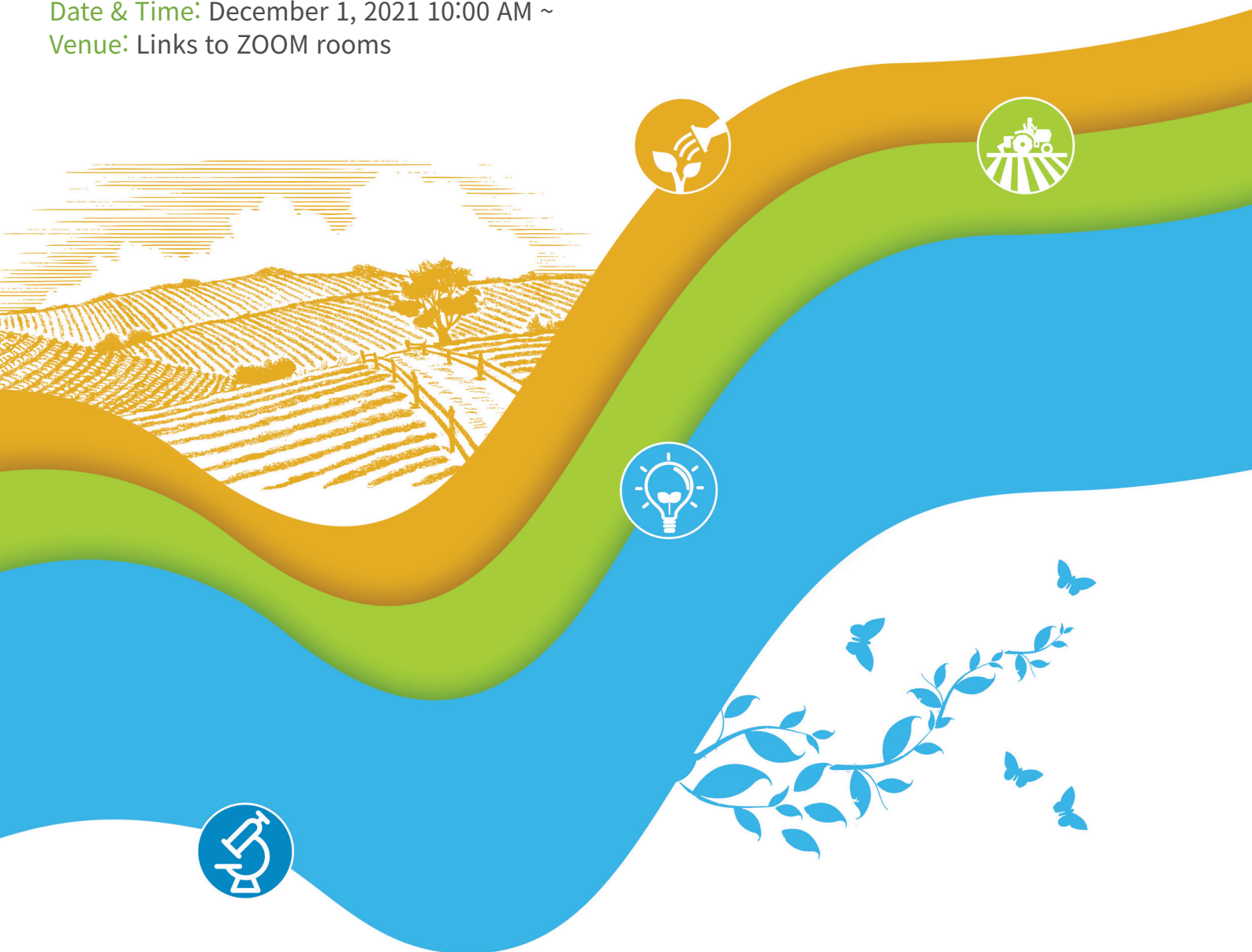# 1ST INTERNATIONAL CONFERENCE ON AGRICULTURAL SCIENCE & RESEARCH

Date & Time: December 1, 2021 10:00 AM ~
Venue: Links to ZOOM rooms

Institute of Agricultural Science, CNU

KSAIA   The Korean Society for Artificial
Intelligence in Agriculture

Welcome Address

Dear respected invited speakers, professors and graduate students, and ladies and gentlemen, on behalf of Agriculture Science Research Institute, Chungnam National University, I am honored to welcome all participants to the 1st International Conference on Agricultural Science and Research.

Agriculture is most important industry to human being, providing not only food but also living environment. We faces rapidly increasing global population and invisible world-war to secure required amount of natural resources and food to maintain the life. Recent surrounding conditions, such as climate change, environmental pollution, limited land for food-crop cultivation, become greater challenges to overcome. Researchers in the world are adopting state-of-the-art available technologies to agricultural science and technology development. Keywords includes artificial intelligence, information and communication, electrics and electronics, big data, block chain, gene editing, and 3-D printing, the elements of 4th revolution. In the era of 4th revolution, fusion and cooperation among multi-disciplinary academic fields is critical for efficient and successful accomplishments. This conference is divided into sessions, representing 12 academic fields in agriculture. Sharing and exchanging research trends and progress would play a role as a "booster-shot" to solve the facing challenges and proceed to the next level.

My special thanks should go to Prof. Jong Myung Choi, Dean of College of Agriculture and Life Sciences, CNU, and the organizing committee members and staffs for making this international conference wonderful and successful. Finally, I wish each of all the participants a productive and fruitful time during this conference.

Sun-Ok Chung
Director, Agriculture Science Research Institute,
College of Agriculture and Life Sciences,
Chungnam National University
President, Korean Society of Artificial Intelligence in Agriculture

Congratulatory Remarks

Dear all participants,

I am honored to be here today and deliver my congratulatory remarks for the opening of 1st International Conference on Agricultural Science & Research. I would like to express my deep appreciation to Prof. Sun Ok Jung, the head of Institute of Agricultural Science, CNU, and the other member of Institute for their work in preparing for today's international symposium.

As you all know, all of us around the world have been fighting COVID-19 for a long time, and now, thanks to vaccination, we are gradually recovering our daily lives and the economy. The world is paying more attention to health than ever before, and as a result, many changes are required in the agricultural industry. The increase in production cost and the shortage of manpower in rural areas are pointed out as obstacles to the growth and development of the agricultural industry. I think it is very meaningful to hold this conference at a time like this.

This conference covers a wide range of research topics and issues in agriculture. I hope that this will lead to a active exchange of ideas and discussion involving important issues and they resulted in the formation of a number of new scientific collaborations. I hope that this conference, which is held for the first time, will not end with this one-time event and will continue to be successful. Once again I have the pleasure and honor of welcoming all of you to this international conference. Thank you.

Jong Myung Choi
Dean and Professor
College of Agriculture and Life Sciences
Chungnam National University

Conference Program

Schedule		Program
	10:00 ~ 10:20	Opening Ceremony
		Crop Science	Crop Science I
		Horticultural Science	Future of climate-smart horticultural science I
		Environment & Forest Recourses	Global Trend on Crop Science Research I
		Applied Biology	Climate change and crop protection I
		Division of Animal	Livestock nutrition
	10:30 ~ 12:00	Dairy Science	Nutrition and Feeding
		Rural & Agricultural Engineering	Agricultural Engineering I
		Biosystems Machinery Engineering	Application of smart agriculture technology as a novel method in biosystems machinery engineering I
		Food Science & Technology	Food Safety
		Bio-Environmental Chemistry	Managing Climate Change and Sustainable Agriculture I
	12:00 ~ 13:00	Lunch Break
2021-12-01(wed)		Crop Science	Crop Science II
		Horticultural Science	Future of climate-smart horticultural science II
		Environment & Forest Recourses	Global Trend on Crop Science Research II
		Applied Biology	Climate change and crop protection II
		Division of Animal	Livestock breeding breeding
	13:30 ~ 15:00	Dairy Science	Waste Management
		Rural & Agricultural Engineering	Agricultural Engineering II
		Biosystems Machinery Engineering	Application of smart agriculture technology as a novel method in biosystems machinery engineering II
		Food Science & Technology	Food Processing
		Bio-Environmental Chemistry	Managing Climate Change and Sustainable Agriculture II
		Agricultural Economics	Agricultural Economy
	15:00 ~ 15:30	Coffee Break
	15:30 ~ 17:00	Bio-Environmental Chemistry	Managing Climate Change and Sustainable Agriculture III

■ Zoom : https://zoom.us/j/98106101538?pwd=dVY0QWZRRUJJdzR0QmI2dGRzYzYxdz09

ZOOM Links

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https://cnu-ac-kr.zoom.us/j/7217209153

Horticultural Science
https://cnu-ac-kr.zoom.us/j/8954376982

Environment & Forest Recourses
https://cnu-ac-kr.zoom.us/j/6889711022

Applied Biology
https://cnu-ac-kr.zoom.us/j/9260269862?pwd=b3dQbk9lSnJRdWZmN254dFpDM2lHUT09
(PW 1234)

Division of Animal
https://cnu-ac-kr.zoom.us/j/4916893804

Dairy Science
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Rural & Agricultural Engineering
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Biosystems Machinery Engineering
https://cnu-ac-kr.zoom.us/j/5321715647

Food Science & Technology
https://cnu-ac-kr.zoom.us/j/84455383558

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Crop Science

Genetic differentiation and signatures of gene flow between regions of traditional rice (*Oryza sativa* L.) from northern Vietnam

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Abstract

Northern Vietnam is one of the most important centers of genetic diversity for cultivated rice. Over thousands of years of cultivation, natural and artificial selection has preserved many traditional rice landraces in northern Vietnam due to its geographic situation, climatic conditions, and many ethnic groups. Despite the abundant genetic resources, a few reports have been published relating to Vietnamese rice landraces and the extent of genetic differentiation between regions and the possible factors affecting the shape and population genetics of rice landraces in Vietnam remain to be determined. In this study, we determined the genetic diversity and population structure of 79 rice landraces collected from northern Vietnam and 19 rice accessions collected from different countries. In total, 98 rice accessions could be differentiated into *japonica* and *indica* with moderate genetic diversity and a polymorphism information content of 0.382. We also detected subspecies-specific markers to classify rice (*Oryza sativa* L.) into *indica* and *japonica*. Additionally, we detected five marker-trait associations and rare alleles that can be applied in future breeding programs. Most interestingly, analysis of molecular variance (AMOVA) found genetic differentiation was related to geographical regions with an overall PhiPT (analog of fixation index FST) value of 0.130. More emphasis was given to provide signatures and infer explanations about the role of geographical isolation and environmental heterogeneity in genetic differentiation among regions in landraces from northern Vietnam. Our results suggest that rice landraces in northern Vietnam have a dynamic genetic system that can create different levels of genetic differentiation among regions, but also maintain a balanced genetic diversity between regions.

Key words: Rice, genetic diversity, population structure, genetic differentiation, marker-trait association, northern Vietnam

Acknowledgements

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Crop Science

Variations in *SBE3* and *GBSS1* synergistically increased the amylose content with changes in the physicochemical properties in rice (*O. sativa*)

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Abstract

Rice is one of the most important resources for staple food and industrial materials in the world. Rice starches contain glucose polymers of primarily linear amylose chains and branched amylopectin chains. Amylose biosynthesis is controlled by granule-bound starch synthase I (GBSSI) and rice *GBSSI* gene (*Wx*) on chromosome 6 is one of the major gene regulating amylose content in rice endosperm. Starch branching enzyme (SBE) is the enzyme that forms branch points in amylopectin, and several *SBE3* mutants showed increased amylose content and resistant starch in rice. In this study, physicochemical properties of rice starches were examined using four genotype lines derived from a cross between Korean elite line Hwayeong and high-amylose cultivar Dodamssal. Sequence variations of *SBE3* and *GBSS1* in Dodamssal synergistically increased amylose content and change physicochemical characteristics in the Hwayeong genetic background. Microscopy analysis, X-ray diffraction, RVA, and starch digestibility analysis were conducted. *SBE3* and *GBSS1* of Dodamssal allele affect starch granule structure, pasting characteristics, starch crystallinity, and digestibility. Further studies are ongoing to reveal the genetic interaction between *SBE3* and *GBSS1*, and difference in amylopectin structure.

