POSTER SESSIONS

Friday and Saturday

Basic science

P 1: Pediatric acute lymphoblastic leukemia with Philadelphia chromosome in Morocco: Experience of BIOLAB Laboratory

Z. Takki Chebihi, A. Belkhayat[1], M. EL-Kababri[2], A. Kili[2], M. Khattab[2]

Department of Biochemistry and Immunology, Faculty of Science, Mohammed V University, [1]Biolab Laboratory, [2]Children's Hospital of Rabat, Morocco. E-mail: zahra_tc@hotmail.com

Philadelphia chromosome-positive acute lymphoblastic leukemia (Ph+ ALL) is a biologically and clinically distinct subtype of ALL. Its incidence increases with age: 2–5% in children and 20–40% in adults, referring an extremely poor prognosis to both groups of age. The Philadelphia chromosome is mainly associated with chronic myeloid leukemia. It's diagnosed by cytogenetic techniques and molecular biology. It results from a reciprocal translocation between chromosomes 9 and 22, respectively at q34 and q11, resulting in the production of a fusion proto-oncogene: BCR/ABL (breakpoint cluster region-Abelson), coding for a chimerical protein with strong constitutive tyrosine kinase activity. The molecular weight of the fusion protein expressed in ALL patients is 190 kDa. In BIOLAB laboratory, we performed a cytogenetic analysis of 70 bone marrow samples referred to us by the children's hospital for an ALL suspicion from the 01/10/2012 to the 24/10/2014 of children aged between 1 and 17 years old. The medullar karyotype had revealed diverse numeral and structural chromosomal abnormalities in 41 cases (59%), among which we detected the Philadelphia chromosome in three cases, representing 4% of the total. It is entirely consistent with the literature. The karyotype in the three cases showed several chromosomal abnormalities in addition to the Philadelphia chromosome. We followed the analysis by FISH (Fluorescent in situ hybridization) in two cases out of three to confirm the diagnosis. This cytogenetic analysis has enabled us to establish the diagnosis of the Ph+ ALL and to point out the ominous prognosis of this disease, in order to encounter an appropriate therapeutic intervention.

Key words: Cytogenetic analysis, pediatric acute lymphoblastic leukemia, Philadelphia chromosome

P 2: The possible involvement of a wide range of viruses in sporadic breast cancer in a Moroccan population

Amal ElAmrani[1,2,3], Tarik Gheit[2], Mustapha Benhassou[4], Sandrine McKay-Chopin[2], Mohamed Attaleb[5], Souha Sahraoui[6], Moulay Mustapha Ennaji[3], Marilys Corbex[7], Massimo Tommasino[2], Meriem Khyatti[1]

[1]Oncovirology Laboratory, Institut Pasteur du Maroc, 1, Place Louis Pasteur Casablanca 20360, Maroc, [2]IARC, Infections and Cancer Biology group, Lyon, 69372 France, [3]Laboratory of Virology, Hygiene and Microbiology, Faculty of Sciences and Technics, University Hassan II Mohammedia-Casablanca, 146 Mohammedia 20650 Maroc, [4]Unité de Biologie et Recherche Médicale, Centre National de l'Energie des Sciences et des Techniques Nucléaires (CNESTEN), Rabat, 10001, [5]Obstetrics Service "A" Maternité Lalla Meryem, CHU Ibn Rochd, [6]Oncology Service, CHU Ibn Roch, Casablanca, 9155 Morocco, [7]Department of Public Health, Institute of Tropical Medicine, Antwerp, 2000, Belgium

Breast cancer (BC) is the most frequently diagnosed cancer and the leading cause of cancer death in women worldwide, accounting for 23% of total new cancer cases and 14% of total cancer deaths. In Morocco, BC is the most common cancer affecting women, with an incidence rate of 17.1/100.000 residents. The International Agency for Research on Cancer stated that 18–20% of cancers are linked to infection, and the list of definite, probable, and possible carcinogenic agents is growing each year. Among them, viruses play a significant role. This is the first study that explored the presence of a wide range of viruses in in 112 patients with BC using Luminex technology. Interestingly, the beta-HPV types were found in 9.1% of subject and gamma-HPV types in 5.7% of cases, while the low-risk and probable/high risk HPV types were present in 6.8% and 4.54% of cases, respectively. High risk mucosal HPV types 16 and 18 were not detected in our samples, but other probable/high risk types were detected (HPV 51, 52, 58, 59 and 66). The low risk mucosal HPV type 11 was the most prevalent type (13.3%). Noteworthy, EBV have been found (EBV1) in a total of 16 patients, twelve of which were carrying the EBV type 1 and four the EBV type 2. In addition, EBV was absent in normal breast samples. MCV is the third most detected virus which was found in 14.47 % of our samples but unlike EBV, the virus was also found in normal breast tissues. On the other hand, the BKV, KIV, JCV, WUV, SV40, TSV, HPyV9, HSV1, MMTV were globally absent or insignificant, while HPyV6 was found in only two cases and HPyV7, CMV and HSV2 found in one sample each. However, despite the presence of some viruses in breast samples further work needs to be done to clarify the role and the risk assessment of this virus in human BC.

