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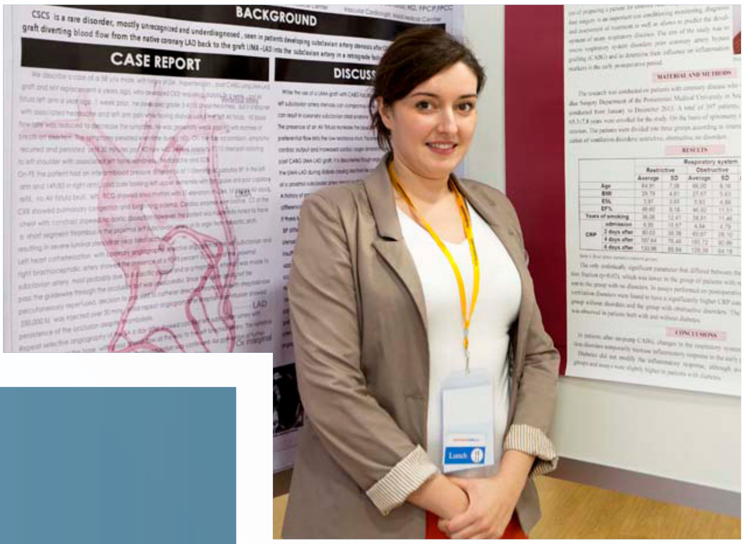

Accepted Abstracts

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Nanobiosensor application in detecting biomarkers in *Candida* infection

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Candida colonization occurs in the oral cavity, gut and reproductive tract in healthy individuals but is a common cause of fungal infection in high risk patients (immunocompromised patients, transplants, diabetes, etc.) with prevalence of 50% in intensive care units. Numerous biomarkers have been anticipated to be of potential use for prognosis in septicemia, including cytokines, cell-surface markers, acute proteins, coagulation factors and apoptosis factors. Sample size is a critical factor and it is unclear if it could predict clinical outcome. This proof of concept study investigated biomarkers of *Candida* immune response from various body fluid samples using a biosensor method. The successful detection of cytokine IL-17A (infection key marker) and Candida-antibody were used as biomarkers to detect infection and immune response in saliva, serum, plasma and semen. A specific, label-free, immunosensor was assembled using polyaniline electropolymerization on a graphene screen-printed electrode base and antibodies covalent binding against IL-17A and Candida. Limits of detection of 0.250 pg/ml (IL-17A) and 7 *Candida* cells/ml were achieved within a linear range of R^2=0.98 and R^2=0.97, respectively. Sample volume used in the nanosensor method was greatly reduced in comparison with the traditional methods. Diverse fluid samples from various body sites from the same participants tested in this study were also detectable. Nanosensors used in the present study were able to detect *Candida* cells and IL-17A level in comparison to gold standard traditional methods. Further studies are needed to characterize specificity and sensitivity of the diagnosis method using nanosensor.

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Characterization and pathological variability of *Exserohilum turcicum* responsible for causing Northern Corn Leaf Blight (NCLB) disease in Malaysia

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Corn is grown primarily for human consumption. It is considered as the second most important cereal crop after rice in Asia. Many diseases affect this crop due to planting of susceptible hybrids. This research is aimed to characterize the causative agent of northern corn leaf blight disease in Malaysia, caused by *Exserohilum turcicum*. Leaf samples were collected from infected farms of two corn growing areas of Peninsular Malaysia in 2015. A total of 5 fungal isolates were examined for cultural, morphological and molecular properties, the five isolates were identified as *E. turcicum*. The conidial shapes were observed to be elongated and spindle. Cultural characteristics showed that variation existed among the isolates in colony growth and color. Mycelia growth rates of the isolates were significantly different on Potato Dextrose Agar (PDA), Corn Meal Agar (CMA) and Potato Sucrose Agar (PSA) media; growth on CMA was faster than on PSA and PDA. The isolates were grouped into three groups based on colony color i.e. light gray, gray and dark gray. The isolates were categorized into two groups based on growth namely, moderate growth and profuse growth. The number of septa ranged from 5-7 to 7-10 representing isolates ET002 and ET003, respectively. Similarly, conidial length varied from 56.7 μm to 89.44 μm for isolates ET002 and ET003, respectively. The pathogenic variability tested on Thai Super Sweet (TSS) corn variety, showed that isolates ET001 and ET003 were more aggressive while isolate ET005 was less aggressive isolate. Both morphology and molecular results showed that, the isolates were identified as *E. turcicum*.