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Crop Science

Mapping of quantitative trait loci associated with amylose and resistant starch content in rice

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Abstract

Studies on starch-related traits such as amylose content (AC) and resistant starch (RS) content have gained interest due to the potential benefits on human health of cereals high in AC and RS content. In our present study, mapping of quantitative trait loci (QTLs) for starch-related traits was carried out using 92 recombinant inbred lines (RILs) derived from a cross between two closely related japonica cultivars 'Dodamssal' and 'Hwayeong', with large differences in their AC and RS content. Three QTLs for AC on chromosomes 2, 6, and 11 and one QTL for RS on chromosome 2 were detected in a two-year field experiment. Among the three QTLs for AC, two QTLs on chromosomes 2 and 6 allelic to starch branching enzyme 3 (*SBE3*) and granule bound starch synthase 1 (*GBSS1*), respectively, were responsible for the high phenotypic variation in both years and the Dodamssal-derived allele increased the AC value at these loci. As *SBE3* and *GBSS1* had mainly elevated the AC value, the interaction between these two genes was analyzed using 210 F_2 plants. The results revealed that the concerted action of these genes in F_2 population showed that both acted in an additive manner in increasing the AC. As revealed by haplotype analysis, a total of 117 rice accessions were categorized into three groups based on two SNPs in *GBSS1*. All *indica*, Korean landrace, and weedy rice accessions had predominantly the Wx^a allele at the 5′ splice site of intron 1 whereas *japonica* accessions had the mutated Wx^b. Thus, the Wx^a allele in landrace or weedy rice accessions could be used in rice breeding programs to alter the AC in cultivated *japonica* rice. Also, the starch-related properties of rice could be regulated through the combined effect of *SBE3* and *GBSS1*.

Key words: Quantitative trait loci, amylose content, resistant starch content, recombinant inbred lines

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Crop Science

Modelling Rice Competition with *Leptochloa fusca*, *Bidens frondosa* and *Ammannia coccinea* in Transplanted Rice Cultivation

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Abstract

Field experiments were conducted to investigate rice - *Leptochloa fusca*, rice - *Bidens frondosa* and rice - *Ammannia coccinea* competition under transplanted rice cultivation in Daejeon, South Korea. Rice yield data were used to predict rice yield as a function of plant densities of *Leptochloa fusca*, *Bidens frondosa* and *Ammannia coccinea* using a rectangular hyperbola. Compared to *B. frondosa* and *A. coccinea*, *L. fusca* significantly reduced number of tillers at early growth stage, resulting in more reduction in number of panicles, and the other yield components such as number of spikelets, ripened grain ratio and ultimate rice yield at later growth stage. Cousens' rectangular hyperbola model predicted that weed competitivity represented by parameter β ranged from 0.0411 to 0.0722 for *L. fusca*, from 0.0168 to 0.0175 for *B. frondosa* and from 0.0043 to 0.0046 for *A. coccinea*, indicating that the competition effect of *L. fusca* on rice yield was greater than that of *B. frondosa* and *A. coccinea*. Our findings will be useful for weed management strategies in transplanted rice cultivation.

Crop Science

Seeds minerals, storage proteins, fatty acids, and squalene composition of new quinoa genotypes grown in hyper-arid desert environments

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Abstract

The Aral Sea Basin (ASB) is a prime example of 'marginal land' and reflects all climate and soil conditions limiting agricultural production. Since decades agricultural production in the ASB and similar marginal land areas is degrading and not sustainable. A successful introduction of crops adapted to these marginal, particularly saline and dry conditions but nonetheless with high value, such as quinoa, would help in the development of a sustainable agriculture. Therefore, the main objectives of the study were the improvement, successful cultivation and use of non-conventional crops such as quinoa in resource-poor farming systems, thus, contributing to alleviate local poverty and malnutrition. A two-year field experiment was laid out in completely randomized block designs with three replications to test the adaptability of this crop to abiotic stresses, grain yield and nutritional quality in marginal areas of the ASB. The vegetation cycle of the investigated five quinoa lines ranged between 107–133 days based on genotype characteristics. Q5 and Q3 lines had early ripening ability of (107 and 113 days), higher seed weight (2.7 and 2.35 g/1000 seeds), better seed germination (68.3 and 56.7%) associated with stress tolerance. All these features reflected in high yield potential of Q5 and Q3 genotypes, exhibiting average grain yields of 2537.8 and 2361.7 kg ha1, respectively. The lowest yield was recorded in Q1 with an average yield of 1551.3 kg ha-1. Nutrition features were similar in the tested quinoa genotypes; however, the highest protein, lignin and lipid contents were recorded in Q5 genotype. Q3 and Q5 genotypes showed higher salinity tolerance than other genotypes when different concentrations (0–500mM) of NaCl and MgSO4 exposed under laboratory conditions. Single steps are planned selecting quinoa as an example of a salt tolerant crop as follows, i) selection of the best quinoa genotypes under marginal conditions, ii) improving the understanding of mechanism on salinity tolerance of quinoa, iii) strengthen non-conventional crop breeding programs iv) developing best agronomic management practices for salt tolerant quinoa and v) understanding of the socio-economic impact on farmers and communities depending on resource-poor farming systems and improving their situation, and vi) addressing nutrition and income-related issues. In collaboration with National Agricultural Research and Extension Services (NARES), partners will build the capacity of farmers and extension workers in salinity-resilient and climate smart agriculture, thus enlarging the available national capacity. To do so, our research focus on characterizing quinoa genotypes in the field and the lab to determine the phenotype measuring different morphological and growth traits. Implementation of innovative technology in cultivation, harvesting, storage and processing will help incorporate quinoa into the ASB's agricultural development and scale up as an alternate crop for food and feed.

Horticultural Science

Quantitative trait locus mapping of Clubroot resistance and Plasmodiophora brassicae pathotype Banglim-specific marker development in B. rapa

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Abstract

Clubroot resistance is an economically important trait in Brassicaceae crops. Although many quantitative trait loci (QTLs) for clubroot resistance have been identified in *Brassica*, disease-related damage continues to occur owing to differences in host variety and constant pathogen variation. Here, we investigated the inheritance of clubroot resistance in a double haploid population developed by crossing clubroot resistant and susceptible lines '09CR500' and '09CR501', respectively. The resistance of '09CR500' to *Plasmodiophora brassicae* pathotype 'Banglim' was controlled as a single dominant gene, with the segregation of resistance and susceptibility being nearly 1:1. $PbBrA08^{Banglim}$ was identified as having a logarithm of odds value of 7.9–74.8, and a phenotypic variance of 26.0%–97.1% with flanking marker '09CR.11390652' in A08. After aligning QTL regions to the *B. rapa* reference genome, 11 genes were selected as candidates. $PbBrA08^{Banglim}$ was located near *Crr1*, *CRs* and *Rcr9* loci, but differences were validated by marker analysis, gene structural variations and gene expression levels, as well as phenotypic responses to the pathotype. Genotyping using the '09CR.11390652' marker accurately distinguished the Banglim-resistance phenotypes in the double haploid population. Thus, the developed marker will be useful in *Brassica* breeding programs, marker-assisted selection and gene pyramiding to identify and develop resistant cultivars.

Key words: Clubroot disease; resistance mapping; Quantitative trait locus (QTL); marker; *Brassica rapa*

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Horticultural Science

The Effects of Plant-Derived Protein Hydrolysates on the Growth, Quality, and Physiology of Greenhouse Crops

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Abstract

Plant biostimulants offer an innovative approach to potentially improve crop yield and quality under various environmental conditions. Particularly, plant-derived protein hydrolysates (PH), a mixture of amino acids and soluble peptides from enzymatic or chemical hydrolysis of agricultural waste, are gaining global interest for their sustainability and significant agronomic value. However, a functional role of the PH in crop yield and quality remains uncertain and is proposed to be associated with its phytohormone-like activities or serve as an additional nitrogen (N) source. Besides, the effects of PH on crop yield and quality are limited in intensive production systems such as greenhouse facilities. The purposes of this research were to examine the effects and mechanisms of PH on greenhouse crops and to assess the potential of PH application to optimize N fertilizer use in greenhouse crop production. The specific objectives were to; 1) elucidate the hormone-like activities of PH in the adventitious rooting formation of in cuttings, 2) evaluate the effects of different PH application methods on yield and quality of lettuce and tomato under different N levels in greenhouse crop production with a commercial root substrate, and 3) examine the effects of PH application methods on yield and quality of hydroponically grown lettuce under different N levels and forms. Three conclusions were determined that 1) the hormonal effects of PH are attributed to BR-mediated processes, and PH has overlapping functions with auxin during adventitious rooting of cuttings in a plant species-specific manner, 2) the root application of PH (PH-R) can be a sustainable method in greenhouse crop production with a commercial root substrate to enhance crop yield, quality, and nutrient use efficiency under both high and low N fertilizations, and 3) PH-R effectively increased hydroponic lettuce root growth, subsequently improving shoot yield and quality with interactions between PH, N level, and NO_3:NH_4 ratio. Also, PH-R counteracted the negative effects of the low NO_3:NH_4 ratios on hydroponic lettuce yield. This research demonstrates the hormone-like activities of PH and provides the optimization of PH application and N fertilization for sustainable production of high-quality greenhouse crops.

Key words: Plant biostimulant, protein hydrolysate, sustainable horticulture, greenhouse crop production

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> **Horticultural Science**

Influence of different nitrogen levels on growth and development of seedlings in vegetative strawberry propagation

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Abstract

This study was conducted to establish the appropriate nitrogen (N) concentration needed as fertilizer for raising of strawberry mother plants in four varieties such as 'Altaking', 'Geumsil', 'Maehyang' and 'Vitaberry'. The peat moss+perlite medium (7:3, v/v) was prepared and mother plants were transplanted. Then, each of nutrient solutions containing five different N concentrations (0, 5, 10, 15 and 20 mM) was applied when plants need watering. The all treatment solutions contained equal concentrations of essential nutrients except N. The growth of mother plants and occurrence of daughter plants were investigated at 90 days after mother plant transplanting. The pH, EC and concentrations of macro-elements in root media were analyzed after removing the plants. The tissue analysis also conducted using oven dried mother plants for nutrient contents. The root medium pHs in all treatments were around 5.65-6.10 and statistical differences were not observed among the treatments. The highest growth of mother plants in terms of numerical data of dry weight and occurrence of daughter plants in 'Altaking', 'Geumsil', 'Maehyang' and 'Vitaberry' strawberries were observed in 10, 20, 10, and 20mM N treatments, respectively. The tissue N contents of these treatments were 2.72, 3.08, 2.71 and 2.94%, respectively, based on the dry weight of above ground tissue. The fresh weights of all daughter plants occurred in each mother plant were the heaviest in N treatments of 10, 15, 15, and 20 mM in 'Altaking', 'Geumsil', 'Maehyang' and 'Vitaberry' strawberries, respectively. However, the statistical differences in terms of dry weight of mother plants were not observed among treatments of 5, 10, 15 and 20 mM N in 'Altaking', 'Geumsil', and 'Vitaberry' strawberries. Above results indicate that 'Geumsil' and 'Vitaberry' strawberries required higher N concentration in fertilizer solution than 'Altaking' and 'Maehyang' for raising mother plants and occurrence of daughter plants in vegetative propagation.

Key words: Soilless culture, N concentration, mother plant growth, daughter plant occurrence

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Horticultural Science

Green synthesis of ZnO nanoparticles for antimicrobial and vegetative growth applications: An efficient strategy forexpandingconcern to human wellbeing

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Abstract

Nanotechnology is a multidisciplinary scientific domain and its promising application unlocked up a new scope and perspective inagriculture.The green synthesis of zinc oxide nanoparticles (ZnO NPs) using the leaf extract of *Parthenium hysterophorus* and its characterization have been investigated. UV–vis, FT-IR, XRD, TEM and SEM investigations were used to study the optical, structural, and morphological properties of produced ZnO NPs. The antimicrobial activity of ZnO NPs tested against bacteria: Gram-positive bacteria (*Staphylococcus aureus*, *Streptococcus pneumoniae*); Gram-negative bacteria (*Escherichia coli*, *Klebsiella pneumoniae*), and fungal strain (*Candida albicans*). The absorption peak of UV–vis spectrum was observed at 380 nm. FT-IR function vibration groups had proved the existence of ZnO NPs. The XRD configuration indicated the pure crystalline nature ZnO NPs formation with an approximate crystalline size 17.63 mm. TEM and SEM images showed the structure of NPs to be a spherical shape with 5–10 nm. The ZnO NPs were revealed strong antimicrobial activity against both bacterial and fungal strains. The ZnO NPs interact with bacterial cells by electrostatic interaction. It has enhanced the surface tension and generates reactive oxygen species (ROS), leading to bacterial lysis. Conveniently, synthesized ZnO NPs can be used against Gram–ve bacteria causing infectious disease in the medical field. The germination of seeds and vegetative growth of *Sesamum indicum* has been greatly improved. Due to the higher antimicrobial efficiency of NPs, future research devoted to postharvest quality of fruits and vegetables with chitosan- nanocomposite edible coating can be a promising technique to extend shelf-life and maintain quality of horticultural crops.

