كلية العلوم
Faculty of Science

جامعة مصراتة
MISURATA UNIVERSITY

Genetic & Biotechnology Department
National DNA Day 25.4.2023

قسم الوراثة والتقنيات الحيوية

Department of Genetics and biotechnology

ملخصات مشاريع التخرج

Abstracts of Research Project

2023 -2022

Genetic & Biotechnology Department
National DNA Day 25.4.2023

كتيب ملخصات مشاريع التخرج
لقسم الوراثة والتقنيات الحيوية

للعام الجامعي 2022 - 2023

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اعداد: أعضاء هيئة التدريس بالقسم

نبذة تارخية :

تأسس قسم علم الوراثة سنة 2015 و تم افتتاحه فصل خريف 2015 و تخرجت أول دفعة في فصل ربيع 2019 ، في سنة 2021 تم تطوير الخطة الدراسية و تغييرمسماه إلى قسم التقنيات الحيوية بناء على المقترح المقدم من كلية العلوم وقرار مجلس الجامعة رقم 21 لسنة2021 ليندرج البرنامج التعليمي لعلم الوراثة كشعبة ضمن قسم الاحياء بكلية العلوم و بعد ذلك تم دمج شعبة الوراثة الى قسم التقنيات الحيوية كقسم واحد تحت مسمى قسم الوراثة والتقنيات الحيوية يبلغ عدد الطلبه فيه حاليا 75 طالب.

عدد الطالب الخريجين حاليا: 93 طالب ضمن خمس دفعات:

الدفعة الاولى: (2018-2019) 18 طالب وطالبة

الدفعة الثانية: (2019-2020) 5 طالب وطالبة

الدفعة الثالثة: (2020-2021) 18 طالب وطالبة

الدفعة الرابعة: (2021 – 2022) 38 طالب وطالبة

الدفعة الخامسة: (2022- 2023)14 طالب وطالبة

أعضاء هيئة التدريس القارين بالقسم واهتماماتهم البحثية:

ا.د. فوزية رجب القرابولي

الكشف الجزئي عن الأمراض الوراثية والتأثير المضاد للمسرطنات والسرطان لمستخلصات الأعشاب والمواد الكيميائية .وايجاد حلول للقضاء على البكتريا المقاومة للمضادات الحيوية.

د. مصطفي محمد مفتاح دراه

الأمراض الوراثية والطفرات الجينية والبصمة الوراثية والمعلومات الحيوية.

د. سعد أبو القاسم عبد الرزاق العربي

Therapeutic protein production, Construction vectors, Extraction of active compounds from plants, and Designing selection and screen system.

ا. أسماء صالح عبد السلام عليلش

Human-microbes (bacteria & viruses) interactions at molecular level, Genetic susceptibility to microbial infection those that related to immunity of host, and Molecular characterization of micro-organisms

ا. مروة الصادق محمد الوش

Virology research, Human-microbes (bacteria & viruses) interactions at molecular level., Medical research in gene therapy, and Bioinformatics.

ا. عفاف إبراهيم اسماعيل البلوز

متابعة النمو الجنيني ودراسة تأثير مختلف أنواع الملوثات على الاجنة الحيوانية والأمراض الوراثية وتأثيرها علي الإنسان ودراسة أسبابها ومدي انتشارها داخل المجتمع و التوعية المجتمعية بالأمراض الوراثية لمجتمع خالي من هذه الأمراض.

ا. محمد يوسف امحمد الوش

Studying the infertility in human, Diabetes in infertile people, and causes of inflammation.

ا. اسماء على محمد أبودبوس

الكشف عن مسببات الامراض سرطانية والامراض وراثية والامراض مزمنة.

ا. احسان محمد ماصدناه ادريس

الوراثة والبيئة Heredity and Environment.

فهرس الملخصات

Table of Abstracts

1.1. Detection of BRCA1 and BRCA2 mutation in some Libyan families with inherited breast cancer.

Omessaaed Ahmed Al-mani, Mustafa Drah

Breast cancers is an important public health problem worldwide. According to American Cancer Society (ACS), nearly 2 million new cases of breast cancer occurred among women worldwide in 2016. Generally, the incidence of breast cancer is increasing in the world. Approximately 5-10% of breast cancer cases are hereditary. Two autosomal dominant genes, BRCA1 and BRCA2, account for most of the cases of familial breast cancer. Women who carry a BRCA mutation have 60 - 80% risk of developing breast cancer in their lifetimes compare with other women which have normal BRCA genes. A total of eleven samples were collected one as control and ten were obtained from patients with breast cancer, who underwent curative surgery at Misurata Cancer Centre (MCC) and diagnosed in the department of histopathology at the centre between December 2018 and March 2019. A new BRCA1 mutation of Libyan families sequenced of those samples by using sanger sequencing. This Mutation was detected a frameshift mutation in exon 10 of BRCA1 (NM_0073300.3), chr17:41,244,195(GRCh37/hg19) from patient with breast cancer history from Tripoli. Sequencing and bioinformatics analysis was done for eleven samples, frameshift (NM_0073300.3) mutation was not found in 11 samples. This result lead us to study the genetic background for this patient and our patients. However more screening of this mutation must be done of all families with breast cancer history in our population, moreover, strongly recommended studying BRCA1 and BRCA2 mutations of all families with breast cancer history.

Key words: BRCA1, Breast cancer, Sanger sequencing, Mutation, NGS

1.2. Genotyping of Epestine Barr Virus (EBV)

Halema Alsead, Thani heba, Safa Huwidy, Ehsan Idrise, AsmaAlilish

Epstein Barr Virus (EBV) and also called Human herpesvirus 4 (HHV4); is one of the most common a strikingly in human and is infecting more than 90% of humanity. EBV is one of eight known types in the herpes family, and the herpesviruses are divided into three families –alpha, beta and gamma. Aims of this study was Detection and Determination the predominat EBV genotype of EBV in Lymphoma. In this study, we have used the molecular techniqueto detect EBV using polymerase chain reaction (PCR). The amplification of EBV Type A and Type B was conducted in 18 tissues of cervical cancer samples. The results of PCR revealed the presence 3of 10(30%)samples have type B and the 7of 10 (70%) samples have type A among cervical cancer sample infected with EBV. The molecular detection of EBV was most of the samples Type A was found in 66.6% (6/9) infection in lymphoma in Libya.

Key words: Epstein Barr Virus, Human herpesvirus 4, polymerase chain reaction.

1.3. Detection of Kras gene mutation in patients with colorectal cancer

Heba Elshara, Mustafa drah, layla Elmajdoub

Colorectal cancer (CRC) is one of the most common cancers in the World, that *Kras* mutation considered as the important point of the cause of colorectal cancer. This study aimed to detect the *Kras* gene in blood isolates from patients at the pathology laboratory in the Misurata Cancer Center during spring 2019. A Total 17 blood samples from patients with the early and late stages based on the patient gender with different ages were collected and Genomic DNA was isolated from patient serum, electrophoresis for DNA extraction and PCR amplification of *Kras* gene. Overall, 58.8% of females and 41.2% males with CRC, 47% of patients with family history and 53% without that. Moreover, the cancer stage in patients showed (47% and 53%) respectively, of the early and late stages of CRC. Genomic DNA concentrations of the 15 samples were recorded between 11.2 ng/UL – 841 ng/UL. The PCR amplification was successful fifteen isolates for the Kras gene, the amplified fragment size was 173 bp. In the Conclusions, this result may suggest determining the point mutation of the *Kras* gene and using DNA sequencing to the presence of *Kras* mutation.

Keywords: Colorectal cancer CRC, Kras gene, DNA sequencing, mutation

1.4. 5-HTT Linked Polymorphic Region Prevalence Among Faculty of Science Students and its Effect on Their General Mental Wellbeing

Manar Agoub, Rowida Altomi, Fatima Alzahra'a Alshebani, Asmaa Alilesh, Marwa El-wash

The short allele of the 5-HTTLPR, located within the promoter of the serotonin transporter gene, has been linked with increased anxiety-related personality traits and affective disorders after exposure to stress. We aim to investigate the relationship between the short allele and the general well-being of Science Faculty students at the University of Misurata who have lived in Libya their whole lives and experienced the unrest of the past eight years. 226 participants were selected randomly, and the Oxford Happiness Questionnaire (OHQ) was used to assess their state of wellbeing. The OHQ results were used to divide the participants into three groups: the highest-scoring individuals, the lowest-scoring individuals, and those within the confidence interval for the mean of the sample. Members of each group were genotyped using conventional PCR analysis. Frequency test analysis showed the presence of a significant association between 5-HTTLPR and the well-being in this sample, where the SS genotype was strongly associated with membership of the first group and LL and LS was just as equally associated with that of the last group.

Key Words: 5-HTTLPR, (OHQ), serotonin, Happiness.

