

Alda Neis Miranda Araujo¹, Danielle Zildeana Sousa Furtado¹, Heron Dominguez Torres Silva², Kelly Polido Kaneshiro Olympio³, Nilson Antônio Assunção²

¹Paulista School of Medicine, Federal University of São Paulo, São Paulo, São Paulo, Brazil.

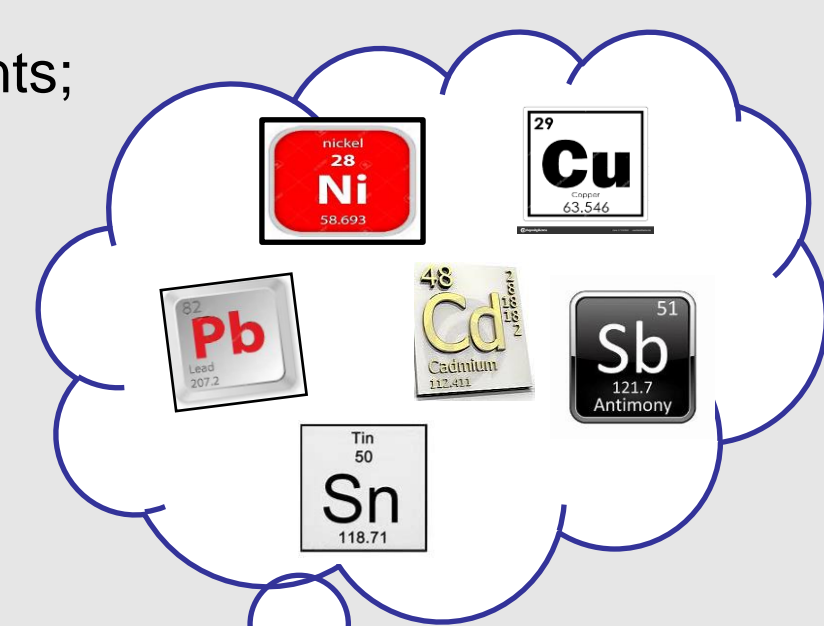
²Department of Chemistry, Institute of Environmental, Chemical and Pharmaceutical Sciences Federal University of São Paulo, Diadema, Brazil.

³Department of Environmental Health, School of Public Health, University of São Paulo, Brazil.

Key findings: Informal, home-based and outsourced work performed by welders is influencing their internal exposure. A significant statistical difference was found for Cu concentrations between the Welders group and Control group. The concentration of Cu, Sn, SB and Pb metals in the blood is correlated with the significant proteins ($p < 0.05$).