Key words: Green Synthesis; ZnO NPs; Reactive oxygen species; *Sesamum indicum*

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Horticultural Science

Accumulating Bioactive Compounds of *Agastache rugosa* by Soaking Root in Hydrogen Peroxide (H2O2) in a Hydroponic System

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Abstract

This study was performed to determine the optimum hydrogen peroxide (H_2O_2) concentration for the plant growth characteristics and the accumulation of the bioactive compounds in *Agastache rugosa* (called Korean mint) cultivated in a hydroponic culture system. *A.rugosa* seeds were sown in an environmental control room for germination and seedling stage. Twenty-eight-days-old seedlings were transplanted into a deep flow technique system with Hoagland nutrient solution at 2.0 dS·m^{-1} of electrical conductivity for thirty-nine days. One week after transplanting, the roots were soaked in diniconazole solution at 120 μmol·mol^{-1} for ten minutes to limit stem length. After 3.5-week from transplanting day, the roots were treated by root soaking with six different concentrations of H_2O_2 solution: 4, 8, 16, 32, 64, and 128 mMol and the control (0 mMol H_2O_2). Plant growth characteristics were measured and bioactive compounds including rosmarinic acid (RA), tilianin, and acacetin concentrations and contents were analyzed after thirty-nine days from transplanting day. The leaf width, number of leaves, leaf area, stem length and shoot fresh weight were not significant differences among all treatments. However, the root fresh weight, shoot dry weight, and root dry weight had a slight reduction when increasing H_2O_2 concentrations and the lowest values were found at 128mMol treatment. Additionally, bioactive compound concentrations and contents in the whole plant were significant differences between H_2O_2 treatments and control. The tilianin and RA concentrations were promoted under 4, 16 and 32 mMol treatments. Especially, the RA content under 16 mMol H_2O_2 was the highest value (98.68 mg/plant DW), and it was 66% higher than the control. Besides that, the tilianin contents at 16, 32, and 64 mMol H_2O_2 treatments were significantly greater compared to the control. The results of tilianin contents were 7.91, 7.68, and 7.75 mg/plant DW under 16, 32, and 64 mMol treatments, respectively. On the other hand, only 32 mMol treatment showed the higher acacetin content than the control. The experiment suggests that soaking the root of *A.rugosa* with *H2O2* at 16mMol will give the best results of the bioactive compounds when growing in the hydroponic culture system.

Key words: acacetin, deep flow technique, Hoagland solution, Korean mint, rosmarinic acid, tilianin

Horticultural Science

Reduced allergenicity of tomato fruits by CRISPR/Cas9-Mediated *Lyc e 1* Mutagenesis

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Abstract

Tomato (*Lycopersicon esculentum*) is a very important dietary component, consumed worldwide. Tomato is a well-known allergen source as demonstrated that tomato allergy prevalence is more frequent in pollen-sensitized patients. The Profilin is a small acting binding glycosylated proteins, contributes to the allergenic potency of various fruits including tomato. Profilin encoded by genes of *Lyc e1.01* and *Lyc e1.02* both have been found as allergens in tomato.So, our aims to generate profilin-free tomato fruits by silencing of both genes in transgenic tomato plants by using CRISPR/Cas9 RNPs to the protoplast system. Firstly we designed five guide RNAs(gRNA) for each profilin gene and two guide RNAs for simultaneous site-directed mutagenesis of two genes. To determine the transfection efficiency, a transient GFP expression system was carried to optimize the concentration of PEG and incubation period. Next the editing efficiency of different sgRNAs was obtained by sequencing. However in the present study, we will develop a DNA-free direct delivery system allowing the efficient mutation of target genes results in production of non-transgenic tomato plants.Research methodologies in this study encompass broad screening of tomato genotypes, selection of candidate genes, designing of CRISPR/Cas9 specific gRNAs, efficient silencing of allergen genes and validation of allergens free tomatoes. Therefore research methods being developed in this study will be applicable to other *Solanaceae* crops and other related species.

Key words: Tomato, profilin, CRISPR/Cas9, Allergen-Free, RNP

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Environment & Forest Recourses

The effect of 16 combinations (N × P) of fertilizer treatment on the Quality Index, soil characteristics and tissue nutrient of *Liriodendron tulipifera*

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Abstract

Liriodendron tulipifera was selected as a "climate tree" in 2021, that will lead to carbon neutrality. *L. tulipifera.* has excellent carbon absorption capacity, and is hence attracting attention as an economic tree that could increase the self-sufficiency of domestic wood usage. Since the fertilization requirements and absorption rates of vary from species to species, our goal was to determine the fertilizer requirement suitable for *L. tulipifera.* production by combining the fertilizer amounts of N and P at four levels, respectively. Two-year-old *L. tulipifera.* were planted (16 seedlings/m2) in a nursery belonging to the Yongmun Cultivation Office of the Northern Forest Service. Urea and Fused superphosphate were applied in 16 regimes along with a no-treatment control, ×1 (N 13.5 g/m^2, P 6.1 g/m^2), ×2 (2 times ×1), ×4 (4 times ×1). The resulting growth and soil characteristics were then measured. Tree height increased as the level of fertilization increased. Root collar diameter (RCD) was the highest in the x2 and the least in the x4. Biomass increased rapidly until the ×2, and decreased gradually in the ×4. The Seeding Quality Index was also the highest in the ×2 (i.e. 10.5) and the lowest in the control (i.e. 6.8). With regards to the soil characteristics, the soil pH significantly decreased as the amount of fertilization increased, and accordingly, the concentration of calcium and magnesium in the soil also tended to decrease. In this study, the N concentration in tissue and total N in the soil increased as the amount of fertilization increased, but it did not affect the P concentration in the tissue while available P increased. The soil EC decreased when the N treatment amount was increased. It however, increased as the P treatment amount increased. This study shows that 2x (N 27.0 g/m^2, P 12.2 g/m^2) is required for the growth of two-year *L. tulipifera.*, while more than that amount may be unnecessary.

Key words: *Liriodendron tulipifera*, Tulip tree, fertilization, nitrogen, phosphorus

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Environment & Forest Recourses

Water stress-induced changes in the leaf anatomy, physiology, and stem biochemistry of two *Quercus* species

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Abstract

Water stress is a major factor affecting the growth and productivity of plants. However, the mechanisms involved in plant responses to water stress are still not clear, especially in forest tree species. Thus, we investigated the changes in leaf anatomy, physiology, and biochemistry of two *Quercus acutissima* Carruth. and *Quercus serrata* Murray under well-watered (WW) and water- stress (WS) conditions. The stomatal density, thickness of palisade and spongy mesophyll, thickness of upper and lower epidermis, trichome density and types, xylem vessel diameter, stomatal conductance (g_s), transpiration (E), water use efficiency (WUE), and stem starch content were measured between WW and WS treatments and species. There were no significant effects on stomatal density, but the thickness of palisade tissue varied considerably between treatments in both species. There were no treatments effects detected in spongy mesophyll and epidermises thickness. Trichome density was significantly higher in WS treatments in *Q. serrata*. Small xylem vessels are more frequent in water-stressed leaves than well-watered ones in *Q. serrata*, whereas no significant difference between treatments in *Q. acutissima*. Physiologically, gs and E decreased significantly in WS in all species and the WUE was significantly higher in *Q. serrata* than *Q. acutissima*. Further, there was no significant variation in starch content between treatments in all species. Water-deficit stress-induced changes in the thickness of palisade tissue, trichome density, xylem vessel diameter, and WUE seem to be the predominant drought responses of the two species, and *Q. serrata* seems to be more tolerant to water stress than *Q. acutissima*. The present study should enhance our understanding on the mechanisms involved in drought responses of forest tree species, particularly oaks.

Key words: drought response mechanisms; drought tolerance; *Quercus acutissima*; *Quercus serrata*; water use efficiency

Environment & Forest Recourses

The influence of socio-economic characteristics on Willingness to pay for conservation of community forest, Myanmar

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Abstract

People's participation in forest conservation is one of the option or solution to reduce deforestation and forest degradation according to REED+. Their willingness to participate in forest management and demographic characteristics are vital for achieving sustainable development objectives, particularly within the context of co-management of forest resources. In Myanmar, approximately 70% of people are rural people and rely on forest resources for their income and livelihood. After initiation of community forestry in 1995, the local people were involved in forest management and own the right for use of forest products. Therefore, this study was carried out to investigate the influence of socio-demographic characteristics on willingness to pay (WTP) for conservation of forest and to assess the benefits contributes by community forestry to members of forest user group. It was a case study of Maing-thauk community forest (MTCF), which was selected based on the criteria: official certification, > 10 years' forest management experience, with one forest consisting of different users and watershed conservation practices. Using the semi-structured questionnaire, responses on socio-demographic, willingness and expectation of forest management for long term questions were obtained from randomly selected at least 35% households in each village involving in the management of MTCF. The result revealed that the distance of village from forest and purposes of extraction of forest products and services significantly influence on WTP for conservation of forest. The significant influence of Ethnicity, gender and education level of forest users varied depending on the onetime payment and long-term payment. The results of this study provide important information to promote sustainable forest management with people participation reducing poverty and conflicts between forest users and authorized organizations in management of forest area and resources as well as reducing deforestation and forest degradation under ultimate goal of REDD+ framework.

Key words: community forestry, willingness to pay, socio-demographic characteristics, people participation, Myanmar

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> **Environment & Forest Recourses**

Seasonal variation in species composition of bird community in urban green space

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Abstract

Urbanization results in decreasing proportion of the native population living in a given geographic area. In addition, urban living limits access to nature and can increase to effect of certain environmental hazards, such as air and noise pollution. The nature-based construction and green space solutions offer innovative approaches to increase the quality of urban settings. Greenspaces are support a number of environmental functions in urban environments, such as the survival of urban-settling species (e.g., bird species). The aim of this study was to investigate the effects of urban habitat, fragmentation, habitat characters and effects on bird's community in an urban environment. This study area was situated in Daejeon, the capital of Korea; embracing the partial area in Yuseong-gu, green space in parts of the urban forest, agricultural, riparian and stream.

Bird surveys were conducted three times a month from dawn to 07:00 and from 17:00 pm, between November 2019 and October 2020. We conducted bird surveys in 1419 observation points where we found 19723 individuals belonging to 72 species that belong to 29 families in 12 orders. A majority of recorded 22 species were observed during all seasons. The species diversity index (Shannon-Wiener index, H) was overall 2.84, and the value was the highest for the winter season in urban sites at 2.92, followed by spring and summer at 2.9 and 2.8, respectively. The species richness index (Evenness Index, EI) was lowest in the autumn season (EI=0.66), where the species number was highest (n=52) whereas the species richness index was highest in the summer (EI=0.81) where the species number was lower (n=34). Species composition was broader in autumn and spring, suggesting that many bird species have use of the urban landscape in migration season. In winter, the amount of birdlife increased in the riparian areas and decreased in crop and urban forests, which suggests that urban riparian and stream areas provide winter habitats for more species. The indicator species for determining seasons include migrant birds such as wading birds and waterfowl species, as well as resident birds such as *Anas zonorhyncha*, *Pica pica*, and *Hypsipetes amaurotis*. Importantly, increases in resident birds' individual counts of these species may also serve as indicators. Our results suggest that urban green space can support a diverse bird community, including species of conservation value.

Key words: Bird communities, Species richness, Urban green space

Acknowledgements

> **Environment & Forest Recourses**

Forest and landscape restoration in Mongolia

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Abstract

Globally, 2 billion hectares of land is degraded, resulted in the annual loss of 24 billion tons of fertile soil and subsequent effects on 1.5 billion of land-dependent population worldwide. As global air temperature rises and the human population expands, the planet is increasingly vulnerable to desertification and land degradation. As a result, combating desertification and land degradation neutrality (LDN) constitute integral parts of SDG15. Mongolia is one of the countries in the world which serious problem with forest depletion, land degradation and desertification. Thus, numerous activities for forest restoration and land rehabilitation had been conducted in Mongolia, but many of the restoration and rehabilitation activities shown poor results due to natural reason, such as harsh climate, and lack of understanding of the ecological characteristics and research capacity. This paper aimed to cover achievements of forest restoration and combating desertification projects conducted recently in Mongolia and to identify the attributes promoting its success in different projects at different part of Mongolia. The success story of northern coniferous forest restoration in Tujiin Nars area and Southern Saxaul forests and reforestation oriented researcher results will be introduced. According to researches on restoration and rehabilitation, water (precipitation) is one of the limiting factors which affect planted seedling growth survival in Mongolia and prevention from of livestock grazing and forest fire is also another important factor. For successful rehabilitation of degraded forests or arid southern conditions of Mongolia, standard techniques for species selection and improvement of rehabilitation effects should be integrated in silvicultural treatments and molecular genetics techniques for increased water use efficiency and stress tolerance is needed.

