (*LpL*) and other lipid transporters, receptors and metabolism genes. Moreover, a decrease in the activity of lipoprotein lipase, as a result of metal inhibition, could also account for the reduced catabolism of very low-density lipoprotein and may explain the elevation of circulating proatherogenic lipid (Afolabi et al. [2012](#page-26-8)).

De novo lipogenesis and lipid accumulation

De novo lipogenesis is a complex and highly regulated biosynthetic pathway by which fatty acids are synthesized from acetyl CoA subunits produced within cells from various sources, especially from carbohydrate catabolism (Song et al. [2018](#page-31-14)). This metabolic process often takes place in

very low-density lipoprotein from triglyceride and cholesterol esters, its efflux from the liver, metabolism, distribution to cells and recycling

the liver when excess sugars, which are not metabolized or stored as glycogen under physiological conditions, are converted into fatty acids and then esterifed into triglycerides (Yilmaz et al. [2016\)](#page-32-12). The process begins with an ATP-dependent carboxylation of acetyl coenzyme A (CoA) subunits to malonyl-CoA, catalyzed by the enzyme acetyl CoA carboxylase. With an acetyl CoA serving as a primer, malonyl CoA's are attached through the action of the multifunctional enzyme complex, fatty acid synthase. The sequential addition of the two-carbon malonyl CoA generates an elongated fatty acid which is then esterifed into triglyceride (Sanders and Griffin [2016\)](#page-31-15).

Initiation of de novo lipogenesis occurs mostly by feeding on hypercaloric or high-carbohydrate diet which results in sugar overload. De novo lipogenesis from carbohydrate, however, is an energetically expensive process due to its ATP-dependent nature and does not signifcantly contribute to total body fat deposit in healthy individuals (Giles et al. [2016;](#page-28-13) Song et al. [2018\)](#page-31-14). Nonetheless, dependence on highly refined carbohydrates, changes in lifestyle and exposure to endocrine disrupting chemicals both alters glucose regulation which infuences de novo lipogenesis, causing a surge in the synthesis of fatty acids where its contribution to total body fat becomes signifcant (Maradonna and Carnevali [2018\)](#page-29-9). A study by Vineeth Daniel et al. [\(2019\)](#page-32-13) indicated that exposure of mice to Pb^{2+} caused an upregulation and transactivation of the carbohydrate responsive element binding protein (*ChREBP*), a transcription factor that regulates the expression of genes responsible for glycolysis and hepatic de novo lipogenesis. Lipogenic markers such as fatty acid synthase (*FAS*) and acetyl CoA carboxylase (*ACC*) were also found to be upregulated and resulted in a dense lipid droplet accumulation in the liver of Pb^{2+} treated mice. Similarly, Zhang et al. [\(2018](#page-32-8)) observed that Cd exposure led to the upregulation of *FASN* and stearoyl-CoA desaturase-1 (*SCD1*), typically involved in de novo lipogenesis through fatty acid and monounsaturated fatty acid synthesis, but its direct efect on inducing de novo lipogenesis was not determined. Present studies on heavy metal-induced lipid dysregulation through de novo lipogenesis however remain sparse indicating that more studies are required to establish this phenomenon.

Heavy metals and plasma lipid dysregulation

In vivo studies in animal models

Maintenance of optimal plasma and cellular lipid homeostasis is pivotal to the normal functioning of an organism. As such, an abnormal deviation from a balanced equilibrium of lipid uptake, metabolism, storage and redistribution may have deleterious lipid-associated health efect on an organism (Małodobra-Mazur et al. [2020\)](#page-29-0). However, as indicated earlier, heavy metals are well known to induce a disturbance in the homeostatic redistribution of dietary lipid by downregulating lipid metabolism and transport genes, thus limiting its uptake by cells and liver. This change in lipid profle results in accumulation of hepatic and serum lipids and cholesterol.

In a study by Samarghandian et al. [\(2015](#page-31-16)), it was shown that the administration of cadmium (2.0 mg/L) in the drinking water of mice for 3 months led to an increase in serum triglyceride, low-density lipoprotein cholesterol and total cholesterol with a decrease in the level of high-density lipoprotein cholesterol. In a similar study by Olisekodiaka et al. [\(2012\)](#page-30-5), rats administered with Cd^{2+} at a dose of 1.0 mg/kg body weight for 4 weeks saw an increase in plasma triglyceride, total cholesterol and low-density lipoprotein cholesterol with a corresponding decrease in high-density lipoprotein cholesterol. In both studies, Cd caused an increase in the levels of malondialdehyde, a product of lipid peroxidation and a decrease in the total antioxidant status. In another study, Oluranti et al. ([2021](#page-30-11)) reported that after exposure of rats to Cd (5.0 and 30.0 mg/kg), the levels of free fatty acid, total cholesterol and triglyceride in the heart increased signifcantly with respect to control, with a reduction in lipoprotein activity among rats exposed to 30.0 mg/kg Cd. Glucose metabolic pathway was also signifcantly impaired in Cd exposed groups with a signifcant decline in serum insulin level, and pyruvate and hexokinase activities (Oluranti et al. [2021](#page-30-11)). These reported fuctuations in lipid and glucose metabolic fuxes in the heart may be a prime contributing factor to the development of cardiac dysfunction and other cardio-metabolic syndromes.

To examine the effect of chronic $As³⁺$ exposure on lipid metabolism alterations and its subsequent efect on murine ofspring in intergenerational study, Rivas-Santiago et al. ([2019](#page-31-6)) exposed Wistar rats to 3 ppm sodium arsenate in drinking water through gestation and lactation until the offspring were 4-months-old. Although no signifcant change was observed in the level of serum adiponectin, an adipocyte-derived hormone that increases insulin sensitivity and regulates lipid metabolism, the serum lipid metabolomic profle of the rats however showed signifcant changes in the metabolism of glycerophospholipid and glycerolipid. A decrease in the levels of phosphatidylcholines and an increase in the levels lysophosphatidycholines were also observed in the animals exposed to $As³⁺$ compared with the control. An increase in lipid peroxidation induced by $As³⁺$ -mediated oxidative stress in treated rats was also reported as indicated by the high malondialdehyde levels (Rivas-Santiago et al. [2019\)](#page-31-6). The fndings from the above studies show that both Cd^{2+} and As^{3+} have the ability to induce dysregulation in lipid metabolism and promote oxidative stress through lipid peroxidation as determined by the increase in malondialdehyde levels, whereas decreasing the antioxidant status through the production and accumulation of reactive oxygen species within cells and tissues.

In mice and rats exposed to MeHg and Pb, though the serum lipids were perturbed, the reported fndings (as shown in Table [1\)](#page-6-0) deviate from the expected and established outcome. While Moreira et al. [\(2012](#page-30-12)), after exposing mice to 40 mg/L MeHg observed an increase in all serum lipid profles, Uzunhisarcikli et al. [\(2015](#page-32-14)) after exposing rats to 1 mg/kg body weight of $HgCl₂$ reported a decrease in triglyceride, total cholesterol and low-density lipoprotein cholesterol. Likewise Wadaan ([2009](#page-32-15)) after exposing rats to 20 ppm HgCl₂ similarly observed a decrease in triglyceride, total cholesterol and high-density lipoprotein cholesterol. These apparent diference in the research outcomes may be attributed to the diferent nature of metal (MeHg and $HgCl₂$) and exposure dosage. Allouche et al. [\(2011\)](#page-26-9) after chronic exposure of rats to diferent concentrations (0.025, 0.5, 0.1 and 0.3%) of lead acetate in drinking water observed that though Pb^{2+} contributed to weight gain and increased obesity risk, no association was found to exist between Pb and serum concentrations of total cholesterol, high-density lipoprotein cholesterol, low-density lipoprotein cholesterol

