Book of Abtract

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CONTENTS

Genomic insights into the diversity of Vietnamese people

Nong Van Hai

Institute of Genome Research, Vietnam Academy of Science and Technology,
Hanoi 100000, Vietnam
**Corresponding author: Nong Van Hai, Email: vhnong@igr.ac.vn*

ABSTRACT. Vietnam is an important crossroads within Mainland Southeast Asia (MSEA) and a gateway to Island Southeast Asia (ISEA). The country has the Kinh (Viet) as the major ethnic nationality together with the other 53 minor ethnic groups, belonging to the five language families (Austroasiatic, Tai-Kadai, Hmong-Mien, Sino-Tibetan and Austronesian). In order to gain comprehensive insights into genetic diversity of Vietnamese people, we analyzed complete mtDNA genome sequences, ~2.3 Mb sequences of the male-specific portion of the Y chromosome (MSY) as well as the genome-wide single-nucleotide polymorphism (SNP-genotyping) data of more than 600 Vietnamese individuals from 17 to 22 ethnic groups of the all five language families. Phylogenetic analysis revealed 111 novel Vietnamese mtDNA lineages and the coalescence time showed a peak of mtDNA diversification around 2.5–3 kya, which coincides with the Dong Son culture. We also found highly variable levels of diversity within and between groups that do not correlate with either geography or language family. Our findings suggested that Vietnamese ethnolinguistic groups harbor multiple sources of genetic diversity that likely reflect different sources for the ancestry associated with each language family. Further genome analyses of more samples from other ethnic groups are now under way.

Studies on Harmful Algae in Viet Nam. Does species identification is a challenge?

Lam Nguyen-Ngoc[1], Jacob Larsen[2]

[1]Institute of Oceanography, Vietnam Academy of Science and Technology, Nha Trang 650000, Vietnam
[2]IOC Science and Communication Centre on Harmful Algae, University of Copenhagen, Copenhagen 2100 Ø, Denmark
**Correspondence author: Lam Nguyen-Ngoc*

ABSTRACT. Red tides' is a concept previously applied by the international scientific community to events of harmful algal blooms (HABs), which is now the preferred terminology. From 2000 up to now, microalgae blooms have been recorded along the coast of Viet Nam, caused by cyanobacteria such as *Lynbya majuscula*, *Trichodesmium erythraeum*; dinoflagellates such as Tripos furca, *Noctiluca scintillans, Alexandrium pseugonyaulax, Peridinium quinquecorrne*; haptophycean alga such as *Phaeocystis globosa;* and diatoms such as *Pseudo-nitzschia* spp., the economic losses of fisheries have not been fully accounted for. However, taxonomic studies based on morphological comparison of potentially harmful species in coastal waters, near and offshore islands of Vietnam showed that there are 19 species of *Alexandrium* can produce PSP toxins (Paralytic Shelfish Poisoning), 12 species of *Pesudo-nitzschia* can produce ASP toxins (Amnesic Shelfish Poisoning), and 3 species *Dinophysis* being responsible for DSP (Diarrehtic Shelfish Poisoning). Recently, a number of benthic algae producing the CP toxins (Ciguatera Poisoning) have been reported, in Vietnam 2 species of G*ambierdiscus* have been confirmed to have ciguatera toxin; and there are 18 species of *Gambierdiscus* have been described over the world. The number of harmful microalgae species could be more accurate if morphological observations under the LM and EM were combined with DNA analysis. *Pseudo-nitzschia* species could not be identified under the LM. Dinoflagellate species such as *Ostreopsis* spp., *Gambierdiscus* spp., *Coolia* spp., *Alexandrium* spp. can change their morphology under the influence of some natural or cultured conditions (cause unknown), so the identification of species belonging to these genera are necessary must be analyzed in combination with genetic analysis. Differences in morphology but sharing a genetic trait or vice versa is a matter of interest to scientists and is a big challenge for harmful algae monitoring programs, as well as for biotechnological and applied researches.

Keywords. HABs, Genetic analysis, Morphology, Vietnamese coast

Taxonomic diversity indices: long-term evaluation on biodiversity and environmental impacts in estuarine plankton

Hai Doan-Nhu, Duyen T.N. Huynh, Hue M. Tran, Van T.L. Tran, Luom P. Tan,
Vinh T. Nguyen, Lam Nguyen-Ngoc

Institute of Oceanography, Viet Nam Academy of Science and Technology,
Ha Noi 100000, Vietnam
**Correspondence author: Hai Doan-Nhu*

ABTRACT. Taxonomic distinctness was popular used due to its better measuring of biodiversity especially for long term assessment of environmental impacts on ecosystems. However, there were few disadvantages of its uses that limit its application in certain conditions. These limits mainly relate to quality of the data sets that require certain level of taxonomic expertise. In Viet Nam, biodiversity was evaluated mostly by number of species, or in higher research by traditional diversity indices (e.g. Shannon, Simpsons indices). In the first case, assuming species number was correct and from taxonomic experts, biodiversity was the simplest presented but not necessary true. In the second case, with the same assuming as in the first case, these indices usually are used with caution e.g. there was on opposite response of these indices observed on long-term data. In coastal waters of Viet Nam, these indices were basically good for indication among the study sites from pollution impact evaluation but not temporal trend or climate variation. The taxonomic distinctness index seems to response to both pollution and climate variability in long-term data. In the Mekong, primitive results indicating possible changes of diversity of phytoplankton under impacts of dams' construction. In the southern South China Sea, the taxonomic distinctness index had positive correlation to production of oil extraction in the area. In the least polluted Nha Trang Bay, the taxonomic distinctness was the only index showed significant responses to ENSO phenomenon. Evaluation of anthropogenic or natural impacts on biodiversity of plankton community can be done using different biodiversity indices. However, there should be quality check on data and with caution on the uses of each index.

Keywords: Taxonomic distinctness, Biodiversity, Mekong, plankton, environment indicators.

Biodiversity research for natural conservation and sustainable development in Vietnam

Nguyen Quang Truong

Institute of Ecology and Biological Resources, Vietnam Academy of Science and Technology, Hanoi 10072, Vietnam
**Correspondence author: Nguyen Quang Truong*

ABSTRACT. Vietnam is located in the Indo-Burma region, one of the 36 global biodiversity hotspot in the world. The country habours a high level of species richness and local endemism with more than 12,000 species of vascular plants, 5,000 species of vertebrates and thousand species of invertebrates. However, biodiversity of Vietnam is under the risk of degradation and many species are under threat of extinction. According to the IUCN Red List of Threatened Species (2021) 1,258 species of plants (19% of the total number of the evaluated species) and 891 species of animals (18.6%) recorded from Vietnam are listed as threatened taxa. Major threats to biodiversity of Vietnam are habitat loss and degradation, population decline of wildlife species, environmental polution and invasive species. This review highlights some achivements of our research work on biodiversity exploration, sustainable use of biological resources, impacts of climate change on biodiversity, and wildlife forensics activities. Research results not only help to fill the knowledge gaps about biodiversity potential of Vietnam, but also provides a scientific basis for management, natural conservation, and sustainable development of the country.

Research and application of insect semiochemicals for crop protection in the Mekong delta of Vietnam

Le Van Vang

College of Agriculture, Can Tho University, Can Tho 900000, Vietnam
**Correspondence author: Le Van Vang, Email: lvvang@ctu.edu.vn*

ABSTRACT. Semiochemicals are chemical compounds carrying signals that function in communication between living organisms. Insect semiochemicals have been extensively researched and applied as a tool for monitoring population dynamics and modifying the behaviors of agricultural insect pests, thereby protecting crops from insect damage throughout the world. In the Mekong Delta of Vietnam, more than 41 semiochemical compounds from 56 insect species have been studied. Amongst these, sex pheromones were predominant with 19 chemical compounds from 14 species. Sex attractants were recorded from 39 species with 17 compounds. Aggregation pheromones and volatile organic compounds with 7 compounds were recorded from 4 species. Because of pest management purposes, most of the studies dealt with insect species that were associated with agricultural insects, including 43 damage and two weed biological control agent species.

Keywords. Agricultural insects; aggregation pheromone; semiochemical; sex attractant; sex pheromone.

AP01

Isolation and identification the antagonistic bacteria against *Xanthomonas* spp. causing the leaf spot from *Rosa* spp.

Le Uyen Thanh

Dong Thap University, Dong Thap 81000, Vietnam
**Correspondence author: Le Uyen Thanh, Email: luthanh@dthu.edu.vn*

ABSTRACT. Three out of 203 bacterial isolates showed high antibacterial activity antagonists by in vitro screening against three strains of *Xanthomonas* spp. causing leaf spot from *Rosa* spp.. Antagonistic bacteria were collected from rhizosphere substrate of potted rose in Sa Dec Flower Village of Dong Thap province, Viet Nam. While three pathogen strains of *Xanthomonas* spp. were stored at Biochemistry Laboratory of Biotechnology Research and Development Institute of Can Tho university. Three effective isolates were identified by Matrix assisted laser desorption ionization time-of-flight (MALDI-TOF) and analysis of 16S rRNA gene sequence. Using MALDI-TOF, these antagonistic bacteria are belong to Bacillus genera. The amplification of 16S rDNA gene is performed using 27F and 1492R primers. The nucleotide sequences of these gene are aligned using GenBank database and BLAST-N program from NCBI site. The isolates identity of BR16, BR37, BR88 were shared the highest similarity values in turn with *Bacillus velezensis* MN160320 (99.11%), Bacillus subtilis MN493770 (99.11%), *Bacillus amyloliquefaciens* KX871898 (99.41%). These *Bacillus isolates* were designed Bacillus velezensis MW677565 (from BR16), *B. subtilis* MW828613 (from BR37), *B. amyloliquefaciens* MW828656 (from BR88). These isolates have shown ability to fight phytopathogenic bacteria of ornamental plant in Dong Thap of Viet Nam.

Keywords: 16S rRNA gene, *Antagonistic bacteria*, Isolation, Identification, MALDI-TOF, *Xanthomonas* spp.,

AP02

Controlling efficiency of the potential rhyzophere bacterial antagonists against leaf spot disease from *Rosa* spp. caused by *Xanthomonas* spp. in vitro and under net-house condition

Le Uyen Thanh[1*], Doan Thi Kieu Tien[2], Huynh Ngoc Tam[3], To Lan Phuong[1],
Nguyen Thi Be Nhanh[1*]

[1]Dong Thap University, Dong Thap 81000, Vietnam
[2] Can Tho University, Can Tho 900000, Vietnam
[3]Tram Chim high school, Dong Thap 81000, Vietnam
**Correspondence author: Le Uyen Thanh, Nguyen Thi Be Nhanh,*
Email: ntbnhanhdt@gmail.com; luthanh@dthu.edu.vn

ABSTRACT. Bacterial leaf spot (*Xanthomonas* spp.) on rose cause great losses to the farming. In vitro condition, the survey of antagonistic density was tested on King's B medium by using three antagonistic isolates (BR16, BR37, BR88) against *Xanthomonas* spp. (XR13, XR9, XR18 strains). Three antagonists and pathogen were diluted separately at 10, 100, 1000 &10000 fold. Results showed that the inhibition abilities was increased with diminishing the population of *Xanthomonas* spp.. In which, three antagonists with populations less than 10^6 CFU/mL are not sufficiently effective or low effective in forming the inhibitory zone against pathogen. Therefore, a density of about 10^7 CFU/mL was selected to be treated in the trials on rose under net-house condition. From that, with foliar application, three isolates (BR16, BR37, BR88) were applied against three strains of *Xanthomonas* spp. above. Results showed that pretreating with antagonistic bacteria achieved high disease control efficiency. In which, BR88 isolate has the highest disease reduction efficiency reaching 70.1%, 72.4%, and 73.3%, respectively, when infecting the XR13, XR9, or XR18, respectively. Furthermore, treatments from applying separately three antagonistic isolates all have AUDPC lower than the treatment with only disease innoculation from 2.4 to 4.7 times. In which, the treatments of BR88 and BR16 isolates got similarly about AUDPC when infecting XR13, or XR9 and lower than BR37. At once, the treatment of BR88 has the lowest AUDPC when infecting XR18. In general, three isolates of antagonistic bacteria BR16, BR37, BR88 can be used to control leaf spot disease caused by *Xanthomonas* spp. on rose. In which, the BR88 achieved the highest disease control efficiency and has the potential to be used as a biological control agent on plants.