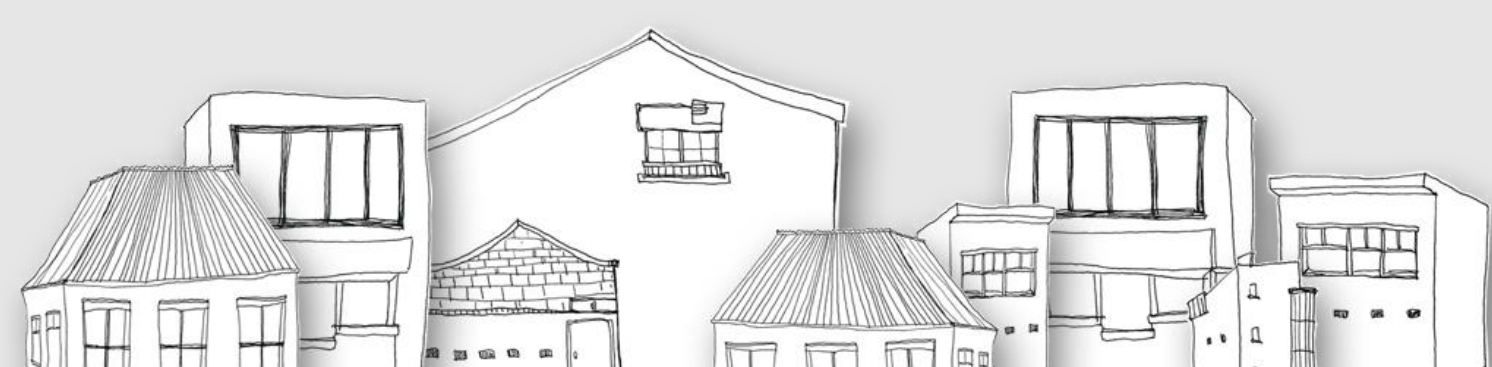
Background

- The soldering process can expose workers to potentially toxic elements;
- The productive chain encompasses the related families;
- This study aimed to evaluate the effects of PTEs exposure and expression performing a proteomic approach.