P3: Molecular detection of hepatitis B virus DNA in ovarian carcinoma in Morocco

Mustapha Benhessou[1,2], Samira Zoa Assoumou[1,3], Anicet Luc M. Boumba[1,3], Mohammed Nabil Benchkrroun[1], Said Bouhya[2] and My Mustapha Ennaji[1]

[1]Laboratoire de Virologie, Microbiologie et Qualité/Eco-toxicologie et biodiversité, Faculté des Sciences et Techniques, Mohammedia, Université Hassan II, Mohammedia-Casablanca, BP: 146 Mohammedia 20650, [2]Service de Gynécologie et obstétrique "A" Centre Hospitalier et Universitaire Ibn Rochd Casablanca, [3]Laboratoire d'Agroalimentaire et Santé, Département de Biologie Appliquée, Faculté des Sciences et Techniques de Settat, Université Hassan 1er Settat, BP 577 Settat, Maroc, Morocco

Background: Epithelial ovarian cancer (EOC) is a major gynecological problem in Morocco represents more than 70% of ovarian cancers. Its etiology remains poorly understood. This study aimed to determine the presence of HBV-DNA in fresh EOC specimens from Moroccan patients. **Materials and Methods:** HBV-DNA was examined from DNA extracts of 50 fresh biopsies specimens from patients with histologically proven EOC by using PCR method. **Results:** HBV-DNA was found to be positive in four patients (8%). All of the positive patients had serous adenocarcinoma (10.3%)

and advanced stage disease. **Conclusion:** The results of this study suggest that hepatitis B virus may be involved in the etiology of ovarian cancer.

Key words: Epithelial ovarian cancer, fresh frozen tissue, HBV-DNA, polymerase chain reaction method

P 4: Study of polymorphisms of CYP1B1 gene in colorectal cancer in Moroccan population

A. Lalami, A. Laraki[1], H. Mouzount[2], F. Azzam, Y. Anjar, H. Errihani, L. Hilal, S. Amzazi, Y. Bakri

Laboratoire De Biochimie-Immunologie, Faculté des Sciences, [1]Hopital Militaire d'instruction Mohammed V HMIMV, [2]Institut National d'Oncologie, Rabat, Morocco

CYP1B1 is an enzyme involved in the activation of procarcinogens to carcinogens and the metabolism of sex hormones and xenobiotics. The enzyme activity is correlated with allele variants resulting SNPs, for this reason, this gene is considered as a candidate gene of interest for studies of susceptibility to colorectal cancer. We genotype a 794pb fragment delimited by the primers 3F- 3R3 at the exon 3 of the gene in 30 patients and 30 controls. We obtain SNPs rs141245683, rs4986888, rs28936701 and rs147535955 associated to a CRC risk demonstrated by Pvalue below the threshold of 5%. There are also three SNPs (rs1056836, rs1056837 and rs1800440), V432L and D449E did not show any significant association by χ^2 test, suggesting that the risk of CCR is not influenced by one SNP alone, association study shows that GC-TT genotype is associated with a risk of developing CCR ($P = 0.03$). Homozygous SNP rs1800440, in contrast, are associated with a protective effect in CCR ($P = 0.02$, $OR = 0.26$, $P = 0.03$).

Key words: CYP1B1, colorectal cancer, polymorphisms

P 5: Molecular analysis of RET and VHL genes in Moroccan patients with medullary thyroid carcinoma and/or pheochromocytoma

Anjar Yousra, El-Annas Abdessamad, CharaibiAbdelmjid[1], Iraqi Hinde[1], Bakri Youssef, Hilal Latifa

Laboratoire de Biochimie et Immunologie Université Mohammed V – Agdal, Faculté des Sciences, [1]Service d'Endocrinologie Diabétologie et Nutrition, Ibn Sina Hospital, Rabat, Morocco