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and triglyceride among lead exposed groups compared to the control group. On the contrary, Heidarian and Rafeian-Kopaei [\(2013](#page-28-15)) observed an increase in triglyceride and very low-density lipoprotein levels and a decrease in low-density lipoprotein and total cholesterol levels with no observable diference in high-density lipoprotein cholesterol after rat were exposed to 500 mg lead acetate/kg diet. Okediran et al. ([2018](#page-30-14)) on the other hand reported that alteration in lipid profile in rats exposed to Pb^{2+} was both time and dosage dependent. They observed that increasing dosage and time increased the serum levels triglyceride, total cholesterol, high-density lipoprotein cholesterol with a corresponding decrease in the serum levels low-density lipoprotein and phospholipids. Though a dysregulation in the lipid profle as induced by heavy metals is indicated, the extent of dysregulation for each metal difers to some extent, and these diferences may be due to factors such as dosage, duration of exposure and the type of model organism used for the study*.*

Heavy metals and plasma lipid dysregulation in humans

Heavy metals remain a major health risk factor in humans due to their ability to induce cardiometabolic syndromes and other life-threatening illnesses. Of this, Steinmaus et al. [\(2015\)](#page-31-17) have reported the association between arsenic exposure and its relation to obesity, increased weight and the risk of cancer. In a study by Shin et al. [\(2018](#page-31-18)) among a population of 1,567 children and adolescents, and Park et al. [\(2017a\)](#page-30-15) from a population size of 200 healthy subjects, a positive correlation between total blood mercury levels, fat deposition, overweight and obesity was observed. A cross-sectional study by Zhou et al. ([2016](#page-32-0)) among Chinese workers with occupational exposure to Cd^{2+} showed a positive correlation between Cd^{2+} levels and dyslipidemia. The prevalence of dyslipidemia was found to increase dose-dependently among subjects. They further found a close association between blood Cd^{2+} levels and body mass index as subjects with a higher Cd^{2+} concentration had a correspondingly higher body mass index. The levels of triglyceride, lowdensity lipoprotein cholesterol and total cholesterol were also found to be higher when Cd^{2+} concentrations were high, with a corresponding lower high-density lipoprotein cholesterol levels. Similarly, a cross-sectional study by Tangvara-sittichai et al. ([2015](#page-31-19)) among 534 volunteered subjects from cadmium contaminated and non-contaminated communities showed similar results as observed by Zhou et al. [\(2016\)](#page-32-0).

Due to the correlation between serum/tissue lipid content and diabetes, other researchers have sought to fnd the relationship between heavy metal exposure and diabetes. In a cross-sectional study conducted among 5,544 volunteers, Nie et al. ([2016\)](#page-30-6) found that subjects who showed higher blood Cd^{2+} level were more likely to be obese or overweight. A comparatively similar cross-sectional studies and evaluations among populations exposed to Hg^{2+} ($n=3951$) (Cho [2017](#page-27-14)), As^{3+} (1160) (Mendez Michelle et al. [2016\)](#page-30-16), and Pb^{2+} (5558) (Wang et al. [2015a\)](#page-32-18) have also been investigated concluding with similar results as that found in individuals with elevated blood cadmium in relation to lipid dysregulation, overweight, obesity and diabetes risks. Among 569 adults with arsenic exposure, Sarker et al. [\(2021\)](#page-31-20) also observed an apparent disparity in arsenic-induced metabolic syndrome between males and females recruited from highand low-arsenic exposure areas. Females were found to be more susceptible to developing metabolic syndrome with hypo-high-density lipoprotein cholesterol, hyperglycemia, high abdominal obesity and insulin intolerance compared to males.

Though metal exposure in the above studies showed lipid profle dysregulation, the pattern of triglyceride, total cholesterol, low-density lipoprotein cholesterol and high-density lipoprotein cholesterol dysregulation difered, with some parameter remaining unafected in some cases. Example, whereas Cd^{2+} is reported to cause a significant increase in serum total cholesterol, triglyceride, low-density lipoprotein cholesterol, with a corresponding decrease in high-density lipoprotein cholesterol, serum high-density lipoprotein cholesterol levels, after As^{3+} and Hg^{2+} exposure, are reported to be higher in some studies (Mendez Michelle et al. [2016](#page-30-16); Sohn et al. [2020\)](#page-31-21). Nonetheless, fndings from other studies indicate no statistically signifcant diferences in serum lipid profle (Cho et al. [2020;](#page-27-10) Kasperczyk et al. [2005](#page-28-16); Sohn et al. [2020\)](#page-31-21), and as well identifed no correlation between metal exposure and changes in lipid profle (Kim [2012\)](#page-29-10) (See Table [2](#page-10-0) for details). Moreover, in spite of the higher antiatherogenic high-density lipoprotein cholesterol levels observed by Mendez et al., individuals with exposure to arsenic were found to be potentially at risk of developing cardiometabolic syndromes (Mendez Michelle et al. [2016](#page-30-16)).

In vivo studies on lipid metabolism gene aberration by heavy metals

a) Heavy metals on lipogenic gene expression

Regulatory genes, enzymes and transcription factors involved in lipid synthesis are reported to be altered by toxic metals which efectively results in the dysregulation of lipid metabolism process and fat accumulation, a precursor for diabetes, insulin resistance and obesity (He et al. [2015](#page-28-7)). The infuence of heavy metals on altering the expression of genes and proteins that modulates lipid and glucose metabolism, synthesis, uptake and storage have been investigated as

^eNo significant changes in concentration of 7-ketocholesterol and blood lipids (cholesterol, high-density lipoprotein, low-density lipoprotein, triglycerides) were found eNo signifcant changes in concentration of 7-ketocholesterol and blood lipids (cholesterol, high-density lipoprotein, low-density lipoprotein, triglycerides) were found^dHigh-density lipoprotein cholesterol and triglyceride® levels were not affected ^dHigh-density lipoprotein cholesterol and triglyceride® levels were not affected

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shown in Table [3.](#page-14-0) The mechanism by which heavy metals cause an increase in serum lipid levels is shown in Fig. [3](#page-18-0).