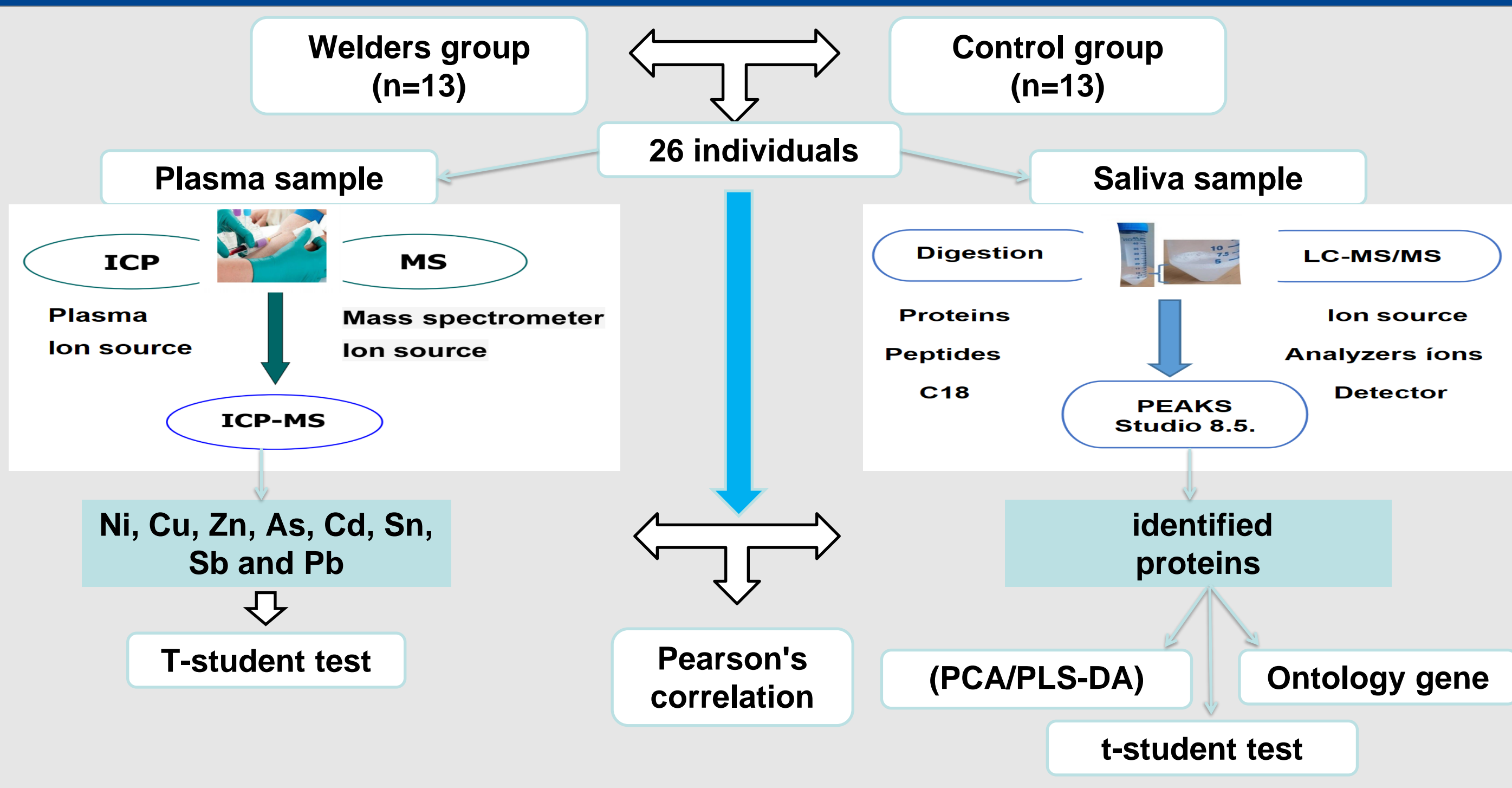


Brazilian city of Limeira

Homemade and informal processes

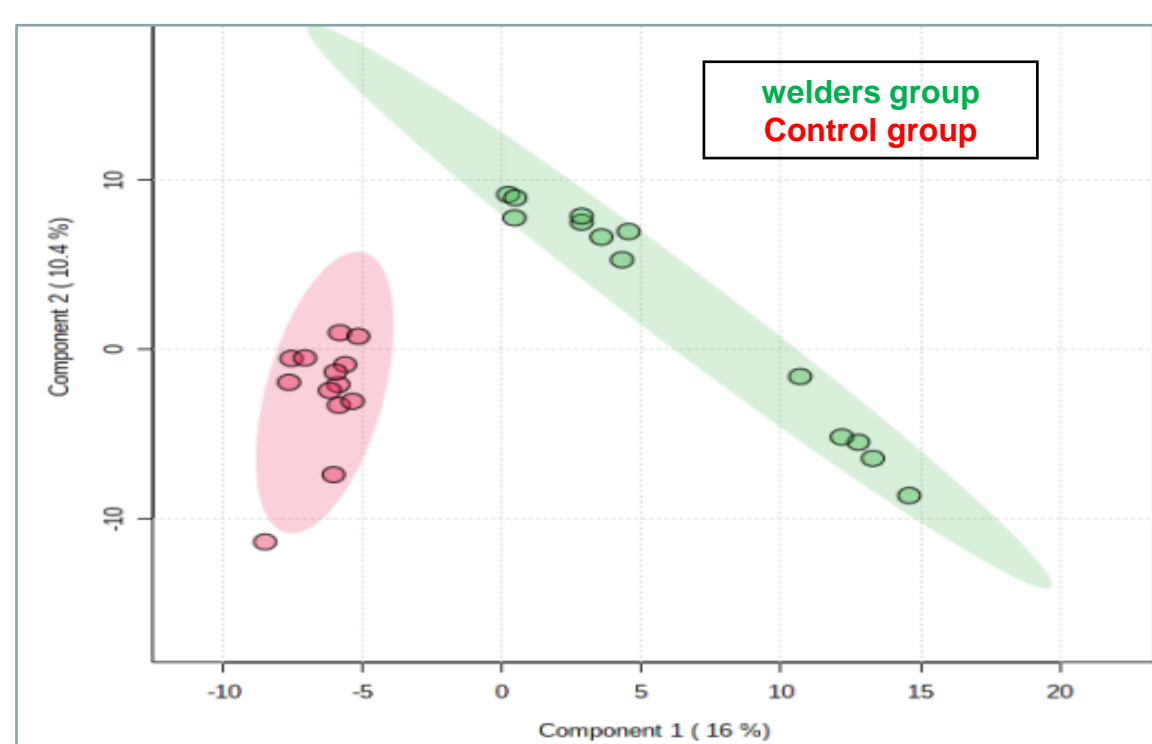


Materials and Methods



Results

- A significant statistical difference was found for Cu concentrations between the Welders group and Control group ($p < 0.0005$).
- Partial least squares discriminant analysis (PLS-DA), shows that proteins are capable of separating control and welding groups.