5.1. تأثير دواء الميزوتاك على أجنة فئران الألبينو

Effect of Misotac drug on embryos of Albino "Rats"

إيمـــان رمضـــان الكـــردي، د. ليـــلى عـــمران الـــمجذوب

يعد أنتشار التشوهات المسخية للأجنة في تزايد وأسبابها عديده , ومن ضمنها تناول الحوامل عـــقاقـــير تضر بتكون الـــجنيـــن بـــصوره سليمة , ومن ضمنها عقار الميزوتاك misotac , وقد أجريت هذه الدراسة في معمل علم الحيوان(بيت الحيوانات) في كليـــة العـلوم مصراتة فـــي الـــفترة الـــممتـــدة من شـــهـــر أكـــتوبـــر 2018- إلى شهر فبراير2019 بحيث اعتمدت هذه الدراسة على دراسة التركيزات المختلفة من عقار الميزوتاك misotacغذا أعطي للـفئران الحوامل , ومدى تأثيرها على الأجـــنة الناتجة حيث تم استخدام 30 فـــأر خمسة فئران ذكور, والفئران (25) المتبقية من الإناث حيث أجريت على خمس فـــئران إناث اختبار تحديد الجرعة القاتلة, والتركيزات التي سـوف يتـم إجـــراء الاختبارات عـــليها. بعـــد تـــحديد الـــتركيزات المناسبة قمنا بإعداد خمس مجاميع بحيث تكون أربعه مـــجاميـــع Treatment, ومجموعة واحدة Control, وقمنا بإدخال أربعة فـــئران إنـــاث فـــي كـــل مجموعة مضافة لها فـــأر لـــتتم عمليـــة الإخـــصاب fertilization بعد 10أيام يتم إخراج الذكور لتبدأ عملية التجريع لمده خمس ايام والجرعات تكون مقسمه كالتالي : مجموعةA (0.04ملجم) مجموعة B(0.06ملجم) مـجموعه C (0.08ملجم) مـــجموعة D (0.1ملجم) كل من التركيزات مذابه في 1مللي ماء مقطر , والمجموعة الأخيرة E تكونControl تظهر لنا الأجـنة الناتجة في كل مجموعة تغيرات في الشكل الـــظاهري من حيث الـــتشوهات الـــعينية مـــنها الرأس الـــمنحني , والـــرأس المسطح مع قـــصر الأطراف , مـــع نمو غـــــــير مـكتمل للعينين , والأذنين تظهر بشكل غير طبيعي مع ملاحظه نقص الوزن , والطول مقارنة مع مجموعة Control , مع ملاحظة أن كلما زاد التركيز زادت التغيرات المسخية للأجنة وأيضا بعد الولادة تمت خسارة الأجنة بنسبه 90% إلى 95%, وأيضا نتائج التحليل الإحصائـــــــي بين شده التركيز, ومدى التشوهات تظهر بوضوح أن كلما زاد تركيز زادت التـــــــشوهات وحالات الوفاة للأجنة.

الكلمات المفتاحية: التشوهات المسخية – ميزوتاك misotac-الإخصاب fertilization

1.6 Study blood group types and their relation to type of cancer

Fatema Egmem, Marwa Alfedh, Ehsan Masdnah

The effect of ABO blood group on the survival of patients with different cancers. The aim of this study was to determine the association of "ABO" and "Rhesus" blood groups with the incidence of cancer. **Methods:** A total 577 cancer patients, different diagnosis of patients. We studied the relationship between ABO blood group and risk of incident cancer patients. **Results:** Blood type A and O have a high incidence of breast cancer and lung cancer; positive Rhesus blood type has a high incidence of breast cancer and the blood type Rhesus negative has a high incidence of stomach cancer. **Conclusion:** The blood type has been studied extensively in terms of human diseases. The frequency of particular cancer may be on the sex type and increase incidence more from of the disease.

Keys words: Blood group ABO, Rh factor and Cancer patients

1.7. Effect of stem cells on kidney inflammation which induced by Herbicide Paraquat in rat

زينب عبد الله المزوغي، مرام فوزي القصير، محمد يوسف الوش

The fundamental principle of stem cell therapy is the replacement of injured cells with stem cells, which holds promise in the treatment of kidney diseases. This study aimed to investigate the effects of stem cells on inflammation in the kidneys of rats treated with paraquat, a substance known to induce renal damage. Paraquat was injected intraperitoneally into the rats to induce renal injury. The rats were divided into four groups: a control group, a group that received two successive doses of paraquat, a group that received paraquat and was later treated with undifferentiated stem cells, and a group that received stem cell treatment alone. Histological analysis revealed signs of paraquat-induced inflammation in the kidneys, including inflamed and atrophied glomeruli, increased endothelial thickness, and areas of inflammatory cell infiltration. Treatment with stem cells demonstrated a reduction in kidney inflammation caused by paraquat. This was evidenced by histological improvement, with the treated group showing normal histology that resembled that of the control group. Additionally, there was a marked improvement observed in the kidney tubules, glomeruli, and endothelium. In conclusion, the exogenous administration of mesenchymal stem cells (MSCs) to rats with acute renal injury could promote both structural and functional renal repair through trans differentiation.

Keywords: mesenchymal, stem cells, kidney inflammation, rat.

2.ملخصات مشاريع التخرج للعام الجامعي 2019 -2020

2.1. A study of down syndrome Rate and Their causing factors in Misurata

هنادي طارق قشوط, سلوي مصطفي عفان, سارة محمد زوبي, د.فوزية القرابولي

Down syndrome is one of the most common syndromes and affects 1 in 319 to 1 in 100 live births. Down syndrome is divided into three types - trisomy, translocation, and mosaicism. This study aims to use genetic methods to identify the most common types. The analysis was conducted on 4 samples ranging in age from 5-15 years, including 2 females and one male, and a control sample for comparison, the karyotyping method and DNA extraction were used for the purpose of using in the polymerase chain reaction (PCR) to detect and determine the type of the syndrome in the samples under study. The equivalent of 25% of the cases was found to be of the trisomy type, 7.5% of the translocation type, and 5% of the mosaicism type, while the rest of the category, which is equivalent to 62.5%, do not know the type of the syndrome they have.

Key words: Down syndrome, trisomy, translocation, the karyotyping method.

3.1. Prediction and analysis of Targeting Libyan Severe acute respiratory syndrome corona virus 2 isolates by Micro-RNA (part 1)

Halima Almahjoub, Yosra Erfida, Zeinab Benzablah, Asma Alilesh, Marwa El-wash.

Coronavirus disease 2019 (COVID-19) cawed by a novel *betacoronavirus* named severe acute respiratory syndrome coronavirus2 (SARS-CoV2) has attracted to health concerns worldwide. Host miRNAs are known as important regulators of virus replication and translation by direct binding of viral RNA. Investigation into miRNA and SARS-CoV2 interaction can reveal novel therapeutic approaches against this virus. The viral genomes of three Libyan SARS-CoV2 isolates along with Wuhan reference strain was analyzed. Through bioinformatic prediction 124 lung miRNA are found to target coding region and 5`UTR of the four studied SARS-CoV2 genomes. There was 29 miRNA with more than four binding site. Mainly, mir-138-5p and mir-574-5p occurred 6 and 4 binding sites respectively and were have ability to binds to 3`UTR of IFN and ACE2 gene in the host cell. However, these miRNA-mRNA interaction need experimental validation to prove it is therapeutic possibilities.

Key words: COVID-19, SARS-CoV2, IFN and ACE2 gene, miRNA.

2.3. تقييم أثار الملوثات البيئية على المادة الوراثية

Assessment of Environmental Pollutants Impacts on Genetic Material

ملاك خليفة صافار، ندي علي كريدان، أ.د.عبد الحميد الحداد، أ.د. فوزية القرابولي

تم جمع عدد 100 ورقة بحثية منثورة جميعها اهتمت بموضوع الدراسة، حيث تم إختيار43 ورقة بحثية منها، والتي تميزت بتحديد ألية وتأثير كل ملوث. صنفت الأوراق البحثية حسب نوع الملوث إلى ملوثات الهواء: غاز الأوزون، الأبخرة، الهيدروكربونات العطرية المتعددة الحلقات، الجسيمات، الضوضاء، الإشعاع غاز الرادون، المعادن الثقيلة: الزرنيخ، الزنك والنحاس، الرصاص، المنجنيز الزئبق، الكادميوم، المبيدات الحشرية. ملوثات مياه الشرب: المعادن الثقيلة. ملوثات الكيميائية: الأستروجين الاصطناعي، ثنائي الفينول أ وإيثينيل استراد يول. وخلصت هذه الدراسة إلى وجود تأثيرات سلبية لملوثات البيئية (هواء، ماء) على المادة الوراثية تراوحت تلك التأثيرات ما بين: مطفرة، فوق الوراثية، مسرطنة.