Adebayo et al. [\(2015\)](#page-26-6) observed that chronic exposure of mice to low dose of arsenic modulates the hepatic expression of genes involved in the regulation lipogenesis. The exposure led to a reduced *SREBP-1c* expression which conjointly resulted in a disturbance of *SREBP-1c* specifc lipogenic genes expression. Arsenic thus downregulated the expression levels of *SREBP-1c*, *FAS*, diglyceride acyltransferase (*DGAT*) and *LDLR* Adebayo et al. ([2015\)](#page-26-6). Wauson et al. ([2002](#page-32-19)) also observed that treatment of C3H 10T1/2 cells with 6 μM arsenic for 2 months signifcantly reduced the expression levels of the adipose modulating genes peroxisome proliferative-activated receptor γ (*PPARγ*), CCAATenhancer binding protein α (*C/EBPα*) and adipocyte fatty acid-binding protein (*aP2*), blocked the upregulation of cyclin dependent kinase inhibitor protein 21 (*p21Cip1/Waf1*) and inhibited the diferentiating efect of the adipogenesis drug, pioglitazone which is clinically used to induce adipogenesis through PPARγ activation. In another study aimed at establishing the role of arsenic on inducing atherosclerosis through altered lipid metabolism, rats exposed to arsenic contaminated water (133 μg/mL), and/or high cholesterol diet showed a transient increase in heat shock protein 70 (*Hsp70*) and high-sensitive C-reactive protein (*hs-CRP*) which are markers of cellular stress and myocardial infarctions. It was further observed that the arsenic signifcantly suppressed the activities of cholesteryl ester transfer protein-1 (*CETP-1*) and liver X receptor β (*LXRβ*) while decreasing the ratio of high-density lipoprotein cholesterol to low-density lipoprotein cholesterol (Cheng et al. [2011](#page-27-7)). Similarly, in zebra fsh, arsenic was found to alter the expression of carnitine O-octanoyltransferase (*CROT*), fatty acid binding protein 3 (*FABP3*), and 3-hydroxy-3-methylglutaryl-CoA synthase 1 (*HMGCS1*), genes required for lipid metabolism and transport (Carlson and Van Beneden [2014](#page-27-15)). Likewise, exposure of diabetic db/m mice to inorganic arsenic downregulated the expression of lipid metabolismrelated genes such as cluster of diferentiation 36 (*CD36*), 3-hydroxy-3-methylglutaryl-CoA reductase (*HMGCR*), fatty acid synthase (*FASN*), ATP-binding cassette transporter A1 (*ABCA1*) and Pparγ coactivator (*PGC*), but upregulated the expression of *PPARR-2*, phosphoenolpyruvate carboxykinase (*PCK1*), Cyclin D1 (*CCND1*) and glycosylphosphatidylinositol-anchored high-density lipoprotein-binding protein 1 (*GPIHBP1*) genes in liver (Liu et al. [2014](#page-29-14)). In male Sprague Dawley rat liver however, arsenic exposure signifcantly elevated the expressions of carnitine palmitoyltransferase 2 (*CPT2*), ecithin–cholesterol acyltransferase (*LCAT*), mitochondrial carnitine/acylcarnitine carrier protein (*CACT*), *CROT* and 5-methyltetrahydrofolate-homocysteine methyltransferase (*MTR*) in high dose groups (sodium arsenite) (Wang et al. [2015b](#page-32-20)). Chronic exposure of C57BL6J male mice to sodium arsenite (300 μg/L for 9 weeks) revealed a signifcant impairment in both glucose and lipid homeostasis which affected the body heat production ability of the mice in cold environments. Although food intake or body weigh was not afected, the arsenic exposed group had an increased total fat mass and subcutaneous inguinal white adipose tissue mass. Expression of genes involved in regulating lipolysis, fatty acid metabolism, adipogenesis, adaptive thermogenesis and infammation were signifcantly decreased in As-exposed group. The study revealed that 6 gene involved in PPAR signaling including, solute carrier family 27 (fatty acid transporter) member 2 (*SLC27A2*), *FABP3*, uncoupling protein 1 (*UCP1*), ATP citrate lyase (*ACSL5*), carnitine palmitoyltransferase 1b (*CPT1B*) and malic enzyme 1 (*ME1*), and as well as 23 other genes responsible for regulating various glucose and lipid metabolic processes were signifcantly reduced by 31–50% indicating that arsenic could be a potent obesogen capable of disrupting normal lipid and glucose homeostasis, and energy balance (Castriota et al. [2020](#page-27-16)).

The lipogenic influence of Cd^{2+} on lipid synthesis and cholesterol redistribution examined by Wang et al. [\(2018a\)](#page-32-7) indicated that Cd^{2+} effectively upregulated the lipid transporter ABCA1 which led to an increase in serum lipid levels of triglyceride, low-density lipoprotein cholesterol and total cholesterol while lowering high-density lipoprotein cholesterol levels in Cd treated HepG2 cells. Although Zhang et al. ([2018](#page-32-8)) also indicated that exposure to Cd^{2+} upregulated the mRNA level of hepatic *FASN*, stearoyl-CoA desaturase-1 (*SCD-1*), hepatic fatty acid uptake genes (*FABP1*, *FABP4*) and hepatic *LpL* among adult female CD1 mice, insulin resistance, obesity and hepatic lipid accumulation were not signifcantly afected. Moreover, the gene profle of mice exposed to sub-chronic dose of Cd^{2+} (10 mg/L for 10 weeks) revealed an alteration in the expression of key genes involved in both glucose metabolism and de novo free fatty acid synthesis and transport pathways. The mRNA levels of glucose metabolism genes such as glucose transporter 2 (*GLUT2*), *ChREBP*, citrate synthase (*CS*) glucose kinase (*GK*) and pyruvate kinase (*PK*) were observed to increase significantly in the liver of mice exposed to 10 mg/L of Cd^{2+} in drinking water. Similarly, the expression of lipid metabolism genes including the hepatic lipogenesis transcription factors (*PPARγ*, *SREBP1-c*), fatty acid synthesis and transport genes (*FAS*, *FAT*, *FATP2*, *FABP1*), triglyceride synthesis genes (*DGAT1/2*, *GPAT*) were signifcantly increased in mice exposed to sub-chronic dose of Cd (10 mg/L) thus perturbing lipid and glucose homeostasis, and hepatic energy metabolism process (Zhang et al. [2015](#page-32-16)). In female CD1 mice administered with a combination of $CdCl₂$ and methylmercury (II) chloride (MeHgCl), Camsari et al. ([2017\)](#page-27-17) reported of an impaired glucose homeostasis, a higher body weight and an increase in abdominal adipose tissue weight in male ofspring of treated females. Genes (*GLUT4*, *IRS1*, *FASN*,

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SREBP1c, sterol regulatory element binding protein-1c; LXR, liver X receptor; PPARy, peroxisome proliferative-activated receptor y; CETP, cholesteryl ester transfer protein; LXRß, liver X
receptor β ; CROT, carnitine O-o *SREBP1c*, sterol regulatory element binding protein-1c; *LXR*, liver X receptor; *PPARγ*, peroxisome proliferative-activated receptor γ; *CETP*, cholesteryl ester transfer protein; *LXRβ*, liver X , 3-hydroxy-3-methylglutaryl-CoA reductase; *FASN*, fatty acid synthase; *ABCA1*, ATP-binding cassette transporter A1; *ABCG5/8*, ATP-binding cassette subfamily G member 5/8; *SCARB1*, Scavenger receptor class B type 1; *PGC*, PPARγ coactivator; *PCK1*, phosphoenolpyruvate carboxykinase; *CCND1*, cyclin D1; *GPIHBP1*, glycosylphosphatidylinositol-anchored high-density drofolate-homocysteine methyltransferase; *GPAT*, glycerol-3-phosphate acyltransferase; *SCD-1*, stearoyl-CoA desaturase-1; *FABP1*, fatty acid-binding protein 1; *LpL*, lipoprotein lipase; *LDLR*, low density lipoprotein receptor; *INSIG2*, Insulin induced gene 2; *OSBP*, Oxysterol binding protein; *PLA2G2E*, phospholipase A2 group IIE; *SLC2A13*, Solute carrier family 2 member 13; *IL4*, interleukin 4 *FATP*, fatty acid transport protein; *GLYCTK*, glycerate kinase; *DGAT*, diacylglycerol O-acyltransferase 1; *CPT-2*, carnitine palmitoyltransferase 2; *MCAD*, medium chain acyl-CoA dehydrogenase; *MTP*, *CYP4A*, cytochrome P450 4A; *ACO*, acyl CoA oxidase; *FADS2*, fatty acid desaturase 2; *FATP1*, fatty acid transport protein 1; *ELOVL5*, methylmercury downregulated fatty acid elongase 5; *PON1*, paraoxonase 1; *APOAI*, apolipoprotein A1; *ACACA*, Acetyl-CoA carboxylase alpha; *PNPLA2*, patatin-like phospholipase domain containing 2; *CPT1A*, carnitine receptor β; *CROT*, carnitine O-octanoyltransferase; *FABP3*, fatty acid binding protein 3; *HMGCS1*, 3-hydroxy-3-methylglutaryl-CoA synthase 1; *CD36*, cluster of diferentiation 36; *HMGCR* 3-hydroxy-3-methylglutaryl-CoA reductase; FASN, fatty acid synthase; ABCA1, ATP-binding cassette transporter A1; ABCG5/8, ATP-binding cassette subfamily G member 5/8; SCARB1, Scavenger receptor class B type 1; PGC, PPARy coactivator; PCK1, phosphoenolpyruvate carboxykinase; CCND1, cyclin D1; GPHBP1, glycosylphosphatidylinositol-anchored high-density ipoprotein-binding protein 1; CPT, carnitinepalmitoyltransferase; LCAT, ecithin-cholesterol acyltransferase; CACT, mitochondrial carnitine/acylcarnitine carrier protein; MTR, 5-methyltetrahymterleukin 4 FATP, fatty acid transport protein; GLYCTK, glycerate kinase; DGAT, diacylglycerol O-acyltransferase 1; CPT-2, carnitine palmitoyltransferase 2; MCAD, medium chain acyl-CoA dehydrogenase; MTP, CYP4A, cytochrome P450 4A; ACO, acyl CoA oxidase; FADS2, fatty acid desaturase 2; FATP1, fatty acid transport protein 1; ELOVL5, methylmercury downregulated fatty acid elongase 5; PONI, paraoxonase 1; APOAI, apolipoprotein A1; ACACA, Acetyl-CoA carboxylase alpha; PNPLA2, patatin-like phospholipase domain containing 2; CPTIA, carnitine lipoprotein-binding protein 1; *CPT*, carnitinepalmitoyltransferase; *LCAT*, ecithin–cholesterol acyltransferase; *CACT*, mitochondrial carnitine/acylcarnitine carrier protein; *MTR*, 5-methyltetrahydrofolate-homocysteine methyltransferase; GPAT, glycerol-3-phosphate acyltransferase; SCD-1, stearoyl-CoA desaturase-1; FABP1, fatty acid-binding protein 1; LpL, lipoprotein lipase; LDLR, low density lipoprotein receptor; *INSIG2*, Insulin induced gene 2; OSBP, Oxysterol binding protein; *PLA2G2E*, phospholipase A2 group IIE; SLC2A13, Solute carrier family 2 member 13; IL4, palmitoyltransferase 1a; GK, Glucose kinase; MTTP, Microsomal triglyceride transfer protein; ACL, ATP citrate lyase; ACC, Acetyl-CoA carboxylase palmitoyltransferase 1a; *GK*, Glucose kinase; *MTTP*, Microsomal triglyceride transfer protein; *ACL*, ATP citrate lyase; *ACC*, Acetyl-CoA carboxylase

