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### GLOBAL AND QUANTITATIVE GENE EXPRESSION ANALYSIS OF THE EFFECTS OF DRINKING WATER EXPOSURE TO LEAD ACETATE IN FISHER 344 MALE RATS LIVER

by

Worlanyo Eric Gato

A Dissertation Submitted to the Faculty of The Graduate College in partial fulfillment of the requirements for the Degree of Doctor of Philosophy Department of Chemistry Dr. Jay Means, Advisor

Western Michigan University Kalamazoo, Michigan April 2007

### GLOBAL AND QUANTITATIVE GENE EXPRESSION ANALYSIS OF THE EFFECTS OF DRINKING WATER EXPOSURE TO LEAD ACETATE IN FISHER 344 MALE RATS LIVER

#### Worlanyo Eric Gato, Ph.D.

### Western Michigan University, 2007

The primary objective of this research is to analyze global gene expression patterns occuring in Fisher 344 rat livers exposed to varying levels of lead and times. The hypotheses were that: 1) effects associated with Pb exposure are both dose and time dependent and 2) several genes will be over-expressed or repressed including transcripts associated with calcium signaling. Initially, the effects of Pb exposures upon morphometric indices, liver and kidney tissue histology, Pb distribution, Pb interaction with other trace metals including Zn, Cu, Co, Fe, Ni and Ca were assessed. Results showed a significant accumulation of lead in blood, liver, kidney and bone marrow in lead exposed groups with the kidney demonstrating greater damage compared to the liver. Potential interactions of calcium, iron, cobalt, copper, zinc and nickel and lead examined showed positive and negative correlation for 30 and 90 days treatment period respectively. Differentially expressed genes included genes cited in the literature and several not previously reported to be affected by lead toxicity. Expression profiles were clustered and gene ontology (GO) revealed 15 GO categories affected by chronic (90d) exposure, while 3 GO categories were affected during (30d) exposures. Pathways emphasized the importance of Pb in modulating various cellular events in a manner similar to calcium regulation, including phosphorylation and dephosphorylation, calcium

signaling, histone acetylation and deacetylation. Conclusions include:

- 1. Pb controls mammalian protein synthesis via regulating phosphorylation or dephosphorylation events of eukaryotic elongation/initiation factors
- 2. Pb regulates gene expression through the regulation of histone acetylases
- 3. Pb regulates calcium dependent transcription factor myocyte enhance factor-2 Quantitative PCR was employed in validating the microarray result and showed that Microarrays and qRT-PCR yield comparable results.

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### Worlanyo Eric Gato

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### CHAPTER I

#### INTRODUCTION

The most ancient and relevant environmental poison to be used by man is lead. According to Jemigan *et al [* 1], hundreds of millions of people have been affected by the toxicity of lead during the last 4500 years either as mining slaves, or as consumers of adulterated wine and food or from breathing urban air. Written archeological evidence exists that lead was used widely in the ancient world. In recent times, lead has been used in gasoline which makes it widely distributed in the environment.

This dissertation is organized as follows; chapter 1: introduction, chapter 2: literature review, chapter 3: assessment of lead toxicity by inductively-coupled plasma mass spectrometry and histopathology, chapter 4: gene expression analysis by microarray DNA gene chips, chapter 5: validation of microarray gene expression data by real-time quantitative polymerase chain reaction (RT-qPCR) and chapter 6: conclusions. In chapter 1, a brief background to the study is provided with project objectives clearly laid out. Chapter 2 provides a review of background knowledge of lead to date. Topics discussed are history of lead production and use, sources of lead contamination and exposure, body absorption and distribution of lead, lead health effects, toxicity mechanisms, ways of remediating lead polluted soils and water and how to reduce lead body burden. Chapter 3 introduces the experiments that were conducted to address goals one through three whilst goals four through seven are addressed in chapters 4 and 5. Finally the study is concluded in chapter 6.

Heavy metals such as lead and its compounds are natural constituents of the environment moving between atmosphere, hydrosphere, lithosphere and biosphere through natural mobilization processes [3, 11]. De Treville [12] estimated the average lead content of the earth's crust to be 16 ppm with acid rocks containing more than basic rocks in the ratio of 20:8. Subsequent distribution of lead in the environment results from natural process and anthropogenic activities [13]. Florea and Biisselberg [13] classified the main anthropogenic sources of lead as fossil fuel combustion, industrial and agricultural processes. The major outdoor sources of lead emissions include aircraft fuel combustion, stationary point and area fuel combustion, autobody refinishing, secondary lead recycling, cogeneration plants, sawmills and paperboard mills, incineration, foundries and steel mills, paints and coatings, battery manufacturing and cement manufacturing [16].

Lead is used in manufacturing storage batteries and alloys of lead are employed in bearings, brass and bronze and some solders, sheets and pipe for nuclear and X-ray shielding, cable covering, noise control materials,, chemical resistant linings, ammunitions, ceramic glazes, plastic stabilizers, caulk and paints [5]. In 2003, primary and secondary lead production was 0.245 and 1.15 million metric tons in the United States respectively whilst world production in 2002 amounted to 2.91 million metric tons [5,21].

Lead as a component of natural minerals is ubiquitous in the environment. It is present in all kinds of soil in a wide range of concentrations. The average lead content of the upper continental metamorphic rock combined with magma intrusions for an unpolluted earth crust is 17 ppm on a worldwide scale [2], Lead background levels have

increased to thousands of ppm soils close to very busy roads or near smelters. Sauvé *et al* [27] notes that most urban soils in industrialized nations have total Pb levels above the geochemical "background levels" of 10-20 mg of Pb per kg as a result of anthropogenic Pb emissions [26]. Lead is sparingly soluble in water but it is capable of forming complexes with chloride, hydroxyl ion and it forms molecules with carbonates, sulfides, phosphates and organics ligands thus increasing the possibility of lead mobility through the soil profile [26-28]. Godelitsas [38] notes that, the chemical mobility of lead in the environment and its harmful effects are mediated via aquatic pathways which include surface and underground waters. They report that major water quality problems are associated with non-point sources of pollution including lead which are comprised agriculture, forestry, mining, construction, livestock feedlots, urban runoffs and roads. In 2004 the EPA [40] reports that a total of 121,760 pounds of lead or lead compounds were discharged to surface waters. Freshwater systems have a greater tendency to transport dissolved lead than marine systems. This is largely due to a higher inorganic and organic suspended material available in fresh aquatic systems. As a result, movement of lead in freshwater is closely linked with turbulent transport of particulate matter [32]. According to Meyer *et al* [44], air in industrial and metropolitan areas is more contaminated with heavy metals than air from rural areas. The presence of lead in the atmosphere is due to both anthropogenic and a variety of natural sources [4, 32, 45]. Lead among other heavy metals such as As, Cd, Co, Ni, Sb, V, Zn are characterized as road-specific metals. Because they are mostly derived from combustion residues and losses from fuels, engines and transmission oils, tire abrasions, brake linings, exhaust catalysts, road pavement and corrosion of galvanized protection barriers [46]. The half-life of lead in the atmosphere is

typically short. This can range from several hours to several days. Lead is removed from the atmosphere via wet, dry or cloud or fog deposition and this deposition is highest near the source as a result of large particle precipitation.

Routes of lead exposure are closely associated with environmental lead sources. Lead entry into the body may be by drinking water, ingestion of food, breathing lead particulates or by dermal contacts. Lead contaminated soil could provide a direct route of lead ingestion for infants or indirectly via contaminated food. According to Romieu *et al* [24], inhalation or ingestion of dust and soil contaminated with lead can play a crucial role in the total body burden of lead in children. In the US, leaded-gasoline contributes significant levels of lead to air and top-soil until it was banned in 1995. It has been estimated that for each  $1\mu\text{g/m}^3$  rise in airborne lead levels, a child's average blood lead level increases by 5-6 µg/dl [5]. Other routes of lead exposure include dishware (i.e. pottery, crystal or commercial dishware), lead based solder cans, children's toys, household products like wicks, and vertical blinds and car keys.

Lead intake and absorption routes are determined by the routes of exposure. Castellino and Castellino [2] summarized the routes of Pb intake and absorption as being via respiratory tract, gastrointestinal tract, skin and placenta. Lead particles absorbed via the respiratory tract are eventually deposited in the lung where they are cleared through sequestration by alveolar cells or through the lymphatic vessels to the lymph nodes or it may dissolve in the tissue fluids and pass into the blood [3]. According to Ragan [69], the primary route of entry metal pollutants into the body is the gastrointestinal tract. Dietary intake of lead from recycled Pb in the form of contaminated meats and plants leads to direct intake of lead. Also, Pb traces may be present in drinking water, milk or beverages

as another direct Pb-consumption. In addition, lead can be ingested by infants in the form of contaminated soil, dust or chipped paint. Pregnancy and lactational periods are probably an important period of lead exposure for both the unborn infant and a child on breast milk [118-121]. Lead is mobilized during pregnancy because the maternal bone is resorbed in order to produce the fetal skeleton.

Although the precise mechanism of lead and other trace metal absorption is not entirely understood it is thought to involve both active and passive transport mechanisms [70-72]. Intestinal lead absorption is observed in all parts of the intestine with the most significant portion occurring in the small intestine [2, 77]. Important parameters influencing the absorption of Pb include ingested metal form, environmental matrix, gastrointestinal tract contents, diet, nutritional status, age and in some cases genotype [78, 79]. The concentration of lead in tissues accumulate in the decreasing order of bone > kidneys  $>$  liver  $>$  brain  $>$  muscle [88]. Lead levels in the body are speciated into two primary pools and these have varied rates of turnover. The slowest and largest pool is found in the skeleton with resident time of more than 20 years. The more labile pool of Pb is found in soft tissues and has a consequent half-life of about 20 days [89, 90]. The primary routes of lead excretion are through the urine or feces though bile and secretions by glands such as salivary, pancreatic, sweat and mammary play a much lesser role in clearing Pb from the body [80, 92-93].

The health effects associated with Pb exposure reported in the literature are numerous. These range from unobservable symptoms to extreme cases of death in exposed victims. Health effects may be manifested via neurobehavioral, cancer, genotoxic, reproductive, developmental and immunological changes [5].

Several molecular and cellular mechanisms of Pb actions have been documented to explain the processes through which lead exerts its negative cellular and molecular influences. Lidsky and Schneider [198] classified Pb neurotoxicity mechanisms as being both direct and indirect while Goyer [196] defined them as being morphological and pharmacological. The neuropharmacological interactions of Pb include substitution for calcium, iron and zinc, increased neurotransmitter release, protein kinase C activation, Na-Ca ATPase inhibition and alterations in energy metabolism. Morphological interactions of Pb on the other hand consist of interference with cellular adhesion molecules, impaired cell: cell programming connections and miswiring of the neurons in the central nervous system. Various studies have examined the role of  $Pb^{2+}$  on messenger RNA (mRNA) expression. These studies have been designed to either explore pathways that involve the production of reactive oxygen intermediates since the literature is emphatic concerning the increased cellular oxidative stress observed due to lead toxicity or the mitogen-activated protein kinase (MAPK) family because activation of some members of this protein family could lead to activation of transcription factors and to apoptosis. Several genes transcripts are reported in the literature to be regulated by Pb exposure either directly or through some other consequential metabolic pathway. In recent years, studies involving Pb have shifted focus to elucidating how Pb regulates mRNA transcription. The greatest challenge of this approach is that until very recently readily available methods allowed the examination of only a single gene at a time. Fortunately, the completion of the human genome project has lead to the emergence of DNA microarray technology. The emergence of DNA chip technology has dramatically increased the number genes that can be studied simultaneously. This technology has

afforded toxicologists the opportunity to study thousands of genes at the same time thereby facilitating the ability to examine pathways and to associate transcription factors with target genes [209]. The acceptance of DNA chip technology for examination of molecular and cellular processes is demonstrated by the increasing number of published literature that employed this technique. The primary objective of this dissertation project is to analyze global gene expression patterns that occur in Fisher 344 rat liver exposed to varying levels of lead for different periods of time, with the hypothesis that effects associated with Pb exposure are both exposure and time dependent and that several genes will be repressed with the most important being mRNA transcripts associated with calcium signaling. The specific experimental goals are;

- 1. Assess  $Pb^{2+}$  distribution in blood, liver, kidney and bone marrow
- 2. Assess  $Pb^{2+}$  interaction with trace metals such as Ca, Zn, Cu, Co and Ni in blood, liver, kidney and bone marrow
- 3. Assess lead effects on the cells of the liver and kidney
- 4. Assess large-scale gene expression profiles
- 5. Determine differential gene expression levels
- 6. Identify likely molecular targets of lead intoxication
- 7. Assess large-scale view of perturbations involving cellular and molecular pathways

Using DNA chip technology, we have been able to confirm the responses of genes already known to be regulated by Pb toxicity but also to identify new mRNA transcripts that are targets of lead poisoning. We have also been able to observe some pathways that

are important in lead toxicity giving us the opportunity to hypothesize new mechanisms by which the toxicity of lead occurs.

### CHAPTER II

### LITERATURE REVIEW

### Lead Background Information

### Historical Background

The most ancient and relevant environmental poison to be used by man from natural processes is lead. According to Jemigan *et al* [1], hundreds of millions of people have been affected by the toxicity of lead during the last 4500 years either as mining slaves, or as consumers of adulterated wine and food or as mere breathers of urban air. There is written and archeological evidence that lead was used widely in the ancient world. For instance in the tribute lists of Pharaoh Thutmosis III (1500 BC), there is a mention of captured lead, which his armies are known to have brought home from Mesopotamia. Jemigan *et al* surmised that it could be used to trace the anatomy and evolution of engineering technology of man since its use can be dated back as far as the beginning of civilization some 12,000 years ago.

Even before the beginning of the metal age around 3500 BC, human activities been associated with metals. This age marked the discovery of copper in its natural state and lead which can be extracted easily from mineral ores [2]. Lead is one of the seven principal metals of antiquity [3] and it has followed the Euro-Asian and American **civilizations at** least **in** part **since their beginning. Copper and lead beads, rings and** pendants were found in Catal Huyuk (Turkey) dating back to the seventh century BC. At about this time, lead minerals such as galena were employed in the extraction of silver

which often is found combined with lead. The oldest known metallurgic process called cupellation was typically used in separating lead from its noble partner silver [1].

It is probable the toxic effects of lead might have been known for almost as long as lead has been used [4, 7], Waldron [7] quoting Pliny says 'For medicinal purposes lead is melted in earthen vessels ... whilst it is being melted the breathing passages should be protected ... otherwise the noxious and deadly vapor of the lead furnace is inhaled; it is harmful to dogs with special rapidity'. Pliny also said 'red lead is a deadly poison and should not be used medicinally'. Also, Vitruvius from the first century wrote 'water is much more wholesome from earthenware than from lead pipes. For it seems to be made injurious by lead because cerruse ( $PbCO<sub>3</sub>$ ) is produced by it; and this is said to be harmful to the human body. Thus if what is produced by anything is injurious, it is not doubtful but that the thing is unwholesome in itself. One symptom exhibited by the workers with lead who had complexions affected by pallor. For when, in casting, the lead receives the current air, the fumes from it occupy the members of the body and rob the limbs of the virtues of the blood. Therefore it seems that water should not be transported in lead pipes if we desire to have it wholesome (quoted by Waldron) [7]. In fact some authors believe the fall of the Roman Empire was due in part to lead poisoning. They report such adverse effects as blindness, insanity and sterility [8, 9].

As Smith [4] rightly wrote, 'the history of lead is that knowledge of lead toxicity and the effects of lead have been periodically ignored and then (on occasions) rediscovered'. McCord [10] describes it as an 'aping disease' because of the wide range of symptoms which it may produce and the number of other diseases which it may

imitate, and this may be the most important reason why the cause was often not recognized.

#### What is Lead?

Lead originally appears shiny silver luster although it quickly weathers taking on its usual dull grey-bluish color. It is naturally occurring element with a chemical symbol of Pb and an atomic weight of 207.2 amu deduced from its stable isotopes with atomic weights 204, 206, 207, 208 amu. Their respective abundances are  $1.35 - 1.5$  %,  $23.5 -$ 27 %, 20.5 - 23% and  $51 - 53$  %. These isotopes are decay products of radioactive elements. Lead 206 from uranium, 207 from actinium and 208 from thorium [4, 5].

Unlike gold, silver or copper, lead does not exist in its metallic form in nature so that all lead is obtained from ores. Galena (lead sulfide) found as a shiny black metalliclooking stone is the principal lead ore. Other weathering products of galena found nearer the surface are cerussite (lead carbonate), anglesite (lead sulfate) and less commonly crocoite (lead chromate) and wulfenite. Approximately 0.002 % of the earth's crust is lead. These are localized into deposits sufficient enough for mining. Lead ore deposits are widely distributed across all five continents [6]. These ores are extremely abundant in the US, Spain, South America and China [1].

All the many forms of lead can be simply divided into lead in metallic form and lead in chemical compounds. Metallic lead form may again be subdivided into unalloyed and alloyed lead. Unalloyed lead is lead with no intentional addition of other metals although there is no such thing as 'pure' lead. Alloys of lead are formed from controlled addition of other metals to lead for example to make tin. Lead compounds are either

inorganic or organic. A principal example of organic lead compounds are tetra-ethyl lead and tetramethyl lead previously used as anti-knock additives in gasoline [4].

All the various forms of lead may exhibit different physical and chemical properties. Lead can be found in Pb(0), Pb(II) and Pb(IV) states, with the Pb(II) state being the most common in the environment. Under extreme oxidizing conditions, Pb(IV) compounds are found whiles organolead chemistry is dominated by the tetravalent oxidation state. Among metals, it is unique in being very soft and malleable but has virtually no elasticity and little mechanical strength. The heavy dense nature of lead coupled with its lack of mechanical strength and softness gives lead a tendency to flow or creep under its own weight. Lead carbonate forms a film on the surface via reaction between lead and air thus making lead resistant to corrosion. This protective film gives lead its dull grey appearance [4, 5]. Metallic lead is solid, melts at 327.4 °C, boils at 1740 °C, at 20 °C has a density of 11.34 g/cm3, at 25 °C is insoluble in water and a vapor pressure of 1.77 mmHg at 1000 °C. lead is commercially valuable because it is easy to cast, density is high, melting point is low, low strength, fabrication is easy, resistant to acid, electrochemical reaction with sulfuric acid and chemically stable in air, water and soil [18-20],

### Sources of Lead in the Environment

Heavy metals and compounds are natural constituents of the environment moving between atmosphere, hydrosphere, lithosphere and biosphere because the earth's crust provides natural mobilization source [3, 11]. De Treville [12] estimates the average lead content of the earth's crust to be 16 ppm with acid rocks containing more than basic rocks in the ratio of 20:8. The subsequent distribution of lead in the environment is as a result of natural process and anthropogenic activities [13].

According to Patterson [14], six most significant natural lead sources in their increasing order of importance are; meteoric smoke, aerosolic sea salts, forest fire smokes, volcanic silicate smokes, volcanic halogen aerosols and silicate dust from natural soils. Some important natural process contributing to lead distribution within the ecosystem include volcanoes, erosion, spring water and bacterial activity.

Florea and Büsselberg [13] classed the main anthropogenic sources of lead as fossil fuel combustion, industrial and agricultural processes. Table 1 below shows the annual lead production in the United States from 1999 through 2003.

### Table 1

### U.S Lead Production (metric tons) from 1999 to 2003 [5].



From this data, the main source of lead to the US market is recycled lead. Han *et al* [15] shows estimates of actual and cumulative global lead production.

These authors estimate that in 2000, the cumulative industrial age anthropogenic global production of lead was 235 million tons whiles lead burdens per capita in the same year was 38.6 kg [15].



Figure 1: (A) Actual global annual industrial age lead production and (B) global cumulative industrial age lead production [15].

The major outdoor sources of lead emissions include aircraft fuel combustion, stationary point and area fuel combustion, autobody refmishing, secondary lead recycling, cogeneration plants, sawmills and paperboard mills, incineration, foundries and steel mills, paint and coatings, battery manufacturing and cement manufacturing [16].

#### Lead Use History

Lead use dates back to ancient times. All the various civilizations from the Egyptians, Phoenicians, Greeks and Romans have found lead useful in everyday life in one way or another  $[1-2, 4]$ .

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For example Lucas and Harris [17] reported that the Egyptians employed metallic lead for small human and animal figurines, sinkers of fishing nets, rings, beads and other small ornaments, model dishes and trays, vessels, tanks and plugs. During these times, the Babylonians used it in building hanging gardens. Lead carbonate or cerussite was used in enamel for glazed pottery and in cosmetics tot whiten the face [2]. Similarly, the Greeks collected water from lead roofs, transported water through lead metal gutters to lead-lined cisterns. They also used iron clamps embedded in lead metal in stabilizing stone building blocks, ships sheathed with lead metal to repel wood-worms and salves, ointments, paints and cosmetics were made from lead compounds. Also, grape sugars were boiled down in lead pots and added to wines to reduce souring and lead-tin alloys were widely being used to line the inside of bronze utensils to keep copper out of foods and liquids [1].

The levels of lead use previously are nothing compared to the Roman era. The Romans were reported to extract lead from several countries of the Empire, Gaul, Britain and Germany but their most important source was Spain. In the  $1<sup>st</sup>$  and  $2<sup>nd</sup>$  centuries, it is estimated the annual lead use in Italy was nearly 0.004 ton of lead/person/year [1, 3]. The Romans extensively used lead in lining their aquaducts and water reservoirs. Like the Greeks their lined their bronze cooking pots with lead. This eliminates the bitterness associated with unlined bronze pots as well producing sweeter tastes in food [3].

With the fall of the Roman Empire, interest in lead declined dramatically until the beginning of the modem era, possibly because no new knowledge with regards to lead applications was discovered. Lead was used in the same applications as in ancient times and also in new areas. Lead sheeting was used in construction to cover public buildings

and cathedrals in France, Italy and England. It was used in the art of glassmaking, printing, medicine, lead smelting, paints, varnishes, pigments and additive in gasoline. Lead is also used in the following areas; low-solubility lead glazes in the pottery industry, lead arsenate in the manufacture of insecticides, borate in the manufacture of certain plastics and pipes, cisterns, roof coverings and metallization of wires [2].

In summary, lead is also used in manufacturing storage batteries, alloys of lead employed in bearings, brass and bronze and some solders, sheets and pipe for nuclear and X-ray shielding, cable covering, noise control materials, chemical resistant linings, ammunitions, ceramic glazes, plastic stabilizers, caulk and paints [5].

### Production. Disposal and Regulations

Galena (PbS) is the principal lead ore. Lead oxide is reducible at temperatures below 800 °C. This process simultaneously results in the reduction of galena to its oxide form with the subsequent reaction with unchanged galena to yield metallic lead. The reaction is shown below [3];

 $2PbO + PbS = 3Pb + SO<sub>2</sub>$ 

The bulk of lead produced currently is secondary lead. Primary lead is lead obtained directly from the mines. Secondary lead is obtained from recycling of manufactured products containing lead such as lead-acid batteries or lead-metal scrap. Table 2 below provides statistics on the current US and global lead production levels **[**21**]-**

The increase in secondary lead production is a useful way of lead disposal. Larrabee [22] points out that no other metal has a recycling rate comparable to lead. For example in 2002, 81 % of refined lead produced in the United States was recovered from recycled scrap. The majority of the lead recycled comes from lead-acid batteries. About 6 % of recycled lead comes from such sources as building construction materials, cable covering, and solder [5].