Pheochromocytomas (PCCs) are rare neuroendocrine tumors derived from the adrenal chromaffin cells. They are often benign tumors that are associated with high morbidity and mortality due to mass effect and high circulating catecholamine. Research studies have reported that about a third of individuals with phaeochromocytoma, have afamilial cancer syndrome. A group of susceptibility genes for syndromicpheochromocytoma were identified (RET, VHL, NF 1 and SDH). They respectively predispose carriers to multiple endocrine neoplasia type 2 (MEN-2), Von Hippel–Lindau disease (VHL), neurofibromatosis type1 disease (NF1) and pheochromocytoma/paraganglioma syndrome (PHEO/PGL). The prevalence of germline mutations in this genes among patients presenting an apparently non-syndromic PCC appears to be much higher than previously supposed. Mutation analysis has shown rates, ranging from 10% to 27% of familial cancer syndrome gene involvement. The purpose of this study is to demonstrate the features of sporadic as well as family PCC interest in genetic testing and we present the contribution of RET and VHL to PCCS in Moroccan patients with different form of PCC. In this report, Peripheral blood from a total of unrelated, consenting six patients participated in this study, five of them were clinically characterized as apparently sporadic cases, two patients with NEM2A, two other with CMT and one with non syndromic PCC. One case of familial MEN2A was tested. We evaluated exon 8, 10, 11, 13, 14, 15 and 16 of RET in cohorts of patients with PCC and or CMT and exon 1, 2, 3 of VHL in patient with non-syndromic PCC. DNA analysis was performed by direct sequencing of PCR product on automated sequencer and/or PCR-digestion. Sequence analysis revealed that 1 of the apparently sporadic cases of NEM2A carried an RET germ-line mutation, C634R, who were reclassified as hereditary form. We have identified the same mutation in patient with familial NEM2A. No mutations were detected in the VHL coding region of individual with a single sporadic PCC. Our study confirms that the gremline mutation can be identified as well as in familial and apparently sporadic PCC. The results further confirm the need of DNA sequencing for identification of hereditary in all PCC cases. In order to confirm that, other candidate genes (SDHB, SDHD) should be analyzed.

Key words: Pheochromocytoma, genetic screening, germlinemutation, RET, VHL

P 6: Development of nano-technological biosensors from tumor markers for early diagnosis of gynecological and breast cancers viral etiology in Morocco

Rahma Ait Hammou, Moulay Mustapha Ennaji

Laboratory of Virology, Microbiology and Quality, Ecotoxicology et Biodiversity, Faculty of Sciences and Technical Mohammedia, University Hassan II-Mohammedia, Morrocco. E-mail: rahma.aith@gmail.com

Breast and gynecological cancers (cervical cancer, ovarian cancer…) represent a real public health problem in Morocco. In 2011 these cancers accounted for 60% of all cancers among women and 50% of cancer among women treated at the National Institute of Oncology. These cancers are often diagnosed at an advanced stage of the disease, especially in rural areas where the awareness and education of the population still represent real obstacles. In spite of significant advances in research on these cancers, with the new tools of molecular biology, viral etiopathology of these cancers is often associated and reported to human papilloma virus (HPV), EBV, MMTV, HBV, and the most affected virus is often the HPV. Therefore their diagnosis is frequently performed late to the metastatic stage. In Africa more than 30% of cancers are caused by infection, and several studies are oriented towards the search of a viral etiology in gynecological and breast cancers. Similarly, in the context of the prevention of cancer, one of the current approaches is the identification of specific biomarkers that allow early diagnosis of these cancers. Among these, the identification of MicroRNAs (miRNAs), which are epigenetic biomarker able to regulate promoters of genes of cancer cells and which are released early in the general circulation, thus providing potential targets for diagnosis. It is in this context that our research project proposes to locate and identify a molecular profile of miRNAs specific to each type of breast and gynecological cancers in the moroccan population, seek the involvement of viral etiology in these cancers from biopsies, and develop a nano-biosensor in order to establish an early diagnosis, better prognosis and improved therapeutic monitoring for patients.

Key words: Breast cancer, biosensor, epigenetic and genetic biomarkers, gynecological cancers, MiRNAs

P 7: Clinical validation of a next-generation sequencing for germline mutations in BRCA1 and BRCA2 genes in breast cancer

Farah Jouali, Nabila Marchoudi[1], Jamal Fekkak[1], Houria Rhaissi

Laboratoire de physiopathologie et génétique moléculaire, Faculté des sciences Ben M'Sick, [1]Laboratoire de Radio-Immuno-Analyse Anoual, Casablanca

Breast cancer is the most common cancer affecting women all over the world. The World Health Organization estimated that 1.38 million breast cancers were diagnosed worldwide in 2008. In Morocco, according to the Greater Casablanca Cancer Registry, breast cancer seems to be the first female cancer with a standardized incidence of 36.4 for an average age of 49.5 years. Germline mutations that inactivate BRCA1 and BRCA2 are responsible for breast and ovarian cancer susceptibility. The prevalence of BRCA1 and BRCA2 mutations where family history shows more than one occurrence of breast cancer under the age of 50 ranges from 8 to 21.2%. High throughput methods such as next generation sequencing are increasingly used in molecular diagnosis. Massive parallel sequencing allows the generation of millions of DNA sequences in a single run with low cost per base. Recently, next generation sequencing methods for the mutation analysis of the BRCA1 and BRCA2 genes in patients with breast and ovarian cancer have been described using both high capacity and bench top platforms. We utilized a workflow using the Ion Torrent Personal Genome Machine (IT-PGM; Life Technologies) an NGS platform, to screen germline mutations in BRCA1 and BRCA2 genes using the Ion AmpliSeq BRCA1 and BRCA2 Community Panel (Life Technologies). Till now, 16 breast cancer patients, considered being at high risk, due to medicinal examination were selected for molecular genetic testing of BRCA1 and BRCA2 genes. Mutations detected by IT-PGM platform were confirmed by traditional mutation detection assay Sanger sequencing. We show that the IT-PGM platform is sensitive and specific and can be used for routine mutational screening of patient with hereditary breast and ovarian cancers.