كلمات المفتاحية: الملوثات البيئية، المثيلة، المادة الوراثية، فوق الوراثية، الطفرات

3.3. Detection of genetic variants of BRCA1 gene in Libyan breast cancer patients

Aisha Shanab, Fatima Godoura, Rawnaq Al-Gzail,. Mustafa Drah

Background and aims: Breast cancer (BC) is the most frequent cancer among women, impacting 2.1 million women each year, and also causes the greatest number of cancer-related deaths among women. BC is an uncontrolled growth of breast cells, occurs as a result of mutations, or abnormal changes, in the genes responsible for regulating the growth of cells. Estimations show that about 5-10% of BCs are linked to gene mutations passed through generations of a family. BRCA1 gene is one of the most common genes that greatly increase the risk of breast and ovarian cancer. Exon11 on BRCA1 gene contain the largest number of variants detected on the gene. The aim of the research was to detect genetic variants in the target region on exon11 of BRCA1 gene in Libyan BC patients. **Method:** Eighteen cases of Libyan BC patients with either a family history of BC or secondary cancer along with BC were selected. PCR and Sanger sequencing were performed to detect genetic variants in the target region on exon11 of BRCA1 gene. **Result:** The sequencing of the fifteen patients tested positive for BRCA1mutations showed twelve different mutations, four of these were previously identified in other researches around the world, and eight were expected to be new mutations. Three out of twelve mutations appeared frequently in cases (c.3531delT, c.3548A>G, and c.3544dupC). **Conclusion:** These mutations that founded in the study, especially the new ones, are considered a dangerous indicator for the women is community in Libya and for patients with BC, as they are likely to be passed on to next generations or lead to second cancers.

Key words: Breast cancer, *BRCA1*, Exon11, Mutation, Sanger sequencing.

3.4. Genotype and its relationship to behaviors in a sample of autistic children in Misurata, using PCR.

Fawzia alqaraboli , Wedad shahout , Hawa ismail , Marwa elshahomii.

Autism is a neurodevelopmental disorder caused by several risk factors, the most important of which are the age of the parents and the health status of the mother and child. This neurological disorder results in adefect in the gene expression of the serotonin transporter. We aim to study the genotype and its relationship to behaviors and alerting to risk factors for autism spectrum disorder. 18 questionnaires were obtained, eleven samples were genotyped using PCR analysis. The results of the study showed that the behavior of repetitive stereotyped movements was of the pattern (L/L), which was 27.27% of the sample, and that the behavior of communication and awareness of the feelings of others was of the pattern (S/L, which was 72.73%). From the sample, the results also showed the effect of the factors surrounding the pregnancy period, both physically and psychologically, in increasing the rate of autism.

Key words*:* Autism, neurological disorder, risk factors, serotonin, serotonin transporter, behaviors, short(S), long(L).

5.3. دراسة بعض العوامل الوراثية المؤثرة على انتشار آفة التدخين داخل مدينة مصراتة

Study of some Genetic Factors the spread of the scourge of smoking with in Misurata

امال عنيبة، زهراء الجطلاوي، حميدة شلغم، احسان ماصدناه، أسماء ابودبوس، مصطفى دراه

تكمن أهمية الدراسة الحالية في الكشف عن الطفرات في جين *OPRM1* باعتباره من الجينات المنظمة لنظام الجسم الداخلي "الألم والسلوكيات التي تسبب الإدمان" ووجود الطفرات فيه مرتبط مع خطر الإصابة بالإدمان. فقد تطرقنا الى معرفة التدخين والأسباب التي تؤدى الى ادمانه، وذلك من خلال الكشف على عدة عينات من أشخاص مدخنين عن طريق استخلاص المادة الوراثية من هذه العينات وقياس كمية ونوعية المادة الوراثية باستخدام جهاز نانو دروب. من ثم تم إجراء عملية البلمرة المتسلسل لتضاعف كمية الجين المدروس OPRM1. باستخدام البادئ المناسب محل الدراسة من ثم إجراء تحليل التسلسل للكشف عن وجود طفرة A 118 G من عدمها لدي الأشخاص المدخنين قيد الدراسة لذلك نوصي بإجراء العديد من الدراسات في هذا المجال.

الكلمات المفتاحية: OPRM1جين، الإدمان، التدخين، عملية البلمرة المتسلسل.

3.6. Phenotypic and genotypic detection of ESBL producing Enterobacteriaceae.

Esra Alsosi, Fatma lsharif, Aisha Elshaikh, Mostafa Mohamed Drah.

Background: Antimicrobial resistance is now proclaimed as the most importantchallenge worldwide being faced by humanity in its fight against infectious diseases. Extended Spectrum b-Lactamases (ESBLs) producing organisms are increasing innumber and causing more severe infections globally and recently among Libyancitizens because of their continuous mutation and multidrug resistance property whichmake its treatment difficult. However, there is a lack of knowledge and data abouttheir presence in Misrata and in Libya in general. This study is aimed at investigatingthe responsible gene of extended spectrum beta-lactamase-producing E. coli and K.pneumoniae. **Materials and Methods**: A total of 32 gram negative isolates of enterobacteriacae isolates (UTI) were collected and identified at Misrata central laboratory. Following antimicrobial susceptibility screening to several antibiotics via disc diffusion, detecting the resistance to cephalosporins and monobactam antibiotics is the identification of ESBL producers. The last step was the genotypic detection of one of the genes responsible for the resistance (**CTX-M**), and followed by the PCR procedure to show the presence of the gene which is detected by the binding of the forward and reverse primers, then finally the PCR products were put to visualization via

gel electrophoreses. **Results:** The phenotypic detection showed that 13/32 samples were ESBL producers, while in genotypic detection only six were tested positive for **CTX-M** gene. **Conclusion:** The findings of this study show that ESBL-producing Enterobacteriaceae are prevalent in Misrata and emphasize the urgent need for optimized infection control and antibiotic stewardship programmers in the Libyan hospitals to prevent further spread of these organisms.

Key work: Phenotypic, genotypic, detection, ESBL, Enterobacteriaceae**.**

3.7. Therapeutic and protective effects of undifferentiated stem cells against liver inflammation induced by Herbicide Paraquat in rat

فاطمة اسماعيل جنات، محمد يوسف الوش

Stem cell therapy is based on the concept that stem cells can replace damaged cells, which has potential implications for the treatment of liver diseases. This study investigated the effects of stem cells on inflammation in the livers of rats treated with paraquat, a chemical that induces damage. The rats were divided into four groups: a control group, a group that received two doses of paraquat, a group that received paraquat and was later treated with undifferentiated stem cells, and a group that received stem cell treatment alone. The presence of liver inflammation caused by paraquat was observed through histological analysis, which showed signs of inflammation, congestion, and infiltration of inflammatory cells. Treatment with stem cells resulted in a reduction of paraquat-induced liver inflammation, as evidenced by improved histological appearance resembling that of the control group. Moreover, there was a significant improvement in liver tubules. These findings suggest that the administration of stem cells could promote structural and functional liver repair in rats with acute liver injury through trans differentiation.

Keywords: Stem cell, rat, Treatment, liver inflammation.

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4.1. Isolation and characterization of lytic bacteriophage against common pathogenic bacteria

Mawaddah Elgawery, Khawla Aween, Tasneem Alswehly, Marwa El-wash, Asma Alilesh.

Regarding their specificity bacteriophages have been widely investigated for combat bacterial infection. Phage therapy is proposed as promising alternative antibacterial agent. The present study was conducted to explore sewage water for the present bacteriophage against clinical bacterial isolates, then to purify and characterize phages with lytic activity against Escherichia coli and Staphylococcus aureus isolates. The sewage water sample were processed and phage screening against six common bacterial pathogens was done by spot assay. Isolation of phages against E. coli and S. aureus as hosts was performed by double layer methods. Characteristics of isolated phages were determined by plaques morphology and host range. Recovery of phage was high from the processed sewage water (66%) against tested bacterial hosts. Four different plaques morphology were observed against E. coli with high lytic activity. In contrast, one small morphology plaques was appeared against S. aureus with low lytic activity. Mean phage titer of phage isolates was 7.7x109 and 2.9x1011 plaque forming unit/ml for S. aureus and E. coli respectively. The isolated phages showed narrow host range when tested against 18 different isolates. To our knowledge, this is the first report on isolation of a bacteriophage from sewage water treatment station in Misurata. The isolated bacteriophages need to be further characterized at molecular level and tested in vivo to be used in one bacteriophage applications.

Key words: bacteriophage, pathogenic bacteria, antibacterial agent, Misurata.

4.2. Isolation and Characterization of Coliphages against Multi-drug resistant Escherichia coli

Sara baitulmal, Kawther kaeiba, Marwa El-wash, Asma Alilesh

Phage therapy present an alternative approach against the emerging multi-drug resistant MDR strains among pathogenic *Escherichia coli* isolates. In the current study, phage-infecting *E.coli* isolated from sewage water with (46.6%) recovery rate. High titer (3.3x109 PFU\ml) of two different morph type phages were characterized by biological and genetic means, they revealed significant tolerance to broad range of PH (5 to 9) and temperature (up to 80 °c) with narrow host range lytic activity. Primary screening for the present of three bacterial virulence factor genes: (stx1,stxf2,eaeA) indicted that isolated phages are negative for all virulence factors assayed, however in vivo test on animal model should be performed to evaluate efficacy of lytic activity of isolated phage.