#### Table 2





There are several federal and state regulations guiding the disposal of waste containing lead or lead compounds. Lead is listed as a toxic substance under Section 313 of the Emergency Planning and Community Right to Know Act (EPCRA) under Title III of the superfund Amendments and Reauthorization Act (SARA). Waste products made of lead comprise storage batteries, lead-based paint, ammunition waste, ordnance, sheet lead, solder, pipes, traps, solid waste and tailings from lead mining, solid waste created by mineral ore processing, iron and steel production, copper and zinc smelting, and production and use of other lead-containing products [5, 23].

### Mode of Toxicity

### Lead in Air

According to Meyer *et al* [44], air in industrial and metropolitan areas is more contaminated with heavy metals than air from rural areas. The presence of lead in the atmosphere is due to both anthropogenic and a variety of natural sources [4, 32, 45], Lead among other heavy metals such as As, Cd, Co, Ni, Sb, V, Zn are characterized as roadspecific metals. Because they are mostly derived from combustion residues and losses from fuels, engines and transmission oils, tire abrasion, brake linings, exhaust catalysts, road pavement and corrosion of galvanized protection barriers [46]. This is shown in the rapid decline in atmospheric Pb deposition to terrestrial and aquatic ecosystems since the ban on lead use in gasoline [49]. The half-life of lead in the atmosphere is typically short. This can range from several hours to several days. A residence time of lead is particle size dependent. Size also accounts for the length of transport of these lead particles and their ability to penetrate into the lungs. Lead is removed from the atmosphere via wet, dry or cloud deposition and this deposition is highest near the source as a result of large particle precipitation. Obviously wet deposition is relatively important during wet seasons as dry deposition accounts for most lead removal from the atmosphere in summer dry seasons. Lead eventually ends up on land or in aquatic systems with the possibility of polluting ground water [4, 32, 45]. Miller and Friedland [49] reporting from several sources showed that lead concentration due to precipitation in the north-eastern U.S. was greater than 30  $\mu$ g/L in the 1960s and early 70s but reduced to 17  $\mu$ g/L by 1982 and further declined to less than  $2 \mu g/L$ .

In fact the residence time of 0.1-2  $\mu$ m size aerosol was estimated between 3 to 7 days with the capacity for atmospheric transport over several thousand kilometers [46]. Miller and Friedland [49] agreed by saying significant amount of Pb is released as volatile compounds or sorbed on fine aerosols which can be circulated into the upper troposphere and transported thousand of kilometers due the relatively long residence time. This is confirmed by elevated Pb levels documented in Greenland and polar snow and accumulated concentrations in sediment, peats and organic horizons of forest soils since the introduction of leaded-gasoline. Lead is reported to fall within this category of heavy metals that closely associate with fine dust. Zereini *et al* [46] found in their study of airborne heavy metal concentration and distribution in Frankfurt am Main, Germany that As, Cd, Pb and V were part of the fine particles of diameter  $\leq 2.1$  µm. It should be noted that fine particles of diameter less than 10 microns are the main fraction of airborne aerosols. This constitutes about 80 % of aerosols [47]. The above observation was also reported by Samara and Voustsa [47] who studied the association between particulate matter and heavy metals. According to them, heavy metals showed three distinct behaviors with regards to size distribution. Lead and cadmium masses resided within the accumulation mode, Ni, Cu and Mn were distributed between fine, intermediate and coarse modes whilst Fe was reported to fall in a diameter larger than  $2.7 \mu m$ . Apart from physical speciation by size, chemical speciation of lead in air include soluble and exchangeable metals, carbonates, oxides and reducible metals; oxidizable and sulfidic metals bound to organic matter and residual metals [48].

### Lead in Soil

Kaste *et al* [26] reports that soils in the northeastern United State receive total atmospheric lead concentrations of 1 to 4 g Pb per square meter in remote environments. According to these authors, the forest canopy serves as an initial recipient of atmospherically delivered Pb or dissolved Pb in rain which is retained. Subsequent litterfall and decomposition leads to enriched lead-organic layer overlying the mineral soil. Forest floor Pb contents have been documented to range from 75 to 300  $\mu$ gg<sup>-1</sup> and this is typically one or two orders higher than parent material Pb concentration [33, 34].

Lead is sparingly soluble in water but it is capable of forming complexes with chloride, hydroxyl, carbonates, sulfides, phosphates and organics thus increasing the possibility of lead mobility through the soil profile [26-28]. Lead has been observed observed to be stable in soil. Experiment have been conducted to determine the stability constant for lead and a host of other metals in their association with anionic microbial surfactant, rhamnolipid, using ion-exchange resin technique. The Pb-complex was found to be more stable than  $Cd^{2+}$ ,  $Zn^{2+}$ ,  $Fe^{2+}$ ,  $Hg^{2+}$  and  $Ca^{2+}$ . Only  $Cu^{2+}$  and  $Al^{3+}$  are stable in the list of metals tested [30]. There is evidence to suggest that some fraction of Pb has been moving into the mineral layer beneath and others have pointed out that lead is moving in association with soil organic matter [26, 33-35], Thus mobilization of organic matter as dissolved or particulate will determine to a great the extent Pb mobility in soil. This was confirmed by Marsh and Siccama [34] who showed decreased lead levels with soil depth and reduced organic matter content. They reported decreasesin Pb concentrations from 350 mg cm depth<sup>-1</sup> m<sup>-2</sup> at 0-2 cm depth to 102-108 mg cm depth<sup>-1</sup> m<sup>-2</sup>  $2$  between 10 and 20 cm depth. At all the sites tested, lead concentrations with depth were
correlated with decline in the amount of organic matter. Also they estimated that 35 % of presumably anthropogenically received lead was in the forest floor and the rest 65 % in the upper mineral layer.

Knowledge of the processes involved in trace metal speciation is essential in estimating metal bioavailability and risk assessment strategies. This is even more important when one realizes that total metal concentrations in soils are poor indicators of metal toxicity because metals exist in varied solid-phase forms [37]. Besides metal bioavailability, biological uptake and ecotoxicological effects on soil biota is better understood by understanding chemical speciation. For example, in contaminated soils, Pb is insoluble, precipitated or bound to soil colloids. Short-term plant available lead is the lead in the soil solution whiles long term bioavailable lead will depend on lead-bearing minerals like carbonates, phosphates or sulfides [27] in addition to the effect of principal soil chemical properties like organic matter and pH. Sauvé and McBride [27] observed that higher solution pH increased organic matter solubility which is likely to induce dissolution of lead phosphate by organic complex reactions. An optimum pH of 5.5 to 6.5 is required to reduce solubility, mobility and bioavailability after soil amendments and lime application [27].

Lead can be toxic to plants and soil microorganisms. Lead is known to cause harmful effects on the physiology and biochemistry of plants and as a result lowering yield [36]. Also laboratory experiments provide evidence that as low as 200 mg kg-1 of lead can disrupt organic matter decomposition and associated N and P mineralization in ecosystems [26]. Mishra and Choudhuri [36] reports that treating rice seeds with lead resulted in decreased germination percentage, germination index, shoot and root length,

tolerance index, vigor index and dry mass of shoot and root but increased percentage phytotoxicity.

## Lead in Aquatic Systems

Godelitsas [38] notes that, the chemical mobility of lead in the environment and its harmful effects are mediated via aquatic pathways which include surface and underground waters. According to them, this is strongly correlated with interactions with different geomedia represented by rocks, soils and their mineral components. Chang and coworkers [39] agreed with this assessment. They reported that major water quality problems are associated with non-point sources of pollution including lead which comprises agriculture, forestry, mining, construction, livestock feedlots, urban runoffs and roads. In 2004 the EPA [40] reported that a total of 121,760 pounds of lead or lead compounds were discharged to surface waters. Surface water includes discharges to streams, rivers, lakes, oceans and other water bodies. The primary sources of lead in rivers are runoff and direct deposition from air (mostly anthropogenic) or erosion (natural). Similarly, most of the lead in oceans is from atmospheric deposition except in estuaries and some coastal waters where riverbome lead, direct dumping of sewage and industrial wastes become the major sources of lead [4, 32].

Freshwater systems have a greater tendency to adsorb dissolved lead than marine systems. This is largely due to a higher inorganic and organic suspended available material in fresh aquatic systems. As a result, movement of lead in freshwater is closely linked with turbulent transport of particulate matter [32]. Much of the lead deposited in seas and oceans end up at the bottom. In fact, this is one way by which past lead use is

determined from sediments. Because of high chloride concentration and lower concentration of particulate matter, much of the lead is in the dissolved form and thus may be bound by salts so that it ends up as marine deposits [4, 32]. In freshwaters, F, Cl,  $SO_4^2$ , OH<sup> $\cdot$ </sup> and  $HCO_3^{\circ}$  are the most important ions responsible for metal uptake. The tendency of these ligands to bind to lead and thus control its bioavailability depends on pH in open waters and electron donor/acceptor in sediments [41, 42, 43]. For instance in sediments, bacteria use oxidized forms of metals as electron acceptors to produce soluble metallic ions.

#### Lead Cycling in Soils and Surface Waters

Lead is considered a good indicator of pollution for the following reasons. It is easy to analyze, non-mobile in natural environmental archives like lake sediments, it is emitted from different kinds of sources such as mining and metal industry and by fossil fuel burning. Analyzing lead in sediment time-series can provide a broad picture of atmospheric pollution as well as chronology of lead pollution [57]. Lead is thought to enter the ecosystem via precipitation and dry deposition in particulate form [50]. As a result, Pb is deposited at places far from the principal source of contamination. There have been documented cases of forests in remote areas and higher elevations showing lead levels greater than expected background concentrations [51, 52]. Wet deposition is primarily in the form of rainfall at low elevations or cloudwater interception at high elevations or dry deposition contributing about 20 *%* of total Pb flux in some regions [50]. Increased lead levels were observed in the organic horizon at high elevations of forest soils because of greater precipitation and deposition at these elevations [50, 53].

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The over 3000 years of metal use in one form or the other has resulted in accumulation of heavy metals in the environment. In the organic horizon overlying the forest mineral soils of podzol (soils that are acidic with characteristics of circumpolar boreal forest coniferous forests that cover large regions of Fennoscandia, Russia and North America. Podzols are stratified into a surficial organic horizon (O horizon), which is a humus layer, also called the mor layer, which covers the mineral soil like a blanket, a gray eluvial horizon (E horizon) where A1 and Fe are leached, a dark illuvial horizon (Bs) where Al, Fe and organic complexes have accumulated below a gradation into unchanged parent mineral soil C horizon) [58], typical Pb concentration values fall between 50 mg  $kg^{-1}$  and 100 mg  $kg^{-1}$  which most authors consider to be about 1000 times greater than natural background Pb content. Lead inventories in Swedish boreal forest soils range from 0.5 to above 3 g Pb per square meter  $[54-57]$ . Natural background Pb concentrations in these soils are assumed to be in the range of 10-15  $\mu$ g g<sup>-1</sup>. Current levels range from 40-100  $\mu$ g g<sup>-1</sup> [55].

Most researchers in the past thought lead was strongly retained in the organic horizons. Data over the last two decades show otherwise. Pb levels on the forest floors of a number of eastern North American sites have decreased by 20-40 % over the last 20 years [49, 59]. This rapid movement loss of Pb from the forest floor has lead to concerns that it might also move rapidly through the soil profile resulting in groundwater contamination. [49]. It has been estimated that the large quantity of Pb deposited in North America after the 1960s might begin to be released into upland streams sometime in the middle of the 21<sup>st</sup> century. Pb transport velocities in forested soils have been documented to range from 0.39 to 0.83 mm year-1 in over 40 sites across Europe, 5 mm year-1 in Mediterranean soils and between 8.2 and 19.7 mm year-1 at Vermont, USA [49, 60-62]. In a study to assess the vertical distribution of lead in Swedish boreal forests, the authors reported that lead was distributed across the profile of an undisturbed forest soil whereas the agricultural revealed completely opposite pattern. Pb concentration was between 60- 100  $\mu$ g g-1 in the mor layer in southern Sweden and about 30  $\mu$ g g-1 in northern Sweden as well as moving down to 20 and 60 cm. According to these authors, the largest pollution of Pb was observed at the Bs horizon. On the agricultural soil, all the lead was evenly distributed in the 20 cm thick topsoil [56].

The key determinant of metal biogeochemical cycling is their chemical form which in turn determines bioavailability and mobility in the various media. Common lead fractions employed in its fractionation include water soluble and exchangeable. Carbonate, Fe-Mn oxides, organic carbon and residual Pb [63, 64]. In site previously employed in discharging batteries, 42.5-44.5 % of the soil surface Pb was associated with the carbonate fraction. Lead in both the carbonate and water soluble and exchangeable fraction was more than 50 % indicating that a substantial portion of the Pb might be available for plant uptake [64].

In a similar study, Huang and Matzner [65] investigated the biogeochemistry of trimethyllead (TML) in a forested ecosystem in NE-Bavaria Germany. Tetraalkyllead compounds undergo the following sequence of decomposition in the environment:  $R4Pb \leftrightarrow R3Pb^+ \leftrightarrow R2Pb^{2+} \leftrightarrow Pb^{2+}$ . They observed lead concentration of 11.56 mg ha<sup>-1</sup> and 222 mg ha<sup>-1</sup> for TML and total-Pb respectively. They estimated the annual total deposition (sum of throughfall and litterfall fluxes) from the atmosphere at 52 g ha<sup>-1</sup> year<sup>-1</sup> <sup>1</sup> for total-Pb and 3.7 mg ha<sup>-1</sup> year<sup>-1</sup> for TML. More than 90 % of the soil storage of TML

was found in wetland soils representing 30 % of the area understudy and it seems to stable under anoxic conditions. TML was observed to degrade relatively rapidly in the forest floor. It had a half-life of 33.5 days in the O-horizon, 421 days in the E-horizon and 612 days in the mineral soil. Adsorption affinity for was highest in E-horizon followed by organic horizon and then the mineral layer. The adsorption capacity of TML and  $Pb^{2+}$ depended on the type of soil. In predominantly organic layers,  $Pb^{2+}$  was more adsorbed thereby increasing the tendency of TML to be mobile. On the contrary, in soils having high cation exchange capacity TML is more strongly adsorbed.

In another investigation in Canada to examine lead biogeochemistry in the littoral zones of south-central Ontario lakes using lead isotopes, the authors concluded that "the exchange of Pb between lakewater and sediment 'carbonate', and subsequently between 'carbonate', 'oxide' and other sediment fractions was the most likely water-sediment pathway of lead movement. pH controlled Pb fractionation within surficial sediments, with the 'organic' pool comprising 80-97 % of total Pb in most acidic lakes and 15-60 % in alkaline lakes. About 28 % of the Pb in Nymphea odorata shoots was accumulated directly from waters and sediments. Plant Pb isotopes strongly resemble the historical Canadian atmospheric (alkyl Pb) signature. A possible explanation is that, like essential trace metals, historically accumulated Pb was highly conserved during the annual growth cycle of this long-lived macrophyte, being stored over-winter in underground rhizomes and recycled into spring growth. Given the low rate of 'new' Pb uptake, historical alkyl Pb may continue to dominate plant tissues for some time, even though it was not detectable in littoral waters and sediment" [66].

#### Human Lead Exposure Routes

Routes of human lead exposure are closely associated with environmental lead sources. Lead entry into the body could be by drinking water, ingestion of food, breathing lead particulates or by dermal contacts.

Lead contaminated soil could provide a direct route of lead ingestion for infants or indirectly via contaminated food. According to Romieu *et al* [24], inhalation or ingestion of dust and soil contaminated with lead can play a crucial role in the total body burden of lead in children. In the US, leaded-gasoline used to contribute significant levels of lead to air and top-soil. It was estimated that for each  $1\mu g/m^3$  rise in airborne lead levels, a child's average blood lead level increases by 5-6 pg/dl [5]. Since the decrease in use of leaded-gasoline in the mid-1970s, there has been a decline blood lead levels [25] but food grown on contaminated soils might have high lead levels. In a study conducted in Mexico, high levels of lead were reported in vegetables. In another study, these authors correlated blood lead levels to canned chili consumption [24]. Lead-based paint provides a direct route of lead ingestion for infants and children. Lead-based paint that is naturally broken down to smaller particles by moisture damage, friction, temperature fluctuations, exposure to acid liquids such as acid rain or by renovation activities can result in contaminated dust, soil and food, or toys [24, 25].

Drinking water provides another exposure route of lead. Drinking water contamination is as a result of plumbing solder. In the US, contamination from lead pipes, lead connectors and lead service lines is rare except in Detroit, Chicago, New York, Philadelphia and most older cities. Potential lead contamination could come from the wire mesh of the faucet when it traps solder particles. Presence of lead due to plumbing can be increased by whether the water is acidic or have mineral content. In Mexico City, lead levels in their drinking water are low due to the high alkaline pH of the water [24, 25].

Many lead-based products are banned in the U.S. but sometimes household items exhibit high lead levels because they were imported from Asia, Central or South America, Eastern European countries or Mexico. These routes provide direct ingestion by hand, dust or food.

Direct occupational exposures to lead can be common for those who work in lead smelting or fabrication into various products. They may also carry lead-contaminated dust on hair, clothing and shoes to their homes. Industries that work with and emit lead can cause lead contamination of air, soil and food produced from contaminated soil [25].

## Lead Remediation

Remediation of heavy metal contaminated soil and water is vital to our survival. This is why the number of articles on this subject has exponentially grown over the last two decades. The approaches to remediation range from engineering through use of plants to chemical means. Adoption of which method to employ depends on extent of pollution, speciation effectiveness of method and cost. Some of these methods are electrokinetic, capping and dredging, phytoremediation or phytoextraction, bioremediation, liming, sorption onto calcium carbonates, iron oxides or humic substances, membrane separation, solvent exchange and recently the application of nanomaterials, among others [151-155].

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Most of these methods, though they have been used for a long time, have one problem or another associated with them. The engineering techniques are simply very expensive and often not tenable on small scale. The other methods either turn to reduce their bioavailability for which long term implications and ever-changing weather pattern effects are still not entirely understood. The rest are not entirely efficient in removing these metals from contaminated media such as water or soil. As a result low cost, accessible and effective remediation alternatives are required. Interestingly, the area of nanotechnology seems to have opened a new chapter and possibilities of research into heavy metal remediation. It is showing a lot of promise with respect to cost, accessibility and efficiency in removing metal ions from polluted water and soil.

# Lead Absorption. Distribution and Excretion

Lead intake and absorption routes are determined by the routes of exposure. As previously mentioned under 'exposure of routes' section; lead entry into the body could be by drinking water, ingestion of food, breathing lead particulates or by dermal contacts. Castellino and Castellino [2] summarize the routes of Pb intake and absorption as via respiratory tract, gastrointestinal tract, skin and placenta.

Lead uptake through the respiratory tract greatly varies from urban to rural areas and to industrial environment. Lead intake via the respiratory tract is a function of particle size distribution, particle shape, solubility and rates of inhalation [2, 3]. Other parameters important in the deposition of lead particulates in the lung include age-related factors for example nose-breathing against mouth breathing, airway geometry and airstream velocity within the respiratory tract [67]. Deposition of particles in the respiratory

tract is determined by the size. In all nasal cavities, particles the size of  $10 \mu$  or greater are removed while particles about  $1 \mu$  in size are not removed that easily [3].

Particles can be deposited in respiratory tract by gravitational sedimentation, inertial impaction and diffusion or Brownian movements [2]. Gravitational deposition is important for large particles and mainly in the large bronchi. Inertial impaction occurs, when a particle undergoing laminar flow encounters and obstacle and suddenly changes direction. It is important for particles within the range of  $2-5 \mu m$ . Particles involved in inertial impaction are deposited on bronchial surface. Brownian movement is important for particles less than  $1-2 \mu m$  in diameter. These particles acquire a casual movement (Brownian movement) as a result of continual collision with other particles that cannot be compensated for and are thus transported to the alveoli by concentration gradient (from high to low). The compartments are first; nasopharynx or the upper respiratory tract; which begins with the anterior pharynx back and down through the posterior pharynx to the level of the larynx. Second is the tracheobronchial compartment that is "the trachea and bronchial tree down to and including the terminal bronchioles". These two constitute the entire of the epithelial area of the respiratory tract. The third is the pulmonary compartment which consists of respiratory bronchioles, alveolar ducts, atria, alveoli and alveolar sacs. These make up the functional areas of exchange space in the lung [2, 65].

Experiments to measure the half-life of submicron lead particle in the lung have reported values ranging from 6-11.5 hours. This lead to one author concluding that submicron lead is cleared from the lung within 24 hours of absorption. Lead particles from the lung are cleared via sequestration by alveolar cells or through the lymphatic vessels to the lymph nodes or it may dissolve in the tissue fluids and pass into the blood [3]. Similarly, Castellino and Castellino [2] categorized the Pb-particle clearance from the lung into two processes which are mucociliary and alveolar clearance. Clearance from the first two compartments nasopharyngeal and tracheobronchial is mainly by mucociliary process. The mucociliary process involves a type of transport in which particles are either shifted from the upper respiratory tract to the gastrointestinal tract or ejected as phlegm. It is a continuous shifting of a layer of mucus toward the esophagus at speeds ranging from mm/minutes or cm/minutes. Larger particles are deposited in the upper tract of the respiratory arbor for quick clearance whilst slower moving mucus particles are cleared slowly from the lower compartments. Alveolar clearing takes place in compartment three. The processes involved include; a) lead particles are transferred form alveolar compartment into mucociliary escalator vial the mechanisms of phagocytosis operated by alveolar macrophages, b) lead particles penetrate through the junctions of the alveolar pneumocytes to interstitial spaces and then into lymph and blood and c) particles pass into the pulmonary tissue where they might remain for a quite sometime [2].

According to Ragan [69], the primary route of entry metal pollutants into the body is the gastrointestinal tract. Dietary intake of lead from recycled Pb in the form of meat and plants leads to direct intake of lead. Also Pb traces may be available in drinking water, milk or beverage for another direct Pb-consumption. In addition, lead can be ingested by infants in the form of contaminated soil, dust and chipped paint. This is particularly important for infants within the ages of 6-24 months. Older infants also have a tendency to ingesting nonfood items which could be Pb-contaminated. Food groups that might be important in Pb transfer include vegetables, cereals, roots, tubers and fruits. Meat products and milk derivatives like cheese might equally be important.