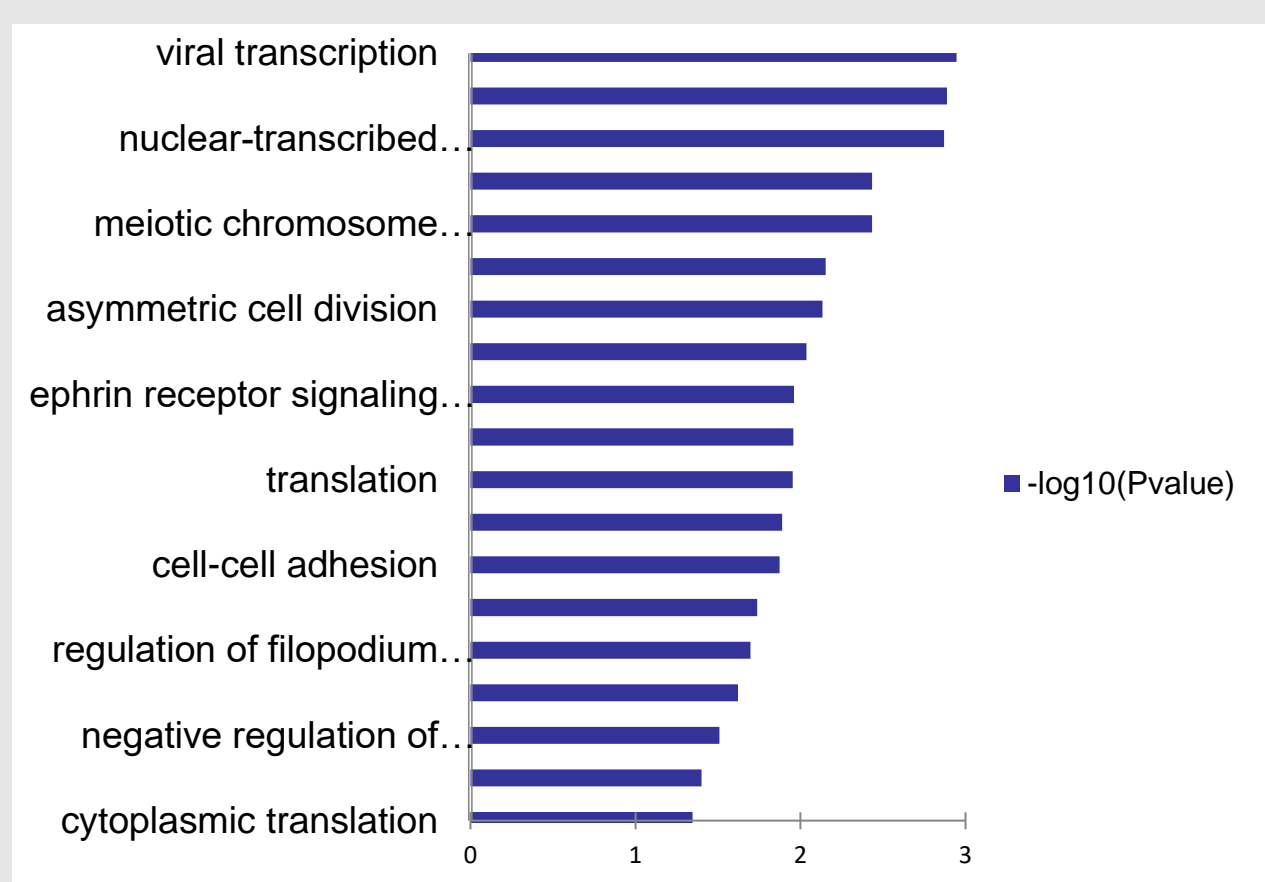


- By t-student test performed, we found 40 significant proteins ($p < 0.05$):