Keywords: AUDPC, Antagonistic bacteria, Disease reduction efficiency, Rose, *Xanthomonas* spp.

AP03

Efficacy of bacteriophages in controlling bacterial vascular wilt caused by *Ralstonia solanacearum* Smith on eggplants

Doan Thi Kieu Tien[1], Lu Chi Thong[1] and Nguyen Thi Thu Nga[1*]

[1]Department of Plant Protection, College of Agriculture, Can Tho University,
Can Tho 900000, Vietnam
[2] Can Tho University, Can Tho 900000, Vietnam
[3]Tram Chim high school, Dong Thap 81000, Vietnam
**Correspondence author: Nguyen Thi Thu Nga, Email: nttnga@ctu.edu.vn*

ABSTRACT. The objective of the study was selection promising bacteriophages for lysis *Ralstonia solannaceum* in vitro and evaluation their ability in prevention of bacterial vascular wilt on eggplants under greenhouse conditions. Primary selection of promising bacteriophages from four bacteriophages as Φ54, Φ60, Φ67 and ΦBT on *Ralstonia solanacearum* isolated from eggplant based on plaque diameter and phage multiplication in in vitro, the result found that three bacteriophages (Φ54, Φ67 and ΦBT) expressed plaque diameter over 7.00 mm at 48 hours, and phage titer with log (pfu/ml) reach over 7.00. Continuing survey, the efficacy of these phages in controlling bacterial wilt on eggplants in greenhouse condition through applying each bacteriophage or cocktail of three phages suspension two times (10^{10} pfu/ pot/ each time) at before inoculating pathogen and 7 days after inoculation through soil drenching. As a result, all bacteriophages either single or mixture of three phages were effective in the prevention of bacterial wilt disease. Specially, phage Φ BT showed highest disease reduction and better than bacteriocide treatment apply with Starner 20 WP.

Keywords: Bacteriophage, eggplant, phage cocktail, *Ralstonia solanacearum*

AP04

Selection and characterization of a yeast strain for the suppression of brown spot on Tru Long pummelo (*Citrus maxima*)

Nguyen Minh Ly[*], Le Thi Mai

Faculty of Biology and Environment Science, The University of Danang -
University of Education and Science, Da Nang 119991, Vietnam
**Correspondence author: Nguyen Minh Ly, Email: nmly@ued.udn.vn*

ABSTRACT. Tru Long pummelo is an endemic plant of Quang Nam province with high economic value. However, many different diseases, especially brown spot disease caused by *Alternaria fungus* on pummelos, have affected the quality of pummelos. Pesticides are overused and misused to the environment and human health. Therefore, there is an urgent need to reduce the use of synthetic chemicals. Biological control offers an alternative to the use of pesticides. Eight yeast strains have been isolated from healthy leaves, pummelo fruits, and healthy mulberries. They were screened for biological activity against *Alternaria* sp. by the dual culture method. The inhibitory potency ranged from 10.46% to 59.86%. The strain with the highest percent (59.86%) was identified as Candida tropicalis using sequence analysis of the ITS region.

Keywords: *Alternaria* spp., biocontrol, candida tropicalis, *Citrus maxima* (Merr.) Burm, Antogonism

AP05

Bulbophyllum tseanum (Orchidaceae) a new record for the flora of Vietnam

Dang Minh Quan[1], Averyanov V. Leonid[2], Dang Van Son[3], Nguyen Tran Vy[3],
Truong Quang Tam[3], Nguyen Quoc Bao[3], Truong Ba Vuong[3*]

[1]School of Education, Can Tho University, Can Tho 900000, Vietnam
[2]Komarov Botanical Institute of the Russian Academy of Sciences, Prof. Popov Petersburg, Moscow 119991, Russia
[3]Institute of Tropical Biology Vietnam Academy of Science and Technology, Ho Chi Minh 700000, Vietnam
**Correspondence author: Truong Ba Vuong, Email: bavuong2019@yahoo.com*

ABSTRACT. *Bulbophyllum tseanum* was found in Quang Nam Province. It is new record for the orchid flora of Vietnam. Previously this species was recorded in Hong Kong and Hainan (South-East China). Living specimens were collected in Quang Nam province and flowering successfully in private garden in Da Lat city, Lam Dong province. Base on morphological characters, *B. tseanum* are very close to *B. lepidum* in the plant habit, shape and color scheme of flowers, but can be distinguished by broadly ovate dorsal sepal, longer lateral sepals, narrow petals with shortly caudate apex, size of stelidia and column wing shape. The description of Vietnamese plants is presented, accompanied with the analytical plate and taxonomic notes.

Keywords: *Bulbophyllum lepidum, Bulbophyllum* sect. *Ephippium*, New record, Plant diversity, Plant taxonomy

AP06

Effect of storage time on quality of fermented total mixed ration (FTMR) from sweet potato by-products

Mai Truong Hong Hanh[1, 2] and Ho Thanh Tham[1]

[1]PhD student in Animal Science, Department of Animal Sciences, College of Agriculture, Can Tho University, Can Tho 900000, Vietnam
[2]Sub-Department of Animal Husbandry and Veterinary Medicine of Soc Trang Taoyuan City 33302, Vietnam
**Correspondence author: Mai Truong Hong Hanh, Email: mthhanh84@gmail.com*

ABSTRACT. The experiment was carried out to establish diet formulations for beef cattle with the main ingredients being sweet potato vines (SPV) and sweet potato tubers type 3 (SPT). The experiment was arranged in a completely randomized design with 3 treatments and 3 replications with 7 evaluation time points. The formulations with the same ratio of SPV and SPT (according to DM) were mixed with some other ingredients such as: rice straw, copra meal, extracted soybean, corn kernel, rice bran, salt, mineral premix and urea. Treatments were evaluated for sensory and chemical composition at 1, 14, 28, 42, 56, 70 and 84 days after enisling. The indicators to evaluate the nutritional content such as: dry matter (DM), ash, crude protein (CP), crude fiber (CF), acid detergent fibre (ADF), neutral detergent fiber (NDF) and ether extract (EE). The pH values starting from 14 to 84 days of storage were all satisfactory for silage, since there is a pH in the range of 4-4.5. The NH_3 content in the same formulation over the incubation times was not statistically significant ($P>0.05$). The results of assessment of changes in nutritional content and sensory evaluation over time showed little change in the formulation, all three formulations met the standards of FTMR mixed feed.

Keywords: beef cattle, Fermented Total Mixed Ration (FTMR), silage, sweet potato by-products, sweet potato vines

AP07

Identification of *Ralstonia solanacearum* species complex causing bacterial wilt in tomato in Vietnam

Nguyen Minh Ly[1*], Kieu Duc Toan[1], Mai Xuan Cuong[2]

[1] Faculty of Biology and Environmental Science, The University of Danang - University of Science and Education, Da Nang 50000, Vietnam
[2] Graduate Institute of Biomedical Sciences, Division of Biotechnology, Chang Gung University, Taoyuan 33302, Taiwan
**Correspondence author: Nguyen Minh Ly, Email: nmly@ued.udn.vn*

ABSTRACT. *Ralstonia solanacearum* species complex (RSSC) is the main pathogen causing bacterial wilt disease in tomato plants. This study applied polymerase chain reaction (PCR) with RSSC's specific and multiplex primer pairs to accurately identify RSSC isolates in Vietnam. The results showed that Vietnamese isolates were identified as *R. pseudosolanacearum*, phylotype I. In addition, a colony PCR technique was developed to rapidly detect and select RSSC strains from isolation samples of diseased tomatoes. This method directly used bacterial colonies on the Petri plate as templates to amplify with primers 759/760 and obtained PCR product with the length of 282 base pairs. This is the first study to recognize *R. pseudosolanacearum* as the cause of bacterial wilt disease in tomatoes in Vietnam.

AP08

Acute toxicity evaluation of methanol, ethanol and aqueous extracts of *Balanophora latisepala* (V. tiegh.) lec.

Nguyen Trong Hong Phuc[*1], Pham Dong Hai[2], Phan Thanh Dat[1],
Nguyen Thi Yen Lan[3], Phung Thi Hang[1]

[1]School of Education, Can Tho University, Can Tho 900000, Vietnam
[2]College of Natural Sciences, Can Tho University, Can Tho 900000, Vietnam
[3]Phan Van Tri high school, Can Tho 900000, Vietnam
**Correspondence author: Nguyen Trong Hong Phuc, Email: nthphuc@ctu.edu.vn*

ABSTRACT. *Balanophora latisepala* has been used in traditional medicine in Vietnam for many years with both proven and unproven scientific proofs. This study aimed to evaluate the acute toxicity effects of *B. latisepala* by testing safety parameters of hot water, ethanol and methanol extracts of *B. latisepala* in *Mus musculus*. The acute toxicity was studied according to the World Health Organisations guideline for the evaluation of the safety and efficacy of herbal medicines. During study, a single dose of 1000, 2000 and 5000 mg/kg of each extract was orally administered to Swiss mice. To determine the median lethal dose, experimental mice were observed in behavior and mortality for 72 hours. Data of organ weight, histopathology, biochemical and hematology were also collected. The results showed that hot water, ethanol and methanol extracts at a dose of 5000 mg/kg did not induce mortality in experimental mice; therefore, LD_{50} is not determined. Insignificant changes were found in relative organ weight at dose 5000 mg/kg for all of the extracts. Similarly, no significant differences were observed in biochemical indices and organ histology. However, changes in hematological indices in both male and female mice were noticed. In male mice, it is likely that all *B. latisepala* extracts induced anemia. Moreover, clotting or bleeding abnormalities were also observed in female mice. Methanol extracts had the highest effect to hematology indices ($p<0,05$). Therefore, *B. latisepala* in different doses was shown its safety under acute toxicity studies with promising applications in drug therapy.

Keywords: *Balanophora latisepala* (*B. latisepala*), acute toxicity, LD50, hot water extract, ethanol extract, methanol extract

AP09

Impact of nanosilver structures on their antibacterial activity against *Bacillus cereus* and *Bacillus megaterium* pathogens

Hoang Nhat Hieu, Nguyen Van Nghia, Nguyen Thi Tho,
Thi Mong Diep Nguyen*

Quy Nhon University, Binh Dinh 590000, Vietnam
**Corresponding author: Thi Mong Diep Nguyen, Email: nguyenthimongdiep@qnu.edu.vn*

ABSTRACT. Silver is a well-known effective antibacterial and disinfectant material with relatively few side effects. Nanosilver are derived from it, have strong antibacterial, antifungal and broad-spectrum antiviral properties. Nanosilver can pass through the bacterial cell wall to change the structure of the cell membrane, even leading to cell death. This study describes the time-dependent microwave synthesis of silver nanoparticles, and their antibacterial activity. The optical properties of the nanosilver were examined through UV-Vis absorption spectroscopy. The morphology of the grain was determined by transmission electron microscopy (TEM), and the crystallinity of the nanosilver was confirmed by X-ray diffraction (XRD). The antibacterial activities were assessed using bacterial pathogens *Bacillus cereus* and *Bacillus megaterium*, and were performed using the disk diffusion method. The obtained results show that (i) the structure and size of the nanosilver change when the microwave time is increased. They are of various sizes but almost all circular in shape when microwaved for 1.5 min, of larger sizes and different non-spherical geometric shapes after 3 min of microwave, and converted to nanowires after 5 min of microwave. (ii) *Bacillus cereus* and *Bacillus megaterium* were sensitive to all nanosilver but the antibacterial activity was more potent when the AgNPs possessed a defined shape (sphere, triangle, square, quadrilateral...) than when they were nanowires.