Although the precise mechanism of lead and other trace metal absorption is not entirely understood it is thought to involve both active and passive transport mechanisms [70-72]. The calcium pump which employs active transport mechanism in channeling  $Ca^{2+}$  ions is reported to be replaced by other divalent cations including Pb and thus actively transported. In fact, Pb has been reported to be actively absorbed in the rat duodenum and also actively transported out of red blood cells [73, 74]. In a study to examine the evidence of Pb-active transport by calcium pumps using efflux from resealed human red cell ghosts, Simons [70] reports that there was an ATP-dependent net lead transfer from the cell interior to the outside. This author also observed that lead efflux was antagonized by internal calcium and is inhibited by vanadate with the same inhibition constant with which vanadate inhibits calcium pumping. These findings seem to be supported by Deane and Bradbury [72] who found evidence for efflux of  $Pb^{2+}$  from brain capillary cells via the  $Ca^{2+}-ATP$ ase. On the contrary, a study by Deane and Bradbury [72] using in vivo perfusion of Pb in rats revealed evidence for passive transport of Pb that is pH dependent and unaltered by the present of calcium ions. According to these authors, the transport species is  $PbOH<sup>+</sup>$ . Other possible mechanisms of Pb transfer reported of in the literature include Pb entry through voltage-gated  $Ca^{2+}$ channels in bovine adrenal medullary cells [75], lead uptake by red blood cells via anion transport probably as PbC**03** [76] or store-operated cation channels due to intracellular depletion of calcium stores [71],

Intestinal lead absorption is observed in all parts of the intestine with the most significant in the small intestine [2, 77]. Several factors are responsible for the extent of Pb absorption in the small intestine, perhaps the most important control level is the

intestinal mucosal cells. Primary absorption of Pb is the duodenum from where it enters the epithelial mucosal cells [69, 80]. Important parameters influencing the absorption of Pb include the ingested metal form, the environmental matrix, the gastrointestinal tract contents, diet, nutritional status, age and in some cases genotype [78, 79]. Increasing intraluminal doses causes a relative block of the mucosa cells and substances that increase the solubility of lead enhance its absorption. Iron, zinc and calcium reduce the absorption of lead without affecting its solubility most probably through the competition for shared absorptive receptors in the intestinal mucosa [77, 80-83]. According to Conrad and Barton [80] Pb does not seem to have a feedback mechanism because its total burden does not affect Pb absorption. Researchers have observed that during periods of rapid growth and in iron-deficient animal, lead absorption is greatly enhanced. Contrarily, the cumulative effect of iron-overload and starvation significant reduces lead absorption. A report by several authors showed that intestinal lead absorption in newborn animals and babies are greater compared to young and adults [83-87]. These authors found that lead absorption was inversely correlated with age by a factor of six- to eight-fold from more than 50 % to approximately 10 % or less between the ages of two weeks to eight years in humans.

The concentration of lead in tissues accumulate in the decreasing order of bone > kidneys  $>$  liver  $>$  brain  $>$  muscle [88]. Lead levels in the body are speciated into two pools and these have varied rates of turnover. The slowest and largest pool is found in the skeleton with resident time of more than 20 years. The more labile pool is found in soft tissues and has a consequent half-life of about 20 days [89, 90]. In a survey of lead levels of 60 corpses (four had occupational Pb exposure history) in 1970 by Barry and

Mossman [91], the authors observed distribution of Pb in soft, bone and blood as follows for the non-occupationally exposed group: adult men  $-$  soft tissues 9.5 mg (range 5.3-21.1), bone 152 mg (range 21.0-340.9), blood 162.2 mg (range 26.6-352.3), adult females - soft tissues 5.6 mg (range 2.6-8.4), bone 106.8 (range 12-236.6), blood 112.5 mg (range 18.8-243.7) and children – soft tissues  $0.55$  mg (range  $0.12$ -1.58), bone  $0.99$  mg (range 0.21-2.4), blood 1.53 mg (range 0.46-3.1). Blood Pb contributions from bone from three groups were 94.1 %, 94.9 % and 64 % respectively. Clearly the important of continuous availability of Pb due to ageing cannot be overestimated.

The most essential routes of lead excretion are through the urine or feces though bile and secretions by glands such as salivary, pancreatic, sweat and mammary play a much less role of clearing Pb from the body [80, 92-93]. Gulson *et al* [94] explains that renal excretion of lead is typically with glomerular filtrate with some renal absorption. Elevated blood levels will lead to augmentation by transtubular transport. Lead may also be excreted with body fluids like milk and for pregnant women; lead crosses the placenta and is transferred to the infant via cord blood. Conrad and Barton [80] employed radiolabeled lead in examining Pb excretion and observed that erythrocytes were important in transporting Pb with excretion occurring in the urine and stool and bile playing an important role in excreting Pb in the gut. Another study by Arai *et al* [92] investigating the excretion of organic lead after injection found that 4 % of administered Pb was excreted in via urine after 7 days post-injection while 68 % was excreted through the feces. According to these authors, approximately 85 % of urinary excretion was diethyllead and 92 *%* was inorganic lead in the feces.

# Lead Toxicokinetics

Toxicokinetic behaviors of lead govern its systemic exposure and associated toxic effects. Understanding the toxicokinetic behavior of Pb requires an interdisciplinary effort in biochemistry, mathematics, physiology and toxicology disciplines [95]. According to Mushak [95], toxicokinetics can be defined in of physico-chemical and mathematical terms or from the perspective of toxicology and epidemiology. The first definition is "the quantification of the rate and extent of lead uptake, distribution/redistribution among transport and deposition tissues, body and tissue retention and finally excretion through various routes". The second is "the biological and toxicological basis for the biological monitoring of lead exposure and the various doseeffect and dose-population response relationships that have been reported".

Lead toxicokinetics is important in quantifying Pb body burden and toxicity. Toxicokinetic models of Pb-uptake are useful in estimating Pb body burden and understanding lead movement between soft and bone tissues. Three models have been most used among toxicokinetic researchers and these include the Leggett model, EPA's integrated exposure uptake biokinetic model (IEUBK) and the O'Flaherty model [95-98]. Both Leggett and O'Flaherty models are physiologically based whilst the EPA's IEUBK is a descriptive model intended to reproduce blood lead concentrations in children up to sevens years of age using urban exposure patterns. A brief description of each of the models is provided below:

The Leggett model is physiologically based model that describes the timedependent distribution and excretion of lead that has been injected or absorbed into blood [98]. This model is implemented as a central plasma diffusible compartment which is linked to other tissues and organs within the body. This diffusible plasma Pb is the key central compartment through which Pb is transferred between other compartments of the body including fetus or breast milk. Some organs can be represented by more than one compartment. These compartments consist of bone ( $n = 6$ ), soft tissues ( $n = 3$ ), liver ( $n =$ 2), brain, kidney, urine, plasma protein, erythrocytes, extracellular fluid [99]. Pb transport between compartments is assumed to follow linear first-order kinetics as long as concentration in red blood cell (RBC) stays below a nonlinear threshold levels. If the RBC concentration of Pb exceeds the threshold value, the transfer rate from diffusible plasma to RBC is assumed to decline linearly with plasma concentration. However deposition fractions in other compartments will increase as a result of reduced competition from RBC but first-order transport between all other compartments are assumed to be maintained at all levels of exposure. Although this model provides a framework to address calcium-like elements, it is considered a starting point for Pb biokinetics in children or adults at high concentrations of exposure but it does not account for sex-related transfers [98, 99],

The US EPA IEUBK model adopts high adult Pb exposure values and applies it to children seven years and lower [100]. This pharmacokinetic model was developed to predict a) risk of elevated blood lead levels in children (under seven years of age) that are exposed to environmental lead, b) the probability that a child exposed to lead via some specified media will have a blood Pb concentration equal to or greater than the threshold value of 10  $\mu$ g/dL and c) preliminary remediation objectives for a contaminated media [97]. Thus this model is structured to relate environmental Pb concentration with potential blood levels in children via exposure, uptake, biokinetic and blood lead

distribution or variability modules [101-103]. Total or net exposure is quantified amount of lead inhaled or ingested from environmental media such as soil, house dust, drinking water, air or food in  $\mu$ g/g,  $\mu$ g/l or  $\mu$ g/m<sup>3</sup> typically multiplied by a term to account of amount of contact represented as  $g/day$ , m<sup>3</sup>/day or liters/day and a term for length of exposure usually days. Uptake refers to the amount of Pb absorbed per unit time from the gut or lung into the systemic blood circulation. Bioavailability or absorption fraction which is the fraction of lead entering the body via respiratory or GI tract is accounted for in the parameterization process. Uptake is measured in  $\mu$ g/day. The biokinetic module employs mathematical expressions to convert total lead uptake rate from the uptake component as an input for the central plasma-extracellular fluid compartment. Then transfer coefficients are used to model transfers between internal components and excretion pathways, thus changing concentration of Pb can be recalculated by combining all the input parameters. Variability in blood Pb distribution is addressed through the lognormal probability distribution [101-103]. Since this model was developed specifically for lead absorption in children, it cannot be used in predicting the impact of Pb exposure on adults Pb kinetics and extrapolations outside of the physiological age will be inaccurate because parameter values used to calibrate the model were strictly kinetic but not physiological [104].

The O'Flaherty model has an age-dependent volume, composition and metabolic activity of liver, kidney, well-perfused, poorly-perfused tissues and bone as compartments [105, 106]. This model uses fractional absorption values; 0.5 at birth to 0.08-0.11 by age 10 in the GI tract. In the lung typical values are 0.5 and these values are independent of exposure level. Pb clearance is set at 30 % from the liver and 70 % from

the kidney. Body clearances, cardiac output, organ and tissue volumes are dependent on body weight and degree of growth. The model takes into account age, body weight by using five-parameter expression that takes into consideration rapid growth at early childhood and accelerated growth at puberty. These values are different for males and females. Lead concentrations in the plasma determine the rate of transfer out blood and this relationship is controlled by capacity-limited Pb binding to erythrocytes. Pb movement between blood and tissues follow flow-limited exchange behavior with deposition in bone or return to plasma via bone resorption or slow exchange throughout bulk bone. Diffusion-limited process describes the slow exchange between plasma and bone. The exposure component of the O'Flaherty is similar to the IEUBK model except the background exposures are date dependent to reflect the marked reduction in Pb levels in air and food since the 1970s. A significant limitation of the model is that it is deterministic and its output does not include estimates of population distribution [96, 104-106].

Lead metabolism in the body is controlled by physiologic and metabolic processes and understanding these processes are crucial for predicting Pb partitioning and toxicity for an organism. Lead is partitioned between blood plasma and the red blood cell (erythrocytes) with this association determining the transport of Pb throughout the body [106, 107]. This relationship can be described as capacity-limited binding of lead by the constituents of erythrocytes. It is reported that Pb binds to constituents of erythrocytes such as hemoglobin, low-molecular weight proteins and to sites on the red cell membrane which are capacity-limited thus leading to changes in blood concentrations [108-109]. In a similar study which is more recent, inductively-coupled plasma mass spectrometry

showed a close association between plasma and red blood cell (RBC) lead with plasma became saturated under high exposure conditions. This situation was attributed to slow gradual saturation of binding sites on the RBC. They also reported that RBC Pb binds to delta-aminolevulinate dehydratase (ALAD), albumin and a-globulin [106,110-111].

Liver and kidney are important excretion pathways of lead as well as exhibiting higher concentration of this toxicant than other soft tissues. Lead rapidly accumulates in the liver between 10-15 % of systemic Pb although much of it is lost within a few weeks. Adults who have been exposed for long periods have 2-3 % of total-body lead in the liver and the ratio between blood to liver is 0.2 [98, 112-113]. Pb is lost from liver by biliary secretion into the gastrointestinal tract and a possible Pb recycled to blood. Rodents and dogs intravenously injected with radio-labelled Pb accumulate about 15-20 % in the kidney within the first 1-2 hours with a substantial portion of the early accumulation is reabsorbed or lost via urine. In the case of rats, the kidneys accumulated approximately 10 % of intravenously injected Pb after day and less than 2 % post-injection. Similarly, baboon kidneys contained 4 % after day 1, 0.6 % after 30 days and 0.1 % after 60 days post-injection of radio-Pb [98, 114-115]. Comparing the rate of Pb clearance from the kidney, it was estimated that the half-life of intravenously injected Pb in baboon kidneys will be one-half that in the liver for the first two months.

Lead is reported in the literature to follow the movement of calcium to a greater degree and that it is physiologically controlled in a manner similar to that of calcium. This is particularly true for its behavior in bone. Pb is found to compete with calcium for bone deposition and similarly distributes among different bones, between trabecular and cortical bone structures [98, 116-117]. Data inferred from healthy adult male humans, baboons and beagles show that the adult skeleton may accumulate 10-15 % of radio-Pb intravenously injected within the first hours of injection. Over the first day or two, there was a decline bone radio-Pb content and then a gradual increase over a period of weeks as Pb is returned from soft tissues through plasma and erythrocytes for deposition in the bone. After 3-4 weeks post-injection, the bone accumulated about 25 % of administered Pb. Also, Pb was reported to initially concentrate in trabecular bone than cortical bone and this is supported by a study in dogs that found five times radioactive Pb in trabecular bone compared to cortical bone [98].

One theme that has been repeated throughout the previous paragraphs of lead toxicokinetics is that age and physiological status significantly influence Pb bioavailability and metabolism. In the following sections these factors are discussed.

Pregnancy and lactational periods are probably an important period of lead exposure for both the unborn infant and a child on breast milk [118-121]. Lead mobilized during pregnancy because the bone is resorbed in order to produce the fetal skeleton. For example when lactating and nonlactating mice were intravenously administered 0.05 mg of Pb, lactating mice had twice the Pb volume in plasma compared to nonlactating. Pb clearance in plasma was 4.25 liter/hr/kg in lactating mice and 1.07 kg/hr/kg in nonlactating mice whilst one-third of injected Pb was excreted via milk [120], In a similar study in Australia, female migrants who were of child bearing age were monitored during gestation and for up to six or more months after pregnancy to examine the effect of lactation on Pb mobilization from the skeleton. Results revealed that breast milk could contribute between 36-80 % infant blood Pb levels and a significant correlation between Pb concentrations and breast milk, blood, urine and diet for infants

and mothers [121]. Pb was reported to be transported to milk by binding to specific and nonspecific carrier proteins [123]. The simple reason for increased blood Pb levels in breast milk is physiology. According to Goyer *et al* [122], bone turnover is affected by pregnancy, lactation, osteoporosis and certain disease states which are likely to produce a rise in lead mobilization from skeleton, thus increasing blood Pb levels. This statement is supported by Franklin *et al* [118] from a study involving monkeys using stable Pb isotopes. They observed a 29-56 % reduction in bone lead mobilization in the first trimester followed by an increase in the second and third trimesters up to 44 %. Also, maternal and fetal bone, brain, liver and kidneys showed substantial transplacental transfer of endogenous Pb. About 7-39 % of fetal skeletal Pb originated from maternal skeleton due to bone resorption to meet the required calcium levels for the developing fetus. Zeigler *et al* [124] investigated the metabolic activity of 12 infants ranging from 14 to 746 days in 1978. The authors report a daily intake of Pb was more than 5  $\mu$ g/kg with an average absorption of 41 % and net retention of 31.7 %. For infants whose daily intake was less than 5 µg/kg had greater fecal Pb excretion than intake with means absorption approximately 5 %.

O'Flaherty [126] stated that bone loss is a natural ageing process. Ageing is accompanied by numerous degenerative processes most of which increase vulnerability to exogenous and endogenous toxicants, an example being lead [125-126]. Bone mass plateaus at ages 25 to 30 years and gradually reduces thereafter for both men and women. Researchers have observed higher blood Pb levels in post-menopausal women which they attribute to bone resorption with age followed by mobilization of lead previously sequestered in bone. Follow up studies by others also reported similar results. They found

Pb in both midfemur and pelvic bone declined steadily with age in the human population from 50 years and above with the most pronounced effects in females [125]. As previously pointed out, lead both competes with and mimics calcium the main constituent of bone. Lead has been shown to be incorporated into the crystalline structure of bone replacing calcium at some sites. It is buried beneath the surface in areas of bone formation and is eventually distributed throughout the bone volume. Bone cell metabolizes Pb similar to calcium. Most of the Pb in bone is rapidly exchangeable and is controlled by the same ions and hormones that modulate bone calcium metabolism, nevertheless, high Pb content will damage bone cells and interfere with bone remodeling [98]. Once in the bone, Pb is slowly diffused by exchange from the bone via canaliculi to blood or by structural remodeling involving resorption of bone by osteoclast cells and then new mineral apposition follows [105].

# Health Effects Associated with  $Pb^{2+}$  Exposure

The health effects associated with Pb exposure reported in the literature are numerous. These range from unobservable symptoms to extreme cases of death in exposed victims. This section is organized into health effects manifested via neurobehavioral, cancer, genotoxic, reproductive, developmental and immunological [5].

#### Neurobehavioral Effects

The early symptoms of lead neurotoxicity in both adults and children include ♦ diffuse muscle weakness, general fatigue, joint pain or arthritis, loss of appetite, headache, insomnia, irritability, diminished libido, decreased attention span and

personality changes [195]. Chronic lead exposure could produce abdominal pain or cramping, nausea or vomiting, depression, short-term memory loss and depression with severe blood Pb over 30  $\mu$ g/dL in victims showing signs of frank paralysis, severe lethargy and abdominal colic. The most reported and severe lead neurotoxic symptom in adults is peripheral neuropathy and encephalopathy (general term to describe disturbance of brain function [195, 197]. Children with blood Pb levels ranging from 10-35  $\mu$ g/dL are at risk of lowered IQ and poor attentiveness. Goyer [196] reported that typically children with blood Pb content below 25  $\mu$ g/dL were found to have reduced IQ scores. In the assessment of children at 4 years of age, the apparent IQ value had reduced between 1 and 5 IQ points for every 10  $\mu$ g/dL increase in blood lead. Järup [197] also made similar conclusions after meta-analysis of four prospective studies in Boston, Cincinnati, Port Pirie and Sydney. The combined evidence from these four studies, show a mean reduction of in IQ of 2 points for 10  $\mu$ g/dL rise in blood lead level at the 95 % confidence interval.

It is quite obvious from the previous paragraph that the neurotoxic effects on children are more severe than on adults. This is likely due to because gastrointestinal absorption of Pb by children is much higher than adults, systemically circulating bioavailable Pb is able to gain a greater access to the brain of children than adults and the vulnerability associated with the developing nervous system [198].

Several neurotoxic mechanisms of Pb actions have been documented to explain the processes through which lead exerts its negative cellular influence. Lidsky and Schneider [198] classed Pb neurotoxic mechanisms as direct and indirect whilst Goyer [196] defined it as being morphological and pharmacological. The neuropharmacological

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interactions include substitution for calcium, neurotransmitter release, protein kinase C, Na-Ca ATPase and energy metabolism. Morphological interactions on the other hand consist of interference with adhesion molecules, impaired cell:cell programming connections and miswiring of the central nervous system. Lead is thought to cross the brain barrier rapidly by disrupting the brains' main structural components as a result of injury to astrocytes and endothelial microvasculature. Once in the brain, lead is found to affect two key proteins involved in learning and cognitive function, protein kinase C and N-methyl-D-aspartate subtype glutamate receptor. Other studies have attributed Pb's neurotoxicity to its ability to influence several biological activities at various levels of regulation due interference on regulatory action of calcium function in cells. So, lead can interfere with homeostatic cellular processes thereby acting as a chemical stressor [199, 200]. Detailed mechanisms of lead toxicity are also discussed under the section on "lead toxicity mechanisms".

The implication of the above observation is that there is apparently no threshold below which lead is without effect on the central nervous system. The only problem associated with this statement is the inability to quantify effects at very low lead exposure. However recent findings have suggested toxicological effects at low dose lead exposure [197, 200].

#### Developmental Effects

This section examines the effect of Pb on growth parameters that are neither neurological nor behavioral. A number of epidemiological studies have investigated the relationship between Pb exposure and growth parameters such as body weight, stature

and head circumference. For example, a study of 223 mother-infant pairs in Mexico found that increasing tibia and patella bone Pb results in decreasing birth length, birth weight and head circumference of newborns respectively, with an estimated increased risk of 1.02  $\mu$ g/g [201, 202]. A similar study was conducted on 329 mother-infant pairs to examine the association between breast milk Pb and anthropometric feature, weight gain. The authors reported that infant Pb content was negatively related to weight gain. They also found that exclusively breast-fed babies had significantly higher weight gains, nevertheless this weight gain declined significantly with rising patella Pb [203]. Other studies carried out in Spain, Russia, Norway and the U.S. have not been consistent. Women from Camden, New Jersey with blood Pb of 1.5  $\mu$ g/dL did not produce any significant association between low birth weight and preterm delivery while the study involving Russian and Norwegian women with maternal and cord blood of 1.2  $\mu$ g/dL negatively impacted birth weight and body mass index. Similar results were reported for Spanish women who had much higher placental blood levels. Birth weight, head, abdominal circumference or shorter length at birth were not affected [5].

One part of the body likely to experience inhibition of growth is the skeleton. According to Ronis *et al* [204], the growth of the skeleton is the primary stimulator of somatic development. It is reported in the literature that Pb can accumulate in the bone throughout the developmental period, localize in regions of bone mineralization and growth, delay growth plate chondrocyte maturation and inhibit bone formation and mineralization [205, 206]. Specifically, male and female rats exposed to lead showed reduced somatic growth, longitudinal bone growth and bone strength during the period of puberty [204],

It has been reported recently that lead exposure might delay growth and pubertal development in girls. A study of 600 non-Hispanic white, 805 non-Hispanic African-American and 781 Mexican-American girls with blood lead concentration of 3  $\mu$ g/dL or less, showed significant delays in breast and pubic-hair development in African-American and Mexican-American girls with no effects at this concentration in white girls. African-American girls were the most affected. Using Tanner staging (as described in the Physician Examiners Training Manual), African-American girls experienced delays in reaching Tanner stages 2, 3, 4 and 5 due to lead exposure of 3  $\mu$ g/dL compared with 1  $\mu$ g/dL at 3.8, 5.3, 5.8 and 2.1 months correspondingly for breast development and 4.0, 5.5, 6.0 and 2.2 months respectively for pubic-hair development. Menarch delay was at 3.6 months [207]. A similar study of 1,706 girls ages 8-16 with blood Pb ranging from  $0.7-21.7 \mu g/dL$  found higher blood Pb to be significantly associated with delayed attainment of menarche and pubic hair but not with breast development [208]. Both study accounted for race/ethnicity, age, family size, residence in metropolitan area, poverty income ratio, body mass index and any other confounding factors that might be important.

# Lead Carcinogenecitv

Lead is considered a probable carcinogen by the EPA [176] whilst the Department of Health and Human Services consider lead and its compounds as posing reasonably anticipated human cancer risk [177]. The International Agency forRresearch on Cancer (IARC) also said inorganic lead is probably carcinogenic to humans though organic Pb could not be classified as to its carcinogenicity to humans [178]. The classification by these agencies reflects the limited evidence of cancer in humans due to lead exposure. Several studies in Britain, Sweden, Italy and Finland among occupationally exposed individuals found limited evidence of brain, spleen, stomach, lung, kidney, bladder and overall cancer risk [179-182].

So far, the most evidence demonstrating the possibility of lead as a carcinogen has come from animal models. The experiments have focused on transplacental or translactational, oral, subcutaneous, intratracheal, intramuscular and intraperitoneal administration of inorganic Pb to rats, mice and hamsters [183]. Most of the tumors that develop from these routes of exposure are renal tumors. The process involves alterations in glomerular function as seen in proteinuria then acute morphological changes that might slowly progress to chronic irreversible nephropathy finally to adenocarcinoma. Initial transformations include the formation of lead-protein inclusion bodies (nuclear inclusion bodies) and ultrastructural damage in cellular organelles particularly the mitochondria.

Although cancinogenic effects of Pb are not obvious, it is thought to play a facilitative or permissive role in cancer induction. In his recent review, Silbergeld [183], stated "epidemiological and mechanistic data are consistent with a facilitative role for lead in carcinogenesis, that is lead by itself may not be both necessary and sufficient for the induction of cancer but at a cellular and molecular level lead may permit or enhance carcinogenic events involved in DNA damage, DNA repair and regulation of tumor suppressor and promoter genes".