Key words: Desertification, land degradation, restoration, Mongolia

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Enhancement of carbon storage and sequestration of mangrove forests: C-PFES implementation toward climate change mitigation and Implications: A case study in Hai Phong Coast, Vietnam

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Abstract

Mangrove forests are important and known as one of the most productive ecosystems in the tropics. They reduce the impacts of extreme events, provide important breeding grounds for aquatic species and build the resilience of ecosystem-dependent coastal communities. They play an important role in carbon sequestration and are identified as one of the most carbon-rich ecosystems, acting as a powerful sink for atmospheric carbon. Continued pressures on mangrove ecosystems, such as increasing demand for timber and firewood, and the expansion of aquaculture and agriculture has exacerbated the problem of global climate change. On the contrary, Mangrove forests are also known as one of the most threatened and vulnerable ecosystems worldwide, which have experienced a dramatic decline due to extensive coastal development during the last half-century. Carbon stocks estimation has received the attention of many countries around the world. With the aim of reducing emissions, mitigating the impacts of climate change, and improving the livelihoods of local people in coastal areas, the current solutions of afforestation and protection of coastal mangrove forests are being considered. This study was conducted to provide the scientific basis for a carbon credit scheme on the coast of Hai Phong by estimating above ground carbon stocks (AGC) and soil organic carbon (SOC). There were 20 plots set up and evenly distributed across Bang La and Dai Hop (only 17 plots for mangrove structure investigation, 20 plots for SOC study). The results showed that AGC stocks were significantly lower than SOC, normally ranging from 9.9 to 29.55 tons ha^{-1}. Using the Walkley-Black method, the total SOC was estimated at the range of 81.76 to 323.83 tons ha^{-1} (with an average of 161.47$\pm$15.85 tons ha^{-1}), which indicated a strong relationship between tree density and SOC. In addition, using the IDW interpolation method, this study estimated that the total CO_2 absorbed by mangrove forests was 1,631,834 tons in Bang La and Dai Hop, including 170,462 tons of CO_2 accumulated in the tree biomass and 1,461,372 tons of CO_2 in the soil, which provided a strong evidence for the potential application of C-PFES and the development of a carbon credit scheme in Vietnam.

Key words: Biomass, carbon stocks, Hai Phong coast, mangrove forests, soil organic carbon

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Applied Biology

A single quantitative trait locus on *Glycine latifolia* chromosome 13 is associated with resistance to *Meloidogyne incognita*

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Abstract

Perennial *Glycine* species are potentially valuable genetic resources that can improve disease resistance in soybean by hybridization or gene transfer techniques. The goal of this research is to discover novel *M. incognita* resistance quantitative trait loci (QTL) from perennial *Glycine* spp. that can be further characterized for potential use in soybean. From our initial screening of 18 accessions of 10 perennial *Glycine* species for resistance to *Meloidogyne incognita*, we discovered that *G. latifolia* plant introduction (PI) 559300 has a higher level of resistance to *M. incognita* than the resistant soybean check Forrest. To identify QTL associated with resistance to *M. incognita* in *G. latifolia*, we have conducted a QTL analysis using recombinant inbred lines derived from resistant (PI 559300) and susceptible (PI 559298) *G. latifolia* accessions and single nucleotide polymorphism markers generated through genotyping by sequencing. The initial analysis identified a single QTL on *G. latifolia* chromosome 13. The QTL interval spans a region from about 824.9 Kbp, explaining 29.1% of the phenotypic variation. This QTL contains at least 37 putative genes that have not been examined for their functions against *M. incognita*. We expect that the QTL on *G. latifolia* chromosome 13 is a major QTL responsible for resistance to *M. incognita* and contains novel genes that confer this resistance. We also anticipate that *G. latifolia* PI 559300 is a good candidate for utilizing genes that are effective against *M. incognita* and could be used to improve soybean resistance to *M. incognita*.

Key words: *Glycine latifolia*, *Meloidogyne incognita*, resistance

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Applied Biology

Screening and testing bacterial effector proteins to identify potential interactors between *Bactericera cockerelli* and *Candidatus* Liberibacter solanacearum

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Abstract

'*Candidatus* Liberibacter solanacearum' (Lso), is a bacterial pathogen which causes serious damage to solanaceous crops, and in potato it causes zebra chip. Presently, nine distinct haplotypes have been found and named depending on their host plants and insect vectors. Among them, two haplotypes of Lso (LsoA and LsoB) are present in North America and both are transmitted by *Bactericera cockerelli* (the potato psyllid) in a circulative and persistent manner. Previous studies in my laboratory showed the Lso manipulates the plant and vector immune responses. Indeed, bacterial pathogens use different approaches to manipulate the host defenses. One of these approaches commonly used by pathogens is the secretion of proteins that can suppress host defenses or hijack specific pathways; these proteins are commonly named effectors. We have identified putative Lso effectors using bioinformatic analyses. I am currently evaluating their secretion using a bacterial surrogate system and testing their ability to manipulate defenses by cell death assays. Finally, I generated a cDNA yeast two hybrid library of potato psyllid which I am screening with the candidate effectors to identify insect interactor proteins. This work will provide new insights into Liberibacter virulence.

Key words: *Bactericera cockerelli*, *Candidatus* Liberibacter solanacerum, bacterial effector

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Applied Biology

Uncovering Symbionts Across the Psyllid Tree of Life and the Discovery of a New Liberibacter Species, "Candidatus" Liberibacter capsica

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Abstract

Sap-feeding insects in the order Hemiptera associate with obligate endosymbionts that are required for survival and facultative endosymbionts that can potentially modify resistance to stress, enemies, development, and reproduction. In the superfamily Psylloidea, the jumping plant lice (psyllids), less is known about the diversity and prevalence of their endosymbionts compared to other sap-feeding pests such as aphids (Aphididae). To address this knowledge gap, using 16S rRNA sequencing we identify symbionts across divergent psyllid host lineages from around the world. Taking advantage of a new comprehensive phylogenomic analyses of Psylloidea, we included psyllid samples from 44 species of 35 genera of five families, collected from 11 international locations for this study. Across psyllid lineages, a total of 91 OTUs were recovered, predominantly of the Enterobacteriaceae (68%). The diversity of endosymbionts harbored by each psyllid species was low with an average of approximately 3 OTUs. Two clades of endosymbionts (clade 1 and 2), belonging to Enterobacteriaceae, were identified that appear to be long term endosymbionts of the psyllid families Triozidae and Psyllidae, respectively. We also conducted high throughput metagenomic sequencing on three Ca. Liberibacter infected psyllid species (Russelliana capsici, Trichochermes walkeri, and Macrohomotoma gladiata), initially identified from 16S rRNA sequencing, to obtain more genomic information on these putative Liberibacter plant pathogens. The phylogenomic analyses from these data identified a new Ca. Liberibacter species, Candidatus Liberibacter capsica, that is a potential pathogen of solanaceous crops. This new species shares a distant ancestor with Ca. L. americanus, which occurs in the same range as R. capsici in South America. We also detected the first association between a psyllid specializing on woody hosts and the Liberibacter species Ca. L. psyllaurous, which is a globally distributed pathogen of herbaceous crop hosts in the Solanaceae. Finally, we detected a potential association between a psyllid pest of figs (M. gladiata) and a Ca. Liberibacter related to Ca. L. asiaticus, which causes severe disease in citrus. Our findings reveal a wider diversity of associations between facultative symbionts and psyllids than previously reported and suggest numerous avenues for future work to clarify novel associations of ecological, evolutionary, and pathogenic interest.

Key words: Candidatus Liberibacter asiaticus; Candidatus Liberibacter capsica; Candidatus Liberibacter psyllaurous; endosymbiont; endosymbiont evolution; long-term endosymbiont; microbiome; psyllid.

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Applied Biology

Developing a RaMV viral vector for genetic study in radish

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Abstract

Cruciferous plants *Raphanus raphanistrum* (Radish) is one of the most important vegetables in Korea, and usually used as the base ingredient of kimchi, the most important component in Korean dishes. Radish mosaic virus (RaMV) is a crucifer-infecting virus from genus Comovirus (family Secoviridae), which naturally infects radish in Korea. From 2014~2017, we collected several RaMV infected radish samples, and three infectious clones of RaMV were generated from isolates collected in mainland Korea (RaMV-Gg) and Jeju Island (RaMV-Aa and RaMV-Bb). Examination of the wild type isolates (Aa, Bb and Gg) and reassortants (Ab, Ag, Ba, Bg, Ga and Gb) between the genomic RNA1 and RNA2 of these three isolates revealed that severe symptoms were associated with RNA1 of isolates Aa or Gg causing systemic necrosis in *Nicotiana benthamiana* (N. b), and mild symptoms were associated with RNA1 of Bb. In order to develop a viral vector for radish genetic study based on RaMV infectious clones, RaMV-Ba which cause mild symptom on N. b was selected vector construction. The genes of interests expressed either between the MP and LCP of Ba-RNA2, or by replacing the LCP/SCP gene sequences of a duplicated RNA2 (named Ba-RNA3). GFP was stably expressed from either RaMV Ba-RNA2 or Ba-RNA3 constructs, size of foreign genes up to 1.6kb was successfully expressed from Ba-RNA3 constructs in N. b, with gene expression in the newly-formed upper leaves demonstrated by RT-PCR. These results show that RaMV is expected to be developed as a promising viral vector for genetic study in N. b and radish.

Key words: Radish mosaic virus, viral vector, foreign protein expression

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Applied Biology

Secreted effectors from *Phytophthora capsici* function as suppressor of INF1- or BAX-induced cell death in N. *benthamiana*

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Abstract

Phytophthora capsici is one of the most destructive hemibiotrophic pathogens; it can cause blight in chili peppers (*Capsicum annuum*), and secrete various effector proteins to infect the plants. These effectors contain an N-terminal conserved RXLR motif. Here, we generated full-length RXLR effector coding genes using primer pairs, and cloned them into the pGR106 vector for in planta expression. Two of these genes, *PcREK6* and *PcREK41*, were strongly induced when the chili pepper plants were challenged with *P. capsici*. This result provides molecular evidence to elucidate the virulence or avirulence factors in chili pepper. Our results also showed that *PcREK6* and *PcREK41* effectors induce hypersensitive cell-death when expressed in chili leaves. Cell death suppression assays in *Nicotiana benthamiana* revealed that most effectors could not suppress programmed cell death (PCD) triggered by Bcl-associated X (BAX). However, PcREK6 fully suppressed PCD triggered by BAX, while PcREK41 partially suppressed PCD triggered by INF1 elicitin. These results suggest that PcREK effectors from *P. capsici* interact with putative resistance proteins in planta, and different effectors may target different pathways in a plant cell to suppress pattern- or effector-triggered immunity.

Key words: *Phytophthora capsici*, chili pepper, RXLR effector, suppressor, programmed cell death

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Applied Biology

The Ecological Characteristics of *Erwinia pyrifoliae*, a Causal Agent of Black shoot blight on apple and pear.

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Abstract

Erwinia pyrifoliae was first reported in 1999 as a causal agent of black shoot blight (BSB) in apple and pear in Korea. BSB is one of the most destructive disease in apple and pear along with fire blight caused by closely related bacteria *E. amylovora*, and recently BSB became epidemic in S. Korea. Symptoms of black shoot blight are almost indistinguishable from fire blight. However, unlike *E. amylovora* the ecological characteristics of *E. pyrifoliae* are not fully understood. In this study, we investigated the ecological characteristics of *E. pyrifoliae* including effects of temperature, pH and bactericides on the growth, motilities, EPS production, biofilm formation. The maximum growth rate of *E. pyrifoliae* were overserved at 28℃. However, their motility, EPS production and biofilm formation were significantly greater at 14℃ than 28℃. Furthermore, *E. pyrifoliae* were treated with several antibiotics to determine minimum inhibitory concentration to identify the dormancy form. The results showed that 0.01 mM of $CuSO_4$ treatment was able to induce the cell dormancy of *E. pyrifoliae* as viable but non-culturable (VBNC). The effect of environmental conditions on ecology of *E. pyrifoliae* and role of VBNC dormancy cell stage will be discussed. This work will provide new insights for developing effective control methods of BSB.

Key words: *Erwinia pyrifoliae*, black shoot blight, apple, pear, VBNC

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Promoting drought stress tolerance in barley seedlings by phenazine producing bacteria *Pseudomons chlororaphis* 30-84

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Abstract

Drought is an important abiotic stress that reduces the quality and yield of barley production. In this study, we investigated the role of phenazine producing plant growth promoting rhizobacteria *Pseudomonas chlororaphis* 30-84 on drought stress tolerance in barley seedlings and compared with a phenazine deficient derivative 30-84 ZN or control (no bacteria). The roots inoculated with the phenazine-producing 30-84 WT showed proliferated root architectures that able to promote water uptake compared to the plants inoculated with 30-84 ZN or no-inoculum control. The water contents of the barley seedlings inoculated with the phenazine-producing strain also showed higher relative water contents than phenazine deficient mutant 30-84ZN and control plants during water deficient and the recovery period. Similarly, after severe drought stress for 15 days, soil moisture contents were greater in the rhizosphere soil of seedlings colonized with phenazine-producing strains. In addition, the chlorophyll content of leaves and the level of MDA and proline, ROS scavenging enzymes of roots were examined. There was no difference in chlorophyll contents between treatments. However, the level of MDA contents in the root were decreased, and the proline contents were increased in the seedlings inoculated with the phenazine-producing strain. These results suggest that seedlings colonized by phenazine-producing bacteria promote drought tolerant by enhanced water uptake of root, increasing soil moisture and ROS scavenging at the root surface. These results support the hypothesis that the presence of phenazine producing *P. chlororaphis* 30-84 promotes drought tolerance in barley.