Keywords: Nanotechnology, silver nanoparticles, nanowires, nanosphere, nanoparticles

AP10

The chemical composition and antibacterial activity of essential oil of *Dysphania ambrosioides* (L.) Mosyakin & Clemants in Lam Dong province

Do Tran Tham Thuy, Huynh Thi Huong Tram, Nguyen Pham Doan,
Do Nguyen Viet Hung, Nguyen Van Phuc, Hoang Thi Binh*

Faculty of Biology, Dalat University, Lam Dong 66000, Vietnam
**Correspondence: Hoang Thi Binh, Email: binhht@dlu.edu.vn*

ABSTRACT. In the present study, chemical composition and antimicrobial properties of essential oil obtained from the aerial parts of the *Dysphania ambrosioides* (L.) Mosyakin & Clemants in Lam Dong province were evaluated. Essential oil was isolated through hydro-distillation. Fifteen constituents comprising 100% of the essential oil were characterized by gas chromatography/mass spectrometry (GC-MS) techniques. The major compounds in the essential oil were α-terpinene (74.70%), ascaridole (17.93%) and o-cymene (3.04%). Moreover, the antimicrobial effects of *D. ambrosioides* essential oil against Staphylococcus aureus (Gram-positive), Escherichia coli (Gram-negative), and Candida albicans (pathogenic yeast) were tested by the inhibition zone diameter test to evaluate the antimicrobial activity. The results showed that the essential oil of *D. ambrosioides* possessed excellent antibacterial activity against all the selected strains, of which Escherichia coli is the most sensitive and resistant strain. In general, this investigation showed that the oil of *D. ambrosioides* is a potent antimicrobial.

Keywords: Antimicrobial, *Dysphania ambrosioides*, essential oil, Lam Dong

AP11

Organogenesis plant regeneration from leaf and stem explants of *Begonia masoniana* irmsch. ex Ziesenh.

Nguyen Ngoc Thao Nguyen*, Lam Thi Minh Chau, Bui Pham Bao Ngoc, Hoang Tran Thao Trang

Faculty of Biology, Dalat University, Lam Dong 66000, Vietnam
**Corresponding author: Nguyen Ngoc Thao Nguyen, Email: 1910204@dlu.edu.vn*

ABSTRACT. *Begonia masoniana* is not only an ornamental houseplant but also a medicinal plant due to its highly effective phytochemicals. For two years, this species was introduced from Hagiang to Dalat. However, the seedling supply is still not enough because of the low propagation rate. In vitro propagation is a well-known method to produce a large number of plants with high quality in a short time. The result obtained from this study showed that the highest induction rate after 6 weeks of culturing (71%) was recorded from TCL of *B. masoniana* ex vitro petiole cultured on MS medium supplemented with 0.25mg/l BA. For shoot multiplication purposes, the in vitro leaf explants grew on MS medium supplemented with 0.4mg/l BA gave the highest shoot induction rate with 72% and 6.76 shoots/explant after 3 weeks. This study is the first step in establishing an efficient method of shoot regeneration through the in vitro culture of *B. masoniana*.

Keywords: Begonia, *Begonia masoniana*, Begonia Iron Cross, Micropropagation.

AP12

Preliminary assessment on chemical composition and investigation on the application for herbal tea of *Launaea sarmentosa* Schultz – Bip.ex Kuntze grown in greenhouse in Dalat

Do Van Duong, Le Thien Hoan, Vo Van Nghia, Hoang Thi Binh*

Faculty of Biology, Dalat University, Lam Dong 66000, Vietnam
**Correspondence author: Hoang Thi Binh, Email: binhht@dlu.edu.vn*

ABSTRACT. The aim of this study is to evaluate the secondary compounds in *Launaea sarmentosa* Schultz-Bip.ex Kuntze grown in greenhouses in Da Lat, and diversify the source of raw materials for making herbal teas. Preliminary survey results on the chemical composition of the aerial parts and roots of plants containing groups of alkaloids, terpenoid-steroids, flavonoids, saponins, cardiac glycosides, tannins and fats, but there's no presence of the sesquiterpene lactone group. Antimicrobial activities of *Launaea sarmentosa* extract were investigated against Gram-negative, positive bacteria and fungi. The results showed that the extracts of *Launaea sarmentosa* were resistant to Escherichia coli, Staphylococcus aureus, Lactobacillus acidophilus and Candida albicans by using disc-diffusion method. In addition, this study created a product of herbal tea and surveyed preferences of consumers for tea mixing ratios and evaluated some physico-chemical criteria of tea quality according to TCVN 7975:2008. The results show that the mixing ratio 4:6 and 6:4 (equivalent to *Launaea sarmentosa* and licorice) are the most popular among consumers, and the herbal tea product mixed from these two ratios achieves the best results and requirements according to TCVN 7975:2008.

Keywords: Chemical composition, Dalat, Herbal tea, *Launaea sarmentosa*, Phytochemical

AP13

Identification of *Ralstonia solanacearum* species complex causing bacterial wilt in tomato in Vietnam

Nguyen Minh Ly[1*], Kieu Duc Toan[1], Mai Xuan Cuong[2]

[1] Faculty of Biology and Environmental Science, The University of Danang - University of Science and Education, Da Nang 550000, Vietnam
[2] Graduate Institute of Biomedical Sciences, Division of Biotechnology, Chang Gung University, Taoyuan 33302 Taiwan
**Correspondence author: Nguyen Minh Ly, Email: nmly@ued.udn.vn*

ABSTRACT. *Ralstonia solanacearum* species complex (RSSC) is the main pathogen causing bacterial wilt disease in tomato plants. This study applied polymerase chain reaction (PCR) with RSSC's specific and multiplex primer pairs to accurately identify RSSC isolates in Vietnam. The results showed that Vietnamese isolates were identified as *R. pseudosolanacearum*, phylotype I. In addition, a colony PCR technique was developed to rapidly detect and select RSSC strains from isolation samples of diseased tomatoes. This method directly used bacterial colonies on the Petri plate as templates to amplify with primers 759/760 and obtained PCR product with the length of 282 base pairs. This is the first study to recognize *R. pseudosolanacearum* as the cause of bacterial wilt disease in tomatoes in Vietnam.

AQ01

The neotenous aquatic duckweeds: Cytogenomics study

Hoang Thi Nhu Phuong[1*], Todd Michael[2], Ingo Schubert[3]

[1]*Faculty of Biology, Dalat University, Lam Dong 66000, Vietnam*
[2] *F J. Craig Venter Institute, Carlsbad, CA 92037, USA*
[3] *Leibniz Institute of Plant Genetics and Crop Plant Research (IPK), Gatersleben, Stadt Seeland D-06466, Germany*
**Correspondence author: Hoang Thi Nhu Phuong, Email: phuonghtn@dlu.edu.vn*

ABSTRACT. Duckweeds are fast growing, free-floating, aquatic, neotenous, mainly asexual monocots on the way becoming crops and show interesting genomic features. There are 36 species belonging to the 5 genera: Spirodela, Landoltia, Lemna, Wolffiella and Wolffia. The genome size of duckweed species has a 14-fold range from 160 Mbp to 1230 Mbp and chromosome number varies from 2n = 20 to 126. We applied sequential multicolor fluorescence in situ hybridization (mcFISH) with 106 BACs together Oxford Nanopore sequencing to validate previous genome maps for *S. polyrhiza* and generate a high-confidence reference genome map of this species. In addition, comparative FISH experiments were performed between *S. polyrhiza* (n=20) and *S. intermedia* (n=18), the only two species in Spirodela genus. With 93 anchored BACs from *S. polyrhiza*, the chromosome homeology between two Spirodela species was investigated and scenarios of karyotype evolution were supposed. Furthermore, cytogenetic map for *S. intermedia* was used as an important anchor point for *S. intermedia* genome assembly with PacBio reads.

Keywords: Antimicrobial, *Dysphania ambrosioides*, essential oil, Lam Dong

AQ02

Morphological variation, chromosome number, and DNA barcoding of Giant Duckweed (*Spirodela polyrhiza*) in Vietnam

Tran Ngoc Bao Tram[1], Tran Thi Nhung[1], Fuchs Jörg[2], Schubert Veit[2],
Schubert Ingo[2] & Hoang Thi Nhu Phuong[1,2*]

[1]*Faculty of Biology – Dalat University, Lam Dong 66000, Vietnam*
[2]*Leibniz Institute of Plant Genetics and Crop Plant Research (IPK), Gatersleben, Stadt Seeland D-06466, Germany*
**Correspondence author: Hoang Thi Nhu Phuong, Email: phuonghtn@dlu.edu.vn*

ABSTRACT. Our present study is the first systematic survey on duckweed biodiversity in Vietnam. More than 100 samples of Spirodela, Lemna, and Wolffia were collected throughout Vietnam and maintained under laboratory conditions. In this report, we focused on studying the morphological variation, chromosome number, and DNA barcoding on Spirodela samples. *S. polyrhiza* and *S. intermedia* are the only two species of Spirodela genus - the most ancient genus among the five duckweed genera. The obtained DNA sequences of atpF- atpH and psbK – psbI regions showed that all 29 Spirodela samples collected from different regions along Vietnam are *S. polyrhiza*. Specific SNPs of individual *S. polyrhiza* clones were identified in the psbK-psbI region. The differences in genome size, frond size, frond shape, and root system among six representative *S. polyrhiza* clones were investigated. The chromosome number of these clones was uniformly 2n=40.

Keywords: Chromosome number, duckweed, DNA barcode, genome size

AQ03

Quality profile of QSU-farm pond irrigation system: Its suitability as irrigation waters

Denson M. Liday, Nobelyn V. Agapito

College of Health Sciences, Quirino State University, Quirino 3401, Philippines
**Correspondence author: Denson M. Liday, Email: densonmarianoliday@gmail.com*

ABSTRACT. The quality of available water must be tested to check its suitability prior to its use. The physicochemical analysis of the QSU-farm pond water system has been done to assess its quality for irrigation needs. The quality analysis was made through the estimation of its temperature, pH, salinity (Total Dissolved Solids and Electrical Conductivity), alkalinity, chloride, hardness, iron, and sulfate as irrigation water criteria. The analytical data were processed and compared with standard permissible limit set for irrigation waters. Regarding the suitability of the farm pond water system for irrigational purposes with the measured quality criteria, the farm pond waters were within the safe limits except for few parameters that did not meet the required irrigation standard limit criteria which need immediate attention. The quality profile results may be used as basis for future management and strategic intervention.