Key words: Breast cancer, BRCA1, BRCA2, next generation sequencing

P 8: Differentiation between primary and secondary glioblastomas: Molecular aspects

N. Senhaji, S. Louati, S. EL-Bardai[1], K. Mikou, A. Amarti[1,2], S. Bennis[1,2]

Laboratory of Bioactive Molecules Structure and Functions, Faculty of Science and Technology, [1]Pathological Anatomy and Molecular Pathology Service, University Hospital Hassan II, [2]Laboratory of Molecular and Cellular Biology, Faculty of Medicine and Pharmacy, Fez, Morocco

Introduction: Glioblastoma is the most frequent and malignant brain tumor with a poor diagnosis, as indicated by a median survival time of only 15 months in optimally treated patients. In spite of a similar histological appearance, primary and secondary glioblastomas are distinct tumor which originate from different precursor cells, develop through different genetic pathways and may require different therapeutic approaches. The aim of this study is to identify the frequency of some genetic markers leading to differentiate between primary and secondary glioblastomas, thing that makes the diagnosis more accurate than the clinical data. **Materials and Methods:** 54 tumor samples were used for this study. They were obtained from patients diagnosed with glioblastoma at the University Hospital Hassan II of Fez between January 2010 and December 2013. DNA was extracted for molecular analysis. We performed a RT-PCR to study EGFR and MDM2 genes amplification and PCR/purification/sequencing techniques to detect mutations in IDH1/IDH2 genes. **Results:** 54 Glioblastomas were studied; 23 patients were male and 22 female. The age of patients was ranged from 8 to 83 years old and the mean was 45.49 IDH1 mutation was observed in 15 cases (27.78%). However, we noted no mutation in IDH2 gene. The detection of EGFR and MDM2 amplifications is in progress with RT-PCR techniques. **Discussion:** Many studies provided evidence that primary and secondary glioblastomas develop through different genetic pathways. Typical molecular markers for primary glioblastoma are EGFR and MDM2 amplifications. Genetic alterations more common in secondary glioblastoma include TP53 mutation and 1p/19q loss. However, the IDH mutations still the most important molecular marker of secondary glioblastoma. This study will focus on the presence and the frequency of these markers. These data should be compared with literature. **Conclusion:** The new molecular technology has allowed better classification of gliomas based on the alteration of specific genes for each tumor subtype. These molecular markers are necessary for accurate and objective differentiation and consequently for a more targeted therapy.

Key words: EGFR, IDH, MDM2, primary and secondary glioblastoma

P 9: Comparison of reverse transcription quantitative real-time polymerase chain reaction, fluorescent in situ hybridization and immunohistochemistry for detection of *MDM2* gene amplification in well-differentiated and dedifferentiated liposarcoma about 14 cases

S. Louati, L. Chbani[1], N. Senhaji, K. Amrani Joutei, A. Amarti Rifi[1], S. Bennis[1,2]

Laboratory of Bioactive Molecules, Structure and Functions, Faculty of Sciences and Techniques, [1]Clinical Pathology and Molecular Pathology Service, University Hospital Hassan II, [2]Molecular and Cellular Biology Laboratory, Faculty of Medicine and Pharmacy of Fez, Morocco

Introduction: Liposarcomas are a heterogeneous group of malignant adipocytic neoplasms that consist of 3 distinct clinicopathological entities: well-differentiated/dedifferentiated liposarcoma, myxoid liposarcoma, and pleomorphic liposarcoma. Dedifferentiated liposarcoma (DDLPS) results from the progression of a well-differentiated liposarcoma (WDLPS) to a nonlipogenic sarcoma of variable histologic grades and morphologic patterns that acquires metastatic potential. The aim of this study is to a correlate between reverse transcription quantitative real-time PCR, fluorescent in situ hybridization and Immunohistochemistry for detection of MDM2 gene amplification in well-differentiated and dedifferentiated liposarcoma. **Materials and Methods:** 14 cases of liposarcoma were selected from the Pathological Anatomy service to make this correlation. Diagnosis is based on a standard histology. Immunohistochemical confirmation was carried out by the antibody anti-MDM2. The amplification of MDM2 gene was performed by fluorescent in situ hybridization technique (FISH) and by reverse transcription quantitative real-time PCR (RT-PCR). **Results and Discussion:** The average age of patients is 54 years, ranging from 27 to 75 years with a slight female predominance. Six cases of tumors are diagnosed well-differentiated liposarcoma, two other cases dedifferentiated liposarcoma and six cases whose diagnosis by immunohistochemistry was not decisive. These tumors are characterized by a heterogeneous aspect of malignant cells and positivity of anti-MDM2 antibody. MDM2 amplification by FISH was found in 7 of 14 liposarcoma cases. Thirty-three percent (2/6) of