Acetyl-CoA carboxylase alpha (*ACACA*), *FATP2*, *CD36* and *G6PC*) associated with maintaining glucose and lipid homeostasis in the liver and abdominal adipose tissues were significantly altered indicating that the effect of heavy metal in females during gestation could persist through their offspring and may amplify the incidence of developing metabolic syndrome.

In lead related studies, Sun et al. [\(2017\)](#page-31-11) observed that Pb^{2+} -induced obesity was as a result of DNA methylation of lipogenic and glucose metabolism genes. DNA methylation regulates gene expression by either inhibiting or suppressing the binding of transcription factors to target sequences and thereby downregulating their expression. Genes that were afected, according to their study, included those relating to fatty acid transport and synthesis (*LDLR*, fatty acid transport protein (*FATP*), glycerate kinase (*GLYCTK*), *DGAT1*, *DGAT2*), fatty acid oxidation (medium chain acyl-CoA dehydrogenase (*MCAD*), *CPT-2*, *CYP4a*, acyl CoA oxidase (*ACOX*)), very-low density lipoprotein-triglyceride assembling (microsomal triglyceride transfer protein (*MTTP*), apolipoprotein-CIII (*APO-CIII*), *APO-V*, *APO-IV*) and *LXR* and *SREBP-1c* transcription factors. The glucose metabolism related genes such as *PKA* and *AKT*, the gluconeogenesis genes phosphoenolpyruvate carboxykinase (*PEPCK*) and *G6pase*, as well as cholesterol metabolism genes such as *CYP51* and acetyl-CoA acetyltransferase (*ACAT*) were also afected. These genetic alterations were found to result in weight gain, glucose intolerance, insulin resistance, elevated serum triglyceride and the accumulation of hepatic lipids. To study the transgenerational effect of a 24 h Pb^{2+} exposure on zebrafsh brain transcriptomics, Meyer et al. [\(2020](#page-30-18)) exposed zebrafsh (*Danio rerio*) embryo to 10 μM after which they were allowed to mature and spawn producing frst and second-generation ofspring. Similar to Sun et al. ([2017](#page-31-11)) observation, Meyer et al. ([2020](#page-30-18)) noticed that Pb^{2+} induced epigenetic changes through DNA methylation across several systemic functions (nervous and endocrine systems) and metabolic pathways. A total of 323 genes associated with endocrine system and 80 genes relating to lipid metabolism pathways were found to be signifcantly altered, indicating that Pb exposure (even acute) could have long lasting generational effect.

In the adipose tissue of C57BL/6 J mice exposed to MeHg $(0.5, 1.0, 5.0 \mu M)$, Ferrer et al. (2018) (2018) (2018) reported that mercury failed to signifcantly afect the adipogenic gene *PPARγ*, lipogenic genes (*ACACA*, *FASN*), lipolytic genes (patatin-like phospholipase domain containing 2 (*PNPLA2*) and *LpL*), and the genes that control β-oxidation (*CPT1a*) and transport (*CD36*). The mRNA expression for *PPARγ*, *FASN* and *PNPLA2* were however suppressed in a dosedependent manner in the liver of male mice with MeHg exposure with a corresponding decrease in hepatic triglyceride. Irrespective of the observation made by Ferrer et al. ([2018\)](#page-28-17), studies on other model organisms subjected to mercury reports of signifcant changes in lipogenic genes. For example, Ferain et al. [\(2018](#page-28-18)) indicated that the phospholipid fatty acid profle in the liver of rainbow trout were afected by methylmercury exposure. The study showed that methylmercury signifcantly downregulated fatty acid elongase 5 (*ELOVL5*), *FATP1*, whereas *FASN*, carnitine palmitoyl transferase 1 (*CPT1*) and fatty acid desaturase 2 (*FADS2*) were upregulated. Similarly, in preadipocytes of rainbow trout cultured with MeHg supplementation, Tinant et al. ([2021](#page-32-22)) observed an upregulation of the lipid metabolism genes, *FAS* and *FABP11a*, as well as several adipocyte-specifc genes including perilipin 2 (*PLIN2*) and apolipoprotein Eb (*APOEB*) inducing an intracellular accumulation of the neutral lipid polyunsaturated fatty acid (PUFA) in MeHg dose dependent manner. Using *Caenorhabditis elegans* as a model organism for studying mammalian response to MeHg due to their shared conserved pathways in synthesizing and oxidizing fatty acids, and regulating lipid homeostasis, Caito et al. [\(2020\)](#page-27-18) treated *C. elegans* with 10 or 20 μM MeHg for 30 min and examined its gene expression profle and triglyceride levels. Out of the 215 diferentially regulated genes, 17 were involved in lipid metabolism and 12 involved in maintaining glucose homeostasis. Expression of the pro-adipogenic transcription factor *C/EBP-1* (a homolog of human *C/ EBP*) known to play a role in the development of metabolic syndrome was upregulated. Other pro-adipogenic transcription factors upregulated by MeHg include *NHR-49* (homolog of *PPARγ*) and *SBP-1* (a homolog of human *SREBP*), the triglyceride synthesizing enzyme acyltransferase (a homolog of human glycerol-3-phosphate acyltransferase, *GPAT*), and the lipid transporter proteins vitellogenins (*VIT-2* and *VIT-*6). The above studies all demonstrate that $Hg^{2+}/MeHg$ is an important environmental contaminant capable of inducing biochemical and metabolic changes in organisms especially, to the lipid profle and thereby leading to metabolic dysfunction. Heavy metals thus largely distort lipid metabolism by infuencing the lipogenic gene expression patterns leading to lipid metabolism dysregulation and redistribution.