Key words: Coliphages, Multi-drug resistant, Escherichia coli.

4.3. Assessment of DNA damage caused by environmental pollutants in lichens. (Control sample characterization)

Nawara Al-Torjman, Shayma El-Hamrush, Doaa Al-Dabiba Asma Alilesh, Marwa El-wash.

Lichens is a stable lasting symbiotic relationship between mycoboit (fungus) and photobiont (algae or cyanobacteria). Because of their wide biodiversity and capability to produce bioactive secondary metabolites, in addition to effective accumulation capcity to air depositions, lichen have agreat potential in biotechnological applications. This study aimed to identify the lichen on the Pinus sp. tree in Misurata and characterize the identified lichen at the physiological and molecular level. Furthermore, isolation of indivisual lichen symbiont in pure culture was conducted by thallus fragments and Ascospre discharge methods. According to the results, folise lichen Xanthoria parientina was found on the trunk of Pinus tree in the studied areas. chlorophyll and protein contents in the control sample were 1.5mg/ml and 0.8µg/mg dry mass respectively. Xparientina fungi was isolated as pure culture within one month. Random amplified polymorphic DNA (RAPD)amplification was obtained from 5 out 7 used decamer primer. Thirteen RAPD bands was observed which its reproducibility need to be tested before approve them as fingerprint pattern to control sample of X.parietina. The present study provides sturtpoint to future investigation in using lichen sample as indicator of genotoxicity of air pollutants.

Keywords: Lichen, Xanthoria parietina, Foliose lichens, bioindicator, (RAPD)PCR, Thallus

5.4. الكشف عن الطفرات في جين لمرضي الصمم الوراثي بمدينة مصراته

4.5. Detection of mutations in GJB2 gene for hereditary deafness patients in Misurata

أماني ذبنون، حنان بلاعو، عائشة ناجي، عفاف البلوز

يوصف الشخص بأنه مصاب بفقدان السمع إذا لم يكن قادرا على السمع بمثل جودة شخص متمتع بسمع عادي، يتراوح ضعف السمع بسبب طفرات GJB2 من خفيف إلى عميق وعادة ما يكون خلقيًا. قد تتأثر شدة فقدان السمع بالعوامل الوراثية وظهور طفرة جينية للجين GJB2, وهو الجين المسؤول عن الحفاظ على المستوى المطلوب لأيونات البوتاسيوم في الأذن الداخلية، بينما قد يعتمد تطور فقدان السمع على عوامل أخرى غير بروتين Connexin 26. تم تجميع 50 استبيان من مراكز تأهيل مختلفة واجريت الاختبارات علي 3 حالات، حيث تم استخلاص DNAمن العينات باستخدام Magic Pure™ Blood Genomic DNA Kit," , و قياس تركيزه وترحيله علي جل الأقاروز للتأكد من جودته، ثم أجري تحليل PCR بعد تصميم البادئ المناسب لتضاعف المنطقة المستهدفة للدراسة، وأرسلت العينات خارج الدولة لإجراء عملية تحليل التسلسل Sequencing analysis، فأظهرت النتائج وجود الطفرة c.35dG في احدى الحالات اي بنسبة 33.3% وكانت من النوع Frameshift mutation.

الكلمات المفتاحية: مصراتة، GJB2، الصمم الوراثي، تحليل التسلسل

4.5. Study of Cytogenetic and molecular methods for the detection of Down syndrome in the city of Misurata

Qamar ALshawish, Ghada ALgnedy, Fauzia ELqarabulli, Afaf lbluz

Down syndrome is the most common chromosomal abnormality in humans affecting 1 in 400 to 1500 live children in different populations, with trisomy 21 being the most common chromosomal abnormality. The current study aimed to detect the most common types of Down syndrome in health care centers in the city of Misurata, where 11 samples for Down syndrome were detected, including 5 females and 6 males, ranging in age from 9 to 16 years, and a control sample for comparison.Through the current study, it was found that 95.7% of cases are ignorant of the type of syndrome and 4.3% are of the mosaic type, and that the mother's age and exposure to environmental pollution are among the main reasons for the occurrence of such a genetic defect. The karyotyping technique and polymerase chain reaction analysis were used to detect the tandem repeat sites of chromosome 21 to determine the number of copies of chromosome 21 present in the studied samples to classify Down syndrome , but due to the difficult circumstances that we encountered in obtaining many samples and the problems of using the molecular genetic technique for detection, the results were not it is clear, but our understanding of this technology and the ability to use it was one of the most important outputs of this research.

Key words: Cytogenetic, Down syndrome, molecular methods, Misurata**.**

4.6. LNPs mRNA vaccines applications and its use against SARS-COV-2 as the first line of vaccination

Fatma Elghtiet, Hanadi Alzergine, Saad Alarabi.

Lipids nanoparticles of mRNA are a new delivery system, to deliver therapeutics oligonucleotide to the human body, to use as a medicine or as a vaccine. And this method was the solution for mRNA instability due to the degradation by the RNAase enzyme which attacks a naked mRNA when it is applying inside the body. Before the outbreak of the Coronavirus in 2019, pharmaceutical companies were working on designing vaccines to adapt to strains of the virus. It has succeeded in developing some COVID-19 vaccines, as shown in the research. mRNA vaccines (Moderna, Pfizer) were the approved vaccine. They are vaccines that use mRNA genetic material, that is encoded spike protein of the virus. Furthermore, these pieces of protein are similar to the virus, which leads to stimulating the immune system, and it recognizes these pieces to be attacked. The mRNA is coated with LNP (Lipid nanoparticle) to prevent hydrolysis via human enzymes, this method has proven to be effective in the COVID-19 pandemic, as well as it was the first emergency approvement by FDA and WHO and from now the best vaccine to obtain final approval. The effectiveness of the Pfizer BioNTech vaccine was 95% and the Moderna vaccine was 94%. After this review research, we assumed that the LNP vaccine will take place in the future of biotechnology in the vaccine field due to its efficacy and short-term production.

Key words: LNPs mRNA, Vaccine, spike protein, Pfizer, and Moderna

4.7. Comparative Sequence Analysis of Severe Acute Respiratory Syndrome CoV-2 in some Mediterranean Sea

Belqis Barras Ali, Noor Asim, Rugia Algouby, Mustafa Drah, Asma Abudabous

Coronaviruses disease (covid19) are positive single stranded RNA viruses belongs to coronaviridae by novel betacoronavirus called severe acute respiratory syndrome coronavirus2 (SARS-CoV2), causing pandemic of worldwide, Libya was the last infected by corona. aims of this study was Comparing the sequence of Libya with the most connected countries (Turkey, Tunisia and Egypt) and also comparing it with the Wuhan reference to find similar mutations and the mutation found in Libya only, this our study focused three genes (*ORF1ab* gene, *S* gene and *N* gene) because these genes used by diagnostic coronavirus disease. In this study, the data available collected by from (NCBI) of (46 of libya,49 of Turkey, 46 of Tunisia, 46 of Egypt) on the whole-genome sequences of SARS-CoV-2 . Through bioinformatics tools we found of *ORF1ab* gene (111 mutations in Libya only, 165 mutations in Tunisia only, 104 mutations in Turkey , and 92 mutations in Egypt), while the *S* gene (38 mutations in Libya only, 40 mutations in Tunisia only, 36 mutation in Turkey only and 31 mutations in Egypt), and *N* gene(13 mutations in Libya only,25 mutations in Tunisia only,24 mutations in Turkey, 16 mutations in Egypt). Also in this study found the core region of three genes in four country was the common mutation Whereas the common mutations in *ORF1ab* , *S* and *N* gene (*ORF1ab* gene 9 mutations, *S* gene 4 mutations, and *N* gene 3 mutations), used The phylogenetic tree to investigate and track the SARS-CoV-2 in Libyan sequence, which shows that Libyan clued to the strain of Tunisian and Turkey.

Key words: Coronaviruses, ORF1ab gene, Libya, RNA viruses, the SARS-CoV-2.

4.8. Evaluation of COVID-19 Vaccines Side Effects among Staff and Students of Misurata University in Libya.

Saad Al Arabi, Mohammed Al Wash, Salem Ebraiek, Fatma Al Tarhouni, Fatima Al Zarrouk.

