# *Comparison of genomic and gene expression profile between cancer and healthy samples*

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**Background:** A variety of chromosomal aberrations underlie developmental abnormalities and cancer. Use of techniques such as microarrays provides an opportunity to perform gene expression analysis. A recent approach is the use of array based comparative genomic hybridization (aCGH) to detect genomic abnormalities in human tumors. The aim of this study is to compare genomic and gene expression profile between cancer patients and healthy individuals.

**Methods:** DNA and RNA were isolated from peripheral blood mononuclear cells from 9 patients, with different types of cancer and 4 normal donors. aCGH (Agilent-60K) and gene expression microarrays (Microarrays Inc.-whole genome platform) were performed using commercial reference samples. Data were analyzed with Array-Pro analyzer and Cytogenomics software.

**Results:** The aCGH data demonstrated the majority of gains and amplifications were observed in cancer samples, while the deletions and losses were higher in normal individuals. Among aberrations, common genes in both types of samples were detected. These genes included *ACAD8, ACP1, B3GAT1, IDI1, IDI2, IGSF9B, IRX1, IRX2, JAM3, MYT1L, NTM, OPCML, PXDN, THYN1, TPO*. However, there were abnormalities that included genes, which appeared only in cancer samples, like cadherins (*CDH11*, *CDH8* and *CDH5*) and *EPHA5*, while genes such as *ACOX1, PTPRN2, TYMS* and genes of zinc-finger proteins were observed only in normal samples. No statistical significant difference in gene expression, between cancer and normal samples, was observed. On the contrary, overexpression was observed in genes that were not detected in aCGH.

**Conclusions:** Whereas it is acceptable that great achievements have been carried out in cancer field, the mechanism of tumorigenesis is not clear understood. The present study demonstrated that even though genomic aberrations exist, these are not always representative at gene expression level. However, the combination of both techniques could be used for more accurate and reliable data. This requires study in more samples including different cancer types so to be used at clinical level.