RESEARCH ARTICLE

CYTOCHROME B AND BETA-FIBRINOGEN IMPLICATION IN THE GENETIC EVOLUTION OF BREAST MALIGNANT TUMOUR IN SENEGALESE WOMEN.

Ahmed Mohamed Mze¹, Fatimata Mbaye¹, Binta Keneme¹ and Mbacke Sembene¹,².
1. Departement de Biologie Animale, Faculté des Sciences et Techniques, Université C.A. Diop, B.P. 5005 Dakar, Senegal.
2. Centre de Biologie des Populations Animales-Sahéli-Soudaniennes (BIOPASS), UMR 022, Institut de Recherche pour le développement, IRD/Bel-Air, Senegal.

Abstract

The International Cancer Centre (CIRC) stated that there is an important increase of breast cancer throughout the world. In Senegal, breast cancer is known as the malicious tumour more developed among women. From thirty (30) Senegalese women were tested, the notice is that a mitochondrial (Cytochrome b) and a nuclear (Beta-fibrinogen) gene evaluated the level of genetic diversity, genetic differentiation and demographic evolution. Our results showed a real diversity of Cytochrome b compared to Beta-fibrinogen. A significant difference has been found between normal tissues and cancerous ones within Cytochrome b. these results showed an implication of mitochondrial DNA compared to nuclear DNA.

Introduction:

Cancer is a sickness characterized by the proliferation of an abnormal cell within a normal tissue of a body. These cells come from all from a same clone, the initiator cell of cancer that has acquired some characteristics that permit it to divide itself and to be able to form metastases (Bertram, 2001). There are two types of tumour: benign tumour and malignant ones. In the first case, the tumour is drowned into conjunctive tissue. This encapsulation permits the considerable slowdown of neoplasm’s growth, making them less dangerous. Beauty spots and warts are examples of this type of tumour easily eliminable by surgical intervention. In the second case, malignant tumours include no capsulated neoplasm. Tumour mass can, then, increase limitlessly what facilitates its infiltration into tissues as well as its invasion by other organs. Contrary to benign tumours, malignant tumours can kill (Voet, 2002). The International Research Cancer Centre (CIRC) valued the new cases of cancer to 14, 1 thousand (CIRC, 2013). It notices an increase of breast cancer throughout the world and with 1,7 thousand of women diagnosed every year. These last years, incidence and mortality have increased respectively of 20% and 14% in the world (OMS, 2013). Breast cancer is the most freqeuent cause of women death by cancer and the most frequent cancer diagnosed among women in the world. It still be the most serious public health problem, particularly among women of less under 35 year’s old where it is aggressive (Axelrod et al., 2008). In Senegal, breast cancer is the second from all the feminine cancers (Dem et al., 2008). Only 5 to 10% of cancers are hereditary ones (Claus et Risch, 1991) attributable, in majority, to BRCA1 and BRCA2 (Dumitrescu-Cotarla, 2005). Mitochondria have been suspected for a long time as playing an important role in the development and the progression of cancers. Many associated mitochondrial alteration have been identified and described in literature. These alterations include modification of mitochondrial genes, structural or quantitative mitochondrial abnormalities, or abnormalities of enzymatic components of

Manuscript Info

Key words: cancer, breast, mutation, DNAm, Senegal.

Introduction:

Cancer is a sickness characterized by the proliferation of an abnormal cell within a normal tissue of a body. These cells come from all from a same clone, the initiator cell of cancer that has acquired some characteristics that permit it to divide itself and to be able to form metastases (Bertram, 2001). There are two types of tumour: benign tumour and malignant ones. In the first case, the tumour is drowned into conjunctive tissue. This encapsulation permits the considerable slowdown of neoplasm’s growth, making them less dangerous. Beauty spots and warts are examples of this type of tumour easily eliminable by surgical intervention. In the second case, malignant tumours include no capsulated neoplasm. Tumour mass can, then, increase limitlessly what facilitates its infiltration into tissues as well as its invasion by other organs. Contrary to benign tumours, malignant tumours can kill (Voet, 2002). The International Research Cancer Centre (CIRC) valued the new cases of cancer to 14, 1 thousand (CIRC, 2013). It notices an increase of breast cancer throughout the world and with 1,7 thousand of women diagnosed every year. These last years, incidence and mortality have increased respectively of 20% and 14% in the world (OMS, 2013). Breast cancer is the most frequent cause of women death by cancer and the most frequent cancer diagnosed among women in the world. It still be the most serious public health problem, particularly among women of less under 35 year’s old where it is aggressive (Axelrod et al., 2008). In Senegal, breast cancer is the second from all the feminine cancers (Dem et al., 2008). Only 5 to 10% of cancers are hereditary ones (Claus et Risch, 1991) attributable, in majority, to BRCA1 and BRCA2 (Dumitrescu-Cotarla, 2005). Mitochondria have been suspected for a long time as playing an important role in the development and the progression of cancers. Many associated mitochondrial alteration have been identified and described in literature. These alterations include modification of mitochondrial genes, structural or quantitative mitochondrial abnormalities, or abnormalities of enzymatic components of
respiratory chain (Wilkieet et al., 1983) and currently thanks to technological development of molecular biology, ADNmt mutations.