Introduction: Covid-19 is a respiratory disease caused by the coronavirus, which spread very quickly in 2019 in Wuhan a Chinese city, which is the epicenter of this pandemic, that represents a global threat and with a high rate of infections in all countries in the world, and this is what led scientists to manufacture vaccines in different ways to combat this epidemic. Furthermore, countries including Libya contracted to obtain these vaccines, such as Pfizer, Sinopharm, Sinovac, AstraZeneca, and Sputnik vaccines. Although some of these vaccines were approved by the American Food and Drug Administration as well as by World Health Organization they are still under clinical study and for a long time to know the adverse effects of these vaccines. **Methods:** Paper questionnaires were distributed to students, staff, and lecturers of some faculties of Misurata University to study the side effects of different COVID-19 vaccines. **Result**: The total number of participants individuals was 238, and the result showed that there were side effects after the first and second doses, and the percentages were 75.1%, and 60%, respectively. and the percentage of the presence of common side effects was fatigue 34.9%, headache 32.4%, injection site pain 28.6%, and fever 20.2% after the first dose**. Conclusion**: In this research, the side effects of Sinopharm and Sinovac vaccines were moderate to mild of headache, injection site pain, and fever. The side effect of Pfizer vaccine was injection site pain, headache, fever, joint pain, and fatigue. in contrast, to Sputnik V and AstraZeneca vaccines, which were the highest number of side effects.

Keywords: Covid-19, vaccines, epidemic, Misurata University, and side effects.

4.9. Bacterial Plasmid as a Vector in Recombinant DNA Technology and its stability

Samer Joudah, Abdulmoneim Al-zrisey, Waleed Khalaf, Saad Alaraby, Asma Abudabous.

Most types of bacteria carrying a genetic element that exists out of its chromosome called plasmid, which can replicate independently inside the bacterial cell. These plasmids have an essential role in many aspects for bacteria to survive as well as to transform genetic elements from cell to cell. This research trying to spot the light on the rule of plasmid to use as a vector in biotechnology field, furthermore the disadvantages of using antibiotic genes as a selectable marker in recombinant proteins production when using *Escherichia coli* as a host cell for recombinant plasmids. Nevertheless, World Health Organization and United States Food and Drug Administration highly recommend to quit using antibiotic-based selection system and find other alternative system, due to its ability to cause spreading of resistance gene as well hypersensitivity to people whom has allergy with β-lactam antibiotics. As well as this research trying to study and compare other alternative selection system such as toxic-antidote selection system, and the effects of this method on the stability of plasmid vectors, on the other hand the effect of addition of *cer* region to increase the stability of plasmid that not using antibiotics selection system in contrast, the toxin-antitoxin system provides the plasmid with stability about 90% instead of 100% of the antibiotic resistance method, then demonstrating the use of Cer-region which can increase the stability to about 94%.

Keywords: plasmid, *Escherichia coli*, antibiotic resistant gene, and toxin-antitoxin selection system.

4.10. Detection of *CACNA1A* gene in stroke patients in Misurata

Eftema Haman, Souad Abuazom, Mustafa Drah, Asma Abudabous

Stroke is one of the main causes of chronic and acquired disability in people all over the world, and is referred to by the World Health Organization as the epidemic of the twenty- first century, resulting from interruption of blood flow to the brain either due to a rupture in the blood vessels or narrowing of the vessels, which reduces The rate of oxygen loaded to the brain, when a mutation occurs in the CACNA1A gene, which is the gene responsible for the transfer of nerve charges in the calcium channel associated with the brain, a disturbance in blood pressure increases the charges in this channel, Shipments in this channel, therefore, this study aims to detect mutations in the CACNA1A gene in Libyan stroke patients, taking into account the risk factors.The study included 10 blood samples from patients with stroke, who's genomic DNA was extracted and amplified by polymerase chain reaction and analyzed by direct sequencing. After analyzing the results, it was found that there were mutations in two different loci in 4 cases out of 10, i.e. 40% of the total studied cases, the substitution mutation in (c.631+6197 C>G) in four cases, and the deletion mutation in(c.621+6216 delC) in one case in addition to the first mutation. This study supports an association between strokes and the CACNA1A gene and suggests that the CACNA1A gene should be analyzed in patients with migraines because they are at greater risk of stroke.

Key words: stroke, calcium channel, *CACNA1A* gene, Migraine, PCR reaction, sequencing**.**

4.11. Detection of MUTYH gene mutations in heredity colorectal cancer patients in Misurata

Eman Kerwad, Fatima Aldeeb, Asma Abudabous, Ehsan Masednah

Colorectal cancer became one of the most dangerous yet spread cancers, as a result of many wrong behaviors people do, in addition to being a hereditary disease. However, Libya was not included in a lot of studies due to the lack of adequate studies on infected CRC Libyan's patients, so this study aims to detection of mutations on *MUTYH* gene in Libyan's families have heredity colorectal cancer. The study included 10 blood samples were collected from patients with hereditary colorectal cancer and they had family history with this disease. Genomic DNA were extracted, amplified by PCR, and analyzed for MUTYH mutational status by direct sequencing. MUTYH mutations were present in 70 % (7\10) of all analyzed samples. A total of 7 patients had a MUTYH mutations in different positions; of which 2\7 (28.6%) they had substitution mutation in c.1140 A>G, 2\7 (28.6%) they had deletion A in c.1140, 1\7 (14.3%) a patient had substitution mutation in c.1149 C>N, 1\7 (14.3%) a patient had substitution mutation in c.1141 G>N, 1\7 (14.3%) a patient had two type mutations, substitution mutation in c.1154 C>T and insertion CT in c.1153. Although this study showed these mutations in small region in *MUTYH* gene, whole gene sequencing screening procedure in *MUTYH* is highly recommended in familial colorectal cancer patients. Additional studies will be helpful to identify of new mutations. We believe that an enlargement of the MUTYH mutation spectrum resulting from these types of studies will contribute to early detection and the prevention of secondary cancer development.

Key words: MUTYH gene, familial, colorectal cancer, hereditary disease.

4.12. Thalassemia, its diagnosis and treatment

Safa San_Alla , Fatma EL_mohashey, Ehsan Idrise

Thalassemia disease, also called hereditary blood disease, is one of the inherited autosomal recessive diseases, where the disease is divided into two types: alpha thalassemia and beta thalassemia. Where the mutation is inherited for the two genes HBA1, HBA2 , either occurs on chromosome 16 and both, when are not inherited genes or inherited only one of them if they are both parents are homozygous of the allele , or one of the two parents is heterozygous for HBA1or HBA2, and these two genes contain a genetic group divided according to the stages of human life. This mutation is deletion of the alpha globin genes leads to a deficiency or absence of the alpha globin chain to lead produce hemoglobin unbalance, causing alpha thalassemia to be divided into several diseases (α Thalassemia trait, HBH disease, Hb Bart's Hydrops Foetalis Syndrome, Alpha thalassemia intermedia). As for beta thalassemia, which is found on the HPB gene located on chromosome 11, one copy is inherited from both parents. Deletion and point mutations occur either if only one gene is called heterozygote, or both copies are inherited, or both genes are deleted and it is called the homozygote allele, and the disease has multiple stages that have been studied are(beta thalassemia trait also called silent, beta thalassemia intermedia, Beta thalassemia major and called zero beta thalassemia also called c`ooly syndrome), Also ,beta thalassemia is associated with hemoglobinopathy, anemia(HB E, HB S , HB C). Through our study, the steps for diagnosing thalassemia were identified, which are: Hematologic diagnosis, Peripheral blood smear, Hemoglobin electrophoresis hemoglobinopathy (HB) (qualitative and quantitative Hb analysis), Complete blood count (CBC). DNA analysis, Genetic testing of amionic fluid, Iron deficiency, high performance

liquid chromatography (HPLC), Diagnosis by amplification LAMP (LOOP – Mediated isothermal amplification) technology, Diagnosis by polymerase chain reaction (by multiplex PCR).

Key words: Thalassemia disease, HBA1, HBA2, multiplex PCR.

4.13. Genotoxicity monitoring using plant bioassay

Mona Rafieda, Nada Almurabet, Fauzia Elgarabulli, Asma Abudabous

With the increase in the spread of diseases significantly, especially cancer in the recent times as a result of the use of many chemicals in daily life. These chemicals have a negative effect on human genome and need to be investigated. This study aimed to illustrate the genotoxicity of environment pollutions means and mechanisms, and different assays. *Allium cepa* plant bioassay as important genotoxic assay was discussed in detail. Meristem cells of onion roots grow in presence of sodium hypo chloride with different concentrations. Genotoxicity end points were recorded but need to be repeated. This study showed a clear existence relationship of toxins in daily life and their impact on the genetic toxicity of living cells which lead to different diseases.