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Effect of antioxidant-rich nutraceutical on serum glucose, lipid profile and oxidative stress markers of salt-induced metabolic syndrome in rats

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Metabolic Syndrome (MS) a high risk condition involving obesity, dyslipidemia, hypertension and diabetes mellitus are prevalent in Nigeria. The study aims to formulate an antioxidant rich nutraceutical from locally available foodstuff (onion, garlic, ginger, tomato, lemon, palm oil, water melon seeds) and investigate their effects on blood pressure, body weight, serum glucose, lipid profile, insulin and oxidative stress markers in salt-induced rats. The rats were placed on 8% salt diet for 6 weeks and then supplementation and treatment with nutraceutical and nifedipine in the presence of salt diet for additional four weeks. Feeding rats with salt diet for six weeks increased blood pressure and body weight of the salt-loaded rats relative to control. Significant ($P<0.001$) increase in serum blood glucose and lipid profile and decrease in High Density Lipoprotein-Cholesterol (HDL-C) was observed in salt-loaded rats as compared with control. Both supplementation and treatment (nifedipine) lowered the blood pressure but only supplementation lowered the body weight. Supplementation with nutraceutical resulted in significant ($P<0.001$) decrease in the serum blood glucose, lipid profile, Malonyldialdehyde (MDA), insulin levels, insulin resistance and increased HDL-C and antioxidant indices. The percentage protection against atherogenesis was 76.5±2.13%. There is strong positive correlation between blood pressure, body weight and serum blood glucose, lipid profile, markers of oxidative stress and strong negative correlation with HDL-C and antioxidant status. The results suggest that the nutraceuticals are useful in reversing most of the component of metabolic syndrome and might be beneficial in the treatment of patients with metabolic syndrome.

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Doxycycline inducible shRNA mediated knockdown of S100A11 impairs the migratory, invasive and proliferative capacity of adenocarcinoma cells

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Non-Small Cell Lung Cancers (NSCLCs) make 85% of lung cancers and adenocarcinomas are the most common type. Currently our understanding of the molecular signatures that drive the progression of lung adenocarcinoma is incomplete. S100A11, a member of the S100 protein family, contributes to the progression of lung adenocarcinoma; however the precise mechanism underlying its implication is unclear. We used doxycycline regulated knockdown of S100A11 to uncover its role in the cellular function of H1975 cells. Knockdown of S100A11 significantly reduced the migratory as well as invasive capability of H1975 cells. Con-focal microscopic analyses suggested a dysregulation in cytoskeletal organization and impaired lamellipodia formation. Further, CCK-8 assay showed high reduction in the proliferative capacity of S100A11 knocked down H1975 cells. Moreover, *in vivo* tumorigenic assay resulted in decreased tumor volumes in mice administered with doxycycline. Together, we report that S100A11 is an important molecule for the tumorigenic properties of H1975 cells and it may serve as a potential therapeutic target to attenuate the progression of lung adenocarcinomas.

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Phytochemicals screening and free radical scavenging potential of leaf and flower extract of *Calotropis procera*

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The aim of the present study was to evaluate the phytochemical constituents and to assess in vitro lipid peroxidation inhibitions and antioxidant activities of different fractions of dried leaves and flowers of *Calotropis procera*. Qualitative analysis of phytochemicals constituent like steroids, saponin, flavonoid, tannin, coumarin, terpenoids and cardiac glycosides was performed by the well-known tests protocol available in the literature. Anti-oxidative efficacy was studied through DPPH, reducing power assay and lipid peroxidation inhibition assay in liver homogenate. The phytochemicals screening revealed the extract richness in tannins, flavonoid, steroids, coumarin and terpenoids. Strong antioxidant scavenging activities were observed in different fractions of leaf and flower extract. Leaf and flower extract of *Calotropis procera* showed lipid peroxidation inhibition against thiobarbituric acid. From the results of the present investigation, it could be concluded that *Calotropis procera* extracts can be explored as a potential source for isolation of natural antioxidant.

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Conjugating activity and substrate specificity of glutathione transferase from organ-pipe mud-dauber wasp *(Trypoxylon politum)*

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Glutathione Transferase (GST) catalyzes the conjugation of glutathione with a large variety of toxic substances thereby rendering them water soluble for elimination from cells. The Organ-Pipe Mud Dauber, *Trypoxylon politum* is a common wasp found beneath the roofs of houses where it builds nest with mud. Since soil, a part of our immediate environment often gets contaminated with chemical pollutants including pesticides. The aim of the study is to evaluate organ distribution of GST in *Trypoxylon politum* as well as determine the substrate specificity of the enzyme. Crude enzyme was prepared from the head, thorax and abdomen of the insect by homogenization and centrifugation. Glutathione transferase activity was determined and purification of the enzyme was carried out by GSTrap 4BTM. Substrate specificity was evaluated with some known substrates of GST. The specific activities of GST from the head, thorax and abdomen of *Trypoxylon politum* were 16.35 µmol min-1 mg-1, 26.29 µmol min^{-1} mg^{-1} and 38.89 µmol min^{-1} mg^{-1} proteins respectively. After the purification of GST from abdomen of *Trypoxylon politum*, the specific activity increased to 193.74 µmol min^{-1} mg^{-1} proteins. This GST showed conjugating activity with ethacrynic acid, p-nitrophenylacetate, haematin, 1-chloro-2, 4-dinitrobenzene and 2, 4-chloro-1-nitrobenzene. The activity and broad substrate specificity of GST in the abdomen of *Trypoxylon politum* suggest possible detoxification of chemical pollutants from soil. Hence, glutathione transferase in organ-pipe mud dauber, *Trypoxylon politum* might be a possible biomarker of chemical pollutants from soil.