Key words: Barley, Drought-stress tolerance, phenazine, *Pseudomons chlororaphis* 30-84

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Applied Biology

Taxonomic study of the subfamily Tortricinae (Lepidoptera: Tortricoidea: Tortricidae) from South Korea

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Abstract

The family Tortricidae is commonly known as leaf-rollers owing to the peculiar habit of the larva to roll leaves of the host plant to create shelter. They are a large group comprising 11,365 species in the world and 434 species in the Korea. The subfamily Tortricinae is one of the three subfamilies of the family Tortricidae with 174 species in the Korea. In this study, we summarize the current research status with information of Korean leaf-roller, and present what to focus on in the future.

Key words: Tortrix moth, Leaf-roller moth

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Taxonomic review of the genus *Hishimonus* Ishihara (Hemiptera: Auchenorrhyncha: Cicadellidae: Deltocephalinae) from Korea

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Abstract

The genus *Hishimonus* Ishihara (Hemiptera: Auchenorrhyncha: Cicadellidae: Deltocephalinae) belonging to the tribe Opsiini and comprising 62 species from Palearctic, Oriental, Australian, and Afrotropical region. The genus can be distinguish ed from other genera in tribe Opsiini by the presence of characters: a large semicircular brown spot on the forewings, when the wings are at rest; bifurcate aedeagus with a pair of gonopores. In Korea, two species, *Hishimonus hamatus* Kuoh, 1976 and *H. sellatus* (Uhler, 1896) have been recorded. In this study, the genus *Hishimonus* from Korea is reviewed with one new species and two new recorded species. Additionally, morphological information such as description, photographs of habitus and genitalia, and a key to the Korean *Hishimonus* species are provided.

Key words: Hemiptera, Cicadellidae, Taxonomy, *Hishimonus*, Leafhopper

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Division of Animal

Alternative antibiotics goes a long way with a successful delivery method to improve gut health in poultry

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Abstract

Emerging concerns on antibiotic resistance steered the legal ban on in-feed sub-therapeutic growth promoting antibiotics usage in the poultry industry to address the consumer's health concerns. As a consequence, many alternatives have been developed to maintain maximum growth performances while reducing gut infections such as coccidiosis and necrotic enteritis in commercial chickens. Even though some alternatives reported were promising as an alternative for antibiotic growth promoters (AGP), most of them were failed to reach the same efficacy as AGPs. Moreover, those alternatives showed inconsistent responses in chickens and the results vary greatly from experimental setup, chicken breeds, and other farm operations. Observed variations might be explained by the lack of proper delivery strategy to bring these alternatives to AGP to the target site of the chicken intestine without losing their functional properties. In recent years, there has been a groundswell of studies to develop new delivery strategies to carry alternative AGPs into the chicken gut. Microencapsulation, in-ovo injection, nanoparticles, and gel vaccination are some of those techniques that reported to be effective in chickens. In comparison, delivery strategies for antimicrobial peptides have attracted considerably less interest in the poultry industry. Such an effective system plays a key role in the development of a potent and safe AMP-based alternative to AGP strategy to chickens. In our recent study, we developed a *Bacillus subtilis*-based delivery system to deliver chicken NK lysin (cNK-2) antimicrobial peptide to the coccidiosis-infected chicken gut. Showing its effectiveness, we observed significantly improved growth performance, gut health, anti-parasitic effect, and major gut microbiota shifts following *Eimeria* infection in chicken treated with *B. subtilis* based cNK-2 peptide compared to its control. Therefore, our study is the first to show the *B. subtilis*-cNK-2 delivery system as a practical and effective delivery strategy to mitigate the negative effects of avian coccidiosis in commercial broilers.

Key words: Alternative antibiotics, delivery method, broiler chicken, chicken NK lysin

Division of Animal

Effects of Brown Rice on Growth Performance and Nutrient Digestibility of Weaned Pigs

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Abstract

This study was conducted to evaluate effects of brown rice on growth performance, nutrient digestibility, and blood parameters of weanling pigs. A total of 60 weanling pigs (6.73 ± 0.77 kg of body weight [BW]; 28 days of age) were randomly allotted to 2 dietary treatments (6 pigs per pen; 5 replicates per treatment) in a randomized complete block design (block: BW and sex): a basal diet based on corn-soybean meal (CON) and the CON replaced 50% of corn with brown rice (BR). Pigs were fed respective dietary treatments for 5 weeks. During the last week of the experimental period, pigs were fed their respective dietary treatments containing 0.2% chromic oxide. fecal samples from randomly selected 1 pig per pen were collected three days during the last week of experiment. Blood was collected from randomly selected 1 pig in each pen on d 0, 3, 7, and 14 for blood parameters. The randomly selected 1 pig per pen was sacrificed to collect ileal digesta. Compared with pig fed CON diet, pigs fed the BR diet were found to have higher ($p < 0.05$) final BW, overall average daily gain, and apparent ileal digestibility (AID), and apparent total tract digestibility (ATTD) of dry matter and energy. However, there were no significant differences between the groups with respect to average daily feed intake, gain to feed ratio, frequency of diarrhea, and the AID and ATTD of crude protein during overall experimental period. Similarly, there were no significant differences in blood parameters between the groups. In conclusion, brown rice could be used to replace 50% of corn in the nursery diet without negatively affecting growth performance, nutrient digestibility, and blood parameters.

Key words: Alternatives, Brown rice, Growth performance, Nutrient digestibility, Weanling pigs

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Division of Animal

Unraveling the Genetic Diversity and Population Structure of Bangladeshi Indigenous Cattle Populations Using High-Density SNP Markers

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Abstract

Indigenous cattle have extraordinary adaptation capability to diverse environments under low input production system. Understanding the genetic basis of locally adapted indigenous cattle populations is essential to design appropriate strategies and programs for their genetic improvement and conservation. Here, we report genetic diversity measures, population differentiation and structure of 218 animals sampled from six indicine cattle populations of Bangladesh those genotyped with Illumina Bovine SNP50K BeadChip along with genotyped data of 505 individuals from 19 zebu and taurine breeds worldwide. The principal component analysis (PCA) showed clear geographic separation between taurine and indicine lineages where Bangladeshi indigenous cattle clustered with South Asian zebu populations. However, overlapped clusters in PCA, heterozygosity estimates and Neighbor-Joining phylogenetic tree analysis revealed weak genetic differentiation among the indigenous cattle populations of Bangladesh. The admixture analysis at K = 5 and 9 suggests distinct genetic structure of the studied populations along with very low proportion of taurine ancestry. Moreover, admixture and phylogenetic analysis highlighting historical gene flow among the studied populations. The effective population size suggesting limited pool of ancestors particularly for Sahiwal and North Bengal Grey cattle. In conclusion, these findings shed insights into genetic architecture of six indigenous cattle populations of Bangladesh for the first time that could potentially be harnessed in future breeding programs particularly for improvement of their production and conservation schemes.

Key words: Genetic diversity, population structure, indigenous cattle, SNP array, Bangladesh

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Division of Animal

Phylogenetic analysis of the BF1 gene in five Korean Native Chicken lines by comparing with allelic sequences in the IPD-MHC database

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Abstract

Korean Native Chicken, an important poultry genetic resource of Korea, is believed to be demonstrated high disease resistance. The advantageous variations in their Major Histocompatibility Complex (MHC), the genomic region for the immune response in chicken, can be the reason behind this phenomenon. Because the BF1 gene of the classical MHC class - I involves this immune response, sequences of the BF1 gene of five Korean Native Chicken (KNC) lines, including KNC red line, yellow line, white line, gray line, and Ogye, were compared with the sequence data in the IPD-MHC database. Firstly, possible homozygous individuals from all the five lines were selected through a variants-based stepwise refinement procedure involved with microsatellites and SNPs-based approaches. Once, apparently homozygous individuals were identified, PCR was used to amplify the BF1 gene and sequences were obtained using Illumina Next Generation Sequencing (NGS), followed by assembling with *Gallus gallus* reference genome and making the consensuses using Geneious prime sequence analysis tools. Meanwhile, the published chicken BF1 allelic query containing 12 alleles (BF1*002:01:01, 004:01:01/02:01/03:01, 005:01:01/02:01, 006:01:01, 009:01:01, 012:01:01/02:01, 017:01:01, 023:01:01) was downloaded from IPD-MHC database. Then, the sequences from the allelic query and the KNC sequences were aligned using MAFFT multiple aligning tools. Finally, the phylogenetic trees were generated addressing both the Maximum Likelihood approach through PhyML, RAxML, and Bayesian approach through MrBayes plugins. After multiple alignment, none of the KNC BF1 gene sequences were perfectly matched with any of the known BF1 alleles, indicating KNC breeds have previously unidentified novel alleles. Based on the results obtained from all three phylogenies, the BF1 gene of KNC gray line, red line, and white line remain closely similar to the BF1*009:01:01, BF1*005:01:01/02:01, and BF1*012:01:01 with identity percentages of 98.30%, 98.18%, and 98.15% respectively. The identity percentages of all the considered alleles reported more than 93% similarity between each other. Further, the yellow line and Ogye share their highest identity percentages with each other rather than any of the known alleles. Correspondingly, the present study concludes that none of the BF1 genes of KNC does follow any known alleles, giving rise to new BF1 alleles, and all the considered alleles have conserved at least 93% of identity between each other.

Key words: KNC, MHC-BF1, NGS, Phylogeny

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Division of Animal

CCL2 regulates prostaglandin circulation and embryo attachment of the bovine endometrium during implantation

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Abstract

CCL2 (C-C motif chemokine ligand 2), which regulates immune cells, has been reported to be expressed in the bovine endometrium during pregnancy. However, the details of how CCL2 is involved in the implantation mechanism of bovine embryos are still unclear. The purpose of this study is to analyze the expression pattern and functional properties of chemokines in the bovine endometrium and embryos. The qPCR analysis of the tissue showed that the amount of CCL2, CCL8 and CXCL10 were high at the implantation stage. The amount of CCL2 was significantly high in IFNa treated bovine endometrial stromal (BES) cells in vitro. In bovine endometrial epithelial (BEE) cells, however, the amount of CCL8 and CXCL10 were significantly high in the treatment group, but not for CCL2. The mRNA of each chemokine receptors (CCR1, CCR2 and CXCR3) was detected in the endometrial tissues and cells by RT-PCR. Cellular proliferation of BEE and BES significantly increased by the CCL2 treatment. The amount of prostaglandin (PG) E2 synthases, PGES1 and PGES2, and PGF2 alpha synthase, AKR1C4, were high at the implantation stage compared with luteal stage. The amount of PGES2 and AKR1B1 were significantly increased by CCL2 treatment does-dependently in BEE. In BES, on the other hand, the amount of PGES3, AKR1A1 and AKR1C4 were increased by CCL2 treatment. The qPCR analysis of the tissue showed that there were no differences in the amount of PGs transporter transcripts (MRP4 and PGT) between the luteal and implantation stages. The amount of MRP4 and PGT were significantly high in CCL2 treated bovine endometrial epithelial (BEE) and stromal (BES) cells in vitro. The mRNA of chemokine receptors (CCR1, CCR2 and CXCR3) were detected in the bovine trophoblastic cells derived from the blastocyst (BT) by RT-PCR. The amount of PCNA and IFNt were significantly high in the BT treated with CCL2 compared to the control. CCL2 significantly increased the attachment rate of BT vesicles to BEE in in vitro co-culture system. The amount of OPN increased in BEE, and ICAM-1 increased both in BEE and BT by CCL2 treatment, respectively. CCL2 treatment did not differ the amount of SELL in BEE and BT. These results indicate that CCL2, which expression increased in bovine endometrium during implantation by embryonic factors, has the potential to regulate the synthesis and circulation of PGs in the endometrium and the embryo growth. In addition, CCL2 has a possibility of regulating the process of bovine embryo attachment to the endometrium by modulation of binding molecules.

Key words: Bovine, CCL2, Endometrium, Prostaglandin, Implantation

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Development of ultra-precise consulting using Big data integration on Hanwoo cattle

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Abstract

Since 1990, the amount of greenhouse gas (GHG) on earth, which causes global warming, has been increasing over years, reaching 5.09 billion tons in 2017. The emission of GHG in livestock production accounts for 18.4% of the total, higher than that from the vehicles. As one of the potential solutions for minimizing the GHG per unit of product but remaining the proficiency of meat production, changes in the cattle breeding system are critical. A highly precise non-contact counseling platform was established using the Hanwoo cattle's pedigree, and genome information, combining with environmental factors for selection of potential calves with high heritability for a particular purpose and prediction of meat productivity at slaughtering through evaluating the abilities in each stage of growth as well. The data system is going to be built with database management by MySQL, and quality control by Plink1.9. Breeding values are estimated using the BLUPF90 family (RENUMF90, AIREMLF90, BLUPF90). A web server linked with the data server was also designed for performing counseling and result displaying. This platform is expected to reduce the nourishing time by 3 months, decreasing the production fee, ameliorating the economic efficiency of the Hanwoo in the beef market and in turn controlling the GHG emission.