## Immunological Effects

Most of the studies examining the influence of lead on immunological parameters have been inconclusive. While some reported negative effects, others did not find any association between blood Pb levels and IgA, IgG, IgM and peripheral blood lymphocyte phenotypes including T cells, B cells, NK cells and CD4/CD8 subsets [5]. A study by Kimber *et al* [170] among workers whose blood Pb levels range from 25 to 53  $\mu$ g/dL found no significant IgA, IgA and IgM concentrations from unexposed group. This finding is supported by Alomran and Shleamon [171] and Basaran and Undeger [172]. These authors report that mean blood Pb concentrations of 64 and 74.5  $\mu$ g/dL produced no significant alterations in IgA and IgM compared to non-exposed control group however IgG was significantly reduced. On the contrary, Ewers *et al* [173] showed a significant decline in serum IgM which they associated with increases in colds and influenza with age. In this study, neither serum IgA or IgG were significantly different. Salivary IgA, a major factor in defense against respiratory and GIT infections, was significantly reduced compared to control group.

Experimental observations involving *in vitro* and *in vivo* models and children reported in the literature appear similar to above results seen in adult human beings. For example, Bauer *et al* [174] employed dynamic light scattering to study the effect of Pb and other heavy metals on aggregation behavior of rat IgGl and antibody-antigen complexation with monoclonal mouse IgGl and found Pb to interact with antibodies and immune complexes thereby inducing large soluble aggregates. The authors also found no effect on antibody-antigen binding activity even at very high concentrations of Pb treatment. Similar results were reported for female pregnant rats exposed to Pb during

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breeding and pregnancy. No alterations were observed in immune function. However, the offspring showed altered cytokine production and a rise in serum IgE [175].

#### Reproductive Effects

There is evidence in the literature supporting an association between occupational and environmental Pb exposure to reproductive anomalies such as abortion and pre-term delivery in women and changes in sperm and a decline in fertility in men [5]. In the past, occupational high Pb exposure in pregnant women in certain parts of Europe showed increases in spontaneous abortions, stillbirths, premature births and neonatal deaths [184]. Fairly recent epidemiological studies in Mexico City, Mexico and Port Pirie, Australia revealed the possibility of moderate blood Pb levels causing spontaneous abortion (loss of pregnancy by gestation week 20) and still birth. Mean blood-Pb content of cases and control were 12.0 and 10.1 pg/dL respectively while that of the Port Pirie were 10.6 and 7.6  $\mu$ g/dL [5, 185] correspondingly. The Mexico study found correlation between increasing blood levels and spontaneous abortion at 1.13-fold. On the contrary, the Port Pirie study did not find any association between blood-Pb levels between exposed and control residents but reported 22 of 23 miscarriages and 10 of 11 stillbirths at Port Pirie compared to 1 miscarriage and 1 stillbirth outside of Port Pirie. Experimental evidence of Pb effects in women from animal models include reduced concentration of progesterone which might be due to impaired luteal function, longer and greater variability in menstrual cycles, shorter menstrual flow, suppressed levels of luteinizing hormone and follicle-stimulating hormone [5, 188].

Men are likely to contribute to spontaneous abortions via passage of Pb through the semen to the mother, lead in work clothes, equipment, hands and changes in sperm [185]. Men exposed to relatively high Pb levels are at risk of male-infertility due to the quantity and quality of sperm production. This has been observed in experimental samples as reductions in sperm concentration which are indications of alterations in sperm chromatin, asthenospermia, hypospermia, teratospermia, reduced seminal plasma constituents, reduced motility, low semen volumes, reduced functional maturity of sperm and most importantly below normal and total sperm count relative to control groups. Most of the studies documenting Pb reproductive effects in men report at least mean blood-Pb levels of 35 pg/dL. Pb minimizes sperm quality and quantity by alterations in chromatin, act directly on the testes causing depression of sperm count and peritubular testicular fibrosis, reduced testosterone, disruption of regulation of luteinizing hormone and DNA-protamine packing [5, 186. Lead is likely to compete with or replace Zn atoms normally bound to nuclear protamines as a result of its binding to free thiols, which might affect disulfide bond formation and thus alter DNA-protamine biding or impair chromatin decondensation during fertilization [187].

# Genotoxic Effects

Experiments testing the genotoxicity of Pb *in vitro* and *in vivo* models have produced inconsistent results, which seems to be the case in humans as well. For example an epidemiological study of battery plant workers in Poland using micronucleus (MN), in situ fluorescence (FISH), analysis of sister chromatid exchange (SCE) and the comet assay found increased incidence of MN in peripheral lymphocytes due to either clastogenic and aneugenic effects. Also, there was a significant rise in the frequency of SCEs and leukocytes with DNA fragmentation relative to controls. Blood Pb concentrations ranged from 282-655  $\mu$ g/dL for the exposed group and 17-180  $\mu$ g/dL for the control population [189]. Contrarily, 78 individuals exposed to mixtures of cadmium, cobalt and lead found no correlation between Pb-exposure and DNA single strand break [190].

The mechanism of lead genotoxicity is considered to be indirect. In the literature, only one article reported that G. C base pairs might be the primary target for lead mutagenesis [191]. Other processes reported include inhibition of nucleotide excision repair [192], production of reactive oxygen species by rapid induction of hydrogen peroxide or stimulation of activities of copper-zinc superoxide dismutase and xanthine oxidase [193]. Although lead is considered by most researchers as a weak mutagen, it could be a potent comutagen and this has been demonstrated *in vitro* by de Restrepo *et al* [194], According to these authors, lead sensitizes cells to damage in order to induce genotoxicity.

## Lead Mechanisms of Action

#### Lead Toxicity Mechanisms

Lead is known to either replace or interact with polyvalent cations such as calcium, and zinc ions in the molecular machinery of cells so that lead can affect diverse **biological processes in living organisms. Examples of these processes include metal** transport, energy metabolism, apoptosis, ionic conduction, cell adhesion, inter- and intracellular signaling, various enzymatic processes, protein maturation and genetic regulation [127, 128]. Essential metal ions in biological systems have functions including charge carriers, intermediates in catalyzed reactions and structural components or elements for stabilization of proteins. These essential metal ions have binding sites that facilitate selectivity and functionality. For instance the binding-sites of calcium are wide, regular charge distribution to facilitate quick ion exchange, oxygen atom conformation and coordination numbers of **6** and 7. Zinc binding-sites on the other hand involve sulfur and nitrogen atoms that have high zinc affinity slowing exchange of zinc and have low coordination numbers [129, 130].

Selectivity of metal-binding sites is limited to essential metal ions in the cell, thus environmental contaminants like  $Pb^{2+}$  which can mimic physiologically important metal ions become a major problem for the cell because there is a lack of specific mechanism to deal with them. In the case of calcium, it does not have a strong enough affinity to bind to zinc-binding sites while zinc cannot be dehydrated by calcium coordinating groups for it to bind to calcium sites. Other ion-specific features like electronegativity, coordination geometry, preference for ligand atom, electric charge and ionic radius ensure that metal interaction with protein targets are specific [129, 130]. The electronegativity of zinc is 1.65 while that of Pb is 2.33.

According to Godwin [131], lead is ubiquitous in its ability to bind several protein targets because it can interact in a flexible coordination number with oxygen and sulfur. In fact zinc binding sites made up of thiols have the most affinity for Pb due to the strong bonds that lead forms with sulfur. Magyar *et al* [132] examined the interaction of Pb(II) with thiol-rich structural zinc-binding proteins using X-ray absorption spectroscopy. The authors found that whilst zinc binds in a four-coordinate mode, Pb(II) binds in a threecoordinate Pb(II)-S**3** mode, which is consistent with trigonal pyramidal Pb(II)-S**3** model. But this is at odds with the small molecule complexation literature that suggested Pb(II)- S**4** as the preferred mode of binding. These authors reexamined the above literature and found that the coordination number of Pb(II)-S4 is 5, **6** or **8** which means Pb avoids the four coordination in sulfur rich environments and instead adapts trigonal pyramidal in  $Pb(II)$ -S<sub>3</sub> or Pb(II)-S<sub>5-8</sub>.

Perhaps the most important metal ion in the body is calcium. It has an ionic radius of 0.99 **A** and is required for bone building, blood clotting, may act as a second messenger in signal transduction, muscle contraction triggering and transmission of nerve impulses [129]. Maintaining a stable level of calcium in the extracellular space and cytosol requires use of calcium pumps which create concentration gradients and selective binding of calcium-binding proteins like calmodulin. Calcium has an electronegativity of 1.0 with a charge distribution that is spherical. Calcium binding motifs are made up of **6** or 7 metal-bound oxygen atoms, though sometimes they can be eight. For instance in the mannose-binding protein complexed with oligosaccharide, calcium motifs within the protein have coordination number of 7 or eight if the substrate is included [129, 133]. Similarly, the calmodulin binding site has seven oxygen atoms at the vertices of pentagonal bipyramid coordinated to the central Ca ion at approximately 2.4 **A** [134]. There is evidence supporting the binding of lead to predominantly calmodulin [135]. This Calmodulin protein is intracellular calcium binding receptor protein that is enriched in neurons and therefore regulates neuronal processes like neurotransmission, axoplasmic transport, cellular cytoskeleton, cAMP metabolism, protein phosphorylation and memory [135]. Calmodulin has an "EF-hand" domain and C2 motifs that have a high affinity for Pb [127, 136-137]. The EF-hand is made up of about 29 amino acid residues and has a

helix-loop-helix arrangement. Binding of calcium and other metals to this site is due to conformational changes that exposes hydrophobic regions of the protein. The C2 domain has approximately 130 residues with its main mechanism of binding to metal ions considered to be an 'electrostatic switch' because domain modifications are electrical rather than conformational and thus C2 motifs interact directly with biological membranes 127, 138-139].

In the bone, a non-collagenous protein osteocalcin has been reported to have a higher affinity for Pb than calcium at similar concentrations. This protein is exclusively synthesized by osteoblasts and odontoblasts and is made up three calcium binding residues y-carboxyglutamic acid. The protein is documented to be involved in bone resorption, osteoclast differentiation, crystal formation and growth and may also play a role in the regulation of bone formation and remodeling [140].

Lead is reported to interact either directly or indirectly with molecules (calcium channels, calcium binding proteins and calcium dependent kinases) involved in signal transduction and gene expression regulation [141-145]. Signal transduction by lead is reported in the literature to be primarily protein kinase C (PKC) or calmodulin II (CaMKII) mediated although some other kinase-dependent mechanisms have been documented [142, 146-147]. PKC belongs to a family of phospholipid-dependent serinethreonine protein kinases crucial to many signal transduction pathways. The interaction of lead with PKC is not straightforward. Low lead levels were observed to replace calcium in PKC whilst high Pb-concentrations inhibited the activity of PKC. At the molecular level, Pb is found to regulate the mRNA expression of PKC via c-fos induction. Similarly, the activity of CaMKII is directly modulated by Pb or indirectly via

the stimulation of adenylyl cyclase and phosphodiesterase. Recently, studies have shown the possibility of lead effecting signaling pathways via not directly linked to PKC and CaMKII pathways. Leal *et al* [143] employed adrenal chromaffin cells and human SH SY5Y cells to investigate the effect of  $Pb^{2+}$  on protein phosphorylation. The authors found a significant rise in the number of proteins phosphorylated and they concluded that lead can modulate the phosphorylation of heat shock protein (Hsp27) through the activation of p3 **8**MAPK pathway.

A few studies have examined the role of  $Pb^{2+}$  on mRNA expression. These studies were designed to either exploit pathways that involve the production of reactive oxygen intermediates since the literature is emphatic on the increased cellular oxidative stress due to lead toxicity or the Mitogen-activated protein kinase (MAPK) family because activation of some members of this family could lead to activation of transcription factors and apoptosis. MAP kinases are grouped into four distinct groups which include extracellular signal-regulated kinases (ERK)- $1/2$ , Jun NH<sub>2</sub>-terminal kinases (JNKs) p38MAPK and ERK5. Ramesh *et al* [142] studied the effect of lead on oxidative stress proteins nuclear factor kappa B ( $NF-KB$ ) and activator protein ( $AP-1$ ) and mitogen activated protein kinase (MEK) and JNK in murine pheochromocytoma cells (PC-12). Their results showed an up-regulation of MEK and JNK. Also,  $NF-KB$  and  $AP-1$  were activated by Pb whilst the inhibitory subunit of NF-<sub>K</sub>B,  $I_K$ B $\alpha$  was degraded. Another study was carried out by Hanas *et al* [141] to elucidate the mechanisms by which Pb might alter the DNA-binding of cysteine-rich zinc finger protein. These zinc finger proteins are thought to play roles in regulating gene expression, signal transduction, cell growth and differentiation and chromosome structure. In this experiment, the effect on Pb

on Cys**2**His**2** zinc finger protein transcription factor IIIA (TFIIIA), transcription factor Spl and another Cys**2**His**2** finger protein that binds GC-rich regions in RNA polymerase II were assessed. Results revealed inhibition of DNA-binding by TFIIA, Spl and another Cys**2**His**2** finger protein with indications that inhibition mechanism minimally involves Nterminal fingers of TFIIIA. A similar study was conducted by Ghering *et al* [169] using spectroscopy to evaluate the binding of  $Pb^{2+}$  to GATA proteins. GATA proteins are considered transcription factors that have affinity for GATA DNA elements via Cys**4** structural zinc binding motifs. These proteins are important in regulating neurological and urogenital development and the onset of cardiac disease. The affinity of Pb for Cterminal domain from chicken GATA-1 (CF) and double-finger motif from human GATA-1 (DF) were assessed spectroscopically.  $Pb^{2+}$  coordination with CF and DF were observed in the near-UV (250-380 nm) spectrum as the appearance of intense bands as lead forms tight complexes with cysteine residues in the zinc-binding sites as well as displacing Zn from CF and DF. The presence of lead also reduced the ability of GATA to bind DNA and subsequently induce transcription.

Lead is known to effect the regulation of the synthesis of heme. Pb is reported to reduce the bioavailability of heme via induction of hepatic expression of heme oxygenase thereby degrading heme and also the inhibition of the enzyme, delta aminolevulinate synthase through heme synthesis pathway [144]. This eventual decline in heme production levels was observed to decrease the function of P450. The cytochrome P450 family of heme containing proteins that are essential for the oxidative metabolism of both and endogenous and exogenous compounds. This family of proteins is responsible for transforming xenobiotics to non-toxic or carcinogenic metabolites [145, 148]. In the liver,
P450 is a major hemoprotein so that the inhibition of heme will interfere with the biogenesis of functional P450. Two ways this is considered to take place include incomplete saturation of P450 apoprotein due to insufficient heme supply or the reduction in the synthesis of P450. Jover *et al* [145] concluded from their study of the role of heme in cytochrome P450 transcription and function in mice treated with lead acetate that, the mechanism involved is two-fold. The first is independent of heme, in that lead reduces the transcription of P450, whilst the second is heme-dependent, in which synthesis of heme is inhibited and consequently decreases the heme saturation of P450 and/or apo-P450 level. Another study by Korashy and El-Kadi [148] revealed the mechanism of heavy metals including Pb regulating the transcription of P450 specifically Cyplal to be aryl hydrocarbon receptor (AhR) dependent. The authors found that the inhibition of AhR degradation enhanced the induction of Cyplal mRNA transcript. Also, Pb and other heavy metals reduced the degradation rate of Cyplal protein, a rise in heme oxygenase-1 (HO-1) with a consequent decrease in cellular heme levels.

Another documented mechanism by which lead toxicity is observed is the interaction with ion channels particularly calcium and potassium channels. This mechanism of action is considered the primary mode by which Pb is a neurotoxin [149, 150]. These authors report that lead acts as a depressant of voltage-operated calcium channels, N-methyl-D-aspartate receptors, adenylate-cyclase and delayed-rectifier potassium currents in neurons. Pb<sup>2+</sup> acts as a competitive antagonist to  $Ca^{2+}$  in blocking  $Ca<sup>2+</sup>$  channels identified in electrophysiological experiments as Pb<sup>2+</sup> induced blocking of end plate potential (EPP) because of reduced amplitude of the EPP and this effect is reversible [150]. Similarly, micromolar concentrations of  $Pb^{2+}$  were reported to be a

reversible blocker of delayed-rectifier potassium currents in hippocampal neurons and this effect is voltage-dependent [149].

# Reducing the Toxicity Effect of  $Pb^{2+}$  Exposure

In this section, a brief description of current strategies that are employed in reducing the toxic effects of lead is provided. Most of the strategies outlined here are reported in the literature, for which some are actual clinical practice, others are experimental evidence which is not proven and therefore should not be considered as a guide for treatment of lead exposure.

As is always the case, prevention is better than cure. Creating conditions that reduce environmental lead levels will continue to be the most effective way of minimizing exposure to lead and its consequent health effects. As pointed out in other parts of this write-up, deficient levels of calcium, iron and zinc enhances the absorption and metabolism of  $Pb^{2+}$  because calcium, iron and zinc have been observed to inhibit the absorption of  $Pb^{2+}$  from the gut. In fact a number of studies involving children, pregnant women and nursing mothers examining the role of dietary supplements of these essential metals and found them to significantly reduce Pb absorption and metabolism [5, 94, 195, 156-158]. Thoroughly washing of skin with soap and water or flushing of eyes with water or saline following acute exposure to lead is recommended. Ingestion of lead compounds is removed by gastric lavage or whole gut lavage using osmotic neutral polyethyelene glycol electrolyte solution (GO-Lytely®) or employing surgical excision to remove lead bullets or shrapnel [5].

To reduce the body burden of lead, chelation agents are typically used. These agents are able to bind inorganic Pb to facilitate its transfer from soft tissues to the circulation system so that excretion is enhanced via the kidney. Obviously extra precaution is need for patients with renal problems. Chelating agents in use currently include dimercaprol (British Anti-Lewiste, or BAL), CaNa<sub>2</sub>-EDTA (EDTA), penicillamine and 2,3-dimercaptosuccinic acid (DMSA; Succimer®) [5, 195, 159-161]. Guilarte *et al* [162] proposed environmental enrichment as an alternative to chelation therapy for childhood lead intoxication. The authors defined environmental enrichment as the "combination of complex inanimate objects and social stimulation" which was found to enhance the recovery of deficits in N-methyl-D-aspartate receptor subunit 1 mRNA and induction of brain-derived neurotrophic factor (BDNF) mRNA in the hippocampus. Long-term potentiation, a cellular model for learning and memory and spatial learning are controlled by N-methyl-D-aspartate type of glutamate receptors (NMDAR) that is also inhibited by Pb. Exposed  $Pb^{2+}$  animals that were provided enriched environments had learning impairments reversed.

#### Lead Regulation of Gene Expression

Several genes transcripts are reported in the literature to be regulated by Pb either directly or via some other consequential means. In the last several years, studies involving Pb have shifted focused on elucidating how Pb regulates mRNA transcription. This section will look at some of the studies designed to understand the role of lead in the expression of genes.

Cabell *et al* [163] stated that one possible means by which lead might induce the synthesis of heme oxygenase-1 (HO-1) is oxidative stress. HO is plays a crucial role in heme catabolism. It oxidatively cleaves the porphyrin to form biliverdin. Heme oxygenases include HO-1, HO-2 and HO-3 iso forms. HO-3 has low heme oxygenase catalytic activity whilst HO-2 though expressed in many cell types is less induced by most stress types. The expression of HO-1 gene is controlled by heat shock element, metal-responsive element, antioxidant response element, AP-1, NFkB and Spl. Lead is reported to cause increases in hydroxyl radicals, lipid peroxidation, enhanced production of reactive oxygen species, increased levels of reduced glutathione (GSH) which is will consequentially induce the synthesis of a number of stress proteins. According to these authors, HO-1 synthesis is induced in astrocytes but not hippocampal neurons, and this induction was reduced by the presence of radical scavengers dimethylthiourea (DMTU) and mannitol but not by inhibitors of calmodulin, calmodulin-dependent protein kinase C or extracellular signal-regulated kinases (ERK), leading them to suggest the importance of oxidative stress as a mediating event in the induction of HO-1 by  $Pb^{2+}$  in astrocytes.

Lead is also cited to effect the expression of inducible nitric oxide synthase (iNOS). NO from iNOS mediates immune defence as well modulating gene transcription, translation and protein function. In this study by Eckhardt *et al* [164], PbCl<sub>2</sub> increased NO production and iNOS activity in a dose-dependent manner in pancreatic  $\beta$  cells. They also found an increase in iNOS mRNA expression and iNOS protein content as determined by semi-quantitative reverse transcriptase-PCR and Western blotting respectively, leading them to conclude that  $Pb^{2+}$  up-regulates iNOS gene expression at the level of transcription.

Other studies have employed cloning techniques to understand the role of heavy in inducing transcription. Cheung *et al* [165] isolated gene sequences of tilapia metallothioneins (tiMT) and characterized them *in vitro* using cultured cell lines PLHC-1. Administration of  $Pb^{2+}$  and other heavy metals showed the induction of tiMT transcription. A similar cloning experiment in which zebrafish metallothionein (zMT) was isolated, characterized in HepG2 cell line and exposed to Pb2+ and other heavy metals revealed the inability of lead to induce zMT transcription *in vitro* [166]. Metallothioneins are low molecular weight cysteine-rich that intracellularly binds proteins for the control of essential and detoxification of non-essential metals. MTs are important metal homeostasis, acts as chelating metal ions via the formation of metalthiolate bonds or provide  $Cu^{2+}$  and  $Zn^{2+}$  reservoirs required in the biosynthesis of metalloenzymes and metalloproteins.

Another investigation to determine the role of the binding activity of AP-1 in PC 12 cells revealed this binding to be dependent on protein kinase C (PKC) [167]. Activator protein-1 complex (AP-1) is a homodimeric complex that has members of jun family or a heterodimer with family members jun and fos. Jun family members are c-Jun, JunB and JunD whilst fos members are c-Fos, FosB, fos-related antigen-1 (Fra-1) and fos-related antigen-2 (Fra-2). AP-1 complex has a high affinity and binds specifically to DNA consensus sequence -TGACTCA- close to the promoter region of the early response gene. Results from this experiment show a rise in AP-1 derived transcription with an increase in AP-1 DNA binding activity that requires PKC. Inhibition and depletion of PKC reduced increase in AP-1 DNA binding in the presence of  $Pb^{2+}$  while

the use of specific antibodies in supershift assay implicated Fra-2 and JunD as the main components responsible for increased activity due to  $Pb^{2+}$ .

Korashy and El-Kadi [168] examined the differential effects of heavy metals mercury, lead and copper on the constitutive and inducible expression of aryl hydrocarbon receptor (AhR)-regulated genes; Cyplal, NAD(P)H: quinone oxidoreductase ( QOR) and glutathione S-transferase Ya (GST Ya) in cultured hepatoma Hepa 1c1c7 cells. AhR is basic helix-loop-helix transcriptional factor that is ligandactivated found in the cytoplasm and bound to 90-kDa heat-shock proteins (HSP90) and AhR interacting protein (AIP). When bound to a ligand, AhR is activated, thus HSP90 and AIP are dissociated subsequently leading to a translocation of ligand-receptor complex to the nucleus where it forms a heterodimer with transcriptional factor protein, aryl hydrocarbon receptor nuclear translocator (ARNT). To initiate mRNA transcription, AhR/ARNT binds to a specific DNA sequence called the xenobiotic-responsive element (XRE) found in the promoter region of Cyplal [148], Lead alone did not change significantly the Cyplal activity and protein content but mRNA expression was significantly increased, however in the presence of a ligand, no  $Pb^{2+}$  effect on Cyplal was observed. Both the activity and mRNA expression were increased by lead in absence and presence of AhR-ligand. Again Pb increased the activity and mRNA of GST Ya.