It was in this framework that we proposed to study Cytb and FGB genetic diversity in malignant breast cancer among Senegalese women.

**Material and Methods:**

**Samples:**
The tissues samples used for this study is obtained but surgery of patients affected by breast cancer. In each patient, normal tissues and cancerous tissues were sampled from Aristide Le Dantec Hospital.

**Genetic Study:**

**DNA Extraction, Polymerase chain reaction and Sequencing of Cyt b and FGB:**
DNA was extracted from patients normal tissues and cancerous tissues using DNA tissue Kit (Qiagen). Cytband FGB were amplified. The amplification has been realized in a reactive volume of 50 µl containing 28.9 µl of Milliq water, 5 µl of buffer (10X) that contain Mg²⁺ ions to an initial concentration of 15 mM, 2 µl of dNTP, Cytb was amplified using: H15915 (TCT-CCA-TTT-CTG-GTT-TAC-AAG-AC) and L14723 (ACC-AAT-GAC-ATG-AAA-AAT-CAT-GGT-T) primers as for FGB: F1 (ATT-CAC-AAC-GGC-ATG-TTC-TTC-AG) and F2 (AAN-GCK-CAC-CCC-AGT-ATC—TG). PCR happened in a thermocycler of Eppendorfin the following conditions: For Cyt b: preliminary distortion to 94°C (3 minutes) followed by a repetition of 40 cycles of initial distortion to 92°C (45 seconds), hybridization to 50°C (1 minute) and complementary DNA strands elongation to 72°C during 1 minute 30 seconds and closed by a final elongation (10 minutes) and for FGB: preliminary distortion to 94°C (3 minutes) followed by a repetition of 40 cycles of initial distortion to 94°C (30 seconds), hybridization to 67°C (1 minute) and complementary DNA strands elongation to 72°C during 1 minute 30 seconds and is closed by a final elongation (10 minutes). An electrophoretic migration 1.5% agarose gel was performed to confine the amplification. Sequencing reactions were performed in a thermocycle MJ Reseeed PTC 225 pettree type with ABI PRISM Big Dye TM terminatos cycle Kit. Each samples was sequenced using the for word primer for each gene (Cytb, FGB).

**Molecular Analysis:**

**Alignment of Cyt b and FGB sequences:**
Cyt b and FGB sequences, of normal and cancerous tissues, are carefully verified, corrected and aligned with BioEdit version 7.0.8 (Hall, 1999) software. The alignment is, in fact an important step of data’s analysis. It is also used to bring to light similarities between sequences in finding the position of deletions or of possible insertions.

**Cyt b and FGB genetic diversity:**
In order to study the genetic diversity of cancerous tissues in the level of each gene, we determined the number of variable and invariable sites, the number of informative sites, the total number of mutations, the number of haplotypes, the average number of various nucleotides, haplotypical (h) and nucleotide (π) diversity using to DnaSP 5.10 (Libradoet Rozas, 2009) software. Nucleotide frequencies, the nature of mutations (% of transitions and transversions) and molecular distances with Kimura 2 parameter (K2P) model were executed in MEGA version 6.00 (Tamura et al., 2013). Nucleotide frequencies and molecular distances were only calculated for Cyt b which is a coding gene in various positions of the codon.

**Study of Cyt b amino acids variability:**
Cyt b nucleotides sequences are transformed into amino acids sequences using to MEGA software version 6.06 5 (Tamura et al., 2013) with the best reading frame. The frequencies of amino acids were stand out for normal and cancerous tissue. Chi² test was realized to see the amino acids that presented significant differences.

**Cyt b and FGB genetic structure:**
Genetic distances between sane and cancerous tissues at intra and inter individual level for the two genes were explained by the genetic distance of Nei (Nei,1978) using MEGA software version 6.06 version software (Tamura et al., 2013).