Key words: Genotoxicity, *Allium cepa*, cancer, bioassay

4.14. Detection of *CYP27B1* Gene Mutation in Exon 2 in Chronic Vitamin D Deficiency Patients

Souror Almheshi, Hanan Abushaalah, Asma Abudabous, Fatma Alzain

Vitamin D deficiency is a global problem, and despite the treatment of the deficiency by all means, including injections and tablets, as well as nutritional supplements and exposure to sunlight, now the deficiency in some cases is chronic even after treatment and is accompanied by pathological symptoms, which necessitated the examination of genetic analyzes of some genes responsible for the formation and transformation of vitamin D in The human body. In this study, a gene *CYP27B1* was detected in reversible cases suffering from chronic vitamin D deficiency with pathological symptoms.The collected 6 blood samples from patients with Vitamin D deficiency all of them female with different ages were collected and Genomic DNA was isolated from patient serum, electrophoresis for DNA extraction, and PCR amplification of *CYP27B1* gene. Genomic DNA concentrations of the 6 samples were recorded between (13.5g/ µl – 115.3 ng/ µl) and 260 nm/280 nm ratios were between (1.57 -1.77). The PCR amplification was successful in isolates for the *CYP27B1* gene, the amplified fragment size was 473 bp. CYP27B1 mutations were present in 100% (6/6) of analyzed samples. all patients had a CYP27B1 mutations in one position, they had deletion A in c.195+571. In the Conclusion, this result may suggest determining the point mutation of the *CYP27B1* gene and using DNA sequencing to the presence of mutation of Vitamin D deficiency patients. There could be a relatively large number of factors that could be linked to the variations in the observed frequencies of CYP27B1 mutations in the different studies. Among these are using different methodologies for detection of the mutations with different ranges of sensitivity and specificity. Environmental factors have a major impact on different populations with diverse lifestyles, dietary habits. In addition, using different numbers and kinds of samples, which might serve as another reason for such diversity.

Key words: CYP27B1 gene, PCR amplification, Vitamin D deficiency.

15.4 تطبيقات تفاعل البلمرة المتسلسل واستكشاف الأخطاء الشائعة ومعالجتها

ابرار الدربالي، هديل رزق، سعد العربي

يعتبر اختراع تفاعل البوليمراز المتسلسل (PCR) حجر زاوية للعديد من مجالات علم الأحياء الجزيئية. سواء كان في الكشف الكمي او النوعي للشفرات الوراثية، أو في مجالات الاستنساخ للجينات. بالرغم من اهمية هذا التفاعل في جميع انحاء العالم، إلا أن مراكز الأبحاث والجامعات في ليبيا مازالت تتحرك على استحياء في استخدام ال PCR، ولعل أكثر استخداماته هو في الكشف عن جينات معينة. وهذا ادى الى تخوف العديد من البحاث في الدخول لهذا المجال والخوف من النتائج السلبية، وايضا عدم توفر المواد المشغلة وصعوبة الحصول عليها. هذا البحث يسلط الضوء على أهم مراحل التشغيل لتفاعل ال PCR أهم تطبيقاته واستخداماته في المجالات المختلفة، بالإضافة الى استكشاف اهم الاخطاء وإصلاحها. هذا البحث سيكون كمرجع باللغة العربية للطلبة والباحثين في هذا المجال، كما سيوفر لهم الإجابات للأسئلة الشائعة التي يمكن ان تواجههم في بحوثهم الأكاديمية.

الكلمات الاستفتاحية: تفاعل، البوليمراز، المتسلسل، الأحياء الجزيئية.

16.4 المؤثرات البيئية وتأثيرها على التعديلات ما فوق الجنينية للجنين

رانيا النبوس، سارة الجمل، احسان ما صدناه

في حين تكون المادة الوراثية ثابتة نوعاً ما، تتغير العلامات ما فوق الجينية المحيطة بالمادة الوراثية وفقا للمؤثرات البيئية، ولا يكون هذا التغيير على المدى البعيد كما في المادة الوراثية وإنما على المدى القصير. تعتبر مرحلة تكوين الجنين مرحلة مهمة وحساسة حيث يتأثر تكوين الجنين بالعوامل البيئية والإشارات الداخلية والخارجية التي يتعرض لها في الرحم. وقد أثبتت الدراسات أن البيئة التي تتعرض لها الأم في فترة الحمل وخصوصاً في الشهور الأولى من الحمل تكون مؤثرة على الجنين تأثيراً كبيراً يتعدى الى ما بعد البلوغ وحتى الأجيال اللاحقة.

الكلمات الاستفتاحية: ما فوق الجينية، المادة الوراثية، الجنين

4.17. Incidence rate of X and Y Chromosomal Aneuploidy in high quality embryos from couples underwent IVF for Gender selection

امل الدنفور، رنيم الزريدي، د.محمد الدنفور

Aneuploidy as a key genetic factor can influence human reproductive ability. Selection of the best embryo for transfer is very important in assisted reproductive technology (ART). **Objective:** The aim of this study was to evaluate the incidence of aneuploidies in sex chromosomes in the high-quality embryos from patients undergoing (ART) for sex selection. **Materials and Methods:** A total of 121 women age of the 35+ 13 years performing consecutive (IVF) cycle in combination with preimplantation genetic screening (PGS) for chromosomes X and Y at the (IVF) and Genetics Centre in Alamal Hospital, Misurata, Libya were included in this study. Embryos of patients were reanalyzed by fluorescence in-situ hybridization (FISH) for chromosomes X and Y. **Results:** Of 237 embryos, 101 (42.6%) embryos were euploidy male (XY), 97 (40.9%) embryos were euploidy female (XX) and 39 (16.5%) embryos were aneuploidy. In this study there was an effect of female age on the aneuploidy produced embryos. There was a significant increase in the number of aneuploidy produced embryos in female age ≥37years (23 aneuploidy embryos (9.9%) compared with female age < 37 (16 aneuploidy embryos (6.9%) P <0.05). **Conclusion:** Chromosomal abnormalities of embryos are one of the most critical reasons for poor (ICSI) outcomes. Therefore, morphological characterization of embryos is not enough method for choosing the embryos without these abnormalities. (PGS) for assessment of embryo quality will increase implantation rate and pregnancy.

Keys words: pregnancy, PGS, ICSI, IVF, ART.

5.1. Identifications of missing persons from Human remain using DNA technology.

Malak Kablan, Kamal Abubaker, Saad Al-araby

The tragedy of missing persons is as old as time. However, there is still a very limited understanding of the diverse nature and significant impact of this global problem. And Following the G-7 Summit in Lyon, France, the International Commission on Missing Persons (ICMP) was established to address the issue of missing people due to the various wars. Before 2011, the missing person file did not exist in Libya, in 2012, Libya called on the ICMP to assist in its efforts to build a sustainable process to find all missing persons, including those missing from the 2011 conflict. The number of missing persons registered in the Commission's family system was 450, and according to the internationally applied protocol, four blood samples were taken from each family, and blood samples were collected on the FTA cards. Among our work in this research is the analysis of some samples from the families of the victims of the missing. This research was conducted in the laboratories of the General Authority for Research and Identification of Missing Persons in Libya (GASIMP). After the results showed the full profile for this family and the entire profile appeared for me as a bone sample and it was matched with all Families victims within the ANFASS system this profile appeared to us for this case and after that, the conformity report was prepared and referred to the competent authorities.

Key Word: DNA technology, ICMP, GASIMP, FTA card, Libya, Missing person

5.2. Prediction and Analysis of Targeting Libyan Severe Acute Respiratory Syndrome Corona Virus 2 isolates by Micro-RNA (Part 2)

Maab Aldeeb, Mona Aborwis, Marwa El-wash, Asma Alilesh.

The Coronavirus disease 2019 (COVID-19) caused by a novel beta-coronavirus named severe acute respiratory syndrome coronavirus 2 (SARS-CoV2), has attracted to health concerns worldwide. Host miRNAs are known as important regulators of virus replication and translation by direct binding of viral RNA. Investigation into miRNA and SARS-CoV2 interaction can reveal novel therapeutic approaches against this virus. The viral genomes of seven Libyan SARS-CoV2 isolates along with Wuhan reference strain were analyzed. Through bioinformatics prediction, 142 lung miRNA are found to target coding region and 5`UTR of the eight studied SARS-CoV2 genomes. There was 38 miRNA with more than three binding sites. Mainly, mir-138-5p and mir-574-5p occupied 6 and 4 binding sites respectively and have ability to binds to 3`UTR of IFN and ACE2 gene in the host cell. However, these miRNA-mRNA interaction need experimental validation to prove it is therapeutic possibilities.

Key words: Coronavirus disease, SARS-CoV2, miRNA, IFN and ACE2 gene.

5.3. Concentration rule in downstream processing of recombinant protein production

Fatima Bayou, Ritaj Alrhet, Saad Alarabi

In protein isolation, proteomic, or peptidomic procedures, protein solutions are often concentrated to remove solvents and undesirable molecules, to separate protein fractions or to increase protein concentrations. Proteins can be concentrated by precipitation from solution with ammonium sulfate, polyethylene glycol, organic solvent, trichloroacetic acid, and three-phase partitioning. Solvents can be removed by passage through a semipermeable barrier where protein solutions are forced against the barrier in a centrifuge tube or with increased pressure concentrating protein in the remaining solution. Precipitation of recombinant proteins, lysed from the host cell, is commonly used to concentrate the protein of choice before further polishing steps with more selective purification columns. Furthermore, membrane ultrafiltration (UF) is a pressure modified, convective process that uses semipermeable membranes to separate species in aqueous solutions by molecular size, shape, and/or charge. It separates solvents from solutes of various sizes. The result of removing solvent from a solution is solute concentration or enrichment. Repeated or continuous dilution and reconcentration are used to remove salts or exchange solvent (in such applications as buffer exchange).