WDLs, 50% (1/2) of the DDLs and seventy percent (4/6) of the cases whose diagnosis by immunohistochemistry was not decisive showed amplification. The search for the amplification of MDM2 gene by QPCR is in progress. **Conclusion:** *MDM2* amplification has been shown to have high sensitivity in characterizing WDL and DDL. Differences in MDM2 amplification profiles among liposarcomas could help further define and predict progression to high-grade neoplasia.

P 10: Novel Fluorescent probe for early detection of some tumor markers

R. EL-Khamlichi, A. EL-Falouji[1], D. Bouchta

University Abdelmalek Essaâdi, Faculty of Sciences, Team of Electrochemistry and Interfacial Systems (ERESI), Morocco, [1]Biotechnology Research Centre, Suez Canal University, 41522 Ismailia, Egypt. E-mail: redkha001@hotmail.com

Cancer is one of the most serious diseases that threaten human life. In the last few decades, there was a significant decrease in the death rate in the US due to cardiovascular, cerebrovascular, and infectious diseases, however non-significant alteration in cancer-related mortalities was achieved since 1950 despite the quick improvement in research methodology and technology. Thus, discovering and developing novel methods for the early detection of cancer has a vital importance. The detection of cancer biomarkers plays an important role in clinical diagnoses and evaluation of treatment for patients. Many immunoassay methods are developed for detection of cancer biomarkers. Early detection of cancer biomarkers plays an important role in clinical diagnoses, oncological medicine and evaluation of treatment for patients. Recent and previous research has shown early detection of cancer increases the odds of patient survival. Different methods have been used for tumor marker detection and determination, in the last five years several reports have appeared where intrinsically fluorescent techniques have been used for tumor markers in cancer patients. In this work the first step towards a molecularly imprinted polymer (MIP) based on star fish compounds for the detection of some tumor markers via fluorescence spectroscopic techniques was presented. The interactions of a new synthesized dendrimer compounds with Alpha-fetoprotein and cancer antigens CA15-3 tumor markers have been studied using spectroscopic techniques.

Key words: Alpha-fetoprotein, CA15-3 tumor markers, fluorescent probe, star fish compounds

P 11: Novel tryptophan ligated lanthanides as natural and effective anticancer agents: Design, synthesis and in vivo and in vitro testing

Abdullah I. A. El-Falouji, Belal H. M. Hussein, Abdelazim Ibrahim, Mohammad S. Gomaa, Hassan A. Azab

Biotechnology Research Center, Suez Canal University, Ismailia 41522, Egypt. E-mail: Faouji@hotmail.com

Although struggling efforts against cancer have grown tremendously in the last few years, cancer is still the second leading cause of death in economically developed countries following heart disease. Therefore, the discovery and development of novel therapeutic agents for the treatment of cancer have a vital importance. The chemotherapeutic cancer treatment through induction of apoptosis has now become one of the most important fields of anticancer research. Recent preclinical studies showed synergistic action between apoptosis and anti-angiogenic therapy. An improved efficacy in lung cancer progression has also been demonstrated through the combination of antiangiogenic and apoptotic effects. In recent years, one of the successful and effective approaches in the search for new chemotherapeutic agents is the development of new rare earth metals-based anti-cancer agents. In this work, a novel erbium (III), samarium (III) complexes containing tryptophan ligand were synthesized and characterized. The anti-tumor effect of these complexes against human liver carcinoma cell line (HEPG2), human breast carcinoma cell line (MCF7) and Ehrlich ascites tumor (EAT) cells was tested in vitro and in vivo, respectively. The results showed an evidence that the new complexes induced apoptosis in EAC cells through P53 and caspase-3 activation. Furthermore, an anti-angiogenic effect of that complex mediated by down-regulation of VEGF receptor type-2 (Flk-1). Knowing that Flk-1 is a tyrosine kinase receptor, molecular docking simulation was used to study the interaction of the complex with different tyrosine kinases known to be associated with cancer pathogenesis to further confirm the antiangiogenic activity of the new complexes.