(b) In vitro and in vivo assessment of possible pathway of lipogenic gene aberration by heavy metals

Since hepatic cells regulate lipid metabolism and governs the whole-body energy metabolism process by serving as the major site for the storage and release of glucose and lipids, determining the expression pattern of lipid metabolism genes after exposure to heavy metals is important to understanding the mechanism and pathways by which metals induce dyslipidemia. The expression of lipid metabolism genes is regulated at the transcriptional level in a coordinated fashion among several transcriptional factors with poly- and mono-unsaturated fatty acids serving as natural

Fig. 3 Lipid metabolism pathway in the liver and the role of heavy ◂metals on inducing lipid profle dysregulation through lipogenic gene aberrations. Alteration in lipid metabolism transcription factor expression signifcantly impairs serum lipid profle. SREBP1c, sterol regulatory element binding protein-1c; LXR, liver X receptor; PPARγ, peroxisome proliferative-activated receptor γ; CETP, cholesteryl ester transfer protein; LXRβ, liver X receptor β; ABCA1, ATPbinding cassette transporter A1; FAS(N), fatty acid synthase; CROT, carnitine O-octanoyltransferase; FABP, fatty acid binding protein 3; CPT, carnitinepalmitoyltransferase; SCD-1, stearoyl-CoA desaturase-1; LpL, lipoprotein lipase; LDLR, low density lipoprotein receptor; CYP, cytochrome P450; ACC, Acetyl-CoA carboxylase; MTTP, Microsomal triglyceride transfer protein; FATP, fatty acid transport protein; ELOVL5, elongase 5; GLYCTK, glycerate kinase; DGAT, diacylglycerol O-acyltransferase 1; CD36, cluster of diferentiation 36; SLC27A2, Solute carrier family 2 member 13; SCARB1, Scavenger receptor class B type 1; PGC, PPARγ coactivator; PNPLA2, patatin-like phospholipase domain containing 2; GPAT, glycerol-3-phosphate acyltransferase; LCAT, lecithin–cholesterol acyltransferase; MCAD, medium chain acyl-CoA dehydrogenase; ACO, acyl CoA oxidase; APOE, Apolipoprotein E; PCK1, phosphoenolpyruvate carboxykinase; CCND1, cyclin D1; GPIHBP1, glycosylphosphatidylinositol-anchored high-density lipoprotein-binding protein 1; CACT, mitochondrial carnitine/acylcarnitine carrier protein; MTR, 5-methyltetrahydrofolate-homocysteine methyltransferase; ACAT, Acyl-coenzyme A: cholesterol acyltransferases; ABCG5/8, ATPbinding cassette subfamily G member 5/8; ACSL5, ATP citrate lyase; HMGCR, 3-hydroxy-3-methylglutaryl-CoA reductase

ligands that activate most of these transcription factors (Ayisi et al. [2018](#page-26-11); Jump et al. [2006\)](#page-28-19).

Studies have indicated that Cd^{2+} (Newairy et al. [2007](#page-30-19); Olszowski et al. [2018](#page-30-20)) and arsenic (Chi et al. [2019b\)](#page-27-2) can signifcantly decrease the levels of PUFA due to their high susceptibility to peroxidation (Gaschler and Stock-well [2017\)](#page-28-20). Decline in poly- and mono-unsaturated fatty acids levels could therefore negatively afect the activation of transcription factors and may account for the downregulation of most lipogenic gene expressions. Several lipogenic gene transcription factors have been identifed among which *SREBPs*, *LXR(α/β)*, *ChREBP* and *PPAR(α/γ)* are most prominent (Cheng et al. [2016;](#page-27-19) Jump et al. [2006](#page-28-19); Vineeth Daniel et al. [2019](#page-32-13); Xia et al. [2018](#page-32-21)). *LXR* transcription factors are nuclear receptors with pivotal role in the transcriptional control of lipid metabolism. The transcriptional activity of *LXR* is induced in response to elevated cellular cholesterol levels. *LXRs* thus binds to and regulates the expression of genes that encode proteins involved in cholesterol absorption, transport, efflux, excretion and conversion to bile acids (Wang and Tontonoz [2018](#page-32-23)). Similarly, *SREBPs* are transcription factors that regulates fatty acid and cholesterol biosynthesis by directly activating the transcription of genes needed for the uptake and synthesis of cholesterol, fatty acid, triglycerides and phospholipids. Though heavy metals have been shown the afect the expression and activity of these transcription factors, differences in their expression pattern have been reported. The expression of *LXR* and *SREBPs* have been shown to be

down-regulated by As and Pb in both in vivo and in vitro studies (Adebayo et al. [2015](#page-26-6); Sun et al. [2017](#page-31-11)). Cheng et al. ([2016](#page-27-19)) showed that $As³⁺$ inhibited the expression of *LXR* at both the mRNA and protein level and subsequently decreased the protein level *SREBP-1c*. The inhibition of *LXR* by As^{3+} resulted in a reduced efflux of cholesterol from HepG2 cell to the extracellular space. Moreover, As also elevated the expression of *C/ETP* involved in reverse cholesterol transport, where cholesterol is transferred from high-density lipoprotein to apolipoprotein B-containing lipoproteins to become low-density lipoprotein and delivering the cholesterol to the hepatocytes to be secreted into bile or bile acid.

Suppression of *SREBP-1c* expression by arsenic was found to inhibit the expression of *FAS*, *LDLR*, *SCD-1* and *DGAT-2* genes but this effect was time dependent as the inhibition observed at 6 h. waned, after which there was an upregulation in the expression levels of *SREBP-1c* and its target genes at 16 h. (Adebayo et al. [2015](#page-26-6)). It has been previously observed that DNA hypermethylation of *SREBP1 c* and *LXR* by Pb^{2+} could have been responsible for the gene repression and downregulation of genes involved in fatty acid transport (*LDLR*, *FATP*, *Glyctk*, *DGAT1* and *DGAT2*) and fatty acid oxidation (*CPT-2*, *MCAD*, *ACO*) and may have thus been responsible for the elevated lipid synthesis in the liver and serum (Sun et al. [2017\)](#page-31-11). Taken together, an inhibition of lipid metabolism transcription factors is a major precursor for the downregulation of most lipogenic genes and may account for the dysregulation in the processes that ensures the maintenance of lipid homeostasis in both hepatic tissue and serum.

The downregulation of lipogenic genes is also closely associated with excess accumulation of cellular and serum lipids, and this could be due to limited protein and enzymes for biosynthesis, absorption, trafficking and cholesterol efflux. In contrast to the findings by Cheng et al. ([2016](#page-27-19)) who reported that As down-regulates lipid transcription factors (*SREBPs* and *LXR*), a study by Xia et al. ([2018\)](#page-32-21) however indicated that chronic exposure to low doses of Pb^{2+} resulted in an upregulation of the transcription factors *SREBP-1c*, *SREBP2*, *PPARα* and *PPARγ* which activate key genes involved in fatty acid transport, β-oxidation, glycolysis, triglyceride synthesis and de novo lipogenesis. Although both authors observed a dysregulation in the lipid profle, Cheng et al. ([2016\)](#page-27-19) attributed the lipid and cholesterol accumulation to the reduced expression level of proteins and enzymes needed for the cholesterol metabolism, transport and efflux of cellular and serum cholesterol, whereas Xia et al. ([2018\)](#page-32-21) on the other indicated that the upregulation of *SREBP* may have induced the genes (*FAS*, *SCD1* and *ACC*) required for de novo lipogenesis, and thus, the accumulated lipids may have been as result of enhanced de novo lipogenesis.

Association of multiple heavy metals on serum lipid dysregulation

Whereas the positive association of each single heavy metal with serum lipid dysregulation is well documented, the correlation between exposure to multiple heavy metals and dyslipidemia show some apparent variations in reported studies. Poursafa et al. [\(2014\)](#page-30-21) observed that a positive correlation between increasing serum Hg^{2+} and Pb^{2+} concentrations with higher triglyceride and total cholesterol in a cross-section of adolescents was linked to a higher risk of developing cardiometabolic syndrome. Xu et al. ([2021\)](#page-32-2) in a retrospective cross-sectional study on humans exposed to low-levels of Cd^{2+} and Pb²⁺ observed no apparent association between the two metals and dyslipidemia. They however reported that, whereas blood Pb was positively correlated with atherogenic serum lipid profles, cadmium did not show any association with serum lipid profles. In a study involving a group of elderly population with or without coronary artery disease, a positive correlation was found to exist between serum metal level and risk of developing coronary artery disease. Patients with coronary artery disease were found to have a significantly higher serum Pb^{2+} , Cd^{2+} and Hg^{2+} when compared with the control population. Moreover, although elevated serum metal level was positively associated with coronary artery disease patients, no signifcant association with triglyceride, high-density lipoprotein cholesterol and total cholesterol/high-density lipoprotein cholesterol was established (Asgary et al. [2017\)](#page-26-12).