Key words: membrane ultrafiltration (UF)**,** proteomic**,** downstream, protein**.**

5.4. Prevalence and risk factors of Cervical cancer

Alaa Alkalefi, Rawand Omar, Afaf AL-ballouz

Cervical cancer is one of the most common cancers among females, and over 200 HPV types have been identified, the highest high-risk genotypes of HPV are 18 and 16. HPV causes over 99% of all cases of this cervical cancer disease. Initial infection by HPV virion occurs in basal epithelial cells, the viral genome is small double-stranded circular DNA particles of about 7-8 kb, and the genome consists of three restricted regions: early gene-coding region € late gene-coding region (L), and long control region (LCR), there are three regulatory proteins and three encoded oncoproteins. This cancer depends on two major oncoproteins E6 and E7, HPV16 E6 is a small essential protein consisting of 151 amino acids, and the HPV16 E7 protein is a 21 kDa nuclear acidic phosphoprotein with no known enzymatic activity, diagnosis is based on histopathological evaluation of cervical biopsy. Diagnostic procedures such as Pap smears have proven to be an effective method in eliminating the oncogenic potential of HPV, vaccination against HPV is one of the most Important strategies against cancer**.**

Keywords: human papillomavirus; cervical cancer; high-risk HPV; diagnosis; vaccination**.**

5.5. Studying the relationship of vitamin D to certain environmental factors and depression in a female sample from Misurata

Assma AL-Haddad, Asma Abudabous, Wafa ElMatoni

Vitamin D deficiency is a global problem, and despite the treatment of the deficiency, including injections and tablets, as well as nutritional supplements and exposure to sunlight, the deficiency is now in some cases chronic even after treatment and is accompanied by pathological symptoms. Recent research suggests a vitamin D deficiency may be associated with an increased risk of depression among the elderly. This study aimed to estimate the prevalence of vitamin D deficiency in a sample of Libyan adult women, investigate factors associated with low vitamin D status, and evaluate the association between vitamin D and depression. 50 women were recruited for this study. A self-administered questionnaire was used to collect data. Vitamin D levels were measured, and depressive status was determined via the Beck Depression Inventory (BDI) scale. The study group's average weight was 68 kg, and their average height was 161.16 cm. The majority of participants were single, aged 20–30, had a B+ blood group, claimed chronic vitamin D deficiency, were born in winter, used sunscreen, slept less than 6 hours a night, and had a family history of vitamin D deficiency. 82% of the women in the study had vitamin D deficiency or insufficiency (20 ng/mL), and 70% of the participants were depressed. No correlation between vitamin D status or depression and weight or marital status was statistically significant; however, there was a correlation between vitamin D status and smoking and between depression and smoking. It was evident that low vitamin D levels are linked to a higher risk of getting depression.

Keywords: Adult women, Vitamin D deficiency, Depression, Environmental factors, Libya.

5.6. Optimization of UV distance and duration to use as bacterial sterilization.

Fatheya Alsoukini, Faiza Abdulrhma, Saad Alarabi, Salem Ebraiek

Ultraviolet is one of the essential methods that used for surfaces sterilization against broad spectrum of microbes. Although the using of some detergents and sanitizers still acceptable for this aim, but still not safe for sterilization of laboratories and operations rooms, for that an alternative method such as UV should be used in these critical cases. This research aimed to determine the activity of UV light that used in water factories to kill or inhibit the growth of bacteria that isolated from the surface of lab bench in molecular biology laboratory in Misurata University. The experiment done using two isolated bacteria as Gram-positive and Gram-negative, and exposed for the UV light in different durations and different distances, then incubated for 24 hours in two groups, first group incubated in dark and the second in light, to give the bacteria chance for DNA repairing. Our results showed conventional bactericidal effect for G-positive bacteria when incubated in dark, but for the rest samples the effect mostly bacteriostatic when the plates still can show growth colonies even if in unsignificant results as one or three colonies. In conclusion, the importance of UV in surface sterilization is really can be alternative method to use in hospitals and labs, moreover, more research should work in to optimize the best duration and distance to have 100 percent of sterilization.

Key words: Ultraviolet (UV), Bacteria (Gram-positive/negative), Resistance, DNA, Antibiotics, Disinfectants and Antiseptics (DA).

5.7. Assessment of DNA damage caused by environmental pollution lichens by RAPD-PCR

Ala Bit Almal, Sundus Altaeb, Asma Alilesh, Marwa El-wash

Lichens are widely used in biomonitoring studies of air pollution, either as bioindicators of air quality or as bioaccumulators of atmospheric depositions. Several molecular techniques have been developed to provide information on genotoxicology. In this study, DNA changes in *X. parietina* transplanted from natural clean habitat to the center area of Misrata City were assessed by random amplified polymorphic DNA (RAPD) analysis to investigate the pattern of genetic variation influenced by the environmental pollution. Results showed changes in RAPD band patterns in transplanted lichen comparing to the control sample, reflecting the presence of DNA damage. The average value of polymorphism obtained from the amplification of the used primer was 30% and the genomic template stability (GTS) ratio was 66.6%. The present results indicate that the lichen species *X. parietina,* which is known for its bioindicator and biomonitor capacity, also has a high capacity as indicator of genotoxicity and provides information about the level of potential genotoxic agents in the studied area. However, this study needs to be extended to include large areas for belonged period with ecological study conducted in parallel to investigate the quality of the air in Misrata City.

Key words: DNA damage, RAPD-PCR**,** environmental, pollution, lichens.

5.8. Detection of *MUTYH* gene mutation of exon 7 in colorectal cancer patients in Misurata

جمانة السنوسي، فاطمة الكميتي، هاجر الاسطى، أسماء ابودبوس، مصطفى دراه

Colorectal cancer (CRC) is one of the most Dangerous cancers in the world, The early diagnosis of CRC is of essential importance as it is one of the most curable cancers if detected early. So, this study aims to detection of mutations on MUTYH gene in Libyan's families have heredity colorectal cancer. The study included 20 Sample (10 from colorectal cancer patients and 10 from healthy people with CRC family history). the genomic DNA from the samples, the specific region in exon 7 of the target gene (MUTYH) was amplified by PCR using the primers. The PCR products revealed a band of the expected size of the MUTHY gene at 173bp, the mutations were present in 10% (2 /20) of all analyzed samples and 60% (12\20) normal and 30% (6/20) exclude, since there is noise present, hence repetitive sequencing is required. A total of 2 patients had a MUTYH mutations in different positions; of which sample number 8 had a Insertion mutation in c.136 Ins C and sample number 17 had 3 substitution mutation in c.113 A>G, c.142 T>C , c.143 G>A and insertion mutation in two positions c.128 Ins TT and c.165 Ins T. Additional studies will be helpful to identify of new mutations. We believe that an enlargement of the MUTYH mutation spectrum resulting from these types of studies will contribute to early detection and the prevention of secondary cancer development.

Key words: MUTYH mutation, Colorectal cancer (CRC), family history, PCR.

5.9. The role of codon optimization in pharmaceutical biotechnology

Khadija albahloul, Wajdin alznigre, Saad Alarabi

Pharmaceutical biotechnology already took a place in medicine therapy against genetic illness, chronic disease such as hormones efficiency and viral infection. For that, the production of heterologous recombinant proteins is now the first line to produce a recombinant human protein in variant host cells. Although, the coding genes are now available in gene bank online, but this wild type of the gene cannot provide a high yield of required protein in manufacturing scale. Here the codons should be optimized according to the chosen host cell. Codon optimization now available as a software, that provide the codon bias that preferable by host cell. Furthermore, this optimization increases the yield of produced protein and enhance the stability as well. This research trying to spot the light on the major step that should be studied well and use it in the biotechnology researchers. As well as the future of drugs production or inventing a new vaccine will be absolutely depending on codon optimization, to guarantee the efficacy and the accuracy of the medical products.

Keywords: Codon, optimization, software, and vaccines

5.10. Bioformatic study 15 losi in short tandem repeat and connection to genetic diseases

Najat Algleb, Nada Alwerfalli, Mustafa Drah, Ismail Taban.