Key words: Apoptosis, antitumor activity, anti-angiogenesis, lanthanide complexes, L-tryptophan

P 12: Pathological and molecular aspects of synovial sarcoma, liposarcoma and tumors of PNET/Ewing group about 79 cases. Experience of the University Hospital HassanII of Fez

S. Louati, L. Chbani[1], N. Senhaji, K. Amrani Joutei, A. Amarti Rifi[1], S. Bennis[1,2]

[1]Laboratory of Bioactive Molecules, Structure and Functions, Faculty of Sciences and Techniques, [2]Clinical Pathology and Molecular Pathology Service, University Hospital Hassan II, 3Molecular and Cellular Biology Laboratory, Faculty of Medicine and Pharmacy, Fez, Morocco

Introduction: The soft tissue sarcomas are rare tumors in which morphological and phenotypic classifications are poorly reproducible. Understanding the molecular mechanisms involved in the genesis of these tumors allowed to classify them in five categories. The objective of this work is to study the molecular aspects in comparison with pathological aspects of soft tissue sarcoma of patients collected in the Pathological Anatomy Service of the University Hospital HassanII of Fez. **Materials and Methods:** This is a retrospective study between February 2008 and October 2014 realized on 79 cases of sarcomas. All tumors are diagnosed in the Pathological Anatomy service and based on histology, 35 cases were classified on PNET/Ewing group, 30 cases on Synovial sarcoma group and 14 cases on liposarcoma group. Immunohistochemical confirmation was carried out by different antibodies anti-MDM2, anti-CD99, anti-cytokeratin and anti-EMA. The chromosomal rearrangement of EWSR1/SS18 genes and the amplification of MDM2 gene were performed by fluorescent in situ hybridization technique (FISH). **Results and Discussion:** The average age of patients is 35 years, ranging from 3 to 75 years with a male predominance. 78% of tumors are grading III FNCLCC with a frequent localization in the lower limbs. Tumors of PNET/Ewing group are composed the proliferation of small round cells. 85%of them show an intense and diffuse membrane positivity ofanti-CD99antibody. EWSR1 gene rearrangement was noted in 63% of cases, confirming the diagnosis of a tumor of the PNET/Ewing group. Most of Synovial sarcoma are characterized by a fusiform appearance of tumor cells and over 60% of cases show a positive staining of anti-cytokeratin and anti-EMA antibody. The SS18 gene rearrangement is detected in more than 50% of cases. Six cases of tumors are diagnosed well-differentiated liposarcoma, two other cases dedifferentiated liposarcoma and six cases whose diagnosis by immunohistochemistry

was not decisive. These tumors are characterized by a heterogeneous aspect of malignant cells and positivity of anti-MDM2 antibody. The search for the amplification of MDM2 gene is necessary for histological confirmation. **Conclusion:** Considering the therapeutic stakes and the non-specificity of the antibodies, the molecular study (FISH and PCR) has become a necessity in the diagnosis of sarcoma.

P 13: Loss of WIF-1 and Wnt5a expression is related to aggressiveness of sporadic breast cancer in Tunisian patients

Fatma Trifa, Sondes Karray-Chouayekh, Emna Jmal, Zeineb Ben Jmaa, Abdelmajid Khabir[1], Tahia Sellami-Boudawara[1], Mounir Frikha[1], Jamel Daoud[1], Raja Mokdad-Gargouri

Laboratory of Biomass Valorisation and Production of Eukaryotic Proteins, Center of Biotechnology of Sfax, University of Sfax, Sidi Mansour Street, BP"K"1177, Sfax 3018, [1]Centre Hospitalo, Universitaire Habib Bourguiba, Sfax, 3000, Tunisia. E-mail: raja.gargouri@cbs.rnrt.tn

Activation of the Wnt/β-catenin signaling pathway is common in various human cancers. The aim of thisstudy was to investigate the expression of two members of the Wnt family (WIF-1 and Wnt5a) in sporadic and hereditary breast cancer tissues. WIF-1, is a secreted antagonist that binds Wnt ligands, and therefore inhibits the canonical Wnt/β-catenin pathway. Wnt5a is one of the members of the noncanonical Wnt family that mainly acts through calcium signaling pathway. The expression of WIF-1 was analyzed by methylation-specific PCR and RT-PCR, and the level of Wnt5a ligand was quantified by RT-QPCR in breast cancer tissues. Methylation of WIF-1 was detected in 71.3 % and 81.8 % of sporadic and hereditary cases, respectively. Aberrant methylation of WIF-1 was associated with advanced TNM stage and triple negative cases in sporadicbreast carcinoma ($P = 0.001$ and $P = 0.037$, respectively). In hereditary cases, methylation of WIF-1 correlated with age at diagnosis ($P = 0.027$) and p53 status ($P = 0.035$). Regarding patients' survival, WIF-1 methylated promoter conferred a reduced overall survival rate, and particularly in a group of patients with advanced TNM stage (p log rank = 0.006). Furthermore, aberrant CpG methylation of the WIF-1 promoter was significantly associated with transcriptional silencing of this tumor suppressor gene in sporadic breast cancer tissues ($P = 0.036$). On the other hand, in sporadic tumor tissues, the level of Wnt5a mRNA was significantly lower compared to normal tissues ($P = 0.031$) and lower still in those showing more aggressive behavior, suggesting that Wnt5a, a ligand involved in the non canonical Wnt/β-catenin Pathway, could act as a tumor suppressor gene in breast cancer.