Keywords: irrigation, water quality, salinity, pH, farm pond, hardness, suitability

AQ04

Morphometric and genetic differentiation in *Butis* species in the Mekong Delta, Vietnam

Tran Thi Huyen Lam[1,2], Ton Huu Duc Nguyen[3], Quang Minh Dinh[3*]

[1]Biotechnology Research and Development Institute, Can Tho University,
Can Tho 900000, Vietnam
[2]Institute of High Quality Biotechnology - Food Technology, Cuu Long University,
Vinh Long 85000, Vietnam
[3]Department of Biology, School of Education, Can Tho University,
Can Tho 900000, Vietnam
**Corresponding author: Quang Minh Dinh, Email: dmquang@ctu.edu.vn*

ABSTRACT. The *Butis* genus has a relatively small body size and broad salt tolerance spectrum, and adapts to the environment. The aims of the research are to find out the influence of salinity, pH, and temperature on the morphometries of three *Butis* species, and to identify species and analyze their phylogenetic relationships through the mitochondrial cytochrome b gene (*Cytb*) sequencing. The Principal Component Analysis results showed that salinity was an environmental factor affect sharply on the measurement and meristic ratio of *Butis* species. The population of *Butis* species has nine haplotypes with a haplotype diversity index of 0.67-1.00. *Cytb* gene sequences were rich in %C (30-32%) and low in % G (14-16%). %AT was always higher than %GC while the AT/GC ratio was constant between *Cytb* sequences. The intraspecific genetic distances were 0.001 - 0.005; meanwhile, the interspecific genetic distances were 0.004-0.2001. All *B. koilomatodon* were in clade I along with the in-group control of the phylogeny with a bootstrap value of 69%. *B. humeralis* and *B. butis* were not grouped by species as *B. koilomatodon* but interspersed in the sub-clades of clade II with bootstrap values as high as 100%. Therefore, it was recommended the simultaneous use of mitochondrial DNA and nuclear DNA barcoding along with morphologies to conduct a more precise identification of *B. humeralis* and *B. butis* in further research.

Keywords: *Butis*; genetic distances; mitochondrial cytochrome b gene; phylogeny; salinity.

AQ05

Effect of heavy metals on duckweed growth

Nguyen Duc Thang, Hoang Le Lan Anh, Pham Thi Thanh Van,
Nguyen Minh Tuan, Nguyen Thanh Hang, Nguyen Huu Phuoc,
Huynh Thuy Van Anh, Tran Thi Nhung, Hoang Thi Nhu Phuong*

Faculty of Biology – Dalat University, Lam Dong 66000, Vietnam
**Correspondence author: Hoang Thi Nhu Phuong, Email: phuonghtn@dlu.edu.vn*

ABSTRACT. In this study, three clones of the duckweed genus Lemna, collected from three different regions of Vietnam are Binh Thuan Bac Giang and Ben Tre, were used to evaluate the growth and development in culture medium containing different concentrations of As^{3+}, Cd^{2+} or Pb^{2+}. During 14 days of incubation, the growth of samples was determined daily by measuring the surface area of all plants of each sample. Experimental results show that the optimal concentration of the investigated heavy metals for the three Lemna clones is 0.3-0.5 mg/L for As^{3+}, 0.15-0.3 mg/L for Cd^{2+} and 0.15 mg/L for Pb^{2+}. At these concentrations, the division rate of the treated clones was several times higher than that of the controls. The highest increase in the surface area was recorded for Lemna BTN (68.47 times higher when cultured in medium supplemented in 0.3 mg/L Pb^{2+} than under control conditions). The surface area of Lemna BTR cultured in medium supplemented with 0.3 mg/L As^{3+} was 54.65 times higher than in medium without arsenic. We also showed that Lemna BGG and Lemna BTR potentially accumulate arsenic and cadmium, while Lemna BTN has a high lead accumulation capacity.

Keywords: Aquatic plants, duckweed, heavy metal, Lemna

AQ06

Initial study of *in vitro* propagation of com chay plants (*Sambucus javanica* Blume)

Vo Ngoc Thuy Van[*], Pham Thi Thanh Van, Truong Thi Nha Uyen,
Tran Nguyen Kim Ngan, Mai Thi Thuy

Faculty of Biology, Dalat University, Lam Dong 66000, Vietnam
[*]Corresponding author: Vo Ngoc Thuy Van, Email: 1911352@dlu.edu.vn

ABSTRACT. *Sambucus javanica* Blume (com chay) is a national medicinal material of Vietnam and commercialized in European countries, it has a lot of potential in providing secondary compounds with high medicinal value. This species originated in Lam Dong, but has not been applied much in Vietnam. In vitro propagation is an effective method for increasing the number of plants in a short time. Research shows that treating young leaves with 1% NaClO for 20 minutes is best to create a sterile source of culture for further experiments. To induce scar tissue, culture the sterilized leaf sample on MS medium supplemented with 0, 0.5, 1.0, 1.5, 2.0, 2.5 mg/l 2.4D and placed in the absence of light, the results showed that the rate of inducing scar tissue formation in the 0.5, 1.0, 1.5, 2.0, 2.5 mg/l 2.4D protocols was above 90%. In order to turn on the buds from the scar tissue of the com chay leaves, uniformly transplant the scar sample from the leaves of the com chay plants on MS medium with the addition of 0; 0.5; 1.0; 1.5; 2.0;2.5 mg/l BA, the results show that the concentration of BA surveyed is not suitable for turning on the buds from the scar tissue. This study is an initial step for in vitro material source creation through scar tissue culture of com chay plants.

Keywords: Com chay, *Sambucus javanica* Blume, Micropropagation.

AQ07

Phylogenics of the genus *Glossogobius* in the Mekong Delta based on the mitochondrial Cytochrome b (*Cytb*) gene

Gieo Hoang Phan[1,2], Tran Thi Huyen Lam[2,3], Quang Minh Dinh[4,*],
Ton Huu Duc Nguyen[4]

[1]Department of Molecular Biotechnology, Biotechnology Research and Development Institute, Can Tho University, Xuan Khanh Ward, Ninh Kieu District, Can Tho 900000, Vietnam
[2]Faculty of Agriculture and Rural Development, Kien Giang University, Minh Luong Town, Chau Thanh District, Kien Giang 920000, Vietnam
[3]Institute of High Quality Biotechnology - Food Technology, Cuu Long University, National Road 1A, Phu Quoi Ward, Long Ho District, Vinh Long 850000, Vietnam
[4]Department of Biology, School of Education, Can Tho University, Xuan Khanh Ward, Ninh Kieu District, Can Tho 900000, Vietnam
**Corresponding author: Quang M. Dinh; Email: dmquang@ctu.edu.vn*

ABSTRACT. The *Glossogobius* species play an essential role in food supply and are distributed widely from the marine to freshwater, especially in the Mekong Delta, Vietnam (VMD). Some of their morphometrics and meristics are observed to vary with species and sampling sites. Therefore, the present study aims to verify if their mitochondrial Cytochrome b (*Cytb*) gene, one of the popular gene sequences used in fish phylogenic variation assessment, is changed with species and sampling site in the VMD. The *Cytb* gene size was 1,300 bp for GcytbH/GcytbL primer pair and 1,045 bp for GluMuq1-F/Mixcyto937-2R. The genetic distance within and among these three fish species groups was 0.00-0.17. The *Cytb* gene sequences' similarity between this study and NCBI database was 85.84-100%. The *Glossogobius* specimens were observed to disperse in small branches of the phylogenetic tree with a low p-value, suggesting that the *Cytb* genetic diversity might be low among species. Therefore, a combination of morphology and DNA barcodes using *Cytb* or marker gene marker is required for accurate classification.

Keywords: *Cytb*; genetic distance; phylogeny; *Glossogobius aureus*; *Glossogobius giuris; Glossogobius sparsipapillus*

AN01

Histopathological characteristics of striped catfish (*Pangasianodon hypophthalmus*) in challenge with *Edwardsiella ictaluri*

Luu Tang Phuc Khang[1*], Nguyen Huu Giau[2], Tran Thi Phuong Dung[1]

[1]Ho Chi Minh City University of Education, Ho Chi Minh 700000, Vietnam
[2]SaiGon University, Ho Chi Minh 700000, Vietnam
**Corresponding author: Luu Tang Phuc Khang, Email: ltpkhcmue@gmail.com*

ABSTRACT. The present study attempted to understand the histopathological index of striped catfish (*Pangasianodon hypophthalmus*) in challenge with Edwardsiella ictaluri, the causative agent of bacillary necrosis of Pangasius. Total of 355 healthy striped catfish juveniles was challenged with E. ictaluri (25 control; 330 infected). After challenge, total of 355 samples of the trunk kidney, liver and spleen were collected at five different time points including just prior to infection, 24, 48, 264 and 312 hours post infection (hpi) to measurements the represented tissue damage of the fish. Results showed that many areas of diseased liver, kidney, and fish organ tissues have been congested and hemorrhaged early at 24 hpi. The number of macrophage centers in kidney and spleen increased at 24 - 48 hpi. Tissue damage (multifocal hemorrhages; necrosis) increased sharply from the period 48 - 256 hpi. The increased number of dead fish throughout the duration of infection, particularly the period from 48 to 200 hpi. At 312 hpi, the histopathological index was highest, so the mortality rate was the highest during the experimental period.

Keywords: *Edwardsiella ictaluri*, disease resistance, histopathology characteristics, striped catfish,tissue damage measurement.

AN02

Cattle fetal sex determination using cell free fetal DNA from maternal blood in the Mekong Detla, Vietnam

Tran Thi Thanh Khuong[1*] Nguyen Dang Khoa[1,4], Nguyen Van Loi[1],
Tran Van Be Nam [1], Tran Gia Huy[1], Lam Phuoc Thanh[2], Cao Thi Tai Nguyen[3]

[1] Biotechnology Research and Development Institute, Can Tho University, Can Tho 900000, Vietnam
[2] Department of Animal Sciences, College of Agriculture, Can Tho University, Can Tho 900000, Vietnam
[3] Biology Genetics Department, Faculty of Basic science, Can Tho University of Medicine and Pharmacy, Can Tho 900000, Vietnam
[4]Department of Life Science in Dentistry, School of Dentistry, Pusan National University, Yangsan 50612, Republic of Korea
**Corresponding author: Tran Thi Thanh Khuong, E-mail: tttkhuong@ctu.edu.vn*

ABSTRACT. At around 5 weeks of pregnancy, cell-free fetal DNA (cffDNA) is identified in the maternal plasma of pregnant cows, accounting for around 10% of the total. Currently, cffDNA is being used as a non-invasive prenatal screening technique for aneuploidy, genetic disorders in humans, early pregnancy diagnosis, and animal fetal sex determination. The goal of this study was to determine the presence of cffDNA in the blood of 13 dairy cows (11 pregnant, 2 non-pregnant, and 1 unmarred) gathered from farms in Can Tho, the Mekong Delta, Vietnam. Plasma/Serum cfc-DNA Purification Midi Kit (Product # 55600) was used to separate CffDNA, and two PCR designed primers named SRY-137 and GAPDH-109, were employed to amplify the Y-chromosome-specific sequences SRY and the housekeeping gene GAPDH, respectively. The fetal sex indicated by PCR data corresponded to the calf's sex at birth in 11 cases. The study's findings first proved the existence of cell-free fetal DNA circulating in the plasma of a pregnant cow in Vietnam, and establishing the calf's sex using simple, high-precision procedures. The use of cffDNA for sex screening brings up the possibility of quickly determining gender and screening for genetic diseases in a big herd of cattle and animals with long gestation periods.

Keywords: Cell free fetal DNA, Dairy cow, Plasma, PCR, SRY, NIPT.