Key words: Hanwoo, big data, consulting

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Dairy Science

Mitigation of gaseous emissions from animal waste with plant-based peroxidase

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Abstract

Confined animal feeding operations impact environment via gaseous emissions to atmosphere. Practical and proven technologies are needed to mitigate emissions. These mitigation technologies require consideration of socioeconomics. Besides the animal production industry, the public and regulatory agencies are concerned and interested in technologies that are proven in farm-scale conditions. This research focuses on developing one such technology from the lab-scale to farm-scale trials. In earlier lab- and pilot-scale studies, we have shown that soybean peroxidase (SBP) mixed with calcium peroxide (CaO_2, a catalyst) was effectively mitigating gaseous emissions from swine manure. Thus, a farm-scale trial was conducted at the university-owned swine barn. The barn had two rooms used for testing, each housing approximately 80 pigs, with shallow manure pit, and mechanical ventilation. The mix of SBP/CaO_2 was applied to manure pit by sprinkling onto surface on Day 1 of the 42-day experiment at 2.28 kg/m2 and 4.2% CaO_2 added by weight. Gas samples were collected from the primary barn exhaust fans. Significant reductions in emissions were observed for ammonia (22%), hydrogen sulfide (80%), and selected odorous volatile organic compounds (VOCs). There were no significant changes to the greenhouse gas emissions. This presentation will highlight the progression of research from lab to farm and suggest directions for future research with plant-based peroxidase.

Key words: Animal waste, Air quality, emissions, waste management

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Dairy Science

Smart Livestock Farming Strategies for the United States

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Abstract

Our food production system is still facing multiple issues that may hamper the prosperity of humankind. Demand for animal-source food has increased since 1970, and it is still predicted to grow another 35% by 2030 and 50% by 2050. Solutions to ameliorate agriculture's impact on the environment are desperately needed to prevent an overall collapse of the production system around the world. We need to reduce livestock production contributions to greenhouse gas (GHG) emissions immediately. Some have proposed the net-zero, carbon-neutral, or climate-neutral concept to avert the situation about livestock impact, but this concept has often been criticized as a manipulation of data and prediction rather than a set of solutions that would deliver real impact. Smart livestock farming (SLF) or precision livestock farming (PLF) technology embraces engineering principles and techniques to automatically monitor, model, and manage animal production within a farm or ranch. In that sense, SLF allows for real-time monitoring of animals equipped with sensors to ensure maximum usage of farm resources while controlling the health and welfare of animals. SLF has the potential benefit of reducing GHG by assisting in selecting energy-efficient animals that can be raised more sustainably. For about 60 yrs in the US, innumerable livestock experimental data have been collected on animal population samples. Decision support systems (DSS) were developed using this collective database. However, modern DSS must be developed to incorporate existing scientific knowledge of livestock production with big data collected via sensors. SLF can become the next generation of tools for sustainable livestock production, but compatibility among sensors, artificial intelligence programming, and standard methods must be employed to allow for the comparison of different production systems.

Key words: Sustainability, Beef Cattle, Production, Artificial Intelligence, Modeling

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Dairy Science

Application of the Hand-Held Laser Methane Detector for Measuring Enteric Methane Emissions from Cattle in an Intensive Farming

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Abstract

A hand-held laser methane detector (LMD) method has been suggested to reduce labor, time, and costs in measuring methane (CH_4) emissions from the enteric fermentation of ruminants in the field. This study aimed to establish a standard procedure of using LMD to assess the CH_4 production of cattle and evaluate the protocol's efficacy to test the difference in CH_4 emissions from cattle fed different forage-to-concentrate (FC) ratios. Experiment 1 was conducted with four Hanwoo steers (584 ± 57.4 kg of BW) housed in a metabolic cage individually. The LMD, installed on a tripod, aimed at the animal's nostril and measured the CH_4 concentration in the exhaled gas for 6 min every hour for two consecutive days. For the data processing, the CH_4 concentration peaks were identified by the Automatic Multi-scale Peak Detection algorithm. The peaks were then separated into those from respiration and eructation by fitting combinations of two of the four distribution functions (normal log-normal, gamma, Weibull). Additionally, the most appropriate time of day and the number of consecutive measurements were determined to represent the daily average of CH_4 concentration. In experiment 2, thirty Hanwoo growing steers (343 ± 24.6 kg of BW), blocked by body weight, were randomly divided into three groups. Three different diets were given to each group: high FC ratio (0.35) with high NDF (44% DM), high FC ratio (0.35) with low NDF (37% DM), and low FC ratio (0.25) with low NDF (35% DM). After ten days of feeding the diets, CH_4 concentrations in all steers were measured and analyzed in duplicate according to the protocol established in experiment 1. The mean correlation coefficient between the CH_4 concentration from respiration and eructation was the highest when a combination of two normal distributions was assumed ($r = 0.79$). The most appropriate measurement times were four times at two hours and one hour before and one hour and two hours after morning feeding. Compared with the low FC ratio and low NDF group, the high FC ratio and high NDF had 49% and 57% lower CH_4 concentrations in the exhaled gas from respiration and eructation, respectively ($P < 0.01$). In conclusion, the LMD method can be applied to evaluate the difference in CH_4 emissions in cattle using the protocol established in this study.

Key words: Hand-held laser methane detector, methane concentration, cattle, respiration, eructation, peak, distribution, forage-to-concentrate ratio

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Dairy Science

Evaluation of enteric methane production from nursery and growing pigs

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Abstract

Among the domestic enteric methane emission, pig enteric fermentation methane emissions account for about 7.4%. Since the enteric methane emission factor for domestic swine operation has not been developed, the IPCC Tier 1 approach default methane enteric fermentation factor, 1.5 kg CH4 $yr^{-1}\cdot head^{-1}$, is used. Therefore, this study was conducted to develop domestic enteric fermentation methane emission factor of pigs according to the growing stage. This experiment was carried out on nursery pigs under two months old and growing pigs up to 2-4 months old using the respiration chamber designed and manufactured to determine the enteric methane emission. The ventilation rate was maintained at 302.4$\pm$8.77L per minute, and methane concentration was measured using a real-time monitoring system. The recovery rate of the enteric methane emission evaluation chamber used in this study was 101.7$\pm$0.90%. This experiment was conducted on 18 pigs for each growing stage using three respiration chambers. Three nursery pigs, average body weight 22.4$\pm$1.45kg, were accommodated in each respiration chamber, and two growing pigs, average body weight 64.2$\pm$1.45 kg, were accommodated in each chamber. The pigs were given free access to water and fed ad libitum throughout the entire experiment period. As a result of the study, the methane concentration was 4.0$\pm$1.14 ppmv for nursery pigs and 5.23$\pm$1.05 ppmv for growing pigs, which was about 1.3 times higher than nursery pigs ($p<0.05$). The methane emission rate was 0.42$\pm$0.14 g/head/day for nursery pigs and 0.86$\pm$0.19g/head/day for growing pigs. The enteric methane emission rate of growing pigs was about twice as high as that of nursery pigs ($p<0.05$). According to 1 kg of body weight, the daily methane emission per head is 13.1$\pm$2.45mg of growing pigs, while the nursery pig was 17.53$\pm$5.59 mg, which was 1.3 times higher than growing pigs ($p<0.05$).

Key words: Enteric fermentation, respiration chamber, methane, growing pig, nursery pig

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Wearable Wireless Biosensor Technology for Monitoring Cattle: A Review

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Abstract

The wearable wireless sensor system (WWSS) plays a crucial role in providing behavioral and physiological data for individual animal in precision livestock farming. This review aimed to collect information about the WWSS for cattle and to conduct a systematic literature review on the accuracy of predicting the physiological parameters of these systems. The WWSS was categorized as an ear tag, halter, neck collar, rumen bolus, leg tag, tail‐mounted, and vaginal mounted types. Information was collected from a web‐based search on Google, then manually curated. We found about 60 WWSSs available in the market; most sensors included an accelerometer. The literature evaluating the WWSS performance was collected through a keyword search in Scopus. Among the 1875 articles identified, 46 documents that met our criteria were selected for further meta‐analysis. Meta‐analysis was con‐ ducted on the performance values (e.g., correlation, sensitivity, and specificity) for physiological parameters (e.g., feeding, activity, and rumen conditions). The WWSS showed high performance in most parameters, although some parameters (e.g., drinking time) need to be improved, and considerable heterogeneity of performance levels was observed under various conditions (average $I^2 =$ 76%). Nevertheless, some of the literature provided insufficient information on evaluation criteria, including experimental conditions and gold standards, to confirm the reliability of the reported performance. Therefore, this review suggested that guidelines for evaluation criteria for research evaluating sensor performance are needed.

Key words: wearable wireless biosensor systems, physiological parameters, sensor performance, meta‐analysis, cattle

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Rural & Agricultural Engineering

Prediction of pollution loads in agricultural reservoirs using RNN-LSTM algorithm

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Abstract

Water is consumed for various purposes such as living, industry, and agriculture. Among them, agricultural water is the most widely used, accounting for 63% of the total water consumption. However, compared to urban areas, the water quality in rural areas is insufficient to invest in environmental basic facilities such as sewage treatment. For water quality management of reservoirs, it is important to establish water quality improvement measures by predicting future water quality changes and to analyze the effects of the measures. Recently, along with the development of computers, research on water quality prediction using artificial neural networks based on big data is being conducted. The recurrent neural network (RNN) algorithm has been widely used in water-related fields such as water level prediction and water quality prediction due to its excellent time series learning. However, application researches on water quality prediction using an RNN algorithm are very limited due to limited water quality data. Therefore, in this study, data was constructed through linear interpolation of data to overcome data limitations. As for the research area, an agricultural reservoir in Nonsan, Chungcheongnam-do, Republic of Korea was selected. In this study, the prediction study was conducted from 7 days to 60 days instead of the daily prediction of water quality items using the RNN-LSTM algorithm. For day prediction, linearly interpolated daily water quality data and daily weather data (rainfall, average temperature, average wind speed) were used. In conclusion, most water quality items can be predicted up to 30 days, but the accuracy of the 45-day prediction is rapidly lowered.

Key words: LSTM(long short-term memory), water quality prediction, COD(Chemical oxygen demand), DO(Dissolved oxygen), SS(Suspended solid)

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Rural & Agricultural Engineering

Analysis of debris flow according to the location of the check dam: suggesting the optimal location by numerical simulation

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Abstract

The shallow landslide-generated debris flow on hillside catchments plays a critical role in the change of landscape features caused by natural hazards. When these debris flows occur in dams or reservoirs, they reduce the efficiency of facilities, and when they occur in residential areas, they cause many casualties and property damage. To minimize such damages, there are methods that can be performed through 1) installation of warning system and 2) construction of check dam. However, in the case of rainfall-induced debris flow, preparation through a warning system is challenging because debris flows very rapidly. Therefore, to reduce the damage caused by debris flow, the check dam should be installed, and for an efficient installment, research through numerical models should be performed. In this study, the mitigation effect through the check dam installation was analyzed using Deb2D numerical model which is a two-dimensional debris flow simulation software based on quadtree-grid. The debris flow was simulated through Voellmy rheology, and the erosion, entrainment, and deposition processes that must be considered for the analysis of debris flow were simulated using the algorithm suggested in our recent study. The Raemian apartment basin debris flow event, which occurred in Mt. Umyeon in 2011, was analyzed, and a check dam installation scenario was constructed by changing the distance from the collapse zone. According to the results, efficient check dam location can be suggested through the simulation results of the erosion depth.

Key words: Debris flow, Numerical model, Check dam, Mitigation effect

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Rural & Agricultural Engineering

Numerical study on delayed failure mechanism of gentle sloping ground

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Abstract

The 2018 Sulawesi, Indonesia, earthquake (Mw7.5) triggered massive flow slide on very gentle slopes of 1 to 5%. Thousands of casualties and missing persons were reported due to such unprecedented disaster. Although detailed mechanism of the flow has yet been speculative, liquefaction is identified as a possible suspect. In-situ microtremor observation results are briefly introduced, which shows that flow slide occurred on the ground where similar dominant frequency of H/V spectrum were observed. In the present study, cause of such a flow slide is numerically investigated using a 2D finite element method (Iai et al. 2011) by simulating the dynamic behavior of the 30 m thick and 200 m long gentle sloping ground (slope angle 2 deg.) of alternating silt and sand layers with the recorded acceleration as an input motion. Flow slide was simulated by varying the permeability of silt (5 m thick) located on top of the saturated loose sand (5m thick). When the permeability of silt (k_{silt}=1×10-6 m/s) is set lower than that of the saturated loose sand (k_{sand}=1×10-4 m/s), the surface layer above the boundary between the silt and sand starts to flow long after the ground shaking ended. In total 1,000 sec of simulation, the ground displacement of about 40 m was obtained. Close observation at the boundary elements revealed that the excess porewater pressure is gradually increasing in the silt layer while that in the liquefied layer dissipates. Mechanism of this type of failure has been studied as the void redistribution mechanism during liquefaction (Boulanger and Truman 1996) or the formation of water film (Kokusho 1999), which may cause delayed failure of the gentle sloping ground (Ishihara 1993). Although this study successfully simulates the delayed failure in 2D model, there is room for further research into seeking causes of the flow slides occurred in specific areas in Palu, Sulawesi, Indonesia.