Like all other cardiometabolic risks, ischemic stroke is a common disease associated with dyslipidemia, diabetes, pressure, obesity and other metabolic syndromes of which heavy metals are implicated as major contributors. Lin et al. ([2018\)](#page-29-15) thus examined the relationship between heavy metals and acute ischemic stroke but found no signifcant association between serum metal level and stroke risk factors such as body mass index, triglyceride and total cholesterol, fasting blood sugar and pressure among both stroke patients and control. After examining the association of 24 metals on blood lipid levels among 1201 participants with history of metal exposure, Li et al. ([2021\)](#page-29-1) observed that the relationship between diferent metal exposure and lipid markers are not identical, and that whereas essential metals showed a positive association with lipid markers (except high-density lipoprotein cholesterol), non-essential metals showed a negative association for lipid markers except for high-density lipoprotein cholesterol and low-density lipoprotein cholesterol. Though in human studies diferent metabolic risk effects are observed after multiple metal exposure, hypolipidemia mediated by oxidative stress and metal interaction was reported for rats exposed to a combination of Pb^{2+} (1.4 mg/kg), Cd^{2+} (0.01 mg/kg) and Mn^{2+} (0.14 mg/kg) for 15 weeks (Oladipo et al. [2017\)](#page-30-22). These fnding together suggest that, even though toxic metals in combination can induce dyslipidemia and other metabolic and cardiometabolic syndromes, the mechanisms and pathways of inducing these metabolic risks may be diferent among diferent host.

Heavy metal, gut microbiome and lipid metabolism dysregulation

The gastrointestinal tract of humans serves as a home to a large community of microbiome known to engage in several metabolic activities which are profoundly intertwined with human health (Gao et al. [2017;](#page-28-21) Lu et al. [2014](#page-29-16)). Accumulating evidence in recent years have demonstrated that ingestion of exogenous toxicant such as heavy metals through food or water can disproportionately shape the nature of the gut microbiome and may increase one's susceptibility to contracting infectious diseases and may also be an underlying cause of metabolic syndromes such as lipid and lipoprotein metabolism dysregulations (See Table [4](#page-20-0) and Fig. [4\)](#page-23-0) (Dabke et al. [2019](#page-27-20); Wang et al. [2020;](#page-32-24) Wu et al. [2016\)](#page-32-25). This is because the gut microbiome has the capacity to perform many complex biochemical and metabolic processes that cannot be performed by the host, including the degradation of undigested carbohydrates through fermentation for the release of microbial metabolites that may function as energy substrates, infammation modulators and signaling molecules (Lu et al. [2014;](#page-29-16) Oliphant and Allen-Vercoe [2019](#page-30-23)). It is commonly observed that among obese individuals, there is a dramatic change in the gut microbiome in relation to the ratio of Firmicutes to Bacteroidetes when compared with healthy lean individuals. Meaning, obese individuals are more likely to have a smaller proportion of Bacteroidetes than Firmicutes (Wu et al. [2016\)](#page-32-25). Moreover, like heavy metals, it is reported that high-fat diet promotes an increase in Firmicutes while decreasing Bacteroidetes population in the gut (Wu et al. [2016\)](#page-32-25).

In mice exposed to cadmium, He et al. [\(2020\)](#page-28-22) observed that cadmium resulted in marked perturbation in gut microbiota which was characterized by a signifcant decrease in gut microbial richness and a lowered abundance in short chain fatty acid-producing bacteria leading to a reduced short chain fatty acid production in the gut. This change in the gut microbiome, as induced by Cd, resulted in substantial changes in the metabolic function of the mice and signifcantly inhibited gene pathways associated with amino acid, carbohydrate, lipid and energy metabolism (He et al. [2020](#page-28-22)). Short chain fatty acid generated from dietary fbers by gut bacteria play an essential role in modulating the hosts immune response, tumorigenesis and energy metabolism and as such a perturbation in microbial richness renders a person immune compromised (Xue et al. [2019\)](#page-32-26).

Xia et al. ([2018](#page-32-21)) also observed that chronic exposure of mice to Pb (0.1 mg/L for 15 weeks) decreased the relative abundance of both Firmicutes and Bacteroides but did not afect the relative abundance of Proteobacteria or Actinobacteria in the cecum. However, whereas the population of Firmicutes decreased signifcantly in the gut, there was a relative increase in the abundance of Bacteroidetes. Since the relative population of Firmicutes/Bacteroides is directly related to serum or hepatic lipid contents, it was observed that Pb signifcantly increased the expression level of key genes related to lipid metabolism in the liver, thus accounting for the elevation of the hepatic triglyceride and total cholesterol levels. This observation indicated that Pb was a potent agent for the disruption of hepatic and serum lipid homeostasis, and this was achieved through gut microbiome dysbiosis (Xia et al. [2018\)](#page-32-21).

To understand the risk factors associated with perturbed gut microbiome, Xue et al. [\(2019](#page-32-26)) examine the serum metabolic profle of mice after exposure to 10 ppm arsenic for 4 weeks. They reported that whereas $As³⁺$ altered the gut microbiome, it also induced drastic changes in the metabolic pathways of fatty acid metabolism, phospholipids, sphingolipids and cholesterols metabolism when compared to the control, suggesting that As-induced gut microbiome perturbation can exacerbate metabolic disorders. It was further noted that when the population of gut microbiome was altered with microbial infection (*Helicobacter trogontum*), arsenic exacerbated the health risk of the host mice through elevated of lipid fux and a disruption of its metabolic function (Xue et al. [2019\)](#page-32-26).

Bridges et al. ([2018\)](#page-27-21) examining how methylmercury induces alteration in intestinal microbiome and metabolome of teleost and mice observed that, the MeHg-altered gut microbiome led to signifcant changes in metabolic precursors related to neuronal function and lipid metabolism. The relative abundance of several long chain fatty acids, including stearic, palmitic, and oleic acids, were observed to have decreased significantly. Moreover, MeHg also significantly altered the availability of serine and phosphocholine precursors required for the generation of bioactive lipids. The MeHg-altered gut microbiome also resulted in changes in the expression of the lipid metabolism genes, *FAS* and *ACOX1*, and the metabolome, indicating that MeHg can infuence the lipid profle of both teleost and mice by altering the microbiome and inducing epigenetic changes in its lipid metabolism genes (Bridges et al. [2018\)](#page-27-21).

In view of the concept of developmental plasticity and a growing body of evidence that suggests that early-life exposure to an environmental toxicant could infuence the establishment of a later-in-life gene dependent health defects through epigenetic dysregulation (Kuo et al. [2018](#page-29-12)), Wu et al*.* sought to fnd the underlying biological mechanism that regulates this event by exposing parental mice to 32 ppm $\rm Pb^{2+}$

Table 4 (continued) **Table 4** (continued)

Fig. 4 Physiological interaction between gut microbiome and lipid produce beneficial health effect to host organism. This effect is however impaired by heavy metal (by ingestion) which perturbs gut

microbiome population, their function in relation to lipid metabolism and may subsequently lead to metabolic syndrome

through gestation to lactation till offspring were 3-weeksold (Wu et al. [2016](#page-32-25)). At 40 weeks of age, it was revealed that Pb^{2+} shifted the gut microbiota in the mice offspring though exposure to Pb^{2+} was ceased when the offspring were 3-weeks-old. A signifcant inverse change in the ratio of Bacteroides/Firmicutes was also observed among obese mice having a higher gut population of Firmicutes than Bacteroidetes. Wu et al. [\(2016\)](#page-32-25) therefore underscored that early-life exposure to Pb^{2+} could induced gut microbiome alteration, suggesting that this may be a contributing factor to the increased adult body weight even when Pb^{2+} exposure is removed at a later point in time. Although the study did not examine the effect of Pb^{2+} on lipid metabolism or serum lipid profile, it was reported that mice exposed to Pb^{2+} showed an increase in body weight but that this observation was sex dependent as weight gain in male mice was more pronounced than in females (Wu et al. [2016](#page-32-25)).