AN03

Effect of oil supplementation on intake, milk yield and composition of dairy cows

Lam Phuoc Thanh[1]*, Pham Truong Thoai Kha[1], Nguyen Thi Thu Ha[1],
Duong Tran Tuyet Mai[1], Mai Hoan Tu[1], Tran Thi Thuy Hang[2]

[1]Department of Animal Sciences, College of Agriculture, Can Tho University, Can Tho 900000, Vietnam
[2]Department of Agricultural Technology, College of Rural Development, Can Tho University, Hau Giang 910000, Vietnam
**Corresponding author: Lam Phuoc Thanh, Email: phuocthanh@ctu.edu.vn*

ABSTRACT. Supplementation of oils rich in polyunsaturated fatty acids and condensed tannin has been known as a feeding approach to improve healthy fatty acids in ruminant milk, but it can cause an adverse effect on intake and animal performance. This study aimed to investigate the effect of feeding oil alone or in combination with grape seed tannin extract (GSTE) on feed intake, milk yield and composition of dairy cows. Sixteen low production dairy cows in mid-lactation fed a basal diet based on agro-industrial by-products were arranged to a completely randomized design for a 6-week duration. Animals were fed basal diet without oil and GSTE inclusion (CON), 2.5% DM soybean oil (SBO), 2.5% DM blend of soybean oil and tuna fish oil at 3:2 w:w (SFO), or SFO plus 0.4% DM GSTE (OCT). The results showed that DM intake was reduced ($P<0.05$) by 14.4% in OCT relative to CON. Milk yield was not affected by oil and GSTE supplementation, but SFO and OCT strongly depressed milk fat, protein and total solids ($P<0.001$). In conclusion, in a low production cow diet based on agro-industrial by-products containing high lipid, supplementation of oil and GSTE should be consider in the aspects of intake and milk composition.

Keywords: Dairy cows, feed intake, grape seed tannin extract, milk yield, milk composition, oil

AN04

Effects of oil and grape seed tannin extract on intakes, digestibility, milk yield and composition of Saanen goats

Nguyen Thi Thu Ha[1], Duong Tran Tuyet Mai[1], Tran Thi Thuy Hang[2],
Lam Phuoc Thanh[1*]

[1]*Department of Animal Sciences, College of Agriculture, Can Tho University, Can Tho 900000, Vietnam*
[2]*Department of Agricultural Technology, College of Rural Development, Can Tho University, Can Tho 900000, Vietnam*
**Corresponding author: Lam Phuoc Thanh, Email: phuocthanh@ctu.edu.vn*

ABSTRACT. An experiment was conducted as a 4×4 Latin square design using 4 lactating Saanen goats, 19 months old and 47.9±1.04 kg of body weight, to evaluate the effect of oil and grape seed tannin extract (GSTE) supplementation on feed intake, digestibility, milk yield and milk composition. Each experimental period lasted for 21 days including 16 days for adjustment and 5 days for sampling. Goats were fed a control diet (Ctrl) consisting of 60% concentrate and 40% fresh Para grass (dry matter, DM, basis) while other 3 treatments were supplementation of 2.5% soybean oil (SO); 2.5% soybean oil + tuna fish oil at 3:2 w:w (SFO); 2.5% soybean oil + tuna fish oil at 3:2 w:w + 0.8% GSTE (OCT). The results showed that oil and GSTE did not affect feed intake, digestibility, milk yield and composition of goats ($P>0.05$). However, digestibility of EE was higher ($P<0.05$) in SFO and OCT diets (85.4% and 84.7%, respectively) compared to Ctrl (76.2%). Combined data suggested that adding 2.5% DM soybean oil alone or a mixture of soybean oil and tuna fish oil with or without 0.8% DM GSTE to the diet is a potential solution to improve the content of beneficial fatty acids in milk without negative effect on intake, digestibility and performance of dairy goats.

Keywords: Digestibility, grape seed tannin extract, milk composition, milk yield, oil

AN05

Impact of heat stress on blood physiological parameters, body temperature, respiratory frequency, antioxidant status, and carcass quality as well as production performance and egg quality of Japanese quails

Nguyen Thi Kim Khang[1], Ngo Thị Minh Suong[2], Masashi Takahashi[3]

[1] *Associate. Professor, College of Agriculture, Can Tho University,*
Can Tho 900000, Vietnam
[2] *Doctor, College of Agriculture, Can Tho University, Can Tho 900000, Vietnam*
[3] *Professor, Dept. of Animal Science, Hokkaido University, Hokkaido 7848, Japan*
**Corresponding author: Nguyen Thi Kim Khang, Email: ntkkhang@ctu.edu.vn*

ABSTRACT. The study was performed with three experiments. The first experiment studied respiratory rate (RR), body temperature (BT), blood physiological parameters (BPP), serum antioxidant enzyme activities (SAEA), and meat quality of 240 quails under three temperatures (38°C, 25°C, and Et-30°C) and two bodyweights (heavy and lighter). Heat stress (HS) increased RR and BT of quails but had no effect on BPP; SOD activity was decreased in group 38°C ($P<0.05$) and a trend of increasing GSH – Px was also observed in group 38°C ($P=0.06$); meat quality was not affected by HS except yellow index of meat color was increased ($P<0.05$). The second experiment was conducted with 168 quails (experiment 1) to record reproductive performance and egg quality. HS affected negatively feed intake, egg weight, egg height, albumen height, yolk weight, yolk color, and Haugh unit ($P<0.05$). The third experiment was performed to evaluate the effect of HS on growth and reproductive performance, and SAEA of the first generation (G1) from 84 quails (experiment 2). Feed intake, weight gain, and feed conversion ratio in 38°C H - G1 quail line were not significantly different from other groups. The higher egg weight and egg production were discovered in heat-stressed G1 groups. The lowest value of SOD and GSH - Px was reported in 38°C H – G1 quail line but no different in CAT ($P>0.05$). The 38°C – G1 quail groups adapted to HS from G0 by expanding feed intake at the growing phase, improving egg weight and egg production, and maintaining the low SAEA.

Keywords: heat stress, quail, growth performance, reproductive performance, antioxidant enzyme

AN06

Prevalence of antibiotic resistance genes and genetic relationship of *Escherichia coli* serotype O45, O113, O121, and O157 isolated from cattle in the Mekong Delta, Vietnam

Nguyen Khanh Thuan*, Nguyen Thanh Lam, Nguyen Tran Phuoc Chien,
Nguyen Phuc Khanh, Ly Thi Lien Khai, Tran Ngoc Bich

Department of Veterinary Medicine, College of Agriculture, Can Tho University,
Can Tho 900000, Vietnam
** Corresponding author: Nguyen Khanh Thuan, Email: nkthuan@ctu.edu.vn*

ABTRACT. A total of 39 *Escherichia coli* strains serotype O45, O113, O121, and O157 isolated from cattle in the Mekong Delta were examined the antimicrobial susceptibility to 13 antibiotics by the disc-diffusion method. Those strains were also analyzed for the presence of antibiotic resistance genes by PCR assay, and their genetic relationship by ERIC-PCR assay. The results of antimicrobial susceptibility testing showed that those strains were sensitive to most of the examined antibiotics, but were relatively high resistance to ampicillin (64.10%), and colistin (53.85%). Those *E. coli* strains could be resistant against one to eight antibiotics with 22 resistance patterns obtained. Moreover, those *E. coli* strains harbored one to seven antibiotic resistance genes. Gene *tetA* (51.28%) and bla_{ampC} (48.72%) were detected frequently while gene *tetB*, bla_{CMY}, and *cat1* were not found in those *E. coli* strains. A total of 21 combined patterns of antibiotic resistance genes were recorded, and the most frequent combined pattern was bla_{ampC}+*tetA* (12.82%). ERIC-PCR analysis revealed that each *E. coli* serotype exhibited various genetic patterns with 40%-100% of similarity. The most elevated number of patterns were in *E. coli* O157 (nine patterns), followed by *E. coli* O121 (six patterns). The prevalence of antibiotic resistance genes and diverse genetic characteristics in those *E. coli* strains originated from cattle constitute potential risks to local health in the Mekong Delta.

Keywords: antibiotic susceptibility, cattle, *E. coli*, genes, genetic relationship

AN07

Effects of organic acid and garlic powder supplementations in the diet on growth and intestinal microflora of the exotic Tam Hoang chickens

Nguyen Thi Thuy[1*], Le Thanh Phuong[2] and Nguyen Cong Ha[3]

[1]Department of Animal Sciences, College of Agriculture, Can Tho University,
Can Tho 900000, Vietnam
[2]Vietswan Poultry Production Joint Stock Company, Binh Duong 820000, Vietnam
[3]Department of Food Technology, College of Agriculture, Can Tho University,
Can Tho 900000, Vietnam
**Corresponding author: Nguyen Thi Thuy, Email: nthithuycn@ctu.edu.vn*

ABSTRACT. An experiment (Exp) was carried out to evaluate the effect of organic acid (OG) and garlic powder (GP) in diets on growth performance, intestinal microflora and carcass quality of the exotic Tam Hoang chickens. The experiment was conducted in a completely randomize design with 3 treatments and 4 replications, each replication was a pen (20 chickens/pen), males and females were raised separately. Each treatment included 2 male and 2 female pens as replications. The control treatment (Cont) was basal diet (BD) without any supplementation; the organic acid supplemented treatment (OG) was BD + 1g Poulacid /kg feed; and the garlic powder treatment (GP) was BD + 1 g garlic powder/kg feed. Results showed that chickens fed Cont diet (1451 g /head) had lower final live weight than that in OG (1568 g/head) and GP (1521 g/head/day). So, the average daily gain (ADG) of chickens in Cont (16.8 g/head/day) and GP (17.7 g/head/day) were lower than in OG (18.2 g/head/day). However, average daily feed intake (ADFI) was not significant different in supplemented diets to compare with control diet. Therefore, feed conversion ratio (FCR) of chickens fed OG (3.04 kg feed/kg gain) was better than that in Cont (3.32 kg feed/kg gain). The density of *Salmonella* bacteria were not detectable in chicken feces at 4th weeks age, but get positive in Cont and GP treatments at 10th weeks age. However, supplementation of organic acid and garlic powder reduced *E. coli* and *Clostridium perfringens* in the feces of Tam Hoang chickens compared to control chickens at both 4th and 10th weeks age. In conclusion, adding organic acid (Poulacid) or garlic powder at the same dose (1g/kg feed) in Tam Hoang chicken diets tended to improve average daily gain, feed conversion ratio, and reduce *E. coli* and *Clostridium perfringens* density in the feces compared to control chickens.

Keywords: Organic acid, Garlic powder, Tam Hoang chicken, Salmonella, *E. coli*, *Clostridium perfringens*

AN08

Detection of Japanese encephalitis virus and its specific antibody in abnormal swine litters in Viet Nam

Ho Thị Viet Thu[1*], Huynh Ngoc Trang[1], Nguyen Duc Hien[1,2,*]

[1]*Department of Veterinary Medicine, College of Agriculture, Can Tho University, Can Tho 900000, Vietnam*
[2]*Department of Animal Health of Can Tho City, Can Tho 900000, Vietnam*
**Corresponding author: Nguyen Duc Hien, Email: ndhien@ctu.edu.vn*

ABSTRACT. Japanese encephalitis is considered an important disease-causing swine reproductive failure in Asian countries; however significant knowledge gaps remain about this problem in actual cases. In this study, 55 cases of reproductive failure in sows including 1 abortion and 54 full-term farrowing litters were examined to find Japanese encephalitis virus (JEV) and specific antibodies against JEV. Haemagglutination test was used to detect specific antibodies against JEV from 63 samples of fetal thoracic fluids and newborn un-suckling piglet sera (54 thoracic fluid samples of dead fetuses, 2 thoracic fluid samples of abortion fetuses, 7 sera samples of weakly newborn un-suckling piglets), viral isolation and RT- PCR technique were attempted from 60 brains of fetuses and newborn un-suckling piglets, histopathology sections of fetal brains which were positive with JEV confirmed by HI test and RT-PCR were also made. The results showed that 17.46% (11/63) of thoracic fluids and sera were positive for JEV. No JEV isolation was found from 60 brain samples of dead fetuses and piglets but RNA of JEV were detected from 5 of them (8.33%). Our results suggest that JEV should be considered to be the important cause of swine reproductive failure in Viet Nam.