Key words: The 2018 Sulawesi Indonesia earthquake, delayed failure, liquefaction, FEM

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Rural & Agricultural Engineering

Effects of a Parapet Structure on an Embankment Dam and Future Challenges

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Abstract

To investigate new methods to prevent the overtopping of embankments due to heavy rainfall, the effects of a newly designed parapet structure constructed on the crest of an embankment dam of a reservoir were investigated in this study. Additionally, other experimental methods for future investigation are proposed herein. To observe the continuous changes in the state of the dam, parapet-fitted and parapet-free embankments were tested under various modes: first seepage mode, earthquake mode, second seepage mode, and low water level mode. A centrifuge was used to model the earthquake conditions, with a seismic acceleration of 1.5 m/s^2 applied to mimic the real-world earthquake conditions in South Korea. The indicators of the experimental evaluation were the embankment deformation, water pressure difference, settlement ratio, and range of cracks at the dam crest, which are factors suitable for representing the effects attributed to the presence or absence of the parapet structure.

In the preliminary experiment, a remarkable difference in the indicator results between the parapet-fitted and parapet-free embankments was observed after the earthquake mode. The settlement ratio of the parapet-fitted embankment was two-fold lower than that of the parapet-free embankment, indicating that the structure had suppressed the development of cracks in the dam crest. In the parapet-free embankment, cracks tended to expand as a result of the increase in water pressure at the crack site after the earthquake mode. These findings suggest that the structural weight of the parapet has the effect of preventing overtopping and the occurrence of seismic disasters. However, more variables related to such disasters and the associated problems need to be investigated. Therefore, in this paper, additional experiments necessary for demonstrating the applicability and reliability of the parapets are specified and the engineering basis for the proposed experiments are discussed.

Key words: Parapet structure, Overtopping, centrifuge model test, dam cracks, seismic performance

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Rural & Agricultural Engineering

Improved heat curing performance of concrete with conductive materials by induction heating system

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Abstract

Recently, the use of concrete has significantly increased and cold-weather construction is inevitable. However, low temperature of concrete curing in cold weather significantly impedes the rate of strength development because of delayed cement hydration. Various heat curing methods, such as combustion heater or electric heater, are used to develop the initial compressive strength of concrete. However, these conventional methods emit a significant amount of hazardous substances, such as carbon monoxide (CO) and carbon dioxide (CO_2). In this study, an accelerating curing method using an induction heating technique was developed. This heating technique is characterized by a high heating rate and high energy transfer efficiency. The optimal induction heating method was determined by comparing the heating curves. Furthermore, the effects of incorporated conductive materials on the heat curing performance of concrete were evaluated. The conductive materials used in this study were steel fiber, amorphous steel fiber, electric arc furnace oxidizing slag, and carbon nano tube (CNT). Test results demonstrated that the induction heat technique can efficiently help strength development of early age concrete even in very cold weather. Furthermore, the incorporation of steel fibers and electric arc furnace oxidizing slag improved heat curing performance of concrete because steel forms and these conductive materials were heated by induced magnetic field.

Key words: Induction heating curing, cold-weather, compressive strength, SF, EAF

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Rural & Agricultural Engineering

Effect of curing temperature on self-sensing performance of concrete incorporating carbon fiber and carbon nano tube

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Abstract

In this study, the effect of curing temperatures on the self-sensing performance of concrete was investigated. Carbon fiber (CF) and Carbon nano tube (CNT) were used as the self-sensing concrete internal fillers, and both CF and CNT (Hybrid, HB) was also performed to evaluate the hybrid effect of the fibers. A cube specimen with a width×length×height of 50×50×50 mm was manufactured, and each specimen was cured for 3 days at temperatures of -20℃, 0℃, 20℃, and 60℃ to evaluate the self-sensing performance according to the curing temperature. The sensing performance of concrete was evaluated as a fraction change of resistance (FCR) by applying a repetitive load to each test subject. The concrete specimens with CF 1.0 vol.% showed the best sensing performance when they cured at 20℃, while the concrete specimens with CNT 1.0 vol.% showed the best sensing performance when they cured at 60℃. In the case of HB (CF 0.1 vol.% + CNT 0.5 vol.%) in which two types of fibers were mixed together, curing at 60℃ had the best sensing performance. In addition, it was confirmed that a reasonable level of sensing performance could be confirmed in all variables (CF, CNT, HB) that were cured at 20℃.

Key words: Self-sensing concrete, fillers, resistance, severe environment

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Rural & Agricultural Engineering

Effect of surface roughness on bond performance between UHPFRC and normal-strength concrete

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Abstract

The demand for ultra-high-performance fiber-reinforced concrete (UHPFRC) for applications in large scale structures and high-rise buildings. However, UHPFRC is an expensive material that is treated as a less economical material. In this study, the experiment was conducted for the manufacture of UHPFRC with the aim of attaching it to the area where the significant stress is applied. This is economical, taking advantage of the structural benefits of the UHPFRC while minimizing the use of expensive materials. In order to attach UHPFRC to normal-strength concrete (NSC), interfacial bond is important. This study evaluated the interfacial bond strength between UHPFRC and NSC by Slant Shear Test. To increase the surface roughness, three types of surface preparation methods (Brushing, Grooving, Shot Blasting) were applied. Two types of steel fibers (smooth fiber, hooked-ended fiber) were used to study the effects of fiber exposure conditions on the interfacial bond strength. Test results indicated that the shot blasting method most effectively increased the interfacial bond strength between UHPFRC and NSC, compared to the brushing and grooving methods. The bond strength was higher when the surface preparation was applied on NSC than when the surface preparation was performed on UHPFRC.

Key words: UHPFRC, Bond strength, surface preparation

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Biosystems Machinery Engineering

Evaluation of Quality of Agro-products by imaging

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Abstract

The quality of agro-products is affected by a variety of factors which, aside from those factors that are also related to food safety problems, may be weighted or flexible depending on customer awareness and current market conditions. Furthermore, agro-products have sample variations among batches or individual units, even when assessing the same product or cultivar type. Thus, evaluation of the quality of agro-products is more difficult than that for industrial products and needs more sophisticated sensing technique. New developments in sensing devices have allowed us to open a world of novel inspection methods. Optical instruments are a prominent example of advanced technologies used for food quality, including techniques such as imaging, spectroscopy, and hyperspectral imaging. In contrast with traditional methods for evaluating food and agro-products, these rapid techniques can deal with high throughput inspection. It is very important to quickly assess the external and internal attributes of agro-products in the product pipeline since those attributes are directly associated with both manufacturer profits and customer safety. As a result, a wide range of evaluation techniques for agro-products has been suggested for assessing appearance, texture and chemical components on agro-products. This presentation targets understanding of the basic principles and concepts of optical techniques, especially imaging, and also broadly presents their application for the assessment of agro-products in different parts of the world.

Key words: Image, Agro-food, Hyperspectral image

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Biosystems Machinery Engineering

Yield monitoring system: A test bench for estimation and mapping of yield through laboratory tests for potato harvesters

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Abstract

A yield monitoring system is one of the essential components of precision agriculture and major interests of the potato producers, providing instant yield and income information. Some commercial yield monitoring systems have been developed for several crops, but very few are available for potatoes. There are several factors that could affect the yield estimation of potato harvesters. Therefore, this research was aimed at establishing a test bench in the laboratory for estimation of potato yield considering different field slopes, forward speeds, and vibrations during harvesting of potatoes with potato harvester. A test bench was designed considering both the components of the mass-based (load cells with impact plate) and volume-based (CCD camera) yield monitoring components. Initially, some basic laboratory tests were carried out to compare the candidate sensors. Different potato dropping heights from the conveyor outlet to the impact plate were tested. Load cell signals due to the plate bending by the impact force were calibrated to the mass of the potatoes. The CCD camera was used to acquire the potato images and image processing techniques were applied to estimate the area and volume from the original images and calibrated to the mass of potatoes. The calibration tests of potatoes showed linear calibrations with R2 of 0.98 for potatoes dropped from a height of 30 cm for the mass-based and 0.37 for volume-based approaches. Different tests will be conducted on the test bench considering variations in the vibration, slope, and operation speed of potato harvesters. This test bench for estimating and mapping yield could provide valuable information for the appropriate design and development of a potato harvester with the yield monitoring system. The proposed yield monitoring test bench could also be used for testing and measuring yields of other specialty crops such as cabbage, carrot, sweet potato, etc.

Key words: Precision agriculture, yield monitoring, test bench, potato harvester

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Biosystems Machinery Engineering

Nondestructive measurement of phenolic compounds in Arabidopsis under different stress conditions

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Abstract

Phenolic compounds form an important class of secondary plant metabolites and is a source of antioxidant and antimicrobial characteristics. Arabidopsis is a small flowering plant which is named as a model plant in microbiology due to its important genetic properties. The plant consists of several phenolic compounds and their extraction were mostly performed using destructive chemical methods like gas chromatography (GC), high performance liquid chromatography (HPLC), and capillary electrophoresis (CE). These methods even though are highly precise and accurate, but they suffer with several limitations i.e. time consuming, expensive and labor intensive. Thus, there is a need to construct a fast and non-destructive analysis methods to solve the aforementioned problems. In this study, we explore the potential of Fourier-transform infrared (FT-IR) spectroscopy for the nondestructive evaluation of phenolic compounds in Arabidopsis under different stress conditions which was validated against reference HPLC method. The spectral acquisition for the plant samples was performed using laboratory based FT-IR spectrometer within 500-3500 cm-1 wavenumber range. For this research, the Arabidopsis plants were grown inside the growth chamber as drought and non-drought for 28 days. Three different lightning conditions i.e. white, blue and combination of red and blue were chosen to observe the change in phenolic compounds in Arabidopsis plants. The prediction analysis was performed using principal component regression (PCR), support vector regression (SVR) and partial least square regression (PLSR) methods in which PLSR acquired a higher prediction results with a correlation coefficient (R^2) of 0.978 and root mean square error of prediction (RMSEP) of 0.063 mg/g. The results therefore concluded that FT-IR spectroscopy when combined with suitable regression analysis method provides a fast, reliable and non-destructive testing of phenolic compounds in Arabidopsis plants under different stress conditions.

Key words: Arabidopsis, Phenolic compounds, Fourier-transform infrared (FT-IR) spectroscopy, Non-destructive

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Biosystems Machinery Engineering

Enhanced viability of freeze-dried Lactobacillus acidophilus using supercooling pre-treatment

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Abstract

Probiotics are living microorganisms that can act as intestinal microflora to offer health benefits to the host. In recent years, the global demand for probiotics has increased significantly, leading to the expansion of the probiotics market size. Most probiotic fortified foods in the market contain strains of *Lactobacilli* and/or *Bifidobacterium*. Probiotics are usually made into dried or frozen culture concentrates for lower distribution costs and to extend storage life. However, probiotics are sensitive to the environment and can be easily killed during a non-optimized manufacturing process. Freeze-drying is often considered the most appropriate drying method for biological materials and has been used to manufacture probiotic powders for decades. However, during the freeze-drying process, the initial freezing step forms ice crystals, which damage cell structure and decrease cell viability. Therefore, additional protective agents are commonly used to stabilize the cell suspension. The concentrations and combinations of protective agents are different for each probiotic strain, and the optimum protective effects need to be determined on a case-by-case basis. As an alternative to the use of cryoprotectant additives, we propose to protect probiotics by strengthening their natural defenses. When *Lactobacillus* culture shifts from its optimum growth temperature to a lower one, a cold-shock response is induced, triggering the production of surface layer protein (SLP). With the help of SLP, cells gradually acclimate to the lower temperature environment. Supercooling is a food processing technique which uses a storage temperature lower than the initial freezing temperature, thus limiting the development of ice crystals, to maintain the qualities of fresh foods. An oscillating magnetic field (OMF) controls ice nucleation and maintains supercooling status by reorientation/vibration of water molecules and/or breaks hydrogen bonds between water molecules, which in turn prevents ice crystallization. Therefore, we investigated the use of OMF-assisted (10 mT, 30 HZ) supercooling to treat *L. acidophilus* for 12 hours and aimed at achieving more SLP to improve the viability of *L. acidophilus*. OMF-assisted supercooling pretreatment effectively increased the production of SLP. Supercooled samples exhibited thicker SLPs than those in control groups and had significantly improved cell viability (78% increase). These results show the protective effect of the SLP during freeze-drying and indicate that OMF-assisted supercooling pretreatment is helpful for enhancing the viability of *L. acidophilus*.