**Signature selection test:**
We have made demo-genetic tests that compare the level of adjustment between the two genes diversity and theoretical expected values under the hypothesis of the evolution under a neutralist model (to mutation-derive
balance). We have, among these tests Tajima D (Tajima, 1989), Fs of Fu (Fu, 1997) and R2 of Ramos (Ramos, 2002). These three tests were realized on \textit{FGB}. These various estimators are obtained using \texttt{DnaSP} version 5.10 (LibradoetRozas, 2009) and \texttt{Arlequin} version 3.5.1.3 (Excoffier et al., 2010). As for \textit{Cyt b}, the existence of any selection was apprehended by report dN/dS thanks to \texttt{MEGA 6} software with using Kimura model. dN is the substitution rate not synonymous and dS the substitution rate synonymous. The level of significance was held to 5% and a bootstrap value of 1000 replications. The distribution disparity analysis (Mismatch Distribution) that is the graphic representation of distances genetic distribution existing between individuals was also determined. Mismatch analysis is accompanied by two indices that test the quality of distribution adjustment. These indices are SSD (squarred sums of deviation) and Rag (irregularity indices). The graphs are built with \texttt{DnaSP} software version 5.10 (Librado et Rozas, 2009). SSD and Rag indices are obtained with \texttt{Arlequin} software version 3.5.1.3 (Excoffier et al., 2010).

\textbf{Results:-}

\textbf{Nucleotides sequences alignment:-}

An area of \textit{Cyt b} and an area of \textit{FGB} were sequenced for normal and cancerous tissues among 30 patients suffering from breast cancer.

\textbf{Study of \textit{Cyt b} and \textit{FGB} genetic diversity:-}

\textit{Cyt b} presents a most polymorphism compared to \textit{FGB}. Transition percentages are more important than that of transversions among \textit{Cyt b} (60%). Contrariwise, among \textit{FGB} percentages of transversions are higher than that of transitions (58.9%) (table 1). The results revealed a predominance of A and T (57.17% for \textit{Cyt b}; 62.6% for \textit{FGB}) with respect to C+G (42.83% for \textit{Cyt b}; 37.4% for \textit{FGB}). Our results revealed a mutation bias in C and G to the third position of the codon. \textit{Cyt b} substitution evolves most rapidly in the third position of the codon with a molecular distance of 0.285+-0.026 compared to the molecular distances to the first (0.161+-0.015) and the codon second position (0.195+-0.019). Genetic diversity indices analysis shows high values of \textit{h} and \textit{π} for \textit{Cytb} and a strong \textit{h} and a weak \textit{π} for \textit{FGB} (table 1).

\begin{table}[h]
\centering
\begin{tabular}{|c|c|c|}
\hline
\textbf{Settings} & \textbf{Cyt b} & \textbf{FGB} \\
\hline
Sample size, n & 30 & 30 \\
\hline
Number of sites, N & 325 & 623 \\
\hline
Monomorphic sites & 108 & 612 \\
\hline
Polymorphic sites & 217 & 11 \\
\hline
Singleton variable sites & 76 & 8 \\
\hline
Parson informative sites & 141 & 3 \\
\hline
Total number of mutations, Eta & 315 & 13 \\
\hline
Number of haplotypes, h & 30 & 10 \\
\hline
Average number of nucleotide differences (k) & 47,030 & 1,467 \\
\hline
Nucleotide frequencies (%) & ATCG & ATCG \\
\hline
1\textsuperscript{st} position & 26.75 30.42 12.13 30.70 & 31.41 31.19 17.50 19.90 \\
\hline
2\textsuperscript{nd} position & 18 13.1 42.8 25.7 & \\
\hline
3\textsuperscript{rd} position & 30 18.3 19.9 32 & \\
\hline
Molecular distances 1\textsuperscript{st} position & 0.161+-0.015 & 2\textsuperscript{nd} position 3\textsuperscript{rd} position \\
\hline
& 0.195+-0.019 & 0.285+-0.026 \\
\hline
Transitions & 60\% & 41.06\% \\
\hline
Transversions & 40\% & 58.9\% \\
\hline
R (Transition rate / Transversion rate) & 1.453 & 0.637 \\
\hline
Haplotypes diversity(h) & 1.000 & 0.800 \\
\hline
Nucleotide diversity(π) & 0.14471 & 0.00235 \\
\hline
\end{tabular}
\caption{Cyt b and FGB genetic parameters for cancerous tissues}
\end{table}