Though toxic metals signifcantly infuence dysbiosis, the gut microbiome responds to the efect of the metal toxicity differently (Wu et al. [2016\)](#page-32-25). Whereas some bacteria are more susceptible to the toxicity of certain metals, others have developed metal-specifc resistance and are been exploited for metal detoxifcation in food processing and in clinical trials (Duan et al. [2020;](#page-27-22) Ibrahim et al. [2006](#page-28-23)). In an attempt to subvert the efect of metal-gut microbiome perturbation and lipid dysregulation, it has been reported in several studies that oral administration of probiotics can inhibit heavy metals absorption, protects the intestinal barrier and limit its efect on negatively afecting lipid metabolism (Zhai et al. [2016\)](#page-32-27). Probiotic bacteria belonging to the *Lactobacillus* genus have been commonly exploited to detoxify cadmium (Afraz et al. [2020](#page-26-13); Bhattacharya [2020](#page-27-23); Gerbino et al. [2014](#page-28-24); Ibrahim et al. [2006\)](#page-28-23), lead (Afraz et al. [2020](#page-26-13); Ibrahim et al. [2006\)](#page-28-23), arsenic (de Matuoka e Chiocchetti et al. [2020](#page-27-24)) and mercury (Majlesi et al. [2017\)](#page-29-20) and several other heavy metals from the gut of animal models, in in vitro studies and in water and also to improve the population of the established microbiome. The detoxifcation ability of these probiotics are pH and dosage (metal concentration) dependent. Gut microbiome and inoculation of probiotics may thus play an important role in the biotransformation of toxic metals through which their toxicity efects are suppressed (Chi et al. [2019a\)](#page-27-13).

Whereas metals perturb lipid profle and gut microbiome, diferent metals at diferent doses have been reported to illicit diferent forms of toxicity, dysbiosis and dyslipidemic efects in mice. Example Richardson et al. [\(2018](#page-31-22)) reports of significant changes in microbiota composition when mice were exposed to high doses of chromium and cobalt whereas signifcant changes in the microbiota composition after exposure to arsenic, cadmium and nickel were dosedependent and were also found to induce a large number of iron-importing gene suggesting the possibility of shared response pattern Richardson et al. ([2018\)](#page-31-22). As reported by (Li et al. [2020](#page-29-17)), diferent doses of cadmium in the form of telluride quantum dots similarly had diferent efect on gut microbiome. While low dose $(0.2 \text{ and } 2 \mu\text{M})$ was reported to signifcantly increase gut microbiota diversity without afect the lipid profile, medium dose (20 μ M) was found to have caused the biggest decrease in Firmicutes/Bacteroides ratio with a corresponding increase in triglyceride, low-density lipoprotein cholesterol and total cholesterol. Though changes in serum lipid profle was not detected, high dose (200 μM) caused toxicities in the liver and intestine and also afected intestinal immunity (Li et al. [2020](#page-29-17)). Particularly lacking is studies on the infuence of mercury on gut microbiome dysbiosis and its relation to lipid metabolism dysregulation of which we recommend more studies.

Heavy metals, hormonal regulation and metabolic syndrome

Heavy metal induced insulin resistance and dyslipidemia

Insulin is a regulatory endocrine hormone that modulates circulating blood glucose. The role of insulin in regulating DNA synthesis and gene transcription of proteins involved in metabolic activities has also been observed (Batista et al. [2021;](#page-27-25) Sears and Perry [2015\)](#page-31-23). One principal function of insulin is to suppress lipolysis of stored fat in adipocytes and gluconeogenesis in the liver. By inhibiting lipolysis, it promotes triglyceride storage and reduces the volume of circulating free fatty acids, and thus regulating very low-density lipoprotein production (Chakrabarti et al. [2013;](#page-27-26) Sears and Perry [2015\)](#page-31-23).

Diabetes and dyslipidemia, common conditions of metabolic syndrome, are among the major disorders that emanate from insulin resistance as a result of accumulation of blood glucose and lipid metabolites. The levels of lipid metabolites in circulation are commonly used as biomarkers for insulin resistance and dyslipidemia and are also used as determinants for cardiovascular related diseases. The ratio of triglyceride to high-density lipoprotein cholesterol and total cholesterol to high-density lipoprotein cholesterol are the generally accepted best marker for insulin resistance (Artha et al. [2019](#page-26-14)). Studies over the years have linked heavy metal exposure to insulin and insulin receptor malfunction. Exposure to arsenic, for example, has been found to induce insulin insensitivity in humans and animals and is implicated as a factor for the onset of diabetes and the progression of obesity (Lin et al. [2014](#page-29-21); Park et al. [2016\)](#page-30-24). Chronic exposure of rats to cadmium has also been reported to impair pancreatic function, and induce insulin resistance in liver, muscle adipose tissue and cardiovascular tissue, thereby resulting in an increase in serum triglyceride, cholesterol, low-density lipoprotein cholesterol and very low-density lipoprotein, and a decrease in high-density lipoprotein cholesterol (Treviño et al. [2015\)](#page-32-28). Findings from studies with arsenic (Afolabi et al. [2015;](#page-26-2) Padmaja Divya et al. [2015\)](#page-30-25), mercury (Jung et al. 2016 ; Kim et al. 2015) and lead (Leff et al. 2018 ; Shyam et al. [2012\)](#page-31-24) indicate similar observations suggesting that these heavy metals have specifc efect on insulin signaling and the metabolism of fat or lipid and glucose and could lead to lipid accumulation, obesity and diabetes.

Role of heavy metals in diabetes

As an environmental and industrial toxicant, heavy metals have no known important biological roles except for their ability to alter the normal physiological function of the body by interfering with hormonal action, for which reason they are classifed as endocrine disrupting chemicals (Lauretta et al. [2019;](#page-29-23) Leff et al. [2018](#page-29-7)). Studies on metal toxicology over the years have explored the hazardous efects heavy metals have on the initiation and progression of type 2 diabetes.

Although current understanding of the direct mechanism by which endocrine disrupting chemicals impair systemic function to promote diabetes initiation remains incomplete, evidence of their inhibitory roles on some endocrine glands and hormones that regulates sugar levels have been reported (Howard [2018](#page-28-26); Sabir et al. [2019](#page-31-12)). Cadmium accumulation, for example, is reported to induce diabetes by competing with zinc, an essential metal required for insulin formation in pancreatic β-cells, thus impairing the function of the insulin producing pancreatic β-cells (El Muayed et al. [2012](#page-28-27); Hong et al. [2021\)](#page-28-28). Cadmium has also been found to reduce the number of insulin receptors and further renders the remaining unresponsive to insulin (Ficková et al. [2003](#page-28-8)). This negative dual effect of cadmium on insulin producing pancreatic β-cells and on insulin receptors may eventually account for the accumulation of blood glucose due to their inability to enter cells and may be a major contributing factor to the initiation and progression of type 2 diabetes. Like Cd^{2+} , the pro-diabetic nature of arsenic (Islam et al. [2012](#page-28-29); Kirkley et al. 2017 ; Liu et al. 2014), Pb^{2+} (Leff et al. 2018) and Hg^{2+} (He et al. [2013;](#page-28-30) Rizzetti et al. [2019\)](#page-31-25) have likewise been investigated in both human and animal models, with a pronounced efect on pancreatic β-cells dysfunction, insulin resistance and an increased gluconeogenesis in the case of arsenic. The pro-diabetic nature of these heavy metals is largely due to their adverse efect on insulin transduction signaling and the inhibition of some genes responsible for glucose metabolism (Islam et al. [2012](#page-28-29)). The initiation of infammation and oxidative stress provoked by heavy metals suppress insulin gene promoter mRNA expression and its activity in pancreatic islet cells thereby evoking an increase in systemic glucose levels and a downregulation in serum insulin levels, thus leading to hyperglycemia and diabetic progression (Khan and Awan [2014;](#page-29-25) Pizzino et al. [2017](#page-30-26)). Even though treatment of diabetes remains complicated, heavy metal chelators such as ethylenediaminetetraacetic acid (EDTA) (Diaz et al. [2018;](#page-27-27) Lamas et al. [2016](#page-29-6)) and lipoic acid (Ibrahimpasic [2013](#page-28-31)) have been found to suppress the progression of metal-induced diabetes and diabetes-associated cardiovascular events.