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# CHAPTER III

# ASSESSING LEAD EFFECTS USING ICP-MS AND HISTOPATHOLOGY

## Introduction to Study

The importance of lead as an environmental chemical species exhibiting various form of toxicity in humans has been well documented. [227-230], As a result of its past uses history, lead is widely distributed in water, soil and air. This is particularly of great importance considering lead use in gasoline and paint was curtailed more than two decades ago. As a result, the potential exposure to significant lead levels, especially infants in the population, is high [5].

Pb exposure targets organ systems such as the skeletal, hematopoeitic, renal, endocrine and nervous systems [231], thereby partitioning between soft and hard tissues in the body with approximately 95 % and 70 % being found in the bones and teeth of adults and children, respectively. Bone then serves as a pool to replenish excreted lead from blood. Some adverse conditions associated with lead poisoning include DNA damage, neurological impairment, abnormal heart function, osteoporosis among others [232-233]. In addition, a weakened immune defense system, sterility in male and females, abnormal fetal development, and glycosuria are also associated with chronic lead poisoning.

Lead **perturbs the functions of enzymes and proteins of varied classes. Studies** have shown that, lead exerts its influence physiologically and biochemically as a mimetic agent substituting for essential elements participating in metabolism such as calcium, iron and zinc. For instance, it directly interferes with zinc and iron in the biosynthesis of heme, in the function sulfhydryl group rich protein enzymes and in protein synthesis in general either directly or indirectly [232-233]. Lead binds to different kinds of transport proteins including metallothionein, transferin, calmodulin and calcium-ATPase. By associating with these proteins, it is transported to specific tissues where it causes its damage. Lead transport and assimilation are optimum when there is the dietary deficiency of iron or calcium, zinc because lead is able to displace these metals in transport proteins and during specific protein-mediated physiologic processes [234],

Liver and kidney damage have been linked to lead toxicity although the exact toxicity mechanism is not entirely understood. Other than the use of histopathology to assess the effects of lead poison in hepatocytes, the use of other methods has been inconclusive. The objective of this study is to assess the interaction of lead with calcium, iron, copper, zinc, cobalt and nickel in blood, liver, kidney and bone marrow using rat model. Histopathology of the liver and kidney will also be examined. ICP-MS is a useful analytical tool for quantifying multi-elements from such matrices as geological, environmental and biological samples at sub parts per billion. That is, it has a detection limit of **1-100** parts per trillion and a linear dynamic range of about eight orders of magnitude. The range of analytes that can be employed in ICP-MS has recently been extended to both metals and nonmetals including radionuclides, rare earths, and some halogens like Br and I. ICP-MS works by generating ions in the plasma which are directed into the ion focusing region using turbomoelcular pumps backed by rotary pumps. Then electrostatic ion and extraction lenses sort the negative and positive ions so that positive ions are directed towards the quadrupole. Ions then enter the separation hardware, the quadrupole mass spectrometer where the electric field forces them into

wavelike motion. Ions with stable trajectories are filtered according to their mass to charge ration (m/z) in the quadrupole. Finally, individual ions are detected by ion counting electron multiplier [298].

The Fisher 344 rat inbred strain was developed in 1920 to address the lack of reproducible animal model for cancer research. In 1970, the National Cancer Institute selected Fisher 344 rat as a replacement for the Osbome-Mendel rat model in cancer bioassay program because tumor latency due to chemical exposure is relatively short whilst maintaining good survivability. Fairly recent literature has indication that F344 rats are prone to exhibit inflammatory effects and mononuclear cell leukemia due to exposure of a range of chemicals and pharmaceuticals. Nevertheless, this animal model has been employed in as many cancer, toxicological, aging, neurological, organ transplant, heart disease etc studies in the literature [243-246].

This experiment is part of a larger project investigating the overall effects of  $Pb^{2+}$ on gene expression in the rat. Results from this investigation will enable us to determine what specific tissue levels of Pb in rat lead to alterations in gene regulation.

## Materials and Methods

#### Experimental Design

Forty-eight six weeks post-weaning male Fisher 344 (F344) rats were exposed to 0 ppm, 50 ppm or 500 ppm of  $Pb^{2+}$ , respectively, in the form of lead acetate through drinking water *ad libitum* for 30 and 90 days, respectively. Control drinking water was distilled water. Prior to commencing treatment, rat diet, control and treated water were

analyzed by inductively-coupled plasma mass spectrometry (ICP-MS) (model # 4202387, serial  $# A0126$ ) for lead contamination and to verify accurate exposure levels. Rats were housed at the Western Michigan University Animal Facility. The animals were treated according to the principles outlined in the NIH Guide for the Care and Use of Laboratory Animals. There were eight rats assigned randomly to each treatment group. After each exposure period, rats were euthanized with CO**2** and blood was collected by cardiac puncture for serum analysis using ICP-MS. Also, some of the liver, kidney and bone marrow were preserved for multi-elemental analysis. A portion of each of the livers and kidneys were also fixed in **10**% neutral buffered saline for subsequent histology analysis.

## Multi-Elemental Analysis

Determinations of lead and other metal ion levels in blood, liver, kidney and marrow, an elemental analysis were carried out by ICP-MS. Approximately 1 g each of blood, liver, kidney and marrow was weighed into Teflon carousels containing 10 ml of 50 *%* nitric acid (ultra trace purity) and digested at high pressure in a microwave oven. After digestion, the samples were transferred to 50 mL conical tubes and diluted with 3 % nitric acid to the 50 mL mark. They were further diluted in a ratio of 1:10, 3 *%* nitric acid for final analysis. A 10  $\mu$ L Yttrium internal standard (10 ug/mL) was added to each sample just prior to inductively-coupled plasma mass spectrometry analysis. There were three replicates for each treatment and each sample was analyzed in triplicate.

# Histopathology

Liver and kidney samples were fixed in 10 % neutral buffered formalin. Fresh fixative was added to the samples and stored at 4 °C until ready for analysis. Briefly, the samples were passed through graded alcohol solutions for dehydration, xylene washed and then embedded in paraffin block cassettes. Then, tissues were sectioned in transverse and deparaffinated and stained with hematoxylin and eosin (H & E). Stained sections were examined under light microscopy to detect structural changes in the cells of the liver and kidney.

#### Data Analysis

Significant differences in lead, zinc, nickel, cupper, cobalt as well as morphometric parameters such as body weight and organ weights were analyzed by student t-test and ANOVA. Regression analysis was also conducted to follow distributions of lead and the other metal ions in blood, liver and kidney as function of time and dose level. Data was presented as means  $\pm$  standard deviation (SD) or means  $\pm$ standard error (SE), and differences were considered significant at  $P < 0.05$  or  $P < 0.01$ . ANOVA and t-test were applied specifically to the data set shown in Tables 3, 4, 5 and **6** . Figures 2, 3 and 4 were analyzed by ANOVA and Figures 5, **6** and 7 by regression analysis. H & E stained slides were observed under low- and high-power optical microscopes at the Biological Imaging Center, Western Michigan University.

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#### Results

#### Lead Effects on Selected Animal Morphometric Parameters

Selected measurements of animal health at time of sacrifice are reported in Table 3. Body weight gains as well as absolute liver and kidney weights were not significantly altered in both the 30-day and 90-day treatment groups relative to controls. The amount food consumed (gram) per gram of body weight gain was also not found to be significant. However, some significant differences were observed for the hepatosomatic and renal somatic indexes (organ wt./body wt.) in both the 30 and 90 days exposure period groups . In the 30-day treated rats, liver and kidney weights and the renal somatic index were decreased. In contrast, in the 90-day treated rats, liver weights, hepatosomatic and renal somatic indices respectively increased **8** %, 11 % and 5 % relative to controls.

## Metal Distribution in Blood. Liver. Kidney and Marrow

In Table 4, lead accumulation in blood, liver, kidney and bone marrow were all increased significantly in lead exposed groups\_relative to the control groups. With the exception of kidney, the 90-day treatment groups also showed markedly higher levels of lead in blood, liver and marrow than the 30-day treatment groups. The amount of lead accumulated in blood was between 6-15-fold greater in the 90-day treated than the 30-day exposed group. This trend is similar to what was observed in the liver and bone marrow. In the kidney, it is a ratio of one-to-one.

# Table 3

Selected organ weights (g) and their indexes (organ wt. X  $10^3$ /Body Wt.) \*P<0.05







VO

#### Table 4



500 PPM 95.17 ±38.90 81.25 ±28.29 666.32 ±155.1 54.67 ±19.33<br>  $(n = 8)**$   $(n = 8)**$   $(n = 8)**$   $(n = 8)**$ 

Lead distribution in selected tissues. \*\*P<0.01

#### Effect of Lead Poisoning on Some Essential Trace Metals

 $(n = 8)$ <sup>\*\*</sup>  $(n = 8)$ <sup>\*\*</sup>

As mentioned to in the introduction, lead exerts its toxic effects through mimicking the behavior of some other essential trace metals. We evaluated the responses of calcium, iron, cobalt, nickel, copper and zinc to varying levels of lead intoxication in some rat tissues. In Figure 1, the levels of zinc are shown in selected tissues as a function of lead exposure and time. The 30-day treatment group showed significant losses of zinc (P<0.05) in the liver at both the 50 ppm and 500 ppm Pb doses, with kidney and marrow levels remaining statistically unaltered. For the 90-day exposure period group, zinc concentrations reduced significantly in liver, marrow ( $P \le 0.05$ ) and kidney ( $P \le 0.01$ ).

Not many significant alterations in calcium and iron levels in blood, liver, kidney or marrow were observed at either time point or in either treatment regime, except calcium was depressed in the blood of 90 day high dose animals (P<0.01) and iron (P<0.05) in marrow in the 90 day high exposure group.

# Table 5



 $476 \pm 105$  $(n = 8)$ 

# Total calcium levels in selected tissues. \*\*P<0.01

## Table 6

 $894 \pm 323$  $(n = 8)$ 

638  $\pm 16.5$  $(n = 8)$ 

Iron content in selected tissues. \*P<0.05



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500 PPM  $114 \pm 19.3$ 

 $(n = 8)$ \*\*



**A**

Figure 2: Distributions of zinc (ppb) due to lead exposure for (A) thirty days and (B) ninety days. Significant decreases in zinc concentration due to lead intoxication were observed at both time points in the various tissues assayed. \*P<0.05, \*\*P<0.01

The concentrations of nickel (ppb) in the selected tissues analyzed are presented in Figure 3. While long-term chronic (D) lead exposure resulted in significant nickel reduction in liver at 50 the ppm dose group only and marrow in the 500 ppm dose group only  $(P<0.05)$ , short -term acute  $(C)$  exposure to lead did not yield any significant changes in nickel levels in liver, kidney or marrow tissues at any dose.



Figure 3: Levels of nickel in blood, liver, kidney and marrow (ppb) as a result of exposure to lead for 30 and 90 days. No significant differences were observed for the shorter (C) time period. On the contrary, significant differences were observed in the liver and marrow for the longer treatment period (D). \*P<0.05.

Similarly, cobalt levels (ppb) were not significant changed for the thirty days treatment group. Though, cobalt in the liver was significantly altered in the groups treated **with lead for ninety days. For the 30-day treatment group, cobalt decreased 34 % in liver,** and increased 12.5 % and 2.5-fold in kidney and marrow respectively. Blood, liver and marrow level cobalt decreased by 84 %, 85 % and 83 % respectively whereas that of the kidney increased by 7 % in the 90-day treatment group (data not shown).



Figure 4: Copper concentration in blood, liver, kidney and marrow (ppb) due to lead poison for 30 and 90 days. Copper levels in the short term treatment group were statistically changed only in the liver (E) whereas the other group was changed both in the blood and kidney. \*P<0.05,  $*P<0.05$ .

Figure 4 shows Cu (ppb) distribution in selected tissues at (e) 30 days and (f) 90 days. The 30-day exposure group showed a significant Cu reduction in the liver  $(P<0.05)$ . Also, rats treated for 90 days showed marked changes in blood, liver and kidney, only in blood and kidney were copper reduced significantly.

The next several figures illustrate the relationship between various lead concentrations and essential trace metals in specific tissues. Though these relationships are too simplistic with respect to the direct influence of lead levels on the levels of these other metals or for explaining mechanisms involved in lead action, they nevertheless provide useful information as to the metal-targets of lead. Figures 5 and 6 shows scatter plots of liver concentrations of lead on the horizontal axis against zinc, nickel and copper concentrations on the vertical axes for 30 day and 90 day exposures, respectively. Both figures were fitted to both linear and polynomial functions and the best fuction selected. The short-term (30d) exposure groups have  $R^2$  values ranging from 0.093 to 0.6109. Similarly, the 90d experimental groups had  $R^2$  values in the range of 0.0245 to 0.2311. The Pb-Ca and Pb-Fe relationships were curvilinear in nature. Although two of the long term treatment groups reveal a weak negative correlation, the majority of the treatment groups showed a quadratic relationship indicative of dose-response, thus, reflecting the most accurate response of the cell to lead toxicity. These results confirm that the response of living organisms to the toxic effects of lead, like many other contanminants, is not likely to be a linear relationship. Whereas some of the treatment groups show positive associations, the others demonstrate negative interactions. Interactions of metals in blood and marrow were all negative. In contrast, some liver associations were positive, in the cases of Ca and Fe (Figure 7) at 90d of exposure Pb-Ca. in the kidney.

In Table 7 above, lead excretion through the feces increased 10 orders of magnitude from the 0 ppm to 50 ppm to 500 ppm treated groups. Clearly, this observation agrees with what we would expect that the more Pb exposure there is in a population to a particular chemical, the greater excretion amounts of that particular chemical.



Figure 5: Plots of Pb (ppb) versus (G) Zn, (H) Cu and (I) Ni (ppb) in liver for 30 days. Data fit to a polynomial function.



Figure 6: Plots of Pb (ppb) versus (J) Zn, (K) Cu and (L) Ni (ppb) in liver for 90 days. Data fit to both linear and polynomial function.





Figure 7: Plots of Pb (ppb) versus (M) Ca and (N) Fe (ppb) in the marrow for 90 days. Data fit to a polynomial function.

 $\mathfrak{S}$ 

## Table 7

Lead, copper, nickel and cobalt levels in feces. \*P<0.05, \*\*P < 0.01



The fecal amounts of zinc, copper, nickel and cobalt extreted were all greater in the control groups than in the the treated groups. All three metals were minimally excreted in the 50 ppm exposure group relative to the controls.

Compared to the controls, zinc, copper, nickel and cobalt excretion were 27 %, 16 %, 38 *%* and 27 % less, respectively, in the low dose treatment group. Similarly, excretion of these metals was reduced by 23 %, 5 %, 34 % and 19 %, respectively, in the high dose group relative to controls

#### Histopathology

Images of H and E stained cells of the liver and kidney are shown in Figure 8. Necrotic tissue which is evidenced by nuclear shrinkage and fragmentation patterns were observed mostly in the long term treated group. The kidney tissues appeared to suffer more damage than the liver even at the same treatment. This is shown by H&E as hydropic degeneration and increase basophilia in renal epithelium.

## Discussion

Generally, the degree and duration of lead intoxication does not appear to be reflected in the body weight gain of the test species, although morphometric indices of tissue weights and their relative contribution to the total body weight gain might prove to be useful measures of frank toxicity to lead. In this study, no alterations were observed in total body weight gain, but rather, kidney and liver weights and their ratios of weights to total body weights at higher lead concentrations were affected. A change in body weight due to lead exposure is not clearly shown in the literature.

A: 30d, 90d Liver Control





Figure 8: H&E staining X 80 (C) necrotic liver showing both pyknosis and karyorrhexis (D) necrosis of the kidney characterized hydropic degeneration and basophilia of the renal tubule epithelia. Both were exposed to  $500$  ppm  $Pb^{2+}$  for 90 days. The 50 ppm treated in liver and kidney respectively (E and F) also shows signs of pyknosis and karyorrhexis, though not as pronounced.



D: 500 ppm 90d Kidney



Figure 8 - Continued





Figure 8 - Continued

For instance, whereas Miller *et al* [235], Corpas *et al* [232] and others did not find reduction in body weight as a result of increasing lead concentration, Adonaylo and Oteiza [236] observed lower body weights of rats intoxicated with lead. According to Corpas and coworkers, lack of evidence with respect to body weight gain does not necessarily mean lead has no effects. Instead the effects are rather intrinsic and continuously affecting the animal during its entire life at the tissue and cellular function level.

Tissue distributions of lead were consistent with applied doses and duration of exposure. In both time points, the 500 ppm exposed group accumulated greater lead levels than either the control or 50 ppm treatment groups in all tissues analyzed. Surprisingly, accumulated lead levels in kidney were almost the same irrespective of treatment time (30d vs. 90d). Lead accumulated in these tissues is a result of conjugation in the liver with metallothionein or other metal chelating proteins which are passed on to the kidney and other tissues, with the balance of the Pb being excreted either in feces or urine [230]. It is generally reported in the literature that a greater proportion of lead is excreted through the feces than urine [5]. The very high fecal content in our experimental animals is consistent with this obervation. Lead either bound to plasma proteins or the free salt form is introduced to the kidney through the apical membrane and in these forms it is cannot readily leave the blood stream through the basolateral membrane [237], Another reason for the relatively high levels of lead accumulation in the kidney might be the indirect activities of metallothioneins and glutathione. These proteins have cysteine in their configuration which has an affinity for heavy metals [238]. Other workers have found that lead bioavailability in kidney and brain relates to binding to a low molecular

weight protein that is rich in aspartic and glutamic dicarboxyl amino acids [242] other than metallothionein. According to Zalups [238], heavy metals such as lead can induce the synthesis of metallothionein and glutathione within the liver which then traps the metal ions within the cell by forming peptide conjugates. During the process of liver cell renewal, the heavy metal-metallothionein or metal-glutathione complexes are released into the systemic circulation and then delivered to the kidney [239]. This type of cycle is likely to result in higher levels of metal ions in the kidney than in most other organ systems.

The importance of trace metals to the normal function of the cell cannot be over emphasized. Essential trace metals exhibit a narrow range of concentrations within which they must function. Deficiencies result when their levels are below that level and when it is greater than that range of concentrations, the metals are toxic. As a result, trace metals are tightly controlled in the body to maintain homeostasis and normal cell metabolism. Levels of cobalt, copper, nickel and zinc were altered in the various tissues analyzed as the result of lead exposure in the corrent expeiments. It appears the metals most affected by lead intoxication are copper and zinc particularly during the long-term exposures. This is supported by the authors Goyer [241] and Peraza *et al* [234].

The interaction of lead with cobalt, cupper, nickel and zinc were all observed in these experiments. Cell homeostasis is maintained by adequate levels of cations such as Zn(II), Cu(II) and others. These metals are involved in various regulatory and physiological activities. Garza *et al* [240] notes that lead is able to substitute for other polyvalent cations that are involved in important molecular processes. According to them, lead has a higher binding affinity for chemical functional groups that would

coordinate divalent cations in proteins. The ionic interaction of lead with these negatively charged acidic amino acid residues making it possible for lead to bind a wide variety of proteins results in a change in the structure and electric charge balance of proteins. The results presented here suggest that the interactions of lead with Zn Cu, Ni and Co are time dependent. The entire 30 day treatment group showed that increasing lead concentration results in no increases of these essential divalent metals in rat tissues. The opposite was however true for the 90 day exposure group. In these animals the levels of Zn, Cu and Co were lowered. These trends are quite different from what was seen in other studies. For example, Goyer [241] reported that lead increases the excretion of zinc and reports a negative correlation between blood lead levels and the activity of zinc-containing heme enzymes. They suggest that lead replaces zinc on the enzyme. Again, he reported that lead exposed rats showed significant reductions in copper levels in the liver.

Examination of hepatic histopathology produced no evidence of necrosis or changes in cellular structure of hepatocytes in the 0 ppm and 50 ppm for the short-term exposure period. In contrast, both necrosis and alterations in cellular structure and cell distribution were observed in the liver and the kidney in both the 50 ppm and 500 ppm  $Pb^{2+}$  90-day treatment groups. Analysis of liver and kidney of long-term exposed lead groups showed varying degrees of necrosis. The 90 day 500 ppm  $Pb^{2+}$  treated group showed signs of pyknosis and karyorrhexis of the liver. In the kidney, hydropic degeneration and basophilia of the renal tubule epithelia were observed. The 50 ppm treated in liver and kidney also revealed signs of pyknosis and karyorrhexis though these effects were not as pronounced as in the high dose groups. Literature reports suggest that the kidney is the most susceptible organ to lead toxicity. The work by Corpas *et al* [232],

found no abnormalities in the liver structure or liver deposition of lead in young neonates intoxicated with lead. On the other hand, Jarrar and Mahmoud [230] found lead to have caused tubular and glomerular alterations in kidney. They observed anisokaryosis, nuclear pyknosis, and vacuolization among other histopathological effects in the kidney.

In summary, effects associated with lead exposure were observed to be both dose and time dependent in our study. Short-term exposures did not produce as serious damage, as did long-term, high dose intoxication levels. Histopathology changes in tissue morphology were consistent with the lead concentration in liver and kidney. For instance, high lead concentration of lead in kidney cells results in pronounced cell necrosis in varied forms. There was a positive correlation between lead levels in tissues and the levels of other trace metals in the short-treatment period. However, a negative correlation between lead levels and other trace element levels in tissues was observed for chronic exposure levels in rat.

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## CHAPTER IV

# GENE EXPRESSION ANALYSIS BY AFFYMETRIX MICROARRAY GENE CHIPS

#### Microarray Background Information

Recently toxicologists have employed molecular tools in the assessment of risk to humans using different animal models. These molecular tools involve the measurement of so-called expression biomarkers. Biomarker levels in an organism can provide indications of contaminant bioavailability (if organism is still in the natural environment), exposure levels and a whole host of possible effects at the molecular level. Biomarkers could be protein levels or activity or enzyme activity and very recently, the expression or suppression of relevant and specific genes. About a decade ago, gene expression analysis was accomplished on a one gene at a time basis. The emergence of DNA chip technology has dramatically increased the number genes that can be studied simultaneously. It has afforded toxicologists the opportunity to study thousands of genes at the same time thereby enabling them to examine entire pathways and associate transcription factors using a suite of selected target genes [209]. The acceptance of DNA chip technology for examination of molecular and cellular processes is demonstrated by the increasing number of published papers in the literature that employed this technique.

The term 'gene expression' refers to the transcription of DNA sequence-encoded information into mRNA that is subsequently translated into proteins that regulate cell function. In brief, gene expression involves transcription which also requires translation [210, 211], DNA templates are transcribed by RNA polymerases into mRNA molecules while translation is carried out by enzymes associated with the ribosomes. Genes that code for mRNAs and other RNAs are regulated in order that they are expressed adequately and appropriately to meet the needs of the cell such as growth, proliferation or at maintenance and this process is dynamic. This highly dynamic gene expression process is controlled by changes within the cell, environment or disease states.

There are currently four main microarray types available in the market. These include expression profiling, single nucleotide polymorphisms (SNP), comparative genomic hybridization (CGH) and resequencing array instruments. Expression profiles are employed to examine gene expression alterations (up or down) due to different disease, intoxication or normal states or to compare gene expression variations in cells over time (growth and differentiation) and these latter measurement have applications in tumor classification, development of predictive or prognostic markers of disease or intoxication or in development of drugs. SNPs are used identify mutations or polymorphisms in a gene sequence that cause genetic variation and they have applications in the investigation of predisposition to genetic disease, disease progression monitoring and selection of DNA-based drugs. Similarly, CGH is used to detect genetic amplifications or deletions of genes or examination of the copy number changes in a specific gene. It can be applied in tumor classification, assessment of risk, prognostic and predictive markers development. Finally, re-sequencing arrays are employed in sequencing portions of the genome. This is used for the assessment of germline mutations or to identify somatic mutations in cancer [211].