\textbf{Cyt b Amino acids variability:-}

We remark that the frequency of \textit{Cyt b} amino acid is lightly difference between sane tissues and cancerous ones without any significant statistic (table 2). However, we observe a significant value on glutamine.
Table 2: Cyt b amino acids frequency

<table>
<thead>
<tr>
<th>Aminoacids</th>
<th>Normal tissues</th>
<th>Cancerous tissues</th>
<th>P- Value</th>
</tr>
</thead>
<tbody>
<tr>
<td>Ala</td>
<td>7.46695</td>
<td>7.07778</td>
<td>0.936</td>
</tr>
<tr>
<td>Cys</td>
<td>4.57306</td>
<td>5.08058</td>
<td>0.868</td>
</tr>
<tr>
<td>Asp</td>
<td>5.25187</td>
<td>4.76524</td>
<td>0.870</td>
</tr>
<tr>
<td>Glu</td>
<td>0</td>
<td>0.42046</td>
<td>0.038</td>
</tr>
<tr>
<td>Phe</td>
<td>1.07181</td>
<td>1.40154</td>
<td>0.795</td>
</tr>
<tr>
<td>Gly</td>
<td>10.11075</td>
<td>9.11002</td>
<td>0.810</td>
</tr>
<tr>
<td>His</td>
<td>1.39335</td>
<td>2.06727</td>
<td>0.697</td>
</tr>
<tr>
<td>Ile</td>
<td>8.71739</td>
<td>8.05886</td>
<td>0.858</td>
</tr>
<tr>
<td>Lys</td>
<td>4.78742</td>
<td>5.95655</td>
<td>0.704</td>
</tr>
<tr>
<td>Leu</td>
<td>7.89567</td>
<td>8.05886</td>
<td>0.958</td>
</tr>
<tr>
<td>Met</td>
<td>10.46802</td>
<td>9.25017</td>
<td>0.775</td>
</tr>
<tr>
<td>Asn</td>
<td>3.00107</td>
<td>2.97827</td>
<td>0.966</td>
</tr>
<tr>
<td>Pro</td>
<td>5.14469</td>
<td>4.87035</td>
<td>0.922</td>
</tr>
<tr>
<td>Gln</td>
<td>2.32225</td>
<td>2.10231</td>
<td>0.923</td>
</tr>
<tr>
<td>Arg</td>
<td>1.89353</td>
<td>1.47161</td>
<td>0.821</td>
</tr>
<tr>
<td>Ser</td>
<td>8.50303</td>
<td>8.51436</td>
<td>1</td>
</tr>
<tr>
<td>Thr</td>
<td>5.71632</td>
<td>6.13174</td>
<td>0.904</td>
</tr>
<tr>
<td>Val</td>
<td>6.64523</td>
<td>6.93763</td>
<td>0.932</td>
</tr>
<tr>
<td>Trp</td>
<td>3.00107</td>
<td>3.43377</td>
<td>0.872</td>
</tr>
<tr>
<td>Tyr</td>
<td>2.03644</td>
<td>2.31254</td>
<td>0.883</td>
</tr>
</tbody>
</table>

Genetic differentiation:
Genetic distances analysis between normal tissues and cancerous ones for each gene revealed an important genetic diversity for Cyt b (d = 0.136), with respect to FGB that has no mutation (d = 0.003). Results are consigned in table III. For Cyt b, the value of genetic distance inside cancerous tissues is superior to that of sane tissues (d = 0.093). Contrariwise, no difference is noticed inside sane tissues for FGB (d = 0.006) and inside cancerous tissues (d = 0.000).

Table 3: intra and inter-group genetic distance

<table>
<thead>
<tr>
<th>Genes amplified</th>
<th>Groups</th>
<th>Genetic distances intra-groupe</th>
<th>Genetic distances inter-groupe</th>
</tr>
</thead>
<tbody>
<tr>
<td>Cyt b</td>
<td>Normal tissues</td>
<td>0.093</td>
<td>0.136</td>
</tr>
<tr>
<td></td>
<td>Cancerous tissues</td>
<td>0.112</td>
<td></td>
</tr>
<tr>
<td>FGB</td>
<td>Normal tissues</td>
<td>0.006</td>
<td>0.003</td>
</tr>
<tr>
<td></td>
<td>Cancerous tissues</td>
<td>0.000</td>
<td></td>
</tr>
</tbody>
</table>

Section signature tests:
Under a neutrality hypothesis (dN = dS) the probability value is -3.16 with a value of p(0.002) which is < 0.05. From this result, the starting hypothesis is accepted. So, substitutions at the level of Cyt b follow the Kimura neutral model evolution. For the whole Cyt b codons, ATA (AUA) triplet that codes for methionine is positively sub selected (dS = 1.618; dN = 8.561, dN – dS = 6.943with a value p. = 0.048). As for FGB, the respective values Fs of Fu (-6.917; P = 0) and of R2 (0.162; P = 0) of Ramos are significantly negativeand positive. However, Tajima D (-0.56656; P >0.3) is not significantly negative (table 4).