Keywords: Japanese encephalitis virus, reproductive failure, pigs, Viet Nam

AN09

The prevalence and associated risk factors of *Spirocerca lupi* in domestic dogs in Mekong Delta of Vietnam

Tran Nguyen-Ho-Bao[1*], Chuc Thi Nguyen[2], Bang Phi Nguyen[3],
Hung Huu Nguyen[1]

[1] Department of Veterinary Medicine, College of Agriculture, Can Tho University,
Can Tho 900000, Vietnam
[2] College of Applied Biology, Tay Do University, Can Tho 900000, Vietnam
[3] An Giang University, Viet Nam National University Ho Chi Minh 700000,
Ho Chi Minh City, Vietnam
**Correspondance author: Tran Nguyen-Ho-Bao, Email: nhbtran@ctu.edu.vn*

ABSTRACT. Spirocercosis is caused by *Spirocerca* spp., which is a chronic disease and might cause life-threatening due to forming cancer in oesophagus in canid carnivores. There are limited studies involving spirocercosis in domestic dogs. Thus, this study aims to investigate the prevalence and analyse risk factors associated with the *Spirocerca lupi* infection in Mekong Delta- Vietnam. A total of 400 fecal samples from domestic dogs were collected from May 2020 to May 2021. The overall prevalence of spirocercosis in domestic dogs in the Mekong Delta was 10.50% by copromicroscope and PCR methods. PCR targeted to the housekeeping gene cytochrome c oxidase I (*cox-1*) was applied to identify species of *Spirocerca* spp. and analyse the phylogenetic tree. Outdoor dogs had 5.487 times (CI 95% = 2.446-11.69, $p < 0.0001$) higher risks of *S. lupi* infection compared to indoor dogs. Besides, seasons and age showed a correlation to the increase in the risk of *S. lupi* infection, while neither dog breeds nor gender influenced the prevalence of this species. The cytochrome c oxidase I (*cox-1*) gene sequence of *S. lupi* in the Mekong Delta showed the high homologues to the *S. lupi* isolates in India, Israel, and the south of Vietnam and belonged to the *S. lupi* genotype 2.

Key words: Cox-1, Mekong Delta, prevalence, risk factors, *Spirocerca lupi*

AN10

The effects of banana flower powder and sodium bicarbonate supplementation on intakes, weight gain and ruminal function in Boer crossbred male goats

Nguyen Thiet[1*], Nguyen Trong Ngu[2] and Sumpun Thammacharoen[3]

[1]Department of Agricultural Technology, College of Rural Development,
Can Tho University, Can Tho 900000, Vietnam
[2]Department of Animal Science, College of Agriculture, Can Tho University,
Can Tho 900000, Vietnam
[3]Department of Physiology, Faculty of Veterinary Science, Chulalongkorn
University, Bangkok 10330, Thailand
**Corresponding author*: *Nguyen Thiet, Email: nthiet@ctu.edu.vn*

ABSTRACT. This experiment aimed to evaluate the effects of banana flower powder (BFP) and sodium bicarbonate ($NaHCO_3$) supplementation on intake, weight gain, ruminal function, and blood electrolytes in Boer crossbred male goats. The experiment was arranged completely randomized with three treatments, a control group (control), a supplement with 4.5% banana flower powder (BF4.5), and a supplement with 4.5% $NaHCO_3$ (Na4.5), with 5 replicates. The results show that DMI, WI, and weight gain from Na4.5 were higher than those from BF4.5 and control groups ($p<0.05$). In addition, goats from Na4.5 and BF4.5 increased ruminal pH, whereas NH_3-N level was similar to among treatments. There were no effects of BFP and $NaHCO_3$ supplementation on body weight and the levels of plasma electrolytes ($p>0.05$). The results from this study indicated that BFP and $NaHCO_3$ have the same effect on ruminal function.

Key words: goats, plant mineral, production, ruminal function.

AN11

Detection of novel transcripts and evaluation of expression levels of *Igf2* in mouse placenta

Van Giang Tran[1*] and Guy Cathala[2]

[1]University of Education, Hue University, Hue 530000, Vietnam
[2]Institut of Genetique Moleculaire in Montpellier, UMR 5535 CNRS-Montpellier II University, Montpellier 34090, France.

** Corresponding author: Van Giang Tran, Email: tranvangiang@dhsphue.edu.vn, tvgiang@hueuni@edu.vn.*

ABSTRACT. The imprinted *Igf2* gene (Insulin-like growth factor 2) encodes a growth factor that plays an important role in the formation of the placenta and embryonic development. This study results showed that several new transcripts of the *Igf2* gene were detected in the placenta of mice, and the new promoter in the placenta P0L and PU2 were found. Expression levels of these promoters as well as of the *Igf2* gene were evaluated in the placentas of mice. The expression levels of these two promoters were investigated in different tissues; P0L is very well expressed in the brain and is clearly expressed in the placenta, tongue, and kidney; P0 is well expressed in the placenta, but also in the kidney and heart; PU2 is expressed in addition to the placenta, tongue, and muscles.

Keywords: Gene expression, placenta, *Igf2*, promoter

AN12

Effect of fluoxetine on cyclic adenosine monophosphate response to follicle-stimulating hormone in HEK cells

Nguyen Thi Tho, Thi Mong Diep NGUYEN[*]

Faculty of Natural Sciences, Quy Nhon University, Binh Dinh 55000, Vietnam
**Corresponding author: Thi Mong Diep NGUYEN,*
Email: nguyenthimongdiep@qnu.edu.vn

ABSTRACT. Fluoxetine is an antidepressant that acts as a selective serotonin reuptake inhibitor. Fluoxetine has exhibited different mechanisms of action on many different cell lines. In this study, the effect of fluoxetine on cAMP production in human embryonic kidney (HEK) cells under the stimulation of bovine follicle-stimulating hormone were examined. HEK cells were incubated for 60 minutes with fluoxetine at different concentrations (0, 12.5, 25 and 50µM), and then cAMP accumulation, ATP level, and AMPK phosphorylation and cell viability were tested. Our results showed that fluoxetine at 25 and 50 µM attenuated cAMP levels in cells after bFSH stimulation. The depletion of cAMP at this concentration is accompanied by a decrease in ATP energy and an increased capacity to phosphorylate AMPK. As such, this study showed that fluoxetine induces a reduction in cAMP accumulation and that it is associated with the AMPK pathway in HEK cells.

Keywords: Adenyl cyclase, adenosine triphosphate, AMPK, cyclic AMP, fluoxetine

AN13

Natural and recombinant equine chorionic gonadotropins past and future in animal reproductive technology

Duong Tien Thach[1,5], Bui Khac Cuong[2], Hoang Van Tong[3], Vo Van Chi[1],
Ngo Kim Khue[1], Nguyen Thi Phuong Hien[1], Nong Van Hai[4,5],
Yves Combarnous[6], Thi Mong Diep Nguyen[1*]

[1]Faculty of Natural Sciences, Quy Nhon University, Binh Dinh 55000, Vietnam
[2]Laboratory Animal Research Center, Vietnam Military Medical University,
Ha Noi 100000, Vietnam
[3]Institute of Biomedicine and Pharmacy, Vietnam Military Medical University,
Ha Noi 100000, Vietnam
[4]Institute of Genome Research, Vietnam Academy of Science and Technology,
Ha Noi 100000, Vietnam
[5]Graduate University of Science and Technology, Vietnam Academy of Science and
Technology, Ha Noi 100000, Vietnam
[6]INRAe, CNRS, Tours University Joint Unit, Physiologie de la Reproduction et des
Comportements, Nouzilly 37380, France
** Corresponding author: Thi Mong Diep Nguyen, Email:*
nguyenthimongdiep@qnu.edu.vn

ABSTRACT: Equine Chorionic Gonadotropin (eCG) previously named Pregnant Mare Serum Gonadotropin (PMSG) has been widely used since the ‘40s in animal reproduction control. It is extracted from the blood of pregnant mares between days 40 and 120 of gestation. Animal welfare organizations have voiced concerns against mares bleeding conditions. There is currently no effective substitute for the natural PMSG. In this review, we summarize the basic knowledge of the structure and biology of eCG, and the research on recombinant eCG production in the past five years.

AN14

Procedure for performing a fixed microscopic specimen of the gonads of fish

Ton Huu Duc Nguyen, Quang Minh Dinh*

Department of Biology, School of Education, Can Tho University,
Can Tho 900000, Vietnam
** Corresponding author: Quang Minh Dinh, Email: dmquang@ctu.edu.vn*

ABSTRACT. This study aims to provide a procedure for performing microscopy in fish gonads. Specimens used in this study were the ovaries and testes of fish collected in the Mekong Delta from April to July 2022. Organs at five different stages for each sex (ovary diameter from 1.16 cm in stage I to 4.04 cm in stage V; testis diameter from 0.42 in stage I to 2.39 in stage V) were studied in this procedure. The results showed that both ovaries and testes needed to be fixed at 4% formol for 24 h and under running water for eight hours. Ovaries and testes were then immersed in 500 ethanol for 24 h to initiate dehydration. Results showed that the time for dehydration and paraffin infiltration was longer in the ovary (26 to 55 h across stages) than in the testis (25 to 26 h across stages). The mean staining time of the ovary was 1.5 min (stage I) to 3.5 min (stage V) in Hematoxylin and 50 s (stage I) to 140 s (stage V) in Eosin. Whereas the staining time of testis was shorter, 1 min (stage I) to 3 min (stage V) in Hematoxylin and 30 s (stage I) to 90 s (stage V) in Eosin. This study provides a reference for further studies on the histological structure of fish gonads. These results could be applied to fish species inside and outside the Mekong Delta.

Keywords: histology, testis, ovary, Hematoxylin, Eosin

AN15

Semi-chronic toxicity study in mice of the extracts from dau Ha Chau (*Bauccaurea ramiflora* Lour.) fruit of Vietnam

Nguyen Hong Xuan[1,2*] and Nguyen Cong Ha[1]

[1]*Food Technology Department, Institute of Food and Biotechnology, Can Tho University, Can Tho 900000, Vietnam*
[2]*Food Technology Department, Faculty of Biological, Chemical and Food Technology, Can Tho University of Technology, Can Tho 900000, Vietnam*
**Correspondence author: Nguyen Hong Xuan, Email:nhxuan@ctuet.edu.vn*

ABSTRACT. This study evaluated of the semi-chronic toxicity of seed, peel and pulp extracts from dau Ha Chau fruit in Swiss albino mice. The ethanolic extract from peels and seeds as well as fruit juice from squeezing pulp were dried under vacuum to obtain the crude extracts. The distilled water (control group) or these extracts at daily dose of 400 mg/kg of body weight were inserted directly into the stomach of each mouse for 90 days. The mice were observed for toxicity signs, external morphological features of organs and histopathology after 45 and 90 days' treatment. The results revealed that there were no toxicity signs and statistically significant difference in body weight gain, ratio of organ weight to body weight and blood glucose level at 45 days of treatment. At 90 days of treatment, the similar results were observed, except the ratio of kidney weight to body weight siginficantly increased in peel extract mouse group as compared to the control. The semi-chronic toxicity assessment showed that DHC seed and pulp extracts were safe at daily dose of 400mg/kg for 90 days in mice, and DHC peel extract was safe as orally administered for a period of 45 days.