P14: Molecular analysis of p53 codon 72 polymorphism among women with cervical cancer in Gabon: A case-control study

Samira Zoa Assoumou[1,2], Anicet Luc M. Boumba[1,2], Angelique Ndjoyi-Mbiguino[3], Abdelkrim Khattabi[2], Moulay Mustapha Ennaji[1]

[1]Laboratoire de Virologie, Microbiologie et Qualité/Ecotoxicologie and Biodiversité, Faculté des Sciences et Techniques de Mohammedia, Université Hassan II Mohammedia Casablanca, BP 146 Mohammedia 20650, [2]Laboratoire d'Agroalimentaire et Santé, Département de Biologie Appliquée, Faculté des Sciences et Techniques de Settat, Université Hassan 1er Settat, BP 577 Settat, Maroc, Morocco, [3]Laboratoire de Référence IST/Sida, Laboratoire de Référence Rougeole, Rubéole et Fièvre Jaune, Département de Bactériologie et Virologie, Faculté de Médecine et des Sciences de la Santé, Université des Sciences de la Santé, BP 4009 Libreville, Gabon

Cervical cancer is the leading cause of cancer related death in Africa and the first most common cancer in Gabonese women due to infection of high risk Human Papillomavirus. However, other cofactors such as genetic factors also come into play. A common polymorphism of the p53 in codon 72 in exon 4 with two alleles encoding arginine or proline is known at this locus. The homozygous arginine form of this polymorphism has been associated to the development of cervical cancer as an increased genetic risk factor. However, the results are still controversial. This study aims to investigate whether the genotype distribution of p53 codon 72 may be a risk factor for cervical cancer among Gabonese women. Samples from 102 Gabonese women, 31 diagnosed with cervical cancer and 71 healthy controls were used. HPV detection was done by nested PCR with MY09/11 and GP5+/6+ primers followed by sequencing for HPV genotyping. p53 codon 72 polymorphism determination was performed by allele-specific PCR assay. Viral DNA was detected in 87.1% of cases and 54.93% of control. HPV 16 was the most predominant in cancer and controls cases. The distribution of Arg/Arg, Arg/Pro and Pro/Pro genotypes was 35.5%, 51.6% and 12.9% in the cervical cancer group and 22.5%, 62% and 15.5% in the control group. No significant association was found between polymorphism of p53 itself as well as in combination with HPV16/18 infection and risk of development of cervical cancer among Gabonese women. Thus, the polymorphism of p53 codon 72 in exon 4 does not seem to play a role in the development of cervical cancer among Gabonese women.

Key words: Cervical cancer, gabonese women, human papillomavirus, p53 codon 72, polymorphism

P 15: Prevalence and specific-HPV genotypes distribution among women attending the General Hospital of Loandjili - Pointe-Noire, Southwestern Congo

Anicet Luc M. Boumba[1,2,3,4], Zineb Qmichou[1,2], Samira Zoa-Assoumou[1,2,3], Mohammed Attaleb[2], Mohammed El Mzibri[2], Mustapha Mouallif[1], Lahoucine Hilali[3], Donatien Moukassa[4], Moulay Mustapha Ennaji[1]

[1]Laboratoire de Virologie, Microbiologie et Qualité/Eco-toxicologie et biodiversité, Faculté des Sciences et Techniques Mohammedia, Université Hassan II, Mohammedia-Casablanca, BP: 146 Mohammedia 20650, [2]Laboratoire de Biologie Moléculaire, Unité de Biologie et Recherche Médicale, Centre National de l'Energie, des Sciences et des Techniques Nucléaires (CNESTEN) B.P. 1382 RP, 10001 Rabat, [3]Laboratoire d'Agroalimentaire et Santé, Département de Biologie Appliquée, Faculté des Sciences et Techniques, Université Hassan 1er Settat B.P. 577 Settat, Maroc, Morocco, [4]Laboratoire d'Analyses Médicales et Morphologiques, Hôpital Général de Loandjili, B.P. 8122, Pointe-Noire, Congo. E-mail: m.ennaji@yahoo.fr