Table 4: signature selection tests value

<table>
<thead>
<tr>
<th></th>
<th>Cyt b</th>
<th>P-value</th>
</tr>
</thead>
<tbody>
<tr>
<td>dN/dS</td>
<td>-3.162</td>
<td>0.002</td>
</tr>
<tr>
<td>FGB</td>
<td></td>
<td></td>
</tr>
<tr>
<td>D de Tajima</td>
<td>-0.56656</td>
<td>0.30600</td>
</tr>
<tr>
<td>Fs of Fu</td>
<td>-6.91799</td>
<td>0.00000</td>
</tr>
<tr>
<td>R2</td>
<td>0.16261</td>
<td>0.0000</td>
</tr>
</tbody>
</table>
Distribution disparity analysis (Mismatch distribution):-

Distribution disparity of base pairs for both genes shows the expected and observed frequencies (full of dotted lines respectively) differences by pairs between samples. Results testify multimodal distributions for both genes (figure 1).

![Distribution disparity analysis](image)

Figure 3: Cyt b and FGB mismatch distribution curb

Cyt b SSD values (0.00336; p > 0.9), FGB (0.02400; p > 0.1), are positive and no significant for both gene (pictures V). Contrariwise, Rag values, Cyt b (0.00368; p > 0.9, FGB (0.18309), are positive and significant in FGB whereas they are negatives and no significant for Cyt b (table 5).

![Cyt b and FGB mismatch distribution curb](image)

Table 5: Values of SSD, Rag and their P-values

<table>
<thead>
<tr>
<th></th>
<th>Cyt b</th>
<th>FGB</th>
</tr>
</thead>
<tbody>
<tr>
<td>SSD</td>
<td>0.00336</td>
<td>0.02400</td>
</tr>
<tr>
<td>P- value</td>
<td>0.96000</td>
<td>0.14000</td>
</tr>
<tr>
<td>Rag</td>
<td>0.00368</td>
<td>0.18309</td>
</tr>
<tr>
<td>P- value</td>
<td>0.95000</td>
<td>0.02000</td>
</tr>
</tbody>
</table>

Discussion:-

In this study, Cyt b which is a mitochondrial gene and FGB which is a nuclear gene were analyzed among 30 Senegalese patients suffering from cancer breast. We proceeded to the study of genetic variability, of genetic differentiation and genetic evolution in order to compare cancerous tissues sequences of Cytb and FGB for the purpose of determining the implication of both genes in the mammary carcinogenesis.

Our results revealed a strong variability of Cytb compared to FGB. This strong variability of Cyt b is in mutual agreement with the works by Mbaye et al., (2014). Several types of explanations can be considered.

It can be mentioned: a sparsely regular replication (Kunkel & Loeb, 1981), mitochondrial polymerase would be less regular than that of the core, a deficiency or an absence of systems of correction and reparation and apparent absence of recombination as well as a rate of renewal and so, of more important replication than that of nuclear DNA (Brown et al., 1982).
Cyt b number of variability (217) and FGB (11) as well as that the substitutions of R, Cyt b (1.453), FGB (0.637) lead to nucleotide variability rate of DNAmt. That rate of substitutions was noticed by (Tan et al., 2002) while examining the presence of DNAmt mutation in breast cancer, of which 58% were the substitutions of gene Cyt b and the no coding area (D-Loop). Among mammal it was accurately estimated, that rate is higher than that described for only nuclear sequence and of a multiplicative factor of 5 or 10 (Brown et al.,1982). That rate is variable following genome area considered but remains globally higher.

DNAmt general characteristics of mutations are transitions C-T and A-G (Beckman & Ames, 1997) that are in correlation with our results with 60% of substitutions that are transitions among Cyt b. They declared that the main reason of DNAmt mutations in tumour is the high level of ROS. On contrast, among FGB transversions types mutations (58.9%) are high with respect to that of transitions (41.06%). These transversion type substitutions wouldn’t have not effect since they happened in an intronic area of FGB.