Heavy metals and the endocrine system

The endocrine system comprises of a network of glands that produce and secrete hormones responsible for regulating cellular and metabolic processes. Several environmental toxicants have been characterized as endocrine disruptors due to their ability to alter hormonal secretion by the glands, as well as their normal functioning and regulatory roles (Mahapatra et al. [2021](#page-29-26); Szkudelska et al. [2021](#page-31-26)). Heavy metals have gained notoriety as endocrine disrupting chemicals due to their hazardous efect on the physiological functioning of both endocrine glands and the body in general. Stahr et al. [\(2021\)](#page-31-27) observed a positive and dose-dependent correlation between postmenopausal women with arsenic exposure and obesity, hinting that high arsenic levels not only suppresses estrogen secretion but may also mimic or abrogate estrogen signaling pathway thereby altering all associated metabolic signaling processes including lipid metabolism. Nadal et al. [\(2017\)](#page-30-27) observed that metabolic disrupting chemicals could regulate nutrient absorption and metabolism by altering intestinal transport and peptides that control food intake. Glucose uptake, for example, is reported to be altered signifcantly after the administration of metabolic disrupting chemicals such as polychlorinated biphenyls and 2,3,7,8-tetrachlorodibenzo-p-dioxin by either increasing the intestinal expression of sodium/glucose co-transporter 1 and glucose transporter type 2 genes, or by reducing insulin stimulated glucose uptake. These alterations together were associated with elevated plasma glucose levels suggesting an increase in intestinal glucose uptake and transport but a decrease in cellular glucose uptake and metabolism (Nadal et al. [2017](#page-30-27)).

In relation to heavy metals, Bell et al. ([1990\)](#page-27-28) reported of an elevated glucose levels in rats exposed to Cd^{2+} (0.84 mg/ kg), whereas Sabir et al. (2019) describes Cd²⁺ and arsenic as hazardous endocrine disrupting chemicals that exhibits deleterious efect on carbohydrate metabolism pathways through modifcation and impairment of relevant key enzyme activity thus contributing to a considerably increase in blood glucose levels. These metals were also found to disrupt hormonal balance by damaging or altering the function of pancreatic islet and adrenal glands. These fndings together indicate that heavy metals together with other endocrine and metabolic disrupting chemicals could infuence the expression and secretion of gastrointestinal peptides and hormones responsible for dietary nutrient absorption of which glucose and lipid processes may be signifcantly afected.

In addition, the hypothalamus is an important region of the brain particularly responsive to hunger and satiety regulating signals and maintaining the overall energy balance by modulating food intake and energy expenditure (Austin and Marks [2009\)](#page-26-15). An alteration in the expression and secretion of any hypothalamic peptide associated with glucose or lipid metabolism and appetite regulation may result in a compulsive eating behavior which could potentially lead to the development of hyperglycemia, hyperlipidemia and an accumulation of total visceral adipose fat (Nadal et al. [2017](#page-30-27)). Heavy metals, acting as endocrine disrupting chemicals, may thus induce obesity by infuencing the hypothalamus and by distorting the expression of peptides that regulates appetite and satiety (Park et al. [2017b\)](#page-30-28). The two major hormones, leptin and ghrelin, produced by adipose tissues and stomach but acts primarily on the hypothalamus to regulates food intake and body weight (Klok et al. [2007\)](#page-29-27), have been observed to be infuenced by toxic metals. Whereas Stasenko et al. ([2010\)](#page-31-28), Ferrer et al. ([2018\)](#page-28-17) and Kawakami et al. [\(2012\)](#page-29-28) reports that Cd^{2+} and Hg^{2+} suppresses the mRNA expression of leptin, other studies have indicate that these two metals induced an elevation of leptin in plasma (Ashley-Martin et al. [2015](#page-26-16); Ba et al. [2017](#page-27-29); Rizzetti et al. [2019](#page-31-25)). Similar investigations on Pb^{2+} (Beier et al. [2015\)](#page-27-30) and arsenic (Penta [2016](#page-30-29)) found that these metals induce an elevation of leptin hormone and implicating it as a factor for weight gain and obesity. Both elevation and suppression of leptin, above or below its optimal threshold, could trigger lipid and glucose dysregulation and potentially lead to the development of metabolic syndrome. This is because elevated leptin levels is directly associated with increased adipose tissue mass and insulin resistance which are factors for inducing obesity (Ashley-Martin et al. [2015\)](#page-26-16), whereas persistently low leptin levels could trigger an incessant craving for food and subsequently lead to hyperglycemia, hyperlipidemia and cardiovascular diseases (Poetsch et al. [2020](#page-30-30)). Heavy metals may thus afect the production, release and function of these hormones in the hypothalamus, and may result hyperphagia leading to excessive food intake, abnormal lipid synthesis, accumulation and obesity.

Conclusion

The pervasive nature of heavy metals is a matter of public health concern due to the multiple cardiometabolic and pathophysiologic efect they induce after exposure, and the high likelihood of increased mortality. Though lipids and lipoproteins are required for carrying out physiological functions such as impulse transmission, formation of cellular or organellar membrane, for energy reserve and for maintaining systemic homeostasis, evidence show that exposure to toxic doses could induce lipid and glucose metabolism dysregulation thus infuencing redistribution and accumulation, which are precursors for developing metabolic syndrome and other life-threatening clinical conditions. Evidence show that heavy metals distort serum lipid profle through lipogenic gene aberration, receptor inhibition, hormonal imbalance and gut microbiome perturbation resulting in high pro-atherogenic lipid levels while signifcantly decreasing anti-atherogenic lipid levels.

The deleterious infuence of heavy metals on altering signifcant lipogenic genes essential for maintaining lipid homeostasis through inhibition of function or causing an increase in pro-atherogenic lipids in serum is illustrated. The transcription factors *C/EBP*, *PPAR*, *SREBP*, *CHREBP* and *LXR* which regulates the expression of a large set of lipid and glucose metabolism processes including β-oxidation, de novo lipogenesis, and the synthesis and transport of fatty acids, cholesterol, phospholipids and triglycerides are the most largely impaired or downregulated genes.

Given that heavy metals perturb gut microflora population, it is found that perturbation in the ratio of *Firmicutes*/*Bacteroidetes* accounts for increased risk of obesity due to the notable decline in glycolysis and lipid metabolism genes. In addition, decline in insulin production, insulin receptor insensitivity, and the decline in ghrelin and leptin secretion are among the many hormonal factors afected by heavy metal exposure, which together contributes to lipid dysregulation. In spite of the availability of several reports on heavy metal induced lipid dysregulation, studies are limited when it comes to de novo lipogenesis, and also Hg^{2+} induced lipogenic gene alteration in model animals. Further studies may therefore be required to accelerate current understanding and insight into their role in dysregulating serum lipid profle.

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Declarations

Conflict of interest The authors declare that they do not have any conflict of interest.

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