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fungi isolated from Olive pomace named *Aspergillus spp LR1-IBT* and *A.spp M9-IBT*. Taking into account substrate and microorganism combination, four SFF essays were carried out: SSF-A (GM + OM with *A.spp M9-IBT*), SSF-B (GM + OM with *A.spp LR1-IBT*), SSF-C (OM+GS with *A.spp M9-IBT*) and SSF-D (OM+GS with *A.spp LR-IBT*). Culture medium was set in petri dishes, inoculated at 10^7 spore/g and incubated at 28 °C, during 15 days. Samples were taken periodically for analytical determinations. An aqueous extract from SFF was prepare for the enzymatic activities detection which includes, Cellulase (Cel), Exo-Polygalacturonase (Exo-PG), Laccase (Lac) and Lignin Peroxidase (LiP). All SSF developed well, since weight loss was detected along the whole incubation period, showing log phase between days 2 and 5. Major weight loss was found when SFF was carried out on OM (SSF-C and SSF-D). Enzymatic activities were detected in all SSF (A, B, C and D). Maximum activities where shown during first seven days, then enzymatic activity was barely detectable. Cel and exo-PG activities were major in SFF on GM (SSF-A and SSF-B). Ligninolytic activities were major in SFF on OM (SSF-C y SSF-D). In the future, the trials will focus on the study of variables to optimize the production of Lac and LiP enzymes in OM substrates and Cel and Exo-PG enzymes in GM substrates.

129. ISOLATION OF TOTAL DNA IN *Hedeoma multiflora* Benth.

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Due to the diverse uses of the native aromatic species from the province of San Luis, "Peperina de las Lomas" (*Hedeoma multiflora* Benth.) is suffering from a high extraction pressure and therefore, it is at risk of genetic variability losses. There is no background on molecular markers in this species for the study of the population genetic structure. The aim of the present work was to obtain *Hedeoma multiflora* genomic DNA with quality, optimal purity, and adequate quantity for subsequent analysis by molecular techniques, such as inter simple sequence repeats (ISSR). Leaves and stems were used as plant material applying the CTAB Protocol 7 for total DNA isolation with modifications of the original protocol. It was possible to extract total genomic DNA with high yield and purity from leaves without the use of liquid nitrogen. A rapid technique was standardized to obtain genomic DNA from this species and to initiate genetic characterization protocols.

130. BACTERIOSIS IN A DIVERSE MAIZE GERMPLASM IN SOUTH CÓRDOBA, ARGENTINA

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The maize is one of the most important crops of the Argentinian pampa region. Plant pathogens, such as fungi, bacteria, and virus can cause serious damage to agriculture and significantly reduce the yield and quality of crops. Diseases caused by bacteria, however, are the few studied. The objective of this work was to identify bacterial pathogens based on symptoms observed in a diverse maize germplasm. Therefore, a population of 200 maize inbred lines developed and provided by the International Maize and Wheat Improvement Center (CIMMYT) were evaluated at Río Cuarto location during the summer cycle of 2017/2018. Light-colored necrotic streaks or yellow irregular blotches were observed on leaves from symptomatic maize inbred lines. The leaves with symptoms were rinsed with sterile distilled water and cut into small bits. These pieces were immersed in 0.85% (w/v) NaCl (physiological solution) and macerated. The samples were serially diluted and plated onto Luria-Bertani (LB) medium, containing dicloran (to prevent fungal growth). Plates were incubated at 30 °C. A total of twenty isolates were obtained from symptomatic maize inbred lines. Gram staining, pigment production in LB medium and catalase reaction were tested in all isolates. In addition, β-galactosidase production was assessed by X-Gal test. Most of the strains were Gram-negative and five isolates were catalase positive. The isolates were distinguished by their different colonial morphologies. Light yellow, orange, red or white convex colonies were observed on LB medium. Moreover, three strains produced blue color colonies on X-Gal containing plates, indicating the presence of β-galactosidase enzyme in those bacteria. Representative isolates were chosen for further identification through the use of phylogenetic analysis of 16S rRNA gene sequences. A single product of about 1.5 kb was amplified by PCR with the primers fD1 and rD1 from each of strains analyzed. The purified PCR products were sent to Macrogen Inc. (Seoul, South Korea) for the sequencing of the gene encoding 16S rRNA. The identification of bacterial pathogenic strains in maize is relevant. Since the study of these emerging diseases in the maize region of Argentina is yet little explored.

131. AGROINDUSTRIAL WASTE FROM THE CUYO REGION REVALORIZATION. PRELIMINARY TESTS USING SOLID STATE FERMENTATION

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The agroindustrial activity of the Cuyo region is based mainly on the processing of two crops: the vine and the olive; and to a lesser extent fruits and vegetables. The wine industry and the olive oil industry generate large amounts of solid waste, such as grape marc, grape stalks and olive mark (OM). At present, the final disposal of these residues is difficult due to their high concentrations of phytotoxic substances, causing environmental problems if they accumulate in large quantities. Due to its chemical composition (carbohydrates, fiber, fats, proteins and mineral salts), agro-industrial residues are suitable substrates for biotechnological proceesing