Our results reveal that each amino acid frequency deriving from cytochrome b sequences are weakly differentiated between sane tissues and cancerous ones without a statistic signification except glutamine. Most of cancers like breast cancer depend on a high rate of aerobic glycolysis for their growth and survival. Paradoxically, some cells lineages of cancer present also the dependence to glutamine in spite of the fact that glutamine is a no essential amino acid that can be synthesized from glucose. The high absorption rate of glutamine by exposed cells depending on glutamine seemed not coming only from its role as nitrogen donor in nucleotides and amino acids of biosynthesis. Instead of that, glutamine plays a role in the required absorption of amino acid essential in the maintaining and the activation of the TOR kinase. Furthermore, in many cancerous cells, glutamine is the primary mitochondrial substrate as well as the support to maintain the potential of the mitochondrial membrane and integrity as well as the support of NADPH production necessary for oxydoreduction control and macromolecular synthesis (Levine etPuzio-Kuter, 2010).

In this present work, we have made a comparative study of genetic distance intra and inter sane and cancerous tissues of both genes. As for Cyt b, inside cancerous tissues the value of genetic distance (d= 0.112) is higher than that of sane tissues (d= 0.093). This can be explained by the fact that, cancerous cells are no longer under the control of cellular division regular mechanisms. One of the characteristics of cancer is the rapid proliferation of abnormal cells (OMS, 2012). And as for FGB, values don’t nearly present a difference inside sane tissues (0.006) and inside cancerous tissues (0.000). This is explained by the aspect of nuclear DNA gene which has a less important replication than that of DNA mt (Brown et al., 1982). On contrat, the weak distance of FGB (0.003), confirms the characteristic of nuclear DNA which has a mutation rate less important than that of DNAmt. Methionine is under positive selection for Cyt b gene (dS = 1.618; dN = 8.561. dN – dS = 6.943 with a value of p= 0.048). In other words, it is advantageous to tumour evolution. Contrary to sane cells, most of tumour cells need a exogenous contribution of Methionine, an essential amino acid (Durando et al., 2008). Molecular mechanisms that help explain their dependence to Methionine are numerous. In vivo, various approaches were realized in order to lack in Methionine. As the main source of Methionine is food, synthetic diet plan lacked in Met have been widely used. Other alternatives were to use metabolism inhibitors of Methionine or anenzymatic degradation thanks to Methioninase. Among animal, deficiency in Methionine permit to limit tumour growth and reduce the height of some tumours. However, some studies also showed a limited effect over time with an upturn of the tumour growth after the interruption of the deficiency. These different modifications suggested the use of a deficiency in Methionine in tumour cells in association with conventional chemotherapy. Many pre-clinical studies showed a synergic effect of a deficiency association in Met and various cytotoxic agents. Currently, little clinical investigations were realized in order to explore this therapeutic strategy.

The observed number of differences between haplotypes doubly taken produced a multimodal distribution. The amount of variances squared SSD, Cyt b (0.00336; p > 0.9), FGB (0.02400; p > 0.1) are positive and aren’t significant for both gene. As for FGB, respective values: Fs of Fu (-6.917; P = 0) and R2 (0.162; P = 0) of Ramos are significantly negative and positive. However, Tajima D (-0.56656; P = > 0.3) is not significantly negative. These positive and negative values of neutrality tests are due to bare mutations. These results suggest a constant height of cancerous cells population for both genes, as show multimodal distribution (Ramos-OnsinssetRozas, 2002).

**Conclusion:**
Cyt b implication in cancers, in particular in breast malignant tumour, is no more demonstrated and is more and more studied. However, FGB is less implicated in breast malignant tumour than Cyt b. As the role of mitochondria
is known in the apoptosis, the presence of these mutations could contribute to alter cellular response to anticancerous agents.

A significant difference of glutamine frequency between normal tissues and cancerous tissues was obtained. These results from Senegalese women suffering from breast cancer should be confirmed in quantifying the level of twenty amino acids from serum or plasma of these patients unpaired to subject of control. Cancerous cells need glucoses for their development and glutamine is a no essential amino acid that can be synthesised from glucose. As glucose comes from carbohydrates, to eliminate carbohydrates, replaced by proteins and same greases, would be less an anticancerous treatment without medicines. Methionine is necessary in carcinogenic processes. So, their inhibition is a means of reducing the growth of cancerous tumour.

References:-
19. OMS : communiqué de presse n° 223, 12 décembre2013. Consultable à l’URL : www.who.int/topics/cancer/fr/