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Effects of estrogen related receptor α inhibition on metabolic adaptations to endurance training in skeletal muscle of male wistar rats

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Fuel consumption is dependent on severity and duration of the exercise. Medium-Chain Acyl-CoA Dehydrogenase (MCAD) and Carnitine Palmitoyl Transferase 1 (CPT1) are involved in this process. MCAD performs the first step in fatty acid oxidation and CPT1 catalyzes the limiting step in mitochondrial beta oxidation. Estrogen-Related Receptor-alpha (ERRα) regulates the genes involved in fatty acid oxidation and mitochondrial biogenesis. The aim of this study was to investigate the effect of 4 weeks of endurance training on the expression of genes involved in lipid metabolism. 30 male wistar rats (8 weeks-old) were randomly divided into four groups: Control (n=7), XCT790 (n=8), trained (n=8) and trained+XCT790 (n=7). Expression of ERRα, MCAD, CPT-1β, PGC-1α, PDK4 and CS genes was measured by Real-Time PCR and quantified by $2^{-\Delta\Delta CT}$ method. The expression of ERRα, MCAD, CPT1β, PGC-1α, PDK4 and CS genes were significantly higher in trained compared to control group. The expression of MCAD and CPT1β genes was significantly lower in tained+XCT790 compared trained and the expression of PDK4, CPT1β and PGC-1α were significantly higher in Trained+XCT790 compared to control+XCT790. Taken together, expression of ERRα is a trainable factor and its changes are parallel with higher expression of the enzymes which involved in lipid metabolism. This indirectly suggests a significant role of ERRα in adaptation of lipid metabolism evoked by endurance training.

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Drug repositioning as an effective therapy for protease-activated receptor-2 inhibition

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Proteinase-Activated Receptor-2 (PAR-2) is a GPCR activated by both trypsin and a specific agonist peptide, SLIGKV-NH2. It has been linked to various pathologies, including pain and inflammation. Several peptide and peptidomimetic agonists for PAR-2 have been developed exhibiting high potency and efficacy. However, the number of PAR-2 antagonists has been smaller. We screened the FDA library of approved compounds to retrieve novel antagonists for repositioning in the PAR-2 structure. The most efficacious compound Bicalutamide bound to the PAR-2 binding groove near the extracellular domain as observed in the *in silico* studies. Further, it showed reduced Ca^{2+} release in trypsin activated cells in a dose-dependent manner. Hence, Bicalutamide is a novel and potent PAR-2 antagonist which could be therapeutically useful in blocking multiple pathways diverging from PAR-2 signaling. Further, the novel scaffold of Bicalutamide represents a new molecular structure for PAR-2 antagonism and can serve as a basis for further drug development.

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Life supporting molecular dynamics under extreme thermal environments

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In the era of global warming, there has been a tremendous concern over as to how life can support itself under extreme temperature regimes. The most primitive bacteria could be used as an ideal model system to look into the molecular dynamics for understanding the biochemical basis of thermophily. The signature molecule of prokaryotes happens to be the DNA which can undergo dynamic change with change in the temperature conditions where bacteria could survive comfortably. The model of nucleotide diversity in psychrophilic, mesophilic and thermophilic bacteria and established that transformation of DNA base composition could enable these organisms to thrive best at their respective optimal growth temperatures, where the frequency of GC base pairs increased with increase in growth temperature from psychrophilic to thermophilic and the frequency of AT base pair decreased with decrease in growth temperature from thermophilic to psychrophilic and vice versa. The other macromolecular attribute, that could support life at high temperature, pertains to rapid turnover of molecules including enzymatic proteins which could serve as the basis for high temperature adaptation, in which macromolecular charged environment and ordered cellular organization contributed significantly for sustainability of life under diverse extreme temperature conditions.