Gene chip DNA microarray provides a rapid means of quantifying the level of messenger RNA (mRNA) abundance in a tissue sample. Quantified mRNA content is an indication of gene expression levels because mRNA is directly transcribed from the DNA

[212]. DNA microarray or "chip" consists of an orderly arrangement of equidistant microscopic DNA spots that are attached to a solid surface like glass or plastic or silicon chip. This chip is made up of thousand of distinct sequences referred to as "probes" found in defined locations on a grid. Complementary DNAs (cDNAs), oligonucleotides of varying length or genomic sequences that are fluorescently or radioactively labeled is hybridized to corresponding probes that recognize and attach to the solid support [211, 212]. Subsequently, an array consisting of thousands of immobilized spots at predetermined grid locations is generated via pins or inkjet technology or *in situ* photolithographic synthesis of oligonucleotides [211-215]. The basic premise is that, nucleic acids molecules show a highly selective binding to their complementary sequences. As a result, the addition of the "target" (pool of mRNAs in the sample-derived nucleic acid sample) to the chip surface leads to a highly parallel searching and sorting of molecular partners, that is, probes linking with their respective complementary targets and this selection process is made quantitative through the presence of millions of identical probes at each single location on the array. A fluorescent-based detection scheme is then employed to quantify mRNA transcript level. This typically involves the excitation of fluorescent-labeled mRNA molecules with a laser. The fluorescence emission is digitized with a fluorescence scanner and the intensity data is subsequently transferred to a computer-linked database [211, 212, 216],

The amount of data generated from microarray experiments is usually large and this has resulted in a parallel growth in the field of bioinformatics. Over the last few years, the mathematical and statistical approaches and corresponding software packages for analyzing microarray data have been increasing rapidly. Irrespective of the software or analysis approach adopted, almost all gene expression studies utilizing microarrays can be grouped into the categories of class comparison, class prediction, class discovery and pathway analysis [216, 217]. Class comparison involves identifying genes that are differentially expressed. It is intended to determine whether gene expression profiles are different among samples selected from predefined classes. Class comparison is similar to class prediction except the latter is focused on developing a statistical model to predict classes to which new samples might belong using expression profiles. Class prediction is useful in medical problems of diagnostic classification, prognostic prediction and disease treatment selection. The purpose of class discovery tools is to identify novel sub-types within a population based on the theory that similar clinical and morphological specimens that vary biologically may be discernible at the molecular level. This tool allows for identifying groups of co-expressed genes and detecting patterns in expression profiles using clusters analysis or classification into sub-groupings. Finally, pathway analysis provides the opportunity for identifying genes that are co-regulated or which are located along the same biochemical pathway [216].

A number of microarray platforms are currently in use. These include Affymetrix, conventional spotted arrays, Agilent and CodeLink™ Bioarray platforms. The Affymetrix GeneChips have extensive genetic content and a high level of reproducibility. The GeneChip contains short single-strand DNA segments, oligonucleotides or "oligos" that are chemically synthesized on the chip itself. High-density arrays are made using lightdirected DNA synthesis which employs a combination of photolithography and solidphase DNA synthesis methods. GeneChips have an advantage over traditional microarrays in that they are synthesized *in silico* so that synthetic management of clone

libraries is insured and this minimizes or eliminates the risk of tube, clone, cDNA or spot misidentification. In addition, they exhibit good signal-to-noise ratios, a wide dynamic range and reduced cross-hybridization because multiple independent oligonucleotides are designed on to the chip surface to hybridize to varied regions of the same mRNA.

Although microarray technology has been demonstrated to be a powerful technology, for studying biological processes in the cell, there are still challenges and limitations that the user should be aware of. For example, understanding the complexity of biological systems with gene expression profiling requires a good understanding of bioinformatics, molecular biology and other fields of study. Also, the huge amount of data generated from typical microarray experiment presents a greater opportunity for user errors or misinterpretation. Thus, the accuracy, reliability and reproducibility of the resulting data depend heavily upon tightly managed good laboratory practices and quality controlled of experiments. Due to their sophistication, microarray experiments are currently expensive [211, 218]. Other sources of error encountered in microarray experiments include the quality and quantity of starting biological tissue samples, chip production, probe hybridization, image quantification, normalization and data interpretation. Currently there are no research community accepted, standardized processes to address inter-experimental variability in microarray studies.

#### Introduction to Study

The importance of lead as an environmental chemical species exhibiting various toxicity symptoms has been well documented. [227-230]. Lead targets diverse organ systems such as the skeletal, hematopoeitic, renal, endocrine and nervous systems [5],
thereby partitioning between soft and hard tissues with approximately 95 % and 70 %, respectively, found in the bones and teeth of adults and children. Bone then serves as a pool to replenish excreted lead from the blood. Some adverse conditions associated with lead poisoning include DNA damage, neurological impairment, abnormal heart function, osteoporosis among others [232-233]. In addition, weakened immune defense system, sterility in male and females, abnormal fetal development, and glycosuria are also associated with chronic lead poison.

Lead perturbs the functions of enzymes and proteins of varying types. Studies have shown that, lead exerts its influence physiologically and biochemically as a mimetic agent for essential elements such as calcium, iron and zinc. For instance, it directly interferes with zinc and iron in the biosynthesis of heme, Pb binds to sulfhydryl group protein enzymes and thus interferes with protein synthesis either directly or indirectly [232-233]. Lead binds to different classes of transport proteins including metallothionein, transferin, calmodulin and calcium-ATPase. By associating with these proteins, it is transported to specific target tissues where it causes its damage. Lead transport and assimilation is optimum when there is the deficiency of iron, calcium, or zinc because lead is able to displace these metals during specific physiologic processes [234]. The interaction of lead and calcium alters the proper functioning of calcium channels and ionic pumps. This leads to inadequate energy generation because of mitochondrial damage. Lead also causes defects in protein folding because of its binding to sulfhyryl groups and it can alter the structure of DNA binding motifs by disrupting their conformation [240].

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Recently toxicologists have employed molecular tools such as microarrays in the assessment of risk to humans using different animal models. These molecular tools involve the measurement of so-called expression biomarkers. Biomarker levels in an organism can provide evidence of contaminant bioavailability (if organism is still in the natural environment), exposure and also a variety of possible effects. Biomarkers can include such parameters as protein levels or activity in cells or enzyme activity in a specific tissue and more recently, the expression of relevant and specific genes.

Until recently, gene expression analysis was limited to the analysis of one gene at a time. The emergence of DNA chip technology has dramatically increased the number of genes that can now be studied simultaneously. Gene chips have afforded toxicologists the opportunity to study thousands of genes at the same time thus enabling them to examine entire metabolic or signaling pathways and associated transcription factors with target genes [209]. The primary objective of this project is to analyze and profile global gene expression patterns in Fisher 344 rat liver exposed to lead  $(Pb^{2+})$  at different doses and over different time periods of exposure using Affymetrix Microarray Analysis.

Lead can alter the function or activity of genes. For instance Korashy and El-Kadi [148] reported the induction of Cyp1a1 gene expression as a response  $Pb^{2+}$  and other metals. This process they attributed to an AhR-dependent process via transcriptional and post-translational mechanisms. Other workers attribute the dysregulation of genes by lead to feedback mechanisms involving interference of Pb with calcium-binding proteins or perturbation of the activity of protein kinase C (PKC) which in turn alters the transcriptional regulation of mRNA transcripts regulated by PKC [252, 253].

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Gene expression analysis of a specific gene provides an estimate of the number of mRNA molecules obtained from DNA transcription of that particular gene in response to a stimulous. The assay process involves mRNA isolation from an organism's tissues, and the mRNA transcripts are then converted to labeled polynucleotides which are placed on microarraysand hybridized with the complimentary sequence tags on the chip. Affymetrix Microarray employs a high-density oligonucleotide arrays that are fabricated using *in-silico* synthesis of short oligonucleotide sequences on small glass chip by lightdirected synthesis. Represented on the chip are known genes or potentially expressed sequences of 11-20 unique oligomeric probes which are 25 bases in length for each gene at different loci on the chip. The target sequence is a group of probes that correspond to a given gene or small group of highly similar genes. Targets are usually labeled enabling them to bind by hybridization to the probes on arrays with which they share sufficient complementary sequence [216].

# Materials and Methods

#### Experimental Design

Forty-eight six weeks post-weaning male Fisher 344 rats were exposed to 0 ppm, 50 ppm or 500 ppm of  $Pb^{2+}$  in the form of lead acetate through drinking water *ad libitum* for 30 or 90 days, respectively. The control drinking water was distilled water. Prior to commencing treatments, the rat diet, control and treatment drinking water were analyzed by ICP-MS for lead contamination and for verification of accurate dose levels. Rats were housed at the Western Michigan University Animal Facility. The animals were treated according to the principles outlined in the NIH Guide for the Care and Use of Laboratory Animals. There were eight rats which were randomly assigned to one of the three treatment groups. At the end of each exposure period (30d or 90d), rats were euthanized with CO**2** and blood was collected by cardiac puncture for serum analysis using ICP-MS. Livers were excised and snap frozen in liquid Nitrogen. Total RNA was isolated from rat livers using a Qiagen RNA Isolation kits for subsequent cDNA syntheses.

# Total RNA Extraction

Total RNA was isolated from rat livers using a Qiagen RNA Isolation kit [247]. Between  $0.05 - 1g$  liver samples were homogenized in RLT buffer. RLT buffer denatures and inactivates RNases. The RNA is then allowed to bind to a silica-gel membrane and finally eluted with RNase-free water. Total RNA was quantified using the UV-vis spectrophotometer at 260 and 280 nm absorbance and control eletrophoretic gels were run for RNA quality assurance purposes.

### Microarrav Experiment

Double stranded cDNA was synthesized from total RNA samples using reverse transcriptase and oligo dT primer. Then, this synthesized cDNA served as a template for T7 polymerase in an *in vitro* transcription (IVT) reaction in which amplified and biotin labeled antisense cRNA molecules were produced. These cRNA molecules were purified, fragmented and hybridized to GeneChip® Rat Expression Array Set 230 (RAE 230A) and subsequently scanned as described in Affymetrix GeneChip™ one-cycle eukaryotic target labeling assay [248]. The RAE 230A chip contains over 30,000 transcripts and variants representing more than 28,000 rat genes which were sensed by the instrument

and incorporated into the data. It consists of 31,042 probe sets with probe pairs of 11 and 25-mer oligonucleotide probe length.

### Data Analysis

The Affymetrix microarray suite (MAS) software was used analyze the image data (.dat files) for computation of single intensity values for every probe locus on the arrays, and saved as .cel files. The fluorescence intensity due to proper hybridization of each target was estimated by examining the difference in fluorescence intensities in perfect match and mismatch probe pairs present at each locus on the chip. Then, intensities were scaled for all valid probes using a default target signal threshold of 500 units resulting in CHP data. These were saved as EXCEL files and imported into Biometric Research Branch - Array Tools (BRB-ArrayTools) software [249] for data collation, filtering, normalization and gene sub-setting. Genes which passed through the above quality assurance process were then analyzed for differential expression by scatterplot analysis. Data collation involved importing data and aligning genes. BRB-ArrayTools converts either EXCEL or CHP files into a tab-delimited format. Individual arrays were filtered using spot filters. Spots on arrays which had signal intensities less than 10 were considered below a threshold and not analyzed further. A log base 2 transformation was applied to all data and each array was normalized to a reference array such that log-intensity differences between any experimental array and the reference array equaled zero over all the genes on the array. The reference was chosen to be the median array. Minimum gene fold-change filter was used to exclude probe sets from all arrays which did not meet the following criteria: the minimum fold change less than 20 %

of expression data values at least a 1.5-fold change in either direction from the gene's median value. Over 2300 genes met these criteria and thus were used in our subsequent analysis of differential gene expression and gene expression profiling.

#### Results

## Differential Gene Expression Analysis

Figure 9 shows all of the greater than 2-fold differentially expressed genes of rats exposed to lead through drinking water. Figure 9A, E and B, F present the data for rat livers treated with 50 and 500 ppm  $Pb^{2+}$ , respectively for 30 days, whereas 9C, G and D, H represent data for rat livers that were exposed to 50 and 500 ppm  $Pb^{2+}$ , respectively for 90 days. Differentially expressed genes are those falling outside (above or below) of the pair of marker lines. These genes indicate expression ratios greater than 2- and 10-fold difference.

The differential gene expression in Fisher 344 rat liver exposed to varied concentrations of lead for both 30 and 90 days are shown in Table 8. At 2-fold expression difference, the number of genes either up/down-regulated appear to be similar for both treatments during the 30-day exposure period. Surprisingly, the 90-day, 50ppm treatment showed less than half the number of differentially expressed genes as compared to the 30 day treatment.



Figure 9: Genes expressed in the liver of Fisher 344 rats exposed to lead through drinking water for 30 days (A) 50 ppm  $Pb^{2+}$ , (B) 500 ppm  $Pb^{2+}$  or for 90 days (C) 50 ppm  $Pb^{2+}$ , (D) 500 ppm  $\rm Pb^{2+}$  at two-fold change and (E) 50 ppm  $\rm Pb^{2+}$ , (F) 500 ppm  $\rm Pb^{2+}$  or for 90 days (G) 50 ppm  $Pb^{2+}$ , (H) 500 ppm  $Pb^{2+}$  at ten-fold change.



Figure 9 - Continued



Figure 9 - Continued

In contrast, the 90-day 500ppm group exhibited over one thousand genes that were differentially expressed at 2-fold threshold level and more than twice the number of genes as the other treatment groups at the 3-, 5-, or 10-fold threshold levels. About 8 % of total transcripts after filtering and gene sub-setting were changed by ten-fold either by up or down regulation (Table 9).

# Table 8



## Transcripts whose expression levels were either suppressed or enhanced as a result of lead exposure.

#### Transcriptional Profiling

### Unsupervised Cluster Analysis

Clustering involves merging or grouping of samples or genes into subgroups that exhibit similar patterns of responses than the other experimental groups. In this study, hierarchical unsupervised clustering algorithm was adapted for comparing the gene expression profiles across all of the set of samples. By defining a measure of pair-wise similarity or distance between expression profiles, hierarchical clustering procedure produces sequentially nested merging of genes that are represented by a "dendogram". A "heat map" image of the log-ratio values with samples sorted according to dendogram order was generated [216, 249]. The results are shown in Figure 10A, B.

# Table 9



Selected genes whose expression levels were either decreased or increased ten-fold.

In Figure 10, snapshots of selected genes obtained via un-centered hierarchical clustering reveal log-ratio values that range from  $+4$  to  $-9$  for the long-term exposed rat group while the short-term treatment group had log-ratio values ranging from +6 to -7. The image plot matches log-intensity values with different colors. Most of the positive log-intensity values are coded red while the negative values are coded blue. In between the extremes of either +4 to -9 or +6 to -7 are yellow, green and light blue. Some of the genes captured by the snapshot are listed in the figure. Correlation coefficients on the dendograms range from  $+1$  to  $-0.2$  and this relates to node width and distance from origin of the gene tree. Increases in correlation among genes leads to declining node width and a reduction in distance from the origin of the gene tree.



Figure 10: Hierarchical clustering using uncentered correlation and average linkage of genes across a set of lead treated hepatic samples. Figure showing dendograms and snapshots of heat map image for (A) 30 days treatment period and (B) 90 days exposure time.



Figure 10 - Continued

Multi-dimensional scaling was used to compare pair-wise similarities between tissue samples. This analysis is similar to clustering analysis because the objective is to determine the relationships between samples without forcing them into specific clusters. The outcome is an un-centered correlation samples shown as a three dimensional rotating cloud of spheres. Samples that have similar expression profiles are close together. Figure 11 is a graphical representation of multi-dimensional scaling of samples.



Figure 11: A graphical representation of multi-dimensional scaling of hepatic gene expression profiles of lead treated rats showing 30-day exposed rats (red spheres) and 90 day treatment groups (purple spheres).

### Gene Ontology Analysis

In order to identify genes that were significantly correlated to such quantitative experimental parameters as dose levels and length of exposure, a Spearman Correlation Univariate Test was conducted. In the test a measure of correlation and parametric pvalues were calculated by employing Spearman correlation coefficients [249]. These results are presented in Table 10.

In the Spearman Correlation Univariate Test at least ten genes were shown to correlate with either length of exposure period or with dose levels with p-values less than 0**.**01**.**

# Table 10

# Transcripts that were significantly correlated with either Pb dose-levels or with duration of exposure.



Some of these genes include Sgk, Atp6apl, Foxa2, Kpna2, RpslO, Gc and Ap2sl and these genes are involved in such gene ontology processes as sodium ion transport, apoptosis, protein amino acid phosphorylation, regulation of transcription, protein binding, protein transporter activity and vitamin D metabolism. For those gene transcripts that correlated with treatment duration, correlation coefficients were either  $+0.87$  or -0.87. The dose level correlated group of genes had correlation coefficients of -0.934, -  $0.856, +0.895$  and  $+0.856$ .

The Gene Ontology (GO) comparison tool was used to show the relationship between and the association of genes with respect to each other in function and biochemical pathways. This analytical tool provides GO categories of differentially expressed genes among samples than would be expected by chance. The procedure uses a functional class scoring approach. For each gene in the GO category, a p-value was calculated followed by using so-called LS and KS statistics to summarize the set of pvalues of a GO category. LS is the average negative natural logarithm of p-values in a class while KS (Kolmogorov-Smimov) statistic is employed in testing for uniform distribution of p-values. To determine the statistical significance of a GO category containing n number of genes, the empirical distribution of these summary statistics in random samples of n genes is computed. A 0.005 default p-value was used in this computation [249]. The results of the GO analysis of the data from the Lead exposed rat tissues are plotted as pie charts for the 30- and 90-day treatments.



Figure 12: Gene ontology category difference of (A) 30-day treatment group and (B) 90 day treatment group.

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Figure 12 presents the gene ontology categories for the two treatment groups. The short-term treatment group showed only three GO categories whereas the long-term exposure group showed 15 categories. The short-term exposure GO categories found were negative regulation of transcription, transcription from Pol II promoter and negative regulation of transcription from Pol II promoter in which each category was represented by 13, 34 and 8 genes, respectively. Some of the categories for the 90 days treatment groups are vitamin biosynthesis and metabolism, porphyrin biosynthesis and metabolism, DNA metabolism, carboxylic acid metabolism and biotin biosynthesis and metabolism. The number of genes in each category ranged from 2 % (11 genes) to 15 % (91 genes). The carboxylic/organic acid metabolism category had the highest number genes affected, whereas S-adenosylmethionine-dependent methyltransferase activity had the lowest percentage of genes affected by lead treatment in its category.

The gene ontology comparison tool provides for the option of grouping genes by metabolic or signaling pathways which are likely to be significantly effected instead of by GO categories. In this case, the affected genes are group by BioCarta pathways. "BioCarta" is a trademark of BioCarta Incoporated. Pathways found to be significantly impacted by lead intoxication include: regulation of eIF4e and p70 S6 Kinase, control of skeletal myogenesis by HDAC and calcium/calmodulin-dependent kinase (CAMK), role of MEF2D in T-cell Apoptosis and regulation of PGC-la (Table 11). The regulation of Eif4e and p70 S6 kinase pathway was observed to have the following genes: Mapkl4, Pdk2, Pdkl, Aktl, Ghr, Pten, Eif4al, Eif4ebpl, Ebp, Mapkl and Eif4e. Those genes found to control skeletal myogenesis are: Ywhah, Mapkl4, Ppp3ca, Aktl, Calml, Igfl, Cabin1, and Pik3r1.

Table 11

Pathways significant at nominal 0.005 levels of LS Permutation test or KS Permutation test.



The pathway "Role of MEF2D in T-cell Apoptosis" has: Ppp3ca, Calml (1369936\_at, 1369937\_at, 1370368\_at, 1387772\_at) and cabinl. Finally, the regulation of the PGC-la pathway has gene components: Ywhah, Ppp3ca (1373479\_at and 1368277\_at), Calm1 (1369936\_at, 1369937\_at and 1387772\_at).

### Pathway Descriptions

### Regulation of eif4e and p70 S6 Kinase

Synthesis of proteins in mammalian systems is controlled by changes in the phosphorylation states of eukaryotic initiation and elongation factors (elFs and eEFs, respectively) as well as other regulatory proteins. The p70 S6 kinase plays a crucial role in regulation of cell-cycle progression, cell survival and control of mRNA translation through phosphorylation of the 40 S ribosomal S6 protein [256-257]. In other words, the phosphorylation/inactivation of p70 S6 kinase and phosphorylation/inactivation of 4E-BP1 is essential for protein translation initiation.

Regulation of eIF4E complex, p70 S6 kinase and eEF2 is linked to the mammalian target of rapamycin (mTOR). mTOR which is composed of several regulatory signaling pathways is a multi-domain protein of 290 kDa with regions that are similar to lipid kinases of the phosphoinositide kinase family [257]. For example, a major mTOR signaling pathway involves the 70 kDa ribosomal protein S6 kinase that is reported to regulate the translation of a set of mRNAs. These have 5' terminal tracts of pyrimidines and encode for ribosomal proteins and elongation factors. A second example involves eIF4E-binding proteins (4E-BPs), which interacts with eIF4E and prevents it from interacting with a scaffolding protein eIF4G that is required for assembly of the

translation-factor complex eIF4F. The presence of insulin activates translation leading to the phosphorylation of 4E-BP1 through a pathway inhibited by rapamycin and as such involves mTOR, thereby leading to dissociation of eIF4E so that it becomes available to bind to eIF4G [257-258].

# Control of Skeletal Myogenesis by HDAC & Calcium/Calmodulin-Dependent Kinase  $(CAMK)$

Differentiation of myoblasts depends on myocyte enhancer factor-2 (MEF2) family of transcription factors association with positive and negative partners. The members of MEF2 family of transcription factors play a central role in skeletal muscle differentiation as well as serving as the end point for diverse intracellular signaling pathway that regulate myogenesis and muscle hypertrophy. MEF2 has four protein types namely; MEF2A, -B, -C, and -D. These proteins share homology in amino-terminal MCM1 agamus deficiens serum response factor (MADS) domain, which mediates DNAbinding, dimerization and cofactor interactions [263].

Histone acetylation/deacetylation is an important process in gene expression regulation. Histones are acetylated by histone acetyltransferases (HATs) leading to nucleosome relaxation so that transcription is stimulated. In contrast, the activity of HATs are inhibited by histone deacetylases (HDAC) resulting in transcription repression. HDACs are classed as I or II depending on size, sequence homology and formation of distinct complexes. In class I are HDACs-1, -2 and -3. These are ubiquitously expressed. Class II HDACs include HDAC-4, -5, -6 and -7 that are most abundant in heart, brain and skeletal muscle. Class II histone deacetylases HDAC4 and HDAC5 are known to repress transcription. Skeletal myogenesis is activated as a result of MEF2 associating with basic

helix-loop-helix transcription factors like MyoD. When these MEF2 proteins interact with HDAC4 and HDAC5 deacetylases, transcription of MEF2-dependent genes are repressed. In contrast, calcium/calmodulin dependent kinase (CAMK) signaling stimulates myogenesis through dissociating MEF2-HDAC complexes [262-265].