STR short tandem repeat the in human genome consists of regions tandemly repeated DNA sequences called short tandem repeats (STRs). STRs, which made up around 3% of the human genome, are repeating DNA sequences 2–6 bp, Tetra nucleotide repetitions with a four base pair (4-bp) repeat exonic STR region located in 15 loci on chromosomes , like loci D21S11 repeat (TCTA), STR fund in non-codon region is intron and Codon region is exon and Aims of this study Determine repeat in loci by bioinformatics Software and Determine location loci on chromosome in normal and studied STR and relationship with diseases the repeat and the number of its repetitions in each lo Variable number Tandem repeat is a form of tandem repeat in which a short nucleotide sequence (10–60 base pairs) is repeated at a specific locus a variable number of times Consequently, VNTR is another name for minisatellites. The chromosomes of the eukaryotic genome are scattered with VNTRs. The impacted genes are involved in diseases including Alzheimer's, obesity and familial cancers, highlighting the importance of VNTRs for understanding the genetic basis of complex diseases. As a result, the length of each individual's array of VNTRs varies. Chromosome variants can be used to identify a person or their parents because they are inherited from parents. The VNTRs of six individuals are shown to differ. (lakna2018). Figure (4) loci were clarified in this study using the NCBI program. FAST was taken for the loci, then the repeat was determined and. result_: in this study, it was verified that the STR is related to diseases and that the STR is present in the intron and the exon it was thougion that the intron region had a function that causes diseases through mutations that occurred in the gene close to the loci. It was proven STR is associated with diseases using Ensembele software. Disease genes are ranked by absolute STR content, separated in 15 STR and STR content in the exons and intron of human.

Key words: Bioformatic, 15 losi, short tandem repeat, genetic diseases.

فاطمة ابوسكساكة، ايمان اجعية، فيروز المحجوب، أ.د. فوزية القرابولي

الملوثات البيئية متنوعة منها ملوثات داخلية مثل الغذاء والدواء وخارجية مثل الأشعة. هذه الملوثات لها تأثير على المادة الوراثية في الكائن الحي مباشرة او غير مباشر. ارتباط هذه المواد مع DNA وتلفه يسمي بالسمية الجينية (GENOTOXICITY) التي تنتج عن ثلاث اليات (MUTAGENIC, EPIGENIC, CARCINOGENIC) فتؤدي الي حدوث خلل في الخلية اثناء نشاطها او انقسامها الي حدوث الأمراض المورثة او الغير مورثه علي حسب نوع الخلية ونشاطها. يعتبر البروجسترون من الهرمونات الصناعية المستخدمة كمثبت لعلاج الاجهاض والعقم. وهو مرشح لمخاطر حدوث لأمرض الوراثية في الاطفال نتيجة لتفاعلها مع DNA . تعالج الحوامل بمثبت الحمل أثناء الثلاثة الأشهر الأولى من الحمل او قبل الحمل بكثرة بالهرمون الصناعي بروجسترون (Duphaston) في ليبيا. ولهذا قمنا بدراسة التأثير السمي للمثبت الحمل الصناعي Duphaston على خلايا جذور القمم النامية للبصل الذي يستخدم بكثرة ل دراسة السمية الجينية للملوثات البيئية والأدوية. تمت معاملة الجدور النامية لمدة 24 ساعة وأقل بتراكيز مختلفة لهذا لعقار ثم فحصه تحت المجهر بعد صبغه لدراسة تأثيره على المادة الوراثية وسلوك كروموسومات اثناء الانقسام الخلوي للخلايا المعاملة والغير معامله. اظهرت النتائج شذوذ في سلوك وتركيب المادة الوراثية شملت تثبيط لمعدل الانقسام وجود طفرات سيتوارثه مثل الجسور في الطور الانفصالي والنهائي وانويه الصغيرة، تلف للأغشية البلازمية. كل هذه التغيرات للمادة الوراثية وسلوكها الطبيعي يدل على السمية الجنيه للمثبت والتحذير من استخدامه الا للضرورة القصوى، خاصة ان له علاقة بحدوث التوحد في الاطفال والتشوهات الخلقية في المواليد لأمهات استخدمنا المثبت اثناء الحمل كما دلت الدراسات المختلفة علاقته بسرطان الثدي.

الكلمات المفتاحية: السمية الجينية، الأدوية، الاجهاض والعقم، المادة الوراثية.

5.12 Molecular mechanisms of Annona muricata anti-proliferative and anti-cancer properties

Fatima shnishah, Malak Ramadan, saad Alarabi, Mohamed Alwash

Annona muricata is a tropical fruit that is rich in nutritional value for humans, as well as its medical use as a traditional therapy as an antibacterial and anti-oxidation. New researches reported the medical use of this fruit as an anti-cancer, and prove its molecular activity to repair the defect in cancer cells. This research tries to review the last studies that were published about the use of Annona muricata for treating different cancer. The result of this research proved the activity of Annona muricata against different cancers in molecular stage, by four pathways, apoptosis, cytotoxicity, oxidative response, and cell cycle arrest. Furthermore, the types of cancer treated by Annona muricata were breast cancer, lung cancer, pancreatic cancer, colon cancer and leukemia. According to the extraction solvent of this fruit, ethanol and methanol extractions had the highest effect extract among the other solvents. Depending on these results, this research recommends patients who started chemotherapy to include this fruit in their diet, when this fruit proved its activity to support other treatment types, as well as the dependents on this fruit to be alternative for other treatment methods not required, because eating fruit alone not proved the treatment yet.

Keys words: leukemia, Annona muricata, cancer, fruit.

تم اعداد كتيب ملخصات مشاريع التخرج من قبل:

جميع أعضاء هيئة التدريس بالقسم

تم تجميع الملخصات وتصميم الكتيب من قبل:

ا. اسماء علي ابودبوس

رئيس قسم الوراثة والتقنيات الحيوية

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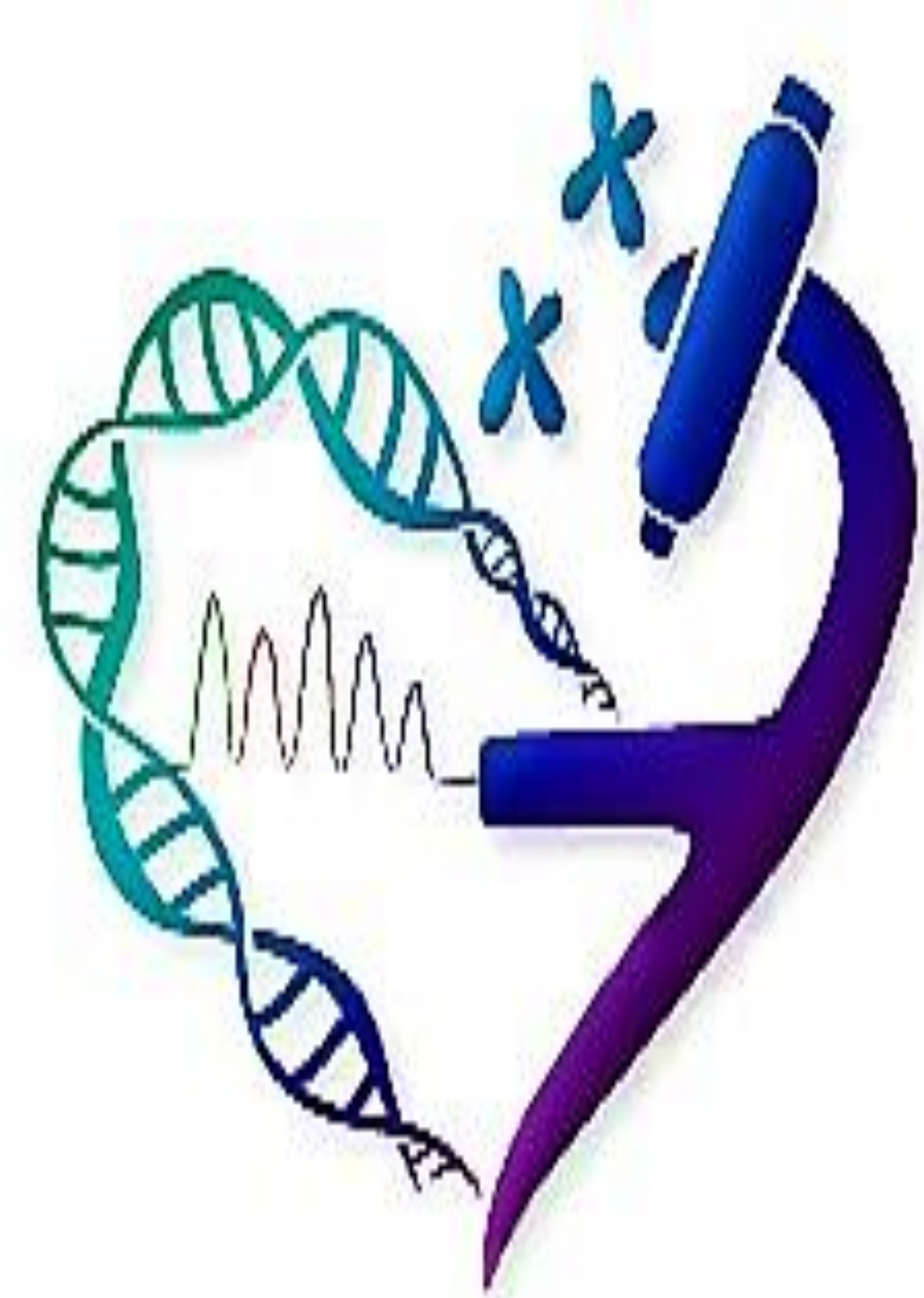

Genetic & Biotechnology Department

National DNA Day 25.4.2023