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Investigating of antibacterial effect of Savory under NaCl and SA treatments

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Savory *(Satureja khuzistanica)* is a medicinal plant from the Labiatae family. It has antifungal and antibacterial properties due to phenolic compounds in its essential oils and tannins in the leaves. The purpose of this study is to investigate the antibacterial properties of leaf and stem extracts of *Satureja* using conventional microbiological methods (measuring diameter of inhibition zone). Also, the effect of salinity and salicylic acid on phenolic components (Rosmarinic acid and Cafeic acid) and relative *RAS* gene expression were investigated. The experiment was carried out with two replications and treatment levels of NaCl (100 and 200 mM) with SA concentration (0.05 Mm). Apical part was tissue cultured on Murashige and Skoog medium and then different salinity levels and SA treatment were treated for 14 days. The methanolic extract impregnated discs was affected on Muller-Hinton agar medium containing the bacteria. The applied bacteria in this study includes *Pseudomonas aeruginosa* (ATCC, 27583), *Escherichia coli* (ATCC, 25922), *Enterococcus faecalis* (ATCC, 25923) and *Staphylococcus aureus* (ATCC, 25923). In conclusion, the medicinal components increased under NaCl and SA treatments. Moreover, relative *RAS* gene expression showed the same results as well. The experiment showed that methanolic extract has antimicrobial effects on *Escherichia coli, Enterococcus faecalis* and *Staphylococcus aureus* that would increase under NaCl and SA treatments. *Staphylococcus aureus* and Escherichia coli was formed in inhibition zone with further diameter. The results of experiments showed that Savory can be used as a medicine plant in the treatment of infections due to *Staphylococcus aureus* and *Escherichia coli.*

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Isolation and molecular identification of halophilic bacteria (Part-II) from saline soil

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The use of phenotypic, chemotaxonomic and genotypic data includes polyphasic approach which is used today in the taxonomy and systematics of the bacteria and archaea. Understanding of 16S rRNA gene sequence has helped us better understand the microbial world and has led to the detailed descriptions of novel taxa especially at the species level. Here efforts to obtain complete genome sequences of all type strains which are critical for the future of microbial systematic were obtained. Coupling the knowledge of genomics along with taxonomy, bacterial systematics and archae systematics together with computational approaches will increase the development of taxonomy in the genomic era. This study covers the isolation and characterization of halophilic bacteria with phylogenetic identification of the halophilic isolates. Halophiles are the salt-loving organisms that thrive in hypersaline environments. Most prokaryotic and eukaryotic microorganisms fall under this category as they have the ability to balance the osmotic pressure of the environment and will resist the denaturing effect of salts. The description of workflows includes outlines of approaches which describes materials and methods for isolation, morphological and cultural characterization, cultivation and phylogenetic analysis of isolates. And the experimental results showing cultural characteristics, growth requirements, phylogenetic trees and discussion are included.

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HER2 breast cancer group in Morocco: A pathological and statistical study

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Background: The molecular classification of breast cancer is based on four parameters: HER2, Ki-67, Estrogen Receptors (ER) and Progesterone Receptors (PR).

Methods: We retrospectively reviewed a series of 1351 cases of infiltrating breast carcinomas in female patients diagnosed in the Pathology Department of Ibn Rochd University Hospital, Casablanca, Morocco, from 1st January 2013 to 30 March 2017. These biomarquers status was assessed by immunohistochemistry and HER2 scores 2+ were subsequently assessed by *in situ* hybridization. We established a molecular classification of the carcinomas and we developed a correlation profile between HER2 status and various parameters. We carried out a bivariate analysis between HER2 overexpression and SBR grade as well, in order to evaluate the degree of correlation between SBR grade and HER2 overexpression.

Results: Based on this study performed on a Moroccan population, we showed that HER2 molecular subgroup represents 11% of the four molecular groups and is correlated to a higher SBR grade and lymph node invasion. Close examination of the HER2 receptor reveals that it is the most overexpressed of all (35%). The average age of patients who overexpress it is 47.36 years and women over 35 years of age are the most affected (89.86%). It is highly related to grade II (52.7%), then to grade III (44.59%), and to the presence of vascular emboli (56.75%). The bivariate study between the overexpression of HER2 and the severity of the SBR grade showed a very significant association. HER2 is correlated to SBR grade with a correlation coefficient of (Kendall tau=0.48). It is also highly and positively correlated with the Ki67 marker (Kendall tau=0.74). While overexpression of HER2 is negatively correlated with hormonal receptors (RE (Kendall tau=-0.16) and RP (Kendall tau=-0.04)).

Conclusion: As expected, we found that HER2-amplified breast tumors are characterized by an increased proliferation rates, high histologic and nuclear grades, low ER and PR levels and a strong correlation between the overexpression of HER2 and SBR grades II or III. This is, to our knowledge, the first statistical study of the kind in Morocco and North Africa.

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