A model published by McKinsey *et al* [262] explains the how HDAC, MEF2 and CAMK interact to allow for myogenesis. This model illustrates the control of signal-dependency of myogenesis. Muscle differentiation is blocked by HDAC through repressing the transcriptional activity of MEF2. CaMK phosphorylates HDAC5 and stimulates its nuclear export thereby freeing MEF2 to cooperate with MyoD to activate genes required for skeletal myogenesis.

### Role of MEF2D in T-cell Apoptosis

Although apoptosis of the T lymphocytes can be induced by multiple signaling pathways, Youn and coworkers [259] report a calcium-dependent expression of steroid receptors Nur77 and Norl that mediate T cell receptor (TCR)-induced apoptosis of thymocytes. The expression of orphan steroid receptor Nur77 requires an increase in intracellular calcium levels. Besides, two calcium regulated DNA elements in the Nur77 promoter were found to be consensus binding sites for MEF2, thus implicating MEF2 as a calcium-dependent transcription factor for Nur77 expression.

Calcineurin, an essential cytosolic calcium transmitting signal is activated by calcium and calmodulin. Cabin1 (calcineurin binding protein) binds to activated calcineurin and also interacts with myocyte enhancer factor 2 (MEF2) and calmodulin in a mutually exclusive way. Interaction of Cabinl with MEF2 suppresses MEF2 transcriptional activity via the recruitment of the mSin3 corepressor complex using the NH**2**-terminal region of Cabinl. Nevertheless, high calcium levels, allows for calmodulin to bind cabinl so that MEF2 is free to recruit coactivator p300 for transcriptional activation of MEF2 targets [259-261]. Similarly, Youn and Liu [260] also reports noted at least two mechanisms by which Cabinl represses the activity of MEF2. First, cabinl recruits mSin3 along with HDAC1 and HDAC2. This inhibition can be reversed by histone deacetylases. Secondly, Cabinl binds to MEF2 at the N-terminal MADS/MEF2 domain leading to competition for against coactivator p300 for MEF2 binding in the absence of calcium.

Youn and Liu stated that TCR-induced expression of Nur77 family of proteins results in thymocytes apoptosis. The absence of TCR signal leads to cause Cabinl silencing Nur77 promoter silent. But this inhibition is relieved by a second messenger calcium in response to TCR signaling. MEF2 is bound to Nur77 at all times and in an unactivated T cells, MEF2 is found bound to transcriptional repression complex made up of Cabinl, mSin3, HDAC1 and HDAC2. TCR signaling and calcium influx then results in activated calmodulin binding to Cabinl, thus relasing it from MEF2, vacating the MADS/MEF2 domain for association with the coactivator p300. Therefore, calciumdependent association and dissociation of two opposing classes of enzymes tightly control Nur77 gene expression so that thymocytes only commit to apoptosis upon TCR signaling [259-260].

### Regulation of PGC-la

Peroxisome proliferators-activated receptor (PPARy)-co-activator 1 (PGC-1) is a transcriptional cofactor involved mitochondrial gene regulation. PGC-1 is highly

expressed in tissues that have high energy demands and mitochondrial content. For example heart, kidney, brain, and brown fat. It was originally identified as important for regulating PPAR gene expression. PGC-1 is now known to also regulate nuclear respiratory factors (NRF-1, -2), uncoupling protein UCP2, hormone receptors; mineralocorticoid and estrogen receptors and MADS-protein MEF2C [266-267]

The coordinated interaction of PGC-1 with NRF-1 and PPAR factors controls program mitochondrial biogenesis and adaptive thermogenesis in brown adipose tissue and skeletal muscle [266-267]. Levels of PGC-1 were up-regulated in brown fat during exposure to cold. Scarpulla [268] reports that PGC-1 is involved in the control of blood glucose levels via the regulation of enzymes involved in gluconeogenesis. This was demonstrated in fasting mice in which PGC-1 was strongly up-regulated in liver. Also, an artificial over-expression of PGC-1 in cultivated hepatocytes and in vivo induced a series of gluconeogenetic enzymes [266, 268]. Scarpulla [268] explains that PGC-1 family members (PGC-1, PGC-1 $\beta$  or PRC) have a tendency to be induced by thermogenic, proliferative or gluconeogenic signaling pathways which can act on the appropriate target tissues. According to him, these coactivators can interact with DNA binding transcription factors leading to the expression of nuclear genes necessary for mitochondrial function and biogenesis. Activator-coactivator interactions can be direct or mediated by other proteins such as HCF and NRF-2 (GABP), so that the complexes formed may facilitate the recruitment of histone-modifying and RNA processing factors that contribute to the proper expression of gene targets.

The pathways outlined above show the importance of Pb in modulating phosphorylation and dephosphorylation events, calcium signaling, histone acetylation and

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deacetylation in gene transcription regulation. Phosphorylation is reported to be particularly important in the case of MAP kinases which are believed to be phosphorylated at the Thr-Glu-Tyr motif. The description of the first pathway affected in our study suggests that this dephosphorylation event might occur via Serine residues. Histone acetylation and deacetylation processes in gene transcription regulation are the main focus of the second pathway outlined in this study. This process is likely to take place in manner dependent on calcium signaling, because CaMK activates mRNA transcription by dissociating myocyte enhancer factor-2 transcription factors from histone deacetylases (HDAC) complexes. Also, the third pathway 'role of MEF2D in T-cell apoptosis' is dependent on the activity of calcineurin (Cabinl), a cytosolic calcium transmitting signal that is activated by calcium and calmodulin. For instance, high calcium content will result in the binding of cabinl to calmodulin so that MEF2 activates transcription. The last pathway identified in this study to be important in the study of Pb toxicity is important in the mitochondria and tissues that require high energy and this pathway was demonstrated to be important modulating gluconeogenesis enzymes. Since this pathway is important in the control of enzymes involved in gluconeogenesis, we might be seeing for the first time why gluconeogenesis is reported to be inhibited in rats exposed to Pb [232].

We can conclude from the above explanations that, the importance of calcium signaling in mediating Pb toxicity cannot be overestimated. This observation is consistent with our study hypothesis that the mRNA transcripts likely to be repressed or enhanced due to Pb exposure are essentially related to calcium signaling. Also, we can hypothesize the following for future study:

- 1. Pb controls mammalian protein synthesis via regulating phosphorylation or dephosphorylation events of eukaryotic elongation/initiation factors
- 2. Pb regulates gene expression through the regulation of histone acetylases
- 3. Pb regulates calcium dependent transcription factor myocyte enhance factor-2 (MEF-2)

## Discussion

The advent of microarray technology has offered molecular biologists and geneticists, toxicologists among others, the opportunity assess several thousands of genes simultaneously. This technology has been employed in studying molecular phenotyping, functional genomics, pharmacogenomics, developmental biology and DNA sequencing and mutational analyses [212]. Since lead is known to cause a broad range of adverse effects upon exposure, this method was adopted in assessing the differential gene expression profiles of Fisher 344 male rat liver due to lead intoxication at different dose levels and over different exposure periods. In the process, it has been possible to outline some pathways that are likely to be affected and thus are important in the continuing study of lead toxicity.

The data scatter-plots of gene expression values with reference to controls and the subsequent follow-up tables reveal that, about 42 % of all genes were up-regulated at 2 fold change. Approximately 8 % of these genes were either up- or down-regulated at 10 fold. For the short-term treatment period, both low- and high-dose groups showed a gene expression in approximately 1:1 ratio for 2-, 3-, 5-, and 10-fold changes, except the 5-

and 10-fold down-regulation values. In contrast, the long-term exposed group revealed a more pronounced pattern gene expression alteration in the high-dose group than in the low-dose group. The ratio of high- to low-dose for 2-, 3-, 5- and 10-fold up-regulation were 2.75:1, 4.33:1, 3.8:1 and 2.46:1, respectively. Those for down-regulation were 5.89:1,29.8:1, 123.75:1 and 119:1 correspondingly.

Comparing the 90-day treatment period to the 30-day period for the 50 ppm  $\rm Pb^{2+}$ group, between one-half and one-third more transcripts were either 2-, 3-, and 5-fold upregulated at 30 days than at 90 days exposure period. Similar trends were observed for down-regulated gene expression values. Interestingly, the 500 ppm  $Pb^{2+}$  group showed a different result between the time points. Chronically exposed rat groups exhibited 47 %, 56 %, 61 % and 71 % of transcripts up-regulated either 2-, 3-, 5-, and 10-fold, respectively. Similarly, 75 %, 85 %, 90 % and 93 % of genes between 30- and 90-day treatment period were either 2-, 3-, 5- and 10-fold down-regulated as a result of chronic lead intoxication. These results are quite different from those reported by Bouton *et al* [251] in their study of gene expression of lead exposed in rat astrocytes in which Clontech microarrays were employed. Of the 418 genes detected in their array, 94 passed the set criteria (ratio expression value  $\geq 1.8$  and t-test value of p<0.05). Eighty (85 %) were up-regulated and 14 (15 %) down-regulated.

Genes already known to be strong targets for lead exposure were observed to be differentially expressed in this study. Some of these are aminolevulinic acid synthase (Alasl, 2), FBJ murine osteosarcoma viral oncogene homolog (fos), heat shock protein 1 (hspdl), zinc finger protein 148 (Znfl48) and protein kinase, AMP-activated, alpha 2 catalytic subunit (prkaa2), vascular endothelial growth factor A (Vegf), zinc finger

protein 189 (predicted) (Znfl89 predicted) and mitogen activated protein kinase 14 (Mapkl4) [145, 167, 251, 254], According to the literature [145, 167, 251, 254], these effects are achieved through the perturbation of PKC activity by lead, the binding of lead to zinc-fmger nucleotide binding proteins or inhibition of ALA dehydratase. This study also revealed other equally important genes that are likely to be affected by lead. Examples of these genes are: proliferating cell nuclear antigen (PCNA), Caspase (Casp 3), solute carrier family 25, member 30 (Slc25a30), ATPase inhibitor (Atpi), polyubiquitin (Ubb) and protein phosphatase 1, catalytic subunit, beta isoform (Ppplcb), GATA binding protein 4 (Gata4), insulin-like growth factor 1 (Igfl), Forkhead box A2 (Foxa2), Karyopherin (importin) alpha 2 (Kpna2), Adaptor-related protein complex 2 sigma 1 subunit (Ap2sl), eukaryotic translation initiation factor 4E (Eif4e), tyrosine 3 monooxygenase/tryptophan 5-monooxygenase activation protein, eta polypeptide (Ywhah), protein phosphatase 3, catalytic subunit alpha isoform (Ppp3ca) and calcineurin binding protein 1 (cabinl).

According to Bouton *et al* [251], the altered regulation of numerous specific genes might produce distinct or diagnostic patterns of gene expression profiles, which can be grouped into clusters based upon similar shared properties. However, the clusters produced from dendograms or heat maps are not necessarily unique to a single toxicant. Patterns of clustering observed in our data across the time points of 30 days and 90 days appear similar though the 30 days exposure group have a  $\pm$ 2-fold lesser or greater number of affected genes than in the chronic treatment group. This observation seems to be confirmed by the multi-dimensional scaling plot. Eight out of the ten arrays aggregate

around the origin except two of the short-term treatment group arrays that are located either far to the right on the x-axis or far down below the origin on the y-axis.

Gene Ontology is useful in organizing differential gene expression information into biological processes, molecular function and cellular components. Results are implemented as GO categories in the form of tables and pathways (KEGG) which correlated to groups of genes [255]. GO analysis using quantitative test parameters dose levels and duration of exposure produced different results. Using dose as a reference parameter yielded such genes as karyopherin (importin) alpha 2, ribosomal protein S10, group specific component and adaptor-related protein complex 2 sigma 1 subunit. Similarly, length of exposure as a reference parameter produced gene markers such as serum/glucorticoid regulated kinase, ATPase,  $H^+$  transporting, lysosomal (vacuolar proton pump) subunit 1, forkhead box A2, casein kinase 1 alpha 1 and sialyltransferase. Both experimental parameters produced both positive and negative correlations to specific gene expression values due to lead exposure.

GO category analysis revealed a significant shift in lead effects from a small group of molecular effects to a broad spectrum of biological and cellular level effects of lead intoxication between 30- and 90-days of exposure. Short-term effects on GO categories involve transcription regulation while chronic lead exposure effects were observed in the biosynthesis and metabolism of carboxylic acid, vitamins, biotin, porphyrin and cofactor. Some of the key gene transcripts involved in the GO category for the 30-day exposure group include Stat3, Taf9, Nabl, Bzwl, Nrbf2, Gata4, Thrsp and Zfp189 predicted. For the long-term group, some of these key genes are Pgd, Pcca, Alasl, Alas2, Gsta5, Gsttl, Pnpo, Mapkl4, Srr, Cyp2c23, Igfl, Egfr, Vegf and Casp3.

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The results of this series of experiments indicate that exposure time is importance in the assessment of dose-response relationships of lead toxicity. Dose levels are not crucial when the exposure period is short when considered based upon the number of genes affected. If exposure to lead becomes chronic, then dose was observed to become a more relevant factor. Responses to lead intoxication were observed to be similar for the short-term treatment period irrespective of lead dose. However, when the dose levels were low over long periods of time, toxic effects seemed to be minimized possibly due to an adaptive response over time. Williams and Iatropoulos [250] explain that the hepatic adaptive response could be beneficial if it leads to the enhancing the capacity of all cellular units to respond to chemical induced stress in order to preserve viability. The process involves modulation of the various cellular and extracellular functions of the cell leading towards homeostasis. Adverse effects often result, when the conditions necessary for homeostasis cannot be maintained. This was seen in the chronic treatment groups in this experiment, particularly at the high dose level.

Garza *et al* [240] pointed out that lead distribution within the cell is typically even and as a result, Pb reaches the endoplasmic reticulum, mitochondria and cell nucleus. This is manifested in the wide range of gene ontology categories and pathways that were identified as being affected by lead from our study. At least forty discrete pathways have been identified as being altered by lead intoxication. These categories ranges from biosynthetic and energy metabolism such as nucleotide synthesis and glycolysis through cell cycle regulation, apoptosis and DNA repair to calcium signaling and protein degradation by ubiquitin.

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In summary, effects associated with lead exposure are dose and time dependent. Response to lead poisoning was observed to be almost similar for the short term treatment period irrespective of lead dose levels. However, when the dose levels were low over long periods of time, toxic effects are minimized due to adaptive response over time. On the contrary, lead exposure for long periods of time results in adverse effects in the form of increase incidence of lead-induced gene expression. Several of the differentially expressed genes are associated with essential pathways such as transcriptional, signaling and metabolism. Clustering patterns appear to be similar for all time points and dose levels. However, the short term exposure group have a  $\pm$ 2-fold less or greater than the sub-chronic treatment group. This was confirmed by multidimensional scaling plot which shows majority of arrays congregate around the origin. Gene ontology analysis revealed 15 GO categories affected by chronic lead exposure whiles three GO categories were observed to be significantly affected for short exposure periods. The following pathways; Regulation of eIF4e and p70 S6 Kinase, Control of skeletal myogenesis by HDAC and calcium/calmodulin-dependent kinase (CAMK), Role of MEF2D in T-cell Apoptosis are significantly perturbed by lead poison in vivo.

### **CHAPTER V**

# MICROARRAY DATA VALIDATION BY QUANTITATIVE REAL-TIME REVERSE TRANSCRIPTION POLYMERASE CHAIN REACTION (qRT-PCR)

## qRT-PCR Background Information

Since its invention in the 1990s, real-time PCR has been increasingly employed to quantify nucleic acids for mutation, genotyping and chimerism analysis, consequently, the number of publications in which real-time PCR has been used in one way or another has also increased exponentially [219]. It has been described by Bustin [220] as the enabling technology of the genomic era and it is now considered the scientific standard for detection and quantification of RNA targets [221, 222]. Real-time PCR is unique in that amplified PCR products are monitored in real time so that information obtained from amplification curves can be used to determine the initial amounts of template molecules with high precision over a wide concentration range [219, 223]. The principle adapted in PCR is one in which target DNA gene sequence is amplified during denaturationannealing-extension over a number of cycles. With conventional PCR, only the final concentration of the amplicon is monitored via a DNA-binding fluorescent dye while in qRT-PCR the amplicon concentration is monitored throughout 30-40 amplification cycles, also using fluorescent dyes. The fluorescent reagents bind to the amplified products without causing damage at the end of each amplification cycle so that amplification can continue. During the process, emitted fluorescence intensity is an indication of amplicon being produced in real time.

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Several detection schemes are currently in use. The notable ones can be divided into three categories namely double-stranded binding dyes (dsDNA), DNA-sequence specific probes and DNA sequence-specific primers [223]. Examples of DNA-sequence specific probes include the Taqman®, molecular beacon and dual hybridization probe. DNA sequence-specific primers have the examples Amplifuor® primer, scorpion primer, Light Upon extension (LUX) and universal template systems [223]. The most widely used of these are SYBR Green I, Taqman® and molecular beacon. SYBR Green is the most frequently used dye in monitoring dsDNA amplification by qRT-PCR. Synthesis of dsDNA from single-stranded denatured DNA occurs during the extension phase of PCR cycle and the binding of this to SYBR green dye makes it possible to track the amount of amplified DNA using the fluorescence intensity of SYBR Green I. Taqman® probes are 5' terminally labeled oligonucleotides with a reporter fluorophor and 3'-sequence terminally labelled with a quencher. Quenching occurs on intact probes so that they do not fluoresce. During the extension phase of the primers, the probe is bound to the singlestranded PCR product. The probe is complementary to the amplicon sequence. TaqDNA polymerase sheers and cuts the probe with an endonuclease to release the quencher from the fluorophor, thus it can be excited and fluoresces. Increasing fluorescence is proportional to the amount of amplicons. Like the Taqman® probe, the molecular beacon is labeled on both ends but the middle end of the probe is complementary to the amplicon sequence while the terminal 10-15 nucleotides are self-complementary. This probe has a "hairpin" (stem-loop) structure in which the reporter is kept close to the quencher. At the annealing stage of the PCR cycle, fluorescence intensity of the reporter increases with distance from the quencher and this indicates the target DNA concentration. The rise in

temperature due to subsequent extension results in the detachment of the DNA segment though the hairpin structure is retained and this can rebind to the target DNA segment in the next cycle. Design and detection of molecular beacon probes are very demanding and are very sensitive to hybridization conditions thus they are difficult to optimize. Nevertheless, they have a high specificity and thermally stable because of the hairpin structure and they can discriminate between DNA sequences that differ by a single nucleotide substitution. These probes are therefore employed in mutation analysis or single nucleotide polymorphism analyses [219, 223].

The difference between RT-PCR and PCR is the preliminary step added to account for the conversion of mRNA into a cDNA template by RNA-independent DNA polymerase (reverse transcriptase). Also, in real-time PCR, the amplified PCR product is measured at each cycle throughout the PCR reaction rather than at the end of the amplification process. Thus, real-time PCR makes it possible to follow the amplification of PCR product over time during the exponential phase of the PCR process so that the precise amount of starting material can be determined. Unlike end-point PCR methods, the result obtained from real-time PCR is independent of the plateau that corresponds to the saturation of the reaction, which causes inaccurate quantification of the products [**221**, 224].

Compared with conventional PCR, qRT-PCR is provides a rapid, sensitive and specific means of detecting nucleic acid sequence targets. In addition, it is quantitative rather than qualitative [219, 221, 222, 224, 225]. RT-PCR is rapid and provides reliable data mainly as a result of the progress made during the last few years in detection instrumentation, such that some machines can accommodate 384 well plates containing

individual reactions as well as the ability que processes over 24h without stopping. This might become important in running high through-put assays. Data from RT-PCR has a wide dynamic range detection  $(>10^7$ -fold) and is reliable because the entire amplification profile is known so that individual reactions that deviate in their amplification efficiency due to the presence of polymerase inhibitors or other inhibitors can be identified. In summary, the combination of DNA sequence amplification and simultaneous detection steps into one continuous assay system reduces the need for post-PCR processing thereby increasing sensitivity. The wide dynamic range means that very low to very high concentrations of gene products can be determined in the same tissue extracts. That means that analysis of target gene abundances in samples that differ by orders of magnitude can be done. Although qRT-PCR has become the benchmark method for analyzing mRNA targets and its use is increasing popular with researchers, there are still a few technical challenges the user should take into consideration. These include issues of template quality, operator variability, reverse transcription step reproducibility, and the potential subjectivity of data analysis and reporting. Furthermore, there are currently no standardized qRT-PCR protocols [226].

### Description of Genes Selected for Validation from Microarray Data

### Calmodulin

Calmodulin (CaM) is considered a small ubiquitous eukaryotic calcium-binding protein that is a principal mediator of calcium signalling via the regulation of CaMbinding proteins [269-271]. Calmodulin which is a heat-stable acidic protein that is involved in such critical cell functions as regulation of cell division and differentiation, control of gene expression, initiation of programmed cell death or apoptosis, DNA replication and repairing and exocytosis of hormone/neurotransmitter [272], This protein is encoded in mammals by three different genes namely Calml, Calm2 and Calm3 [270- 273]. Knaup and Roemer [271] report that the three genes are located on different chromosomes with 20 % divergence in their coding regions. The structure of CaM is characterized by four calcium-binding motifs called helix-loop-helix EF-hands [272].  $Ca<sup>2+</sup>-ATPase$  which is responsible for calcium transport is regulated by calcium concentrations that are mediated by the activation or auto-inhibition of calmodulin (CaM) [275-276]. CaM may exist in both the active and inactive form in cells depending upon cell free-calcium levels. At high calcium levels,  $Ca^{2+}$  binds to calmodulin to form a calcium-calmodulin complex which is activated, and subsequently this complex binds to the domain of  $Ca^{2+}$ -ATPase so that calcium-ATPase is activated [275]. According to Lee and East [274],  $Ca^{2+}$ -ATPase crystal structure exhibits ten trans-membrane  $\alpha$ -helices attached to three clear globular domains on the cytoplasmic end of the membrane whereas the lumenal end of the protein is made up of small loops. The transport of calcium is thought to occur according to the following scheme: first, E complexes with calcium and ATP to form a "high energy" intermediate  $E \sim P.2Ca^{2+}$ ; second, there is the relaxation of this intermediate to its "low-energy" conformation E-P resulting in the release of calcium outside of the cell. Third, phosphate is hydrolyzed yielding E and finally making it possible for calcium binding-capacity recovery for another cycle of the reaction [275].

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## Aminolevulinate Synthase

Heme and heme proteins are important for the metabolism and transport of oxygen in vertebrates [277]. Aminolevulinate synthase, a protein located in the mitochondria, catalyzes the first and rate-limiting reaction in the biosynthesis of heme as well as playing a key role in heme biosynthesis pathway [277-279]. The reaction involves condensation of glycine and succinyl-CoA to form aminolevulinate. This enzyme is encoded by two genes ALAS1, which is ubiquitously expressed in tissues and ALAS2 that is expressed only in erythroid cells. ALAS1 is the drug-responsive, housekeeping gene that provides hemes for CYPs and other hemoproteins. On the other hand, ALAS2 is responsible for the generation of functional hemoglobin in erythrocytes [279]. Though the catalytic regions of these two proteins are similar and highly conserved in various genomes, their amino-terminal ends are different. The cellular expression and localization of both genes are regulated by heme itself. Regulation of ALAS2 is uncomplicated as compared to the regulation of ALAS1. ALA2 is typically controlled by the availability of iron that regulates the interaction with iron-binding proteins and the iron-responsive element in ALAS2-mRNA in order to control gene translation. ALAS1 is believed to be controlled by a feedback mechanism by heme itself however, the exact process by which this takes place is not fully understood.

