**Characterization of 331G/A polymorphism of RP gene and identification of viral oncogene HMTV virus as genetic markers for the improvement of breast cancer management in Cameroon.**

**NIELS NGUEDIA KAZE1,****nnguediakaze@yahoo.com****, (237)690336493, N.N.K.,** JEAN PAUL CHEDJOU1,J.P.C., WILFRED MBACHAM1,2, W.M.

1. University of Yaoundé I (Department of Biochemistry / Biotechnology Center, Yaounde, Cameroon)
2. Faculty of medicine and Biomedical Sciences

**Background:** Breast cancer is a real public health problem in Cameroon, where more patients with this cancer usually die a year after diagnosis, as it is still based on histological examination, mortality due to cancer is far from decreasing. Since cancer is an accumulation of molecular changes, the +331 G/A polymorphism of PgR gene (progesterone receptor) and viral oncogene HMTV (Human Mammary Tumor Virus) has been recently considered as a molecular markers associated with breast cancer. Due to that we fixed our objectives to characterize these markers.

**Aim and objectives**: characterization of +331 G/A polymorphism of PgR gene (progesterone receptor) and viral oncogene HMTV (Human Mammary Tumor Virus) by semi-nested PCR to understand etiological factor of that cancer in Cameroon.

**Method**: We carried out a case control study, in which 26 cases diagnosed positive for breast cancer at the CHU of Yaounde were recruited through the identification of archived biopsies. Blood samples were also collected from 20 women recruited using a questionnaire and a inform concern sign by each of them. +331 G/A polymorphism in the PgR gene was identified using NIaIV endonuclease by PCR-RFLP, and HMTV viral oncogene by hemi-nested PCR. The data were analyzed using Microsoft Excel and SPSS v20.

**Results:** We got a mean age of 57,73 +/- 9,87 in our cancerous group with the predominance of infiltrant duct carcinoma at grade II of SBR. An Odd Ratio of 1.268 with Confident Interval of 95% 1.004-1.664 proving that there is a significant association between 331G/A mutation and breast cancer with P-value of 0.026, obtained by comparing the mutant group (AA) 28,5% and wild genotype (GG). In addition, 3 cases were detected with the HMTV virus, one was found in the cancer group and two in the control group.

**Conclusion**: These results indicate that, HMTV is considered as viral cause and can predispose to breast cancer, beside 331 G/A polymorphism is an associated risk factor of that cancer.

**Key words**: Breast cancer, progesterone receptor,+331G/A PgR gene polymorphism, Human Mammary Tumor Virus.