# A289 - IN SILICO STUDY FOR CERVICAL CANCER DIAGNOSIS: A NOVEL GENE PANEL

MARIA SENRA CARDOSO[1]; DANYELLY BRUNESKA GONDIM MARTINS[1]; CARLOS HENRIQUE MADEIROS CASTELLETTI[1]; JOSÉ LUIZ LIMA-FILHO[1]; JOSÉ ANTONIO COUTO TEIXEIRA[2]

*1.LIKA-UFPE, RECIFE, PE, BRASIL; 2.DEB- UMINHO, BRAGA, PORTUGAL.*

## Abstract:

Cervical cancer (CC) is the second cause of death cancer related among women worldwide. Nowadays,it is also done visual inspection with acetic acid to aid in detection of cervical lesions.Pap smear exam is insensitive, and false negatives occur. So, more accurate methods are needed to avoid problems with late diagnosis, once that it makes more likely the tumour spread, making the treatment more challenging.

Genetic aspects like SNPs (single nucleotide polymorphisms) presence and methylation events can be related to CC development. SNP presence also can affect gene expression by altering promoter activity or by changing a coding codon. Methylation is related to gene expression, once the hypermethylation of the promoter region prevents gene transcription, while hypomethylation increases gene expression. This information can be used to have a more reliable diagnosis, as well be used to predict treatment efficacy or prognosis for the cancer evolution.

Our work goal was to discover genes that have deregulated expression, which could be caused by methylation or SNPs. Then, this gene panel could be used as diagnosis or prognosis approach for CC patients. The in silico analysis was performed with Metacore® software database (Thomson Reuters, USA), with the follow word combinations: "cervical cancer" and "methylation", "cervical cancer" and "polymorphisms" and "cervical cancer" and "gene expression". The three sets of results were combined so that only genes that were affected in all aspects were considered.

For methylation there were 54 genes, while 3003 genes were linked to expression deregulation and 4095 linked to SNPs. The intersection of these genes

resulted in 16 genes. This gene list included genes such as CDKN2A (ciclin-dependent kinase inhibitor 2A), CDKN1A (ciclin-dependent kinase inhibitor), TP53 (tumor protein p53) and TP73 (Tumor protein p73) are related to cell cycle. Both TP73 and TP53 are tumor suppressor proteins, having their expression reduced when hyper-methylated, which is consistent with cancer development. Several other tumor suppressor proteins were found, for instance: FHIT (Fragile histidine triad), PTEN (Phosphatase and tensin homolog) and RB1 (Retinoblastoma 1), RASSF1 (Ras Association domain-containing protein 1). This indicates that CC development requires extensive damage to cells mechanisms of regulation. APC (adenomatous polyposis coli) also appears in the gene panel, once it was found hypermethylated and downregulated in CC, meaning that it has it's activity reduced. APC is antagonist of the WNT signaling pathway. In colorectal cancer, loss of this function is associated with cancer progression. It is interesting to notice this gene presence in cervix samples probably due to epithelial cells similarity between cervical and colotectal regions. Further *in vitro* studies are needed in order to confirm these *in silico* results, but the use of genetic markers looks promising for a more reliable and accurate diagnosis of CC.

José Osvaldo B. Carioca • Levi Moura Barros • André L. Coelho

# Biotechnology for the Development of a Green Economy

**IBS** 2014

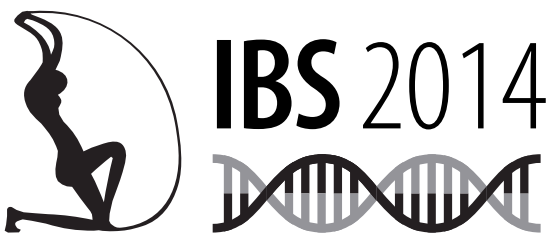
Proceedings of the **16th International Biotechnology Symposium and Exhibition**, held in Fortaleza, Ceara, Brazil
September, 14-19th, 2014

IUPAC
INTERNATIONAL UNION OF PURE AND APPLIED CHEMISTRY

UNIVERSIDADE FEDERAL DO CEARÁ

José Osvaldo B. Carioca • Levi Moura Barros • André L. Coelho

# Biotechnology for the Development of a Green Economy



Editorial Coordination
**José Osvaldo Beserra Carioca**
**Rafael Dias Bezerra**

Secretary
**Elke Montenegro**

Reviser
**Lúcia M. Martins do Vale Carioca**
**Rafael Dias Bezerra**

Graphic design and publishing
**Eduardo Freire**

Printed version
**Expressão Gráfica Editora**

ISBN
**978-85-420-0788-6**
**Biotechnology for the Development of a Green Economy**