# ATP Synthase,  $H^+$  Transporting, Mitochondrial F1 Complex, O Subunit

The FlFo ATP synthase complex plays a vital role in cellular energy metabolism. This type of protein complex is found in bacteria, plant chloroplasts and mitochondria [280-284] and it acts to synthesize ATP from ADP and inorganic phosphate employing a

proton motive force that is generated across the mitochondrial membrane by electron flow [282-283]. Tucker *et al* [284] report that the general structure of this multi-subunit enzyme is highly conserved and composed of a globular FI domain protruding out of the inner side of the membrane, Fo, a membrane-spanning proton channel and a stalk linking FI to Fo [281-284]. Substrates, inorganic phosphates and ADP, are located in the catalytic binding site, FI domain. Chen and coworkers [283] note that, energy is transferred to the catalytic site most probably via a proton flux through Fo as a result of conformational changes through the stalk.

## Protein Phosphatase-3, Catalytic Subunit Alpha Isoform

Protein phosphatase is a calmodulin-regulated protein that plays a vital role in signal transduction. Phosphatases are important in controlling protein function via reversible phosphorylation-dephosphorylation cycles, especially those cellular processes that are in response to extracellular stimuli. Grove *et al* [287] estimates that nearly onethird of intracellular proteins phosphorylate. Protein phosphatase is one of the major cellular serine/threonine phosphatase proteins. Phosphatases are classified as 1, 2A, 2B, and 2C based upon preferences for different phosphoprotein substrates, their sensitivity to selective inhibitors and their specific  $Ca^{2+}$  or  $Mg^{2+}$  requirements. They are reported to be involved in such regulation processes as energy metabolism, receptor and ion channel functioning, transcription, RNA splicing, and cell growth and transformation [285-287]. According to Wang *et al* [285], these enzymes are heterodimers with molecular weights of 58-59 kDa and comprised of a calmodulin binding catalytic subunit and a small  $Ca^{2+}$ binding regulatory subunit. The B form of the enzyme is conserved in all tissues except

the testes and is encoded by a single gene. The A form of the protein on the other hand has three isoforms (alpha, beta and gamma) which are encoded by genes on three different chromosomes.

### Cytochrome P450, Family 3. Ssubfamilv A. Polypeptide 13

Cytochromes P450 (CYPs) enzyme system plays a vital role in the oxidation of structurally diversified compounds, for example pharmaceutical agents, chemical carcinogens, lipophilic xenobiotic chemical and endogenous steroids, fatty acids, prostaglandins and vitamin D**3** [288-291]. Though the CYPs comprise a very large family of heme thiolate proteins, CYP3As are the most abundantly expressed sub-family in humans and account for ~50 % of clinically active drugs metabolized via this enzyme system. In the liver, about 30 % of P450s expressed are CYP3As and they are particularly important in the metabolism of pharmacologically, physiologically and toxicologically important agents. Although the CYPs are expressed in very limited amounts in the brain, they are reported to show evidence of involvement in brain development and its basic functions. The CYPs show gender-, tissue-, and age-dependence in their expression. Isoforms present in different species that are classified as part of the CYP3A subfamily are four human, five rat, six mouse gene iso forms and many more in other species [288- 289].

# Mitogen Activated Protein Kinase 1

Mitogen-activated protein kinases (MAPK) are proline-directed Ser/Thr protein kinases that are controlled via external signals such as growth factors, mitogens and

cellular stress. In other words, they are activated by dual phosphorylation on Tyr and Thr residues within the motifs of Thr-Glu-Tyr (ERK), Thr-Pro-Tyr (JNK) or Thr-Gly-Tyr (p38). The three most well characterized MAPKs are grouped as extracellular signalregulated kinases (ERKs), c-Jun amino-terminal kinases (JNKs) that are critical regulators of transcription and the p38 MAPKs that are activated by inflammatory cytokines and environmental stress [292-294]. The cascade of these three modules is successively activated by phosphorylation events. Therefore, MAP kinase is phosphorylated and activated and in turn activates other kinases. For example, JNK is known to activate mapk4 and mapk7, while p38 is activated by mapk3, mapk**6** and mapk4, and ERK is activated by mapkl and mapk2 [294].

# Materials and Methods

### Total RNA Extraction

Total RNA was isolated from rat livers using a Qiagen RNA Isolation kit [247]. Between 0.05-1g liver samples were homogenized in RLT buffer. RLT buffer is responsible for denaturing and inactivating RNases. The RNA is then allowed to bind to a silica-gel membrane and finally eluted with RNase-free water. Total RNA was quantified using the spectrophotometer at 260 and 280 nm absorbance and gel electrophoresis was also ran for quality assurance purposes.

### Quantitative Real-Time Polymerase Chain Reaction (qRT-PCRl

To validate gene expression data from microarray experiments, quantitative realtime polymerase chain reaction (qRT-PCR) was employed to quantify the mRNA

expression of seven selected genes and a control gene  $\beta$ -Actin. Using the National Center for Biotechnology Information (NCBI) database, the FASTA mRNA sequence of  $\beta$ -Actin, calml, calm2, Alasl, Atp5o, Ppp3ca, Cyp3al3 and Mapkl were obtained for *Rattus norvegicus* and employed in the Taqman® Assay-on-Demand™ system provided by Applied Biosystems [295], thus offering us optimized probe and primer in a single tube. Synthesized cDNA from total RNA as described in Taqman® Gold RT-PCR kit [295] was diluted to different three concentrations each with three replicates per concentration assayed and loaded together with Taqman® Universal PCR Master Mix and the optimized probe and primer in the form of Taqman® Gene Expression Assay Mix in a 25  $\mu$ L volume and run on ABI Prism® 7700. PCR temperature cycling conditions were 95 °C for 10 minutes DNA polymerase activation, followed by 40 cycles of 15s at 95  $\mathrm{^{\circ}C}$  and 1 minute at 60  $\mathrm{^{\circ}C}$  for denaturation and annealing, respectively.

Raw fluorescence intensity data were exported for normalized gene expression (NGE) analysis using data analysis for real-time PCR (DART-PCR) and relative expression software tool (REST©) which are both implemented in Excel [296-297]. Reaction efficiency was calculated by DART-PCR. Peirson *et al* [296] suggested that DART-PCR is a simple tool and reliable tool for analyzing PCR data from raw fluorescence data. Theoretical values of  $R_0$  are calculated from raw data on the basis the fluorescence is proportional to DNA concentration. The normalized theoretical value is the ratio of the target gene theoretical value to reference gene theoretical value. Efficiency is determined according to the following equation:

$$
Efficiency = 10^{\left(\frac{1}{\cancel{5}}\right)} - 1 \,\,(1).
$$

Expressions of genes relative to  $\beta$ -Actin were conducted by REST. Pfaffl and coworkers [297] report that such relative expression is increasingly employed in analyzing the expression of target genes after standardizing to a non-regulated reference gene(s). This statistical model employs a pair-wise fixed reallocation randomization test. Normalized gene expression values were calculated according to the equation as implemented in REST©.

$$
NGE = \frac{\left(E_{target}\right)^{\Delta C_{target(control-sample)}^{CP}}}{\left(E_{ref}\right)^{\Delta C_{ref(control-sample)}^{CP}}}
$$
(2)

Where E is PCR efficiencies, CP is threshold cycle and  $\Delta$  is the difference of unknown sample verses a control.

### Results

In order to validate gene expression data obtained by the Affymetrix Microarray assays, we used Taqman RT-qPCR to quantify the expression of nine selected genes that are crucial in studying potential lead toxicological effects. The selected genes were: calmodulin, aminolevulinate synthase, ATP synthase,  $H^+$ -transporting, mitochondrial F1 complex-O subunit, Protein phosphatase-3 (catalytic subunit alpha isoform), Cytochrome P4503A13, Mitogen activated protein kinase-1, Insulin-like growth factor-1 and Pyruvate dehydrogenase kinase-1. The gene expression levels of these genes as determined from Affymetrix Microarray are re-shown in Table 12.

# Table 12



# The expression of selected transcripts determined from Gene Chip Affymetrix Microarray.

Most of the transcripts in the 30d exposure group were up-regulated whilst most in the 90d treatment were down-regulated. Calml, Calm2, Atp5o, Ppp3ca and Mapkl were all up-regulated in the short treatment regime.



Figure 13: Expression of genes determined by QRT-PCR exposed to (A) 90d 50 ppm, (B) 90d 500 ppm, (C) 30d 50 ppm and (D) 30d 500 ppm.







**B: 90d High Dose**

For the chronic exposure group, Calml, Calm2, Atp5o, Ppp3ca, Mapkl were all downregulated except Calm2 in the 50 ppm treatment group. Similarly, Alasl was negatively regulated in all treatment groups except the 90d 50 ppm group. Cyp3al3 was negatively regulated in all treatment groups during all time points.

The relative comparison of gene transcripts analyzed by microarray gene chips and qPCR are shown in Table 13. Most of the mRNA transcripts favorably compare between the two analytical methods although the magnitude of expression varies.

### Table 13

Comparison of transcripts determined by both Microarray Gene Chips and quantitative PCR. The first column indicates gene expression by microarray while the second shows the relative expression of genes evaluated by QPCR.



### Discussion

Quantitative PCR was employed in validating the microarray results. This approach has been used in practically every microarray experiment for such purposes. Transcripts chosen for validation are involved in processes such as regulation of cell division and differentiation, metabolism and transport of oxygen in vertebrates, cellular energy metabolism, signal transduction, metabolism of pharmacologically, physiologically and toxicologically important agents, transcription regulation, activation of signal transduction pathways involved in the expression of transcriptional regulators of tumorigenesis and glucose metabolism.

From our study, gene expression as determined by microarray gene chips and qRT-PCR are comparable although the relative expression values are somewhat different. For example, in the higher dose chronically-exposed group, almost all mRNA transcripts evaluated by qPCR had greater fold-change values relative to the ones determined by Gene Chips. Apart from Calml and Mapkl transcripts measured by gene chips in the 30d/50ppm and 90d/50ppm, respectively, all the mRNA transcripts showed expression levels. Most of the selected gene transcripts in the chronically exposed (90d) rats were down-regulated in the high dose group. The effects were less pronounced for the Calml and Cyp3al3 genes than for the others assayed. Chronic low dose exposures to lead yielded a mixture of gene regulation responses. Calm2, Alasl and Mapkl were upregulated in this group while all other genes were slightly down-regulated except for Ppp3ca which was strongly down-regulated. Ppp3ca was actually more strongly downregulated at the 50 ppm dose than at the 500 ppm dose.

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In this study, we employed  $\beta$ -actin as an internal control because studies by Jover *et al* [145] found that the expression of  $\beta$ -actin is independent of dose or time of treatment lead acetate although dependent on RNA level in liver tissues of mice. In their experiment, they found that the injection of lead acetate results in about 45 % decrease Cyp3all mRNA levels after 12 hours. Instead of mRNA expression, other studies have examined the activities and protein levels associated with p38<sup>MAPK</sup> and calciumcalmodulin-dependent protein kinase II (CAMKII) in the brains of rats or zebra fish due to Pb exposure. The results indicate the phosphorylation of  $p38^{MAPK}$  and a decrease in CaMKII levels in exposed rats. Also observed were a 40 % decrease of CaMKII  $\beta$ expression in hippocampal cytosolic fractions with no alterations in CaMKII a protein content [143, 299].

## CHAPTER VI

### **CONCLUSIONS**

The most ancient and relevant environmental poison to be used by man is lead and as such; it is ubiquitous in the environment. It is present in all kinds of soil and aquatic media in a wide range of concentrations, as a result lead can enter into the body by drinking water, ingestion of food, breathing lead particulates or by dermal contacts. Lead contaminated soil could provide a direct route of lead ingestion for infants or indirectly via contaminated food.

Lead is reported to be absorbed by both active and passive means with the most absorption occurring in the small intestine. The absorption of lead is influenced by several factors including ingested metal form, environmental matrix, gastrointestinal tract contents, diet, nutritional status, age and in some cases genotype. Lead is distributed in both soft and hard tissue. Its concentration increases in the order of muscle < brain < liver  $\leq$  kidney  $\leq$  bone. Lead can reside in the bone for as long as 20 years. Lead is essentially excreted via the urine or feces.

The health effects associated with Pb exposure reported in the literature are numerous. These range from unobservable symptoms to extreme cases of death in exposed victims. Health effects may be manifested via neurobehavioral, cancer, genotoxic, reproductive, developmental and immunological.

Several molecular and cellular mechanisms of Pb actions have been documented to explain the processes through which lead exerts its negative cellular and molecular influence. Lidsky and Schneider [198] classed Pb neurotoxic mechanisms as direct and

indirect whilst Goyer [196] defined it as being morphological and pharmacological. The neuropharmacological interactions include substitution for calcium, iron and zinc, neurotransmitter release, protein kinase C, Na-Ca ATPase and energy metabolism. Morphological interactions on the other hand consist of interference with adhesion molecules, impaired cell:cell programming connections and miswiring of the central nervous system. At the molecular level, lead is reported to regulate mRNA transcription. Several genes transcripts are reported in the literature to be regulated by Pb either directly or via some other consequential means. In the last several years, studies involving Pb have shifted focused on elucidating how Pb regulates mRNA transcription.

Experimental results from our study show that the effects associated with lead exposure and dose and time dependent. Short time span exposures do not produce serious damage, as long high dose intoxication levels. Histopathology results are consistent with lead concentration in liver and kidney as well other trace metals measured. For instance, high lead concentration of lead in kidney results in pronounced cell necrosis in varied forms. There was a positive correlation between lead and other trace metals for the short treatment period and a negative correlation for chronic exposure levels. ICP-MS results showed a significant accumulation of lead in blood, liver, kidney and bone marrow in lead exposed groups. With the exception of kidney, the 90-days treatment groups showed markedly high levels of lead in blood, liver and marrow than the 30-days exposed groups. Potential interactions of calcium, iron, cobalt, copper, zinc and nickel and lead examined showed positive and negative correlation for 30 and 90 days treatment period respectively. Hepatic histopathology produced no evidence of necrosis nor changes in architecture of hepatocytes in the 0 ppm and 50 ppm for the 30-day duration of exposure

in the case of the liver. In contrast, necrosis and alterations in the structure and disposition of the liver and kidney tissues were observed for the 500 ppm treatment group.

A total of over 2300 genes were then used in differential gene expression analysis by scatterplot with regards to the microarray experiment. The scatterplot data suggest a greater number of genes were differentially expressed in the 90 days 500 ppm  $\rm Pb^{2+}$ treatment than the other dose groups. Using a 2-fold expression difference threshold, genes either up/down-regulated appear to be the same for both treatments during the 30 days exposure period. Interestingly, 90 days 50 ppm treatment showed less than half the number of genes expressed compared to the 30 days treatment. In contrast, the 90 days 500 ppm group had over one thousand genes differentially expressed at 2-fold and more than twice the number of genes of the other treatment groups at 3-, 5-, and 10-fold levels. Gene precursors for proteins such as FBJ murine osteosarcoma viral oncogene homolog, heat shock protein, protein kinase and proliferating cell nuclear antigen were ten fold up/down-regulated. Our study showed genes such as aminolevulinic acid synthase (Alasl, 2), calmodulin (Calm 1 and 2), mitogen activated protein kinase 14 (Mapkl4) that are reported in the literature to be lead targets and Caspase (Casp 3), solute carrier family 25, member 30 (Slc25a30), ATPase inhibitor (Atpi), polyubiquitin (Ubb) and protein phosphatase 1, catalytic subunit, beta iso form (Ppplcb), GATA binding protein 4 (Gata4), insulin-like growth factor 1 (Igfl) identified from this study to be potential targets of lead. Expression profiles were analyzed by clustering and gene ontology (GO). Clustering patterns appear to be similar for both time points and dose levels. However, the short term exposure group (30d) showed far fewer genes being affected by  $\pm$ 2-fold

than in the sub-chronic treatment group (90d). This was confirmed by multidimensional scaling plot which shows majority of arrays congregate around the origin. Gene ontology analysis revealed 15 GO categories affected by chronic (90d) lead exposure, whiles three GO categories were observed to be significantly affected for short exposure (30d) periods. The following pathways; Regulation of eIF4e and p70 S6 Kinase, Control of skeletal myogenesis by HDAC and calcium/calmodulin-dependent kinase (CAMK), Role of MEF2D in T-cell Apoptosis are significantly perturbed by lead poison in vivo.

To validate gene expression data acquired by Affymetrix Microarray, Taqman RT-qPCR was used to quantify the relative expression levels of selected genes already known to play important roles in mediating  $Pb^{2+}$  toxicity and others identified in our study that might be equally important in this process. Using Taqman RT reagents and Assay-On-Demand offered by Applied Biosystems, the expression of calml, calm2, Alas1, Atp5o, Ppp3ca, Cyp3a13 and Mapk1 were measured relative to  $\beta$ -Actin. Most of the transcripts in the 30d exposure group were up-regulated while most transcripts in the 90d treatment were down-regulated, relative to controls. Calml, Calm2, Atp5o, Ppp3ca and Mapkl were all up-regulated in the short treatment regime. For the chronic exposure group, Calml, Calm2, Atp5o, Ppp3ca, Mapkl were all down-regulated except Calm2 in the 50 ppm treatment group, relative to controls. Similarly, Alasl was negatively regulated in all treatment groups except the 90d 50 ppm group. Cyp3al3 was negatively regulated in all treatment groups during all time points. Confirming microarray results are the down-regulation of Calm2: -3.886, Alasl: -1.616, Atp5o: -2.706 and Cyp3al3: -1.79 genes in the long term exposure group.

Our results indicate the importance of time in the assessment of dose-response relationships of lead toxicity. Dose levels are not crucial when the exposure period is short. If exposure to lead becomes chronic, then dose becomes a relevant factor. Response to lead poisoning was observed to be almost similar for the short term treatment period irrespective of lead concentration. However, when the dose levels are low over long periods of time, toxic effects are minimized due to adaptive response over time. Williams and Iatropoulos [250] explains that, hepatic adaptive response could be beneficial if it leads to the enhancing the capacity of all units to respond to chemical induce stress in order to preserve viability. The process involves modulation of the various cellular and extracellular functions of the cell towards homeostasis. Adverse effects often result, when the conditions necessary for homeostasis cannot be achieved. This is seen in the sub-chronic treatment group.

Garza *et al* [240] pointed out that lead distribution in the cell is even and as a result, it reaches the endoplasmic reticulum, mitochondria and cell nucleus. This is manifested in the wide range of gene ontology categories and pathways that have noted to be affected by lead from our study. At least forty pathways have been outlined. The categories range from metabolism such as nucleotide synthesis and glycolysis through cell cycle regulation, apoptosis and DNA repair to calcium signaling and protein degradation by ubiquitin.

Summarily, effects associated with lead exposure are both dose and time dependent. Response to lead poisoning was observed to be almost similar for the short term treatment period irrespective of lead dose levels. However, when the dose levels are low over long periods of time, toxic effects are minimized due to adaptive response over

time. On the contrary, lead exposure for long periods of time results in adverse effects in the form of increase incidence of lead-induced gene expression. Several of the differentially expressed genes are associated with essential pathways such as transcriptional, signaling and metabolism.

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#### APPENDIX A

Institutional Animal Care and Use Committee Approval Form

# WESTERN MICHIGAN UNIVERSITY

**Institutional Animal Care and Use Committee** 

#### **ANNUAL REVIEW OF VERTEBRATE ANIMAL USE**

**PROJECT OR COURSE TITLE:** Investigation of Markers of Cell Death and Immune Function in Rats Exposed to Selected Chemicals



Revised 10/01 WMU IACUC All other copies obsolete.

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### APPENDIX B

## Gene Annotation List





















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1371934\_at Tmem9\_predicted RGD:735141 \_predicted 10230\_predicted RGD:727884 \_predicted 303130 edicte predicted 2422 \_predicted **8** 08463\_predicted aa\_predicted oredicted RGD: 1302 11955\_predicted 27866 predicted **Paox**\_pre RGD1304 706\_predi

RGD1309 198\_predi cted Peflin Prkca Mocs2 Hpcal1 Sdc3 Rpa1\_pre dicted Pfkp Kpnal RGD:6204 Aqp4 Impact Tnnc2\_pr edicted<br>LOC3043 61 Pink1\_pre dicted RGD: 1303 014 978 RGD1310 553\_predi cted RGD1307 475\_predi cted Brd8\_pred icted Cops5\_pr edicted<br>Mospd3\_p redicted<br>Mafk dicted dicted

![](_page_235_Picture_518.jpeg)

1372427\_at Dnajc4\_predict 1372675\_at

p1

RGD:735230

RGD1305638\_predicted p2b Ddx3x Ncorl Cab39\_pr

าร2

1dc1\_predicted

1dc1\_predicted

101

b\_predicted

b\_predicted

b7 1372806 at Cdw92 1372807\_at LOC3134 p11\_predi 1372808\_at cted 95 8l2\_predic 1372809\_at Hnrpdl\_pr Snx15\_predict 1372811\_at LOC2961 ed the 15 and 16 an D1311532 1372812\_at RGD1306 edicted 682 predi

n 1372831\_at gcp3\_pred 1372832\_at Wdr7 Tbl3\_predicte 1372833\_at Vps4b\_pr o34\_predi 1372834\_at Rhoj\_pred cted icted icted icted in the set of  $\sim$ f2\_predicte 1372851\_at MGC94797 1372852\_at RGD:7278 D1307682 1372855\_at edicted<br>C317214 1372856\_at Pacsin2 Qprt\_predicte 1372859\_at MGC9509 d 2 D1306954 1372860\_at Pip5k1c edicted

Wbp1\_pre dicted Sdbcag84 \_pred icted Sgca\_pre dicted Oaz1 edicted Cab39\_pr edicted Ciao1\_pre dicted Ddost\_pre dicted Sesn1\_pr edicted Rbm5\_pre dicted Trappc1\_ predicted Clcn<sub>2</sub> 10 LOC2905 edicted cted Epim

cted

edicted Rps6kb2

89 Hdgfrp2

RGD1304560 1372861\_at Rab22a\_p

![](_page_236_Picture_401.jpeg)

![](_page_237_Picture_402.jpeg)

![](_page_238_Picture_394.jpeg)

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![](_page_239_Picture_391.jpeg)

![](_page_240_Picture_681.jpeg)

 $licted$ ct1\_predi cted LOC3160 09 Grca\_pred cted Pde9a Cops7a\_p edicted Zdhhc4\_p edicted Kifap3\_pr edicted Qki Tfg\_predic ted  $AGC1057$ 97 Prkce rap1 RGD:7350  $3<sup>13</sup>$ Dhx57\_pr edicted Cpne2\_pr edicted LOC2907 75 Ceacaml LOC3614 **20** Galnt11 Hes6\_pre licted

225

![](_page_241_Picture_407.jpeg)

![](_page_242_Picture_473.jpeg)

![](_page_243_Picture_410.jpeg)

![](_page_244_Picture_391.jpeg)

![](_page_245_Picture_614.jpeg)

![](_page_246_Picture_333.jpeg)

![](_page_247_Picture_378.jpeg)

![](_page_248_Picture_399.jpeg)

![](_page_249_Picture_497.jpeg)

![](_page_250_Picture_478.jpeg)

![](_page_251_Picture_619.jpeg)


























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RGD1308 813\_predi cted<br>Usf1 313\_predi cted RGD1310 905\_predi cted Tmp21 Pprf18 Clk1\_pred icted RGD.7279 57 Scyl1\_pre dicted 09

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