Background: Infection with HPV is associated to cervical cancer and its precancerous lesions. A good vaccination strategy is based on the perfect knowledge of HPV genotypes distribution in a given population. **Objective:** To characterize the HPV genotypes in Southwestern Congo, we investigated the HPV prevalence and genotype distribution associated with cervical lesions from women attending the General Hospital of Loandjili. **Methods:** A cross-sectional study was conducted and completed with a standardized questionnaire on 321 women aged 16 to 72 years. Cervical samples

were obtained using a cytobrush and HPV infection was assessed by nested-PCR using MY09/MY11 and GP5+/GP6+ primers followed by direct sequencing. Multiple infections were assessed by type-specific PCR for HPV 6, 11, 16, 18, 31 and 33. **Results:** HPV-DNA was detected in 41.1% (95% CI, 35.8–46.5) of the study population. High-risk genotypes (HR-HPV + pHR-HPV) were found in 84.8% of positive samples, of which 15.9% involved multiple-type infections. The five commonest genotypes were HPV16 (35.6%), HPV33 (16.7%), HPV70 (6.0%), HPV18 (5.3%) and HPV31 (3.8%). The prevalence of HPV infection increased with the severity of cervical lesions from 11.7% in N/BRCC to100% in HSIL/ICC). HPV infection was significant associated with age, number of sexual partners, and number of pregnancy, education level and first sexual intercourse age ($P < 0.05$). **Conclusion:** Based on the high prevalence of HPV infection found in this study, the necessity of cervical cancer prevention program in Congo is entirely justified.

Key words: Genotypes distribution, General Hospital of Loandjili, HPV prevalence, pointe-noire, Southwestern Congo

P 16: Low level of consanguinity in Moroccan families at high risk of breast cancer

M. Mansouri[1,2], S. Chafai Elalaoui[1,2], I. Cherkaoui Jaouad[1,2], F.Z. Laarabi[1,2], N. Benjaafar[3], A. Sefiani[1,2]

[1]Centre de génomique humaine, Faculté de Médecine et de Pharmacie, Université Mohammed V Souissi, [2]Département de Génétique Médicale, Institut National d'Hygiène, [3]Service de Radiothérapie, Institut National d'Oncologie, Rabat, Marocco

Breast cancer is the most common malignancy affecting women worldwide. 5–10% of all breast cancer cases that show strong familial history are caused by inherited mutations in many genes mainly BRCA1 and BRCA2. The development of cancer in women from families at high risk is probably more related to genetic than environmental factors, and a possible relationship between consanguinity and cancer should be examined. Different types of consanguineous marriages impart in offspring a different probability of homozygosity by descent. In spite of a large consanguineous population in Africa and Arab Countries, the effect of inbreeding on developing breast cancer in these countries is still unclear. In this study, we examined the parental consanguinity level and the possible effect of inbreeding on the risk of breast cancer in Moroccan families at high risk. The present study showed that the rate of parental consanguinity was lower in breast cancer patients (9.72%) than in Controls (15.25%), with an Odds ration of 0.59 (CI: [0.27; 1.2]). These results indicate that consanguinity might be a protective factor against breast cancer in families at high risk.

17: Pre-symptomatic diagnosis of breast cancer in two Moroccan family

M. Mansouri[1,2], S. Chafai Elalaoui[1,2], FZ. Laarabi[1,2], A. Sefiani[1,2]

[1]Centre de génomique humaine, Faculté de Médecine et de Pharmacie, Université Mohammed V Souissi, [2]Département de Génétique Médicale, Institut National d'Hygiène, Rabat, Morocco

Breast cancer is one of the most common diseases affecting women. Inherited susceptibility genes, BRCA1 and BRCA2, are considered in breast, ovarian and other common cancers etiology. BRCA1 and BRCA2 genes have been identified that confer a high degree of breast cancer risk. Our study was performed to identify germline mutations in some exons of BRCA1 and BRCA2 genes for the early detection of presymptomatic breast cancer in females. Presymptomatic diagnosis was carried out using DNA genetic testing in three healthy Moroccan female individuals from two families with an elevated risk of developing breast cancer. These are the first Moroccan families reported to be affected by breast cancers associated with BRCA mutations. One family was the first reported incidence of the founder mutation Ashkenazi BRCA1-185_186delAG in Moroccan patients. The second family carried the known BRCA2 mutation c.5073dupA/p.trp1692metfsX3. . Two sisters from family 1 carried the BRCA1-185_186delAG mutation, whereas the third female individual from family two carried the c.5073dupA/p.trp1692metfsX3 mutation. This study found BRCA mutations in three asymptomatic subjects, suggesting that this is the first step towards the development of persistent medical monitoring of females from families with a history of breast and ovarian cancers. Consequently, it is crucial for oncologists in Morocco to initiate the supervision of healthy female individuals with genetic defects which may lead to hereditary cancers.