Keywords: dau Ha Chau, fruit composition, morphological feature, histopathological study, semi-chronic toxicity

AN16

Sex discrimination based on morphological traits in *Mystus mysticetus* Roberts, 1992

Thu Quynh Phan, Anh Ngoc Tran, Lam Thi Thao Vo, Quang Minh Dinh*

Department of Biology, School of Education, Can Tho University,
Can Tho 900000, Vietnam
**Correspondence author: Quan Minh Dinh, Email: dmquang@ctu.edu.vn*

ABSTRACT. This study supplemented the way of sex determination of fish based on the regression relationship of some morphological indicators of *Mystus mysticetus*. A total of 425 fish specimens were collected by trawl nets at Cai Rang - Can Tho and Long Phu - Soc Trang from January to July 2022. After collection, the fish were transferred to the laboratory to determine their total length (*TL*), standard length (*SL*), eye diameter (*ED*), eye distance (*DE*), body height (*BD*), head length (*HL*), and mouth width (*MD*) before anatomy for sex determination based on gonads. The regression analysis results of *TL-SL, TL-ED, TL-DE, TL-BD, TL-HL,* and *TL-MD* showed that *SL, DE,* and *MD* could be used to determine the sex of this fish species because *SL* and *DE* were dominant in growth in males, and *MD* was prevalent in females. In addition, SL could be used to determine the sampling time and HL to determine the distribution environment.

Keywords: Fish body height, Fish head length, Mekong Delta, *Mystus mysticetus*

AN17

Morphometrics allometry changes and sexual dimorphism in *Caragobius urolepis* (Gobiiformes: Gobiidae)

Phuc Le Hoang Nguyen, Ly Thi Cam Tran, Thu Thi Anh Phan,
Thoai Kim Nguyen, Lam Thi Thao Vo, Quang Minh Dinh*

Department of Biology, School of Education, Can Tho University,
Can Tho 900000, Vietnam
**Correspondence author: Quan Minh Dinh, Email: dmquang@ctu.edu.vn*

ABSTRACT. The present study reported an alternative way of sex-determining for scaleless worm goby *Caragobius urolepis* based on the regression relationship of some morphological parameters. A total of 328 samples were collected at the trawl nets in two coastal regions in Bac Lieu and Ca Mau from April to August 2022. After collection, the samples were transported to the laboratory in order to measure the total length (*TL),* body height (*BD),* head length *(HL*), the distance of eye *(DE),* and mouth width *(MD)* before surgery for accurate sex determination based on gonads. Regression analysis results of *TL-BD* (growth pattern A+ in females and I in males), *TL-HL* (growth pattern A+ in females and A- in males), and *TL- MD* (growth pattern A- in females and A+ in males) could be used to determine the sex of this fish. Moreover, *TL-DE* and *TL-BD* could be used to estimate when the samples were collected, e.g., in the dry or wet season, because *DE* and *BD* displayed A+ in the wet season but A- in the dry one. The findings could be used as an alternative way to determine fish sex and catching season for this species and others in the Mekong Delta.

Keywords: *Caragobius urolepis*, Mekong Delta, regression relationship, sex discrimination

GE01

The chromosome numbers of *Panax vietnamensis* Ha et Grushv

Dinh Xuan Tu[1], Le Huynh Thi Diem Suong[3], Nguyen Minh Ly[2*]

[1]Incubation and Support Center for Technology and Science Enterprises – Ministry of Science and Technology, Da Nang 550000, Vietnam
[2]Faculty of Biology and Environment Science, The University of Danang – University of Education and Science, Da Nang 550000, Vietnam
** Correspondence author: Nguyen Minh Ly, Email: nmly@ued.udn.vn*

ABSTRACT. The somatic chromosome number of *Panax vietnamensis* Ha et Grushv. was determined to be 2n = 24, based on the hypotonic shock method by potassium chloride solution. In this study, we investigated the effect of potassium chloride and colchicine solutions on chromosome dispersion of Panax vietnamensis at different concentrations. The treatment using 0.2% KCl solution in 45 minutes combined with 0.05% colchicine solution in 2 hours subsequently resulted in proper hypotonia. The result showed that chromosomes were evenly dispersed. The hypotonic shock method seemed to be effective in equally distributing chromosomes. The result can be applied in cell genetic studies and selective breeding programs for *Panax vietnamensis*.

Keywords: hypotonic shock, potassium chloride, colchicine, chromosome, *Panax vietnamensis*.

GE02

Creation of Variation through *In-vitro* Mutagenesis using *Gamma* radiation in Rose (*Rosa hybrida* L.) Variety 'Lửa'

Le Nguyen Lan Thanh[1*], Nguyen Van Son[2] and Le Van Hoa[3]

[1] Vegetables, Flowers and Ornamental Division, Southern Horticultural Research Institute, Tien Giang 860000, Vietnam
[2] Agronomy Division, Southern Horticultural Research Institute, Tien Giang 860000, Vietnam
[3] College of Agriculture, Can Tho University, Can Tho 900000, Vietnam
**Correspondence author: Le Nguyen Lan Thanh, Email: lnlanthanhsofri@gmail.com*

ABSTRACT. *Rosa hybrida* L. cv. Lửa has been one of the most important roses for a long time and is most often used for ornamental purposes in Sa Dec city, Dong Thap province. The study aimed to induce variation through in- vitro gamma radiation in the rose variety 'Lửa' for further improvement in rose breeding in Dong Thap province. In-vitro single node cuttings (25 in vitro cuttings per treatment with four replications) were irradiated with different doses of γ-rays (0, 5, 10, 15, 20, 25 or 30 Gy) using a ^{60}Co source (India) at Da Lat Nuclear Research Institute. The γ-irradiated explants were then cultured aseptically on Murashige and Skoog's basal medium supplemented with 1.0 mg/L BAP to induce sprouting, shoot proliferation and acclimatization at Division of Vegetables, Flowers and Landscaping of Southern Horticultural Research Institute (SOFRI). The results showed that these doses affected the multiplication rate, growth in-vitro and ex-vitro survival rate. The LD_{50} dose was determined to be 20 - 25 Gy treatments. In-vitro proliferated cultures and non-irradiated (control) plants were transferred to plastic pots 1 month after acclimatization under laboratory conditions and examined for their morphological traits. Three types of flower color mutants with altered or novel flower color in comparison to original flower clolor were isolated. The flower color of plants were different with control plants such as 0.5-8 with orange-pink (Red 52C), 1.5-79H with pink (Red 54B) and 1.5-79H with Red 45AB with Red 54B bicolor.

Keywords: gamma radiation, *in vitro*, mutagenesis, *Rosa hybrida*, variation

GE03

Lithocarpus encleisocarpus (Korth.) A. Camus a newly recorded from Vietnam and its phylogenetic relationship based on genome-wide SNPs

Nguyen Van Ngoc*, Hoang Thi Binh

Faculty of Biology, Dalat University, Lam Dong 66000, Vietnam
**Correspondence author: Nguyen Van Ngoc, Email:ngocnv@dlu.edu.vn*

ABSTRACT. A newly recorded *Lithocarpus* (Fagaceae) species for the flora of Vietnam, namely *Lithocarpus encleisocarpus* (Korth.) A.Camus was reported in this study. This species is most morphologically similar to *L. dahuoaiensis* Ngoc & L.V. Dung in having completely entire leaf margin, solitary cupule, long stalks of fruits, deeply cup-shaped or turbinate cupules, with a number of horizontal filiform lines, but it differs from the latter by having cupules almost completely covering the nut, surface of the cupule densely fulvous tomentose by stellate hairs, secondary veins 8-10 pairs. This study provides the phylogenetic relationship of *L. encleisocarpus* with its close species based on genome-wide SNPs. Taxonomic treatment, photographs, information on distribution and habitat, and the GenBank accession number for DNA barcodes of the species are also provided.

Keywords: Fagaceae, Flora, Lam Dong, MIG-seq, NGS

GE04

Diversity of medicinal plant resources in Lai Son island, Kien Giang province

Nguyen Trong Hong Phuc[1], Hu Thi Phi Yen[2], Dang Minh Quan[1]

[1]Department of Biology, School of Education, Can Tho University,
Can Tho 900000, Vietnam
[2]Derparment of Biology, College of Natural Sciences, Can Tho University,
Can Tho 900000, Vietnam
**Correspondence author: Dang Minh Quan, Email: dmquan@ctu.edu.vn*

ABSTRACT. This study was conducted with the aim of assessing the diversity of medicinal plants in Lai Son Island, Kien Giang province, that is as a scientific basis for more effectively using, managing, and preserving this medicinal plant resource in this province. In this study, the PRA (Participatory Rural Appraisal), field investigation, morphological comparison and classification, with the aid of specialized medicinal plant books were used. The results showed a total of 353 species of medicinal plants belonging to 264 genera of 112 families in 4 divisions. Among them, Magnoliophyta was the most diverse division with 94.90% % species, 95.08% genera, and 90.18% families. Seven species were listed in "Red List of Vietnamese medicinal plants" (2006), "Vietnam Red Book" (2007), and the Decree 06/2019/ND-CP. The medicinal plant species were divided into ten life forms and distributed in six biotopes. The most species diversity was recorded in the natural forest on rocky mountain biotope. Ten parts of plants were used to medicate for 36 disease types. Twenty-four species were commonly used by local people.

Keywords: Biotope, diversity, medical plant, Lai Son island of Kien Giang province

GE05

Prevalence of Marek’s disease virus in unvaccinated healthy backyard chickens in Cantho city, Vietnam and genetic characterization of *meq* gene

Huynh Ngoc Trang, Nguyen Tran Phuoc Chien, Ho Thị Viet Thu*

Department of Veterinary Medicine, College of Agriculture, Can Tho University,
Can Tho 900000, Vietnam
**Corresponding author: Ho Thị Viet Thu, Email: htvthu@ctu.edu.vn*

ABSTRACT. An investigation was carried out to survey the prevalence of Marek’s disease virus serotype 1 (MDV-1) on unvaccinated healthy backyard chicken flocks from four districts in Cantho city and to analyze the genetic characterization of the *meq* gene. A total of 353 feather follicle samples were collected from 50 unvaccinated chicken flocks for Marek’s disease to investigate prevalent MDV-1 by polymerase chain reaction (PCR). The four represent strains were chosen for *meq* gene sequencing. The results revealed that 26 out of 353 samples were positive for MDV-1 accounting for 7.37%. There were significant differences in the prevalence of MDV-1 on chickens among districts ($P<0.05$). The Meq protein of the four strains (VT, CD, PD, and TL) contained 20.14% proline and three regions of proline repeats. Besides, all four strains occurred with amino acid point mutations. These strains had only a substitution of proline at position 217 as well as interruption of consecutive proline at site 2. Phylogenetic analysis indicated that these strains were within a group relating to virulent Italian isolates.