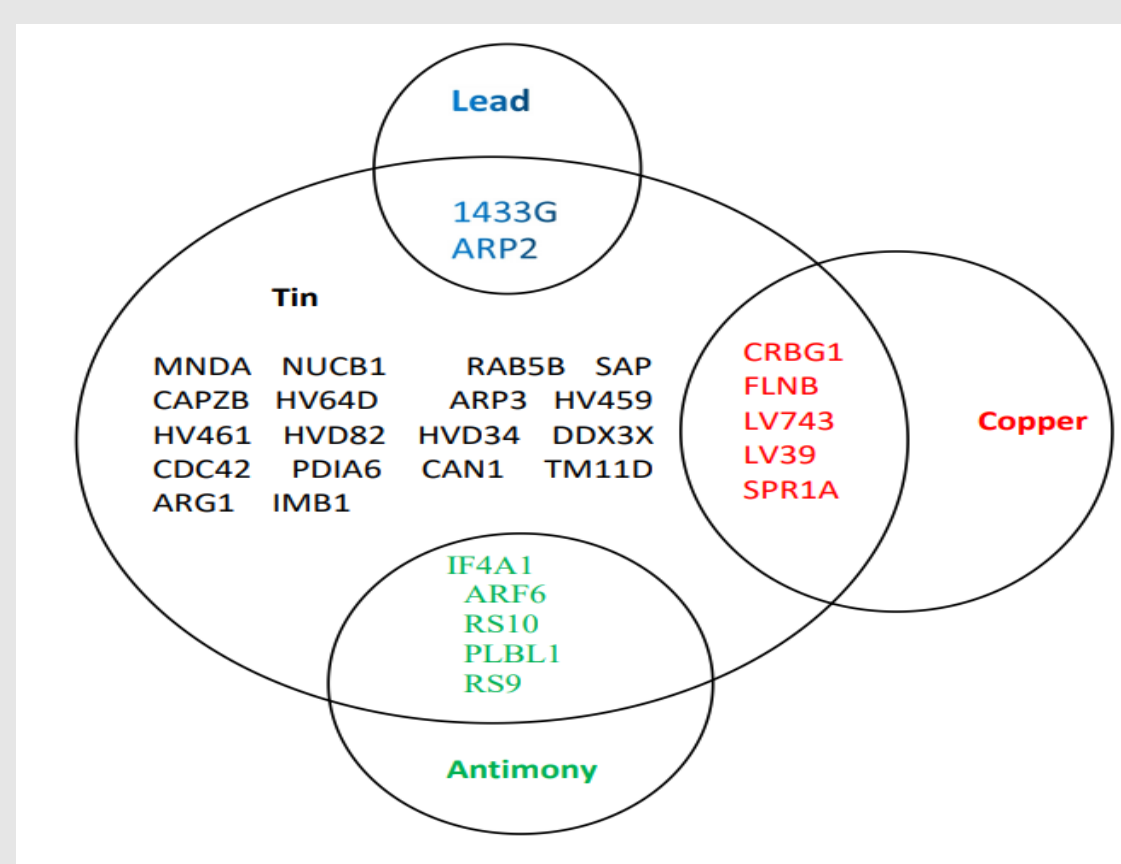
CRBG1, RAB5B, NUCB1, MNDA, 1433G, SNAA, FLNB, PDIA6, RLA2, TM11D, CAN1, IF4A1, CPNS1, FM25A, FM25C, VDAC1, ARP3, SAP, RS10, SPTN1, ARP2, AL9A1, RS9, ARF6, RL22, PLBL1.

Additional Results

- Gene ontology analysis - Biological process



- Pearson correlation showed 28 significant proteins correlated with metals ($p < 0.05$).



Conclusions

- The identification of differentially expressed salivary proteins in informal workers provides new insights into PTEs poisoning.
- This study shows that gene expression profiles can comprise biological responses induced by PTEs.
- Proteins LV39, SPR1A, CRBG1, LV743, FLNB, RAB5B, CAN1, ARP2, 1433G, IF4A1, ARF6, RS10, PLBL1, RS9, MNDA, SAP, NUCB1, CAPZB, HV64D, IMB1, ARP3, SPR1A, HV459, HV461, HVD82, HVD34, DDX3X, CDC42, PDIA6, TM11D can be candidates for biological markers of PTE intoxication in future studies.

ACKNOWLEDGMENTS:

