LINE-1 methylation profile in Adolescents Living in the Industrialised Area of Milazzo-Valle del Mela (Northern Sicily)

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Environmental pollutants as the heavy metals deriving from industrial plants can affect human health deregulating hormonal status and increasing oxidative damage to DNA. It is known that children are more susceptible to environmental pollutants, because their detoxification enzymes are less competent, and this may lead to alterations in chromatin structure or of DNA causing, in turn, epigenetic modifications.

Transposable non-coding elements, such as long interspersed element (LINE), short interspersed elements (SINE), and the repetitive Alu sequences, constitute about 45% of the human genome. These sequences could interfere with gene expression regulation and genome structure by insertions, inversions, translocations and deletions of genomic sequences. However, high levels of CpG methylation effectively silence these repetitive regions, thus reducing the potential genomic damage. LINE-1 or L1 is a repetitive DNA retro-transposon that duplicates *via* a copy-and-paste genetic mechanism. LINE-1 constitutes a substantial portion (approximately 17%) of the human genome, and the extent of LINE-1 methylation is considered as a surrogate marker of global DNA methylation. Additionally, LINE-1 methylation (increased as well as decreased) was predicted to be an indicator for the influence of environmental conditions and lifestyle habits on the genome.

Recently the use of methylation sensitive-high resolution melting (MS-HRM) is widespread for specifically detect methylation levels of bisulphite-treated DNA. In this research we focused on the methylation status of LINE-1 evaluated in whole blood of children living in areas exposed to heavy metals pollution (Interdonato et al., 2014; Pizzino et al., 2014). As control population we used blood samples from children living in non-exposed areas, and from young healthy adults. The exposed and not-exposed population have been previously screened for the presence of heavy metals in urine and blood. Our previous results showed that exposed children had high levels of metals, especially cadmium, that have been reported to affect DNA methylation. MS-HRM was performed on bisulphite-converted DNA samples, using methylation independent primers (MIP) designed according to Wojdacz et al. (2007 and 2009) by using Methyl Primer Express Software v 1.0 (Applied Biosystems). The methylation profile of children exposed to heavy metals was significantly different as compared to non-exposed children and healthy young adults. These results suggest that exposure in the early life could represent a trigger for future diseases.

References

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