Keywords: Cantho, backyard chickens, Marek’s disease, *meq* gene, unvaccinated

GE06

Multiplex PCR for simultaneous identification and differentiation of methicillin-resistant *Staphylococcus aureus* and *Staphylococcus pseudintermedius* isolated from dogs

Nguyen Pham Thao Nhi[1], Bui Nguyen Thanh Vy[1], Nguyen Thuy Y Vi[1],
Nguy Ho Hoang Tho[2], To My Quyen[1], Nguyen Khanh Thuan[1],
Nguyen Thi Lan Anh[3], Lam Thanh Nguyen[1]*

[1] Department of Veterinary Medicine, College of Agriculture, Can Tho University, Can Tho 900000, Vietnam
[2] Department of Applied Biology, College of Agriculture, Can Tho University, Can Tho 900000, Vietnam
[3] Faculty of Veterinary Medicine and Animal Husbandry, HUTECH University, Ho Chi Minh 700000, Vietnam
** Corresponding author: Nguyen Thanh Lam, Email: ntlam@ctu.edu.vn*

ABSTRACT. Methicillin-resistant *Staphylococcus aureus* (MRSA) and methicillin-resistant *Staphylococcus pseudintermedius* (MRSP) have been opportunistic pathogens causing important diseases in human and veterinary medicine in recent decades. Rapid and accurate diagnosis is one of the key strategies for the control of infection caused by MRSA and MRSP. In the present study, we applied a simple cost-effective DNA extraction and established a multiplex PCR assay for identification and differentiation of MRSA and MRSP isolated from dogs in Vietnam. Result of this study indicated that DNA extraction of MRSA and MRSP using Tris-EDTA-NaCl-Triton X100 (TENT) yielded comparable DNA extraction efficacy as using the commercial kit, and TENT method was more cost-effective. In addition, a multiplex PCR assay with four primer pairs including 27F/1492R, mecA_F/mecA_R, au-F3/au-nucR and pse-F2/pse-R5 successfully identified and discriminated between MRSA and MRSP. The multiplex PCR showed highly specificity with desired amplification of targeted amplicons and no cross-reaction. Furthermore, applicability of the diagnostic procedure was demonstrated by identification of field MRSA and MRSP isolated from clinical samples of dogs in Vietnam. Our study, therefore, provides an effective identification procedure for MRSA and MRSP. This diagnostic procedure can be a prompt countermeasure against rapid emergence of MRSA and MRSP in Vietnam.

Keywords: DNA extraction, dogs, methicillin resistance, multiplex PCR, Staphylococcus aureus, Staphylococcus pseudintermedius

GE07

Molecular Phylogeny and Taxonomical Insights of *Lithocarpus elegans* Complex (Fagaceae) in Vietnam and adjacent countries Based on Multiplexed ISSR Genotyping by Sequencing

Nguyen Van Ngoc[1*], Hoang Thi Binh[1], Shuichiro Tagane[2], Hironori Toyama[3], Yoshihisa Suyama[4], Tetsukazu Yahara[5]

[1]Faculty of Biology, Dalat University, Lam Dong 66000, Vietnam
[2]The Kagoshima University Museum, Kagoshima University, Kagoshima 890-8580, Japan.
[3]Center for Environmental Biology and Ecosystem Studies, National Institute for Environmental Studies, Tsukuba, Ibaraki 311-3101, Japan.
[4]Kawatabi Field Science Center, Graduate School of Agricultural Science, Tohoku University, Naruko-onsen, Osaki, Miyagi 980-8577, Japan.
[5]Department of Biology, Kyushu University, Fukuoka 6-10-1, Japan.
**Correspondence author: Nguyen Van Ngoc, Email: ngocnv@dlu.edu.vn*

ABSTRACT. *Lithocarpus* is the second largest genus of the family Fagaceae, with approximately 350 species in the world. The center of species diversity is mainly in continental Southeast Asia, especially China (123 spp.) and Vietnam (117 spp.). In Vietnam and adjacent countries, there is a group of *Lithocarpus* species having many similar and confusing morphological characters, so we designate these species as *L. elegans* complex hereafter. In this study, to assess the phylogenetic relationship and revise the taxonomy of *Lithocarpus elegans* complex and their close relatives in Vietnam and adjacent countries, we made a molecular phylogeny analysis based on multiplexed inter-simple sequence repeat (ISSR) genotyping by sequencing (MIG-seq) on our recent collection of Lithocarpus mainly collected from Vietnam and partly from Cambodia, Indonesia, Laos, Myanmar, and Thailand. The evidence obtained from phylogenetic analyses and subsequent morphological observations on 72 samples and herbarium specimens including types showed that *L. elegans* s. lat. is not a single widespread species but a group of cryptic species including *L. auriculatus*, *L. blaoensis, bokorensis*, sp. nov., *L. elegans* s. str., *L. syncarpus,* and *L.* sp. The morphologically distinct species *L. harmandii* and *L. harmandi* var. malachotricus are sisters to *L. elegans* s. str. and *L. bokorensis* in the MIG-seq tree, respectively. *Lithocarpus blaoensis* treated as a synonym of *L. elegans* is not close to *L. elegans* s. str. but is sister to *L. auriculatus*.

Keywords: Flora, MIG-seq, Taxonomic, Phylogenetic, Southeas Asia

GE08

Genetic characterization of African swine fever viruses circulating in Can Tho city, Vietnam during 2019–2022

Le Trung Hoang[1,2], Lam Thanh Nguyen[1], To My Quyen[1], Nguyen Minh Tu[1],
Nguyen Phuc Khanh[1], Nguyen Duc Hien[1,2]*

[1]Department of Veterinary Medicine, College of Agriculture, Can Tho University, Can Tho 900000, Vietnam
[2]Can Tho Sub-Department of Animal Health, Ministry of Agriculture and Rural Development, Can Tho 900000, Vietnam
** Corresponding author: Nguyen Duc Hien, Email: ndhien@ctu.edu.vn*

ABSTRACT. African swine fever (ASF) is a highly contagious and deadly viral disease in domestic and feral pigs. Since 2018, the disease has spread and caused huge consequences to pig industry in many Asian countries including China, Vietnam, and South Korea. The objective of this study is to determine genotype, serotype and genetic variation of representative African swine fever viruses (ASFVs) responsible for the outbreaks during 2019–2022in Can Tho city, a central administrative province in the Mekong delta. For outbreak investigation, presence of causative ASFVs was tested using conventional PCR targeting B646L gene. Subsequently, sequencing of DNA fragments of the putative B646L gene encoding the major capsid protein p72, EP402R gene encoding the viral hemagglutinin CD2-like protein (CD2v) and intergenic region (IGR) between l73R and I329L genes were performed for the genetic characterization. The phylogenetic analyses based on B646L and EP402R genes confirmed that all the ASFVs detected in Can Tho city belonged to the genotype 2 and serotype 8. In addition, this study revealed that at least two variants of ASFVs, IGR II and IGR III based on nucleotide variation of IGR sequence, co-circulate and caused outbreaks in Can Tho city. This molecular investigation provides great significance for understanding on evolution of ASFVs and tracing possible sources of infection in Can Tho and Mekong delta.

Keywords: African swine fever, Can Tho, genotype, serotype, variant, Vietnam.

GE09

Perspectives on the application of next-generation sequencing in agriculture in Vietnam

Thuy Duong HO HUYNH

KTest Co. Ltd., 17, Route No. 4, Gia Hoa Residental Area, Phong Phu, Binh Chanh, Ho Chi Minh 700000, Vietnam

ABSTRACT. Persistent problems of soil exhaustion and pollution due to overuse of fertilizers and pesticides, emerging diseases in animal rearing, uncontrolled utilization of antibiotics in aquaculture, to name a few, negatively impact the sustainable development of agriculture in Vietnam. These challenges require the application of innovative technologies to effectively manage crop and livestock production together with environment protection. Next-generation sequencing technology, including whole genome sequencing (WGS), metagenomics, and transcriptomics analysis, is a powerful tool for better understanding and exploitation of natural resources. WGS of microorganisms, plants, and animals, terrestrial and aquatic, provides genetic information for the selection of novel species with improved traits. WGS also contributes to the conservation of endangered species with valuable properties. Transcriptomics analysis, focusing on gene expression, exposes differential responses of host genome to changing environmental conditions and identifies transcriptional variants with promising characteristics. Shotgun metagenomics and 16S metabarcoding analyses reveal diverse microbiota present in soil, water, animal gut,… that have a crucial role in health and growth of plant and animal hosts. An appropriate monitoring of these microbiota, based on the knowledge of their composition and functions, could increase the productivity and quality of agricultural products without causing excessive harmful environmental effects.

GE10

Study on antioxidant and *in vitro* anti-diabetic activities of *Peperomia pellucida* (L.) Kunth extract

Tran Thanh Men[1], La Thi Kim Tu[2], Nguyen Thi Kim Anh[2], Huynh Hong Phien[1],
Nguyen Thi Bich Nhu[3], Nguyen Thi To Uyen[3], Ngo Thi Anh Thu[2],
Tran Ngoc Quy[2], and Do Tan Khang[2,*]

[1]*Department of Biology, College of Natural Sciences, Can Tho University,*
Can Tho 900000, Vietnam
[2]*Department of Molecular Biotechnology, Biotechnology Research and*
Development Institute, Can Tho University, Can Tho 900000, Vietnam
[3]*Can Tho Science and Technology Application Cente, Can Tho 900000, Vietnam*
[*]*Corresponding author: Do Tan Khang, Email: dtkhang@ctu.edu.vn*

ABSTRACT. *Peperomia pellucida* (L.) is known as a herbal plant used in folk medicine to treat many inflammatory diseases, digestive disorders, and cancer in tropical and subtropical regions. However, this plant species in Vietnam has not been studied widely, especially its biological activities. This study was carried out to evaluate the antioxidant capacity in the fruit fly model *Drosophila melanogaster* and the ability to inhibit α-amylase enzyme activity in *Peperomia pellucida* extract. The results showed the in vitro antioxidant activity of *Peperomia pellucida* extract in four methods, including DPPH, $ABTS^{\cdot+}$, RP and TAC had EC_{50} values (effective concentration) of 730.34 µg/mL, 84.33 µg/mL, 95.28 µg/mL, respectively, and $Abs_{0.5}$ value of 114.73 µg/mL. The total polyphenolics and flavonoid contents of *Peperomia pellucida* extract were determined to be 359.91±0.77 mg GAE/g extract and 200.28±1.23 mg QE/g extract, respectively. Similarly, under H_2O_2-induced oxidative stress, fruit flies reared in the feed medium supplemented with a concentration of 1 mg/mL *Peperomia pellucida* extract had a mean lifespan, 50% survival, and maximum lifespan were 1.6 times, 1.8 times, and 1.62 times, respectively higher than the control without extract. In addition, the ability to inhibit the α-amylase enzyme activity in *Peperomia pellucida* extract was reported with an EC_{50} value of 115.32±2.65 µg/mL compared with the acarbose control of 18.67±0, 01 µg/mL.

Keywords: antioxidant, anti-diabetic, *Peperomia pellucida* (L.)

GE11

Identifying candidate SNPs and genes related to amylose content in the medium-grain rice

Bui Phuoc Tam[1], Pham Thi Be Tu[2], Nguyen Thi Pha[2] and Vu Anh Phap[2]

[1]PhD Student of Can Tho Univerisity, Can Tho 900000, Vietnam;
[2]Can Tho University, Can Tho 900000, Vietnam
[*]Corresponding author: Bui Phuoc Tam

ABSTRACT. Amylose content (AC) is one of the key traits related to rice grain quality. This is a single-gene trait and is controlled by the *Waxy* gene located on chromosome 6. Genetic studies related to amylose content in medium-grain rice varieties underpin the identification of genes and linked molecular markers that few previous studies mentioned. The purpose of this study is to investigate the genetic characteristics of AC in the medium-grain rice on 12 chromosomes. The results showed that the AC in this study had a large range from 10.83 to 30.12%, however, the group of varieties with low AC (less than 20%) accounted for 21.9%. The genome-wide association study (GWAS) for AC in medium-grain rice varieties identified 9 significant SNPs on chromosomes 1, 2, 4, 8, 9, 11, and 12. The frequency of alleles widely ranged from 0.94% to 56.60%. On chromosome 6, 74 significant SNPs had allele frequencies ranged from 3.8% to 67.0%. In which, two SNPs *fd7* (1764762 bp) and *fd8* (176707 bp) are located on the *Waxy* gene region. Based on the RiceFREND and ePlant databases, two candidate genes, *LOC_Os02g01610* on chromosome 2 and *LOC_Os12g06250* on chromosome 12, were selected. These genes connected the AC-related genes and QTLs in previous studied and controlled the mature of rice grain.

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