to obtain value-added products. The objective of this work was to carry out a preliminary study of the production of hydrolytic enzymes using *Aspergillus niger* in Solid State Fermentation (SSF) using solid regional wastes. The following residues were used: red grape marc (RGM), olive mark (OM) and mixture RGM-OM (50% w/w of each one). SSF were carried out in Petri´s dishes at 27°C, with solid medium initial moisture content of 60% w/w and an inoculum size of $1x10^7$ spores*g dry^{-1} of *A. niger*. Two samples of culture were taken per day during one week for subsequent analytical determinations. The enzymatic activities that were measured in the aqueous extracts of SSF were: α-L-arabinofuranosidase (α-L-arf), α-L-rhamnosidases (α-L-rha), exopolygalacturonase (exo-PG), laccase (lac) and lignin peroxidase (LiP). The maximum enzymatic activity values were obtained for α-L-arf and exo-PG. The maximum activities for both enzymes were: 2.62U/g for α-L-arf, at 58 hours of cultivation and 4.53U/g for exo-PG at 70 hours, in SSF of RGM-OM. As for lac and α-L-rha activities, lower values were obtained. No significant amounts of LiP activity were determined. The results obtained indicate that it is of interest to optimize the SSF tests with the mixture of the two solid substrates to maximize the values of the enzymatic complex, investigating the culture conditions and nutrient additions.

132. DETECTION OF IMPORTANT GENE POLYMORPHYMS IN SWINE PRODUCTION

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Applied genetics allows increasing the production of pork meat and improving its quality. Some of the most wanted production parameters in pigs are litter size, number of piglets born alive, feed conversion, backfat thickness and meat quality. For litter size and number of born alive, two genes that have the greatest impact are the estrogen receptor (*ESR1*) and the prolactin receptor (*PRLR*). For the pork meat quality one of the important factors is related to a polymorphism of the ryanodine receptor gene (*RYR1*). The objectives of this work are: 1) to establish the frequency of favorable polymorphisms for the estrogen receptor gene and for the prolactin receptor gene in gestating sows and 2) to establish the frequency of the HAL-1843 polymorphism of the *RYR1* gene in juvenile pigs, sows and boars. All specimens come from small and medium-sized establishments in the UNNOBA area of influence. The end is to contribute to the knowledge of breeders to achieve a genetic improvement, increasing productivity. A total of 51 samples were analyzed for *ESR1* and 50 for *PRLR*, from 2 porcine establishments and 154 samples for *RYR1* from 11 establishments. The study of the different genotypes was carried out by PCR followed by RFLP. Hair bulb samples were washed with ethanol, incubated with Proteinase K; DNA was extracted by phenol-chloroform-isoamylalcohol and amplified by PCR. The fragments were digested for the three genes in question, using the restriction enzyme *Pvull* for the *ESR1* gene, *Alul* for the *PRLR* gene and *BsiHKAI* for the *RYR1* gene. For the estrogen receptor gene, where the B allele is preferred 54.9% was detected with the AB genotype and 3.9% with the BB genotype. For the prolactin receptor gene, which the A allele is favorable, 38% was registered with the AA genotype and 40% with the AB genotype. The genotypes found for the *RYR1* gene were: 88 NN: 6 boars, 52 sows, 4 young males and 26 young females; 64 Nn: 8 boars, 31 sows, 7 young males and 18 young females; nn: 2 young males. We detected 1.3% of recessive homozygotes and a heterozygosity of 41.5%, corresponding the 25.3% to breeding animals. The report to the pig breeders allows them to know the presence of gene polymorphisms in order to maximize better crosses avoiding unfavorable alleles. The HAL-1843 mutation permits also to detect the presence of animals susceptible to Swine Stress Syndrome and to understand the variability observed in the meat quality, so to control the crosses of heterozygotes will contribute to reduce the incidence of the mutation.

133. LOOP-MEDIATED ISOTHERMAL AMPLIFICATION (LAMP): A SIMPLE METHOD EARLY DETECTION OF THE *Xanthomona arboricola* SPECIES

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Xanthomona arboricola (Xa) species are the major cause for premature drop fruit in walnuts, hazelnuts, almonds and other dried fruits, and responsible to of great economic losses throughout the world. On the other hand, Loop-mediated isothermal amplification (LAMP) is a simple, specific, economic and rapid nucleic acid amplification method compared to the conventional PCR assay. This study aims to develop methods that allow early diagnosis, anticipate infection by microorganisms and act quickly on plants health and control strategies. For this purpose, different target genes such as *XopA*, *XopAH* and *XopG* were studied together with various primers for both isothermal amplification and conventional PCR using *Bioedit* and *PrimeExplore V4* software respectively. Thus, samples of bacteria were isolated from infected tissues, the genomic material was extracted using column purification techniques and direct isolation of colonies, and kept at -20°C until use. For LAMP-PCR assays external primers (F3-B3), inside primers (FIP-BIP) and *Bst* 2.0 warm start polymerase. Conventional PCR assays, common primers and *Taq* polymerase were used. Amplifications were detected in 1.8% agarose gel, which showed two characteristics fragments that were compared with a ladder. To compare results, were used conventional PCR primers (LF and LB), the latter was also performed to verify the functioning of the primers to be used in LAMP-PCR. Amplifications for LAMP-PCR were detected by simple visualization with the turbidimetric method (magnesium pyrophosphate precipitate formation), and the fluorometric method by addition of ethidium bromide in both reaction tubes. The results of LAMP-PCR assay obtained during the analysis of nut samples from different regions of the Rio Negro valley showed that *XopA* and *XopAH* genes were positive after 25 minutes reaction and *XopG* gene negative. Moreover, the same genes showed positive results in conventional PCR assay, with a similar specificity. Thus is possible concluded that the LAMP-PCR qualitative assay can be