Key words: Supercooling, probiotics

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Nutrient stress detection of lettuce seedlings grown in a plant factory using convolutional neural network

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Abstract

Rising health awareness influences people to consume fresh vegetables, especially those, which contain health-promoting components and prevent diseases. The yields of vegetables need to be increased to meet the increasing demand, but biotic and abiotic stresses of the plant affect the yield intrinsically. The objective of this study was to detect the nutrient stress of lettuce seedlings grown in a hydroponic system using a convolutional neural network. Plant stress results in constriction and reduction of plant leaf area along with discoloration. So, object detection, area calculation, and color determination are the fundamentals for stress phenotyping. In this study, a model was developed using the convolutional neural network and used to detect lettuce leaves. Leaf area was calculated through segmentation and pixel counting. Finally, leaf color was analyzed, and stress symptoms were determined. Lettuce plants were grown in the plant factory under five different EC (0.5, 1, 1.5, 2, and 2.5 dS/cm) conditions for four weeks, where the ambient environmental variables (i.e., temperature, humidity, light types, intensity, photoperiod, CO_2, and pH) were kept constant. Raspberry pi cameras were installed at the top of the plant beds to capture RGB images automatically. Image analysis was performed using the python and OpenCV platforms. The developed model detected the lettuce plants with an accuracy of 90%. The average accuracy of leaf area calculation was 93%. Although a satisfactory level of output was observed, the color-based stress detection algorithm needs to be improved. Overall, the obtained results demonstrated the reliability of the proposed framework for plant stress detection.

Key words: Lettuce, plant phenotyping, stress detection, artificial intelligence

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> **Biosystems Machinery Engineering**

Spatial analysis of potential distribution of gypsy moths (*Lymantria dispar*) with application of ensemble species distribution modeling

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Abstract

The gypsy moth, *Lymantria dispar* is a forest-damaging pest occurred in the Northern Hemisphere. It has damaged more than 100 trees as host plants, and many of them commonly found in South Korea, causing concerns of domestic forests with the recent outbreak. For this reason, this study developed a species distribution model for evaluating the potential distribution of gypsy moth to provide a data useful for determining where needs to be intensive. In this study, CLIMEX (version 4.0, Hearne software, Australia) and MaxEnt, two different species distribution modeling algorithms, were used to develop models for evaluating climatic suitability and occurrence possibility, respectively. Then, two models were integrated on the map to by overlaying the results of two models. Specifically, CLIMEX model was developed by estimating parameter values based on previous studies and worldwide occurrence records, while MaxEnt model was operated with uncorrelated bioclimatic variables extracted from coordinates of actual distribution. The climate change scenarios used in each model are RCP8.5 and SSP5-8.5, which are scenarios in which greenhouse gases continue to be emitted according to the current trend. Ensemble model was then developed with fuzzy overlay function in ArcGIS (version 10.4.1; ESRI, Redlands, USA) to identify consensus areas where both models showed high climatic suitability and occurrence possibility. Result showed all regions where reported actual occurrence of gypsy moth would be suitable under the current climate. However, it was expected that 42.5% and 12.5% of occurrence coordinates were expected to be suitable in 2060, and 2100, respectively, when applying climate change scenario. Hence, it is conclusive that high risk of gypsy moth occurrence predicted under the current climate will be decrease with climate change, but risk that is be concentrated in a specific area may occur with climate change.

Key words: Climate change, CLIMEX, ensemble modeling, gypsy moth, MaxEnt, spatial distribution

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Biosystems Machinery Engineering

Analysis of exhaust gas emissions by harvesting of combine harvester

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Abstract

Recently, the development of emissions reduction technology for agricultural machinery has gradually strengthened emission standards in advanced countries such as the U.S. and Europe. In Korea, the U.S. Tier 4 Final emission standards have been applied to construction and agricultural machinery since 2015. Also, research on emissions is actively conducted as emission standards for non-road transport pollutants have been gradually strengthened. This study was conducted to analyze the emission characteristics of a combine harvester during rice harvesting. A 67 kW class 5-row combine harvester (CX955, TYM Co. Ltd., Korea) was selected for measuring emissions during rice harvesting. Emissions were measured using Horiba's PEMS (Portable emissions measurement system) equipment which was certified worldwide. The emissions measurement test was repeated three times at each gear stage in harvesting. Engine rotational speed and torque were measured using CAN data, and engine power was calculated using engine rotational speed and torque data. The results show that exhaust gas emissions such as CO_2 and CO increase as engine power increases. NOx (Nitrogen oxide) and PM (Particulate matter) affected by exhaust gas reduction devices such as DPF (Diesel particulate filter) and SCR (Selective catalytic reduction) were decreased during rice harvesting. In this study, emissions are increased or decreased if the engine power changes. In the future, it is possible that research on emissions characteristics associated with the agricultural workload.

Key words: Combine harvester, Rice harvesting, Emissions, PEMS, Agricultural machinery

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> **Biosystems Machinery Engineering**

Development of Vacuum-Thermal Combination Pasteurization System for Barely Grass Powder

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Abstract

Recently, the sprout vegetable powder has a gain from consumers as a nutrition regulation supplement. However, pathogenic coliform detection issues have arisen in the several barely grass powder products. In this study, experiments and simulations were performed for the development of vacuum thermal combination pasteurization system that can reduce microorganisms without the deterioration in quality. As a result of the preliminary experiment, the quality index (water activity, CIE color change) of the barley grass powder treated by vacuum thermal combination system were not significantly changed. The reduction of microbes in the powder has been shown to be associated with an intermediate medium that can transfer heat to the powder (e.g moisture). Through the discrete element method simulation, it was found that the conical double helical shaped blade was effective for uniformly mixing the powder. Vacuum thermal combination pasteurization system was consisted of a steam injection, a band heater (water jacket), a vacuum system (100L, withstand up to ±10 bar) and a mixing unit. 5 kg of powder was heated up to 85℃ and temperature was maintained. The injected steam amount was controlled using time relay and PID controller. As a result of the treatment, it was confirmed that the number of coliform populations was significantly reduced to about 5 log CFU/g. Additional moisture from the steam could be effectively evaporated by vacuum heating. These results are expected to improve the storage stability of products and the safety of powdered foods.

Key words: Vacuum thermal combination, Discrete element method simulation, heat transfer, steam thawing, Coliform

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Biosystems Machinery Engineering

A comparison of statistical and neural network methods for growth prediction of ice-plants grown in a plant factory

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Abstract

Effective plant growth and yield prediction is an essential task for plant factory or greenhouse growers as well as for agriculture in general. Growth prediction can help growers to improve the environmental management for better production, match supply, market demand, and lower costs. The objective of this study was to compare the accuracy of growth prediction of ice-plants grown in a plant factory using multiple regression analysis and artificial neural network methods. Ice-plants were grown in a plant factory for four weeks under three different types of EC (1, 2, and 3) dS/cm and LED (Red:Blue) combinations (R5:B5, R7:B3, and R9:B1), where the temperature, humidity, CO2, photoperiod, and light intensity were kept constant. The sample collection was performed each week, and plant physical parameters (i.e., leaf area, number of leaves, areal part area, fresh weight, and length of the root) were measured and recorded. A regression- and ANN-based growth models were prepared using the measured growth data over the three weeks of cultivation. Both the plant physical parameters as well as the ambient environmental variables were used to prepare the ANN model. The relative growth rates of the considered growth parameters at the 4th week were predicted and compared to the measured value. According to the comparative study, the ANN-based model predicted a relatively low growth rate in some treatments, however, the overall performance of the ANN-based growth prediction was better compared to the regression-based growth prediction model.

Key words: Ice plant, growth, physical variables, prediction, artificial neural network

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> **Biosystems Machinery Engineering**

Pig diseases monitoring based on sound recognition using convolution neural network (CNN)

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Abstract

In livestock production, disease detection, responses, and prevention are critical and difficult. Early diseases detection is an efficient way to avoid large-scale diseases outbreaks and their associated financial cost. Coughing, sneezing, snuffing, and other pig sounds are common indications of respiratory diseases. The anomaly in pig sound detection gives us a way to construct an intelligent system for early disease detection. In this study, we proposed a convolution neural network (CNN) based sound detection algorithm to recognize abnormal pig sounds in the pig farm. Sound sensors were installed in the pig farm to record the sample sound and saved as WAV sound file format at 44.1 kHz. Then the sound files were visualized and converted into spectrogram as image format. We used 20 recording's spectrogram image files as data set for the proposed algorithm. A total of 100 images of spectrogram were used as training datasets and labeled corresponding to each image and another 20 images of spectrogram were used as test data sets with the labeling corresponding to each image. After training our CNN architecture, we evaluated the performance. The results showed that the proposed algorithm was capable of detecting abnormal sounds such as screams and overall recognition accuracy was acceptable. The performance of our method is affected when there is very high background noise. More data sets with many variations and avoiding misclassification would increase the accuracy of the proposed method. Further development is required to enhance the proposed architecture so that all the abnormal sounds are detected efficiently in a robust manner.

Key words: Smart farming, diseases monitoring, sound detection, convolution neural network, pig farm

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Biosystems Machinery Engineering

Study on sementic segmentation for seperating corn and weeds in field images by using U-Net algorythm

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Abstract

Recently, with the development of deep learning technology, studies for application in many agricultural fields are being actively conducted and put into practical use. Weed control during upland crop cultivation like corn is an important issue at begining stage of growth, and it is important to diagnose weeds at corn field for optimal control. In this study, a predictive model was built to analyze the weed images in the middle of corn images using deep learning, and the semantic segmentation among weed generation images and corn growth images was conducted for identifying weed and corn images in the field by using U-Net algorythm, which is one of deep learning algorythms. In the corn field for deep learning model, growth images of maize during the cultivation period were taken with a digital camera or drone. The original image was used as the X value, the image from which weeds were artificially removed was used as the Y value image, and the image generated through the model was used as the P value. The area of weeds can be converted by subtracting the P value of the image generated through the prediction model from the X value. In this study, a model for generating the prediction image (P value) was built. The algorithm used in this model used U-Net and the SGD optimizer was used to calculate the cost function.The image-processed image was converted into a black-and-white image, the image corresponding to the weed was deleted with an image editing program, and the removed black-and-white image was set as the Y value. The same pair of X and Y images were divided into training and validation images at a ratio of 85:15 (483:86), and training and validation processes were performed. When the original digital image was driven again using the model generated through training, a predicted black-and-white image was generated, and the predicted image has a similarity to the black-and-white image processed by removing the pre-weeds. In this way, learning was repeated 50 times(epoch), and if the cost function and accuracy of the traing data did improve early times, but cost and accuracy was not more improved after 35th epoch. After the final traing was repeated 50 times, the cost function for the final learning was 0.007 and the accuracy was 99.4%. Meanwhile, as a result of validation all the tested data using the constructed model, the cost function was 0.014 and the accuracy was 99.4%. The actual original image, the artificial weeding image, and the predicted weed image were checked by driving the model. Base on the results, Early detecting of weeds in the corn fields can be established with images of corn fields. However if we are to apply to practical use, it will be more to collect more sample images, and to develope related technology related such as computer vision.

Key words: U-Net, semantic segmentation, corn, weeds

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> **Food Science & Technology**

A Study for Microbiota Structure on Farm-raised and Wild-caught Dotted Gizzard Shad (Konosirus punctatus) for Microbiological Risk Assessment

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Abstract

Dotted gizzard shad (*Konosirus punctatus*) is mainly consumed along the coast of Asia, and is widely consumed as raw sliced fish without heating process, which is vulnerable to cross-contaminate by potential food-borne pathogens. Illumina Miseq 16S rRNA gene sequencing method was used to analysis microbiota structure of samples. The total bacterial loads and the diversity indices of the microbiota on dotted gizzard shads were significantly different between farm-raised and wild-caught samples. The predominant microbiota on farm-raised samples were Proteobacteria, Bacteroidetes, and Firmicutes, whereas Firmicutes was rarely found in wild-caught samples. Bacteroidetes was mainly composed of family Flavobacteriaceae in both groups. While Vibironaceae was most dominant family in wild-caught samples, Moraxellaceae was the dominant family in farm-raised samples. At the genus level, potential pathogenic genera *Vibrio*, *Pseudomonas*, *Staphylococcus*, and *Acinetobacter* were observed. Within those genera, *V. parahaemolyticus* have been quantified in wild-caught dotted gizzard shad samples by qRT-PCR (5.26×10^2 CFU/g, ratio 64.71%). To measure the colonization of *V. parahaemolyticus* over time on different origin of farm-raised and wild-caught dotted gizzard shad microbiota structure, artificial infection model experiment has been conducted. Amount of *V. parahaemolyticus* was statistically higher in infected wild-caught samples than those of farm-raised samples after 8h. These results can be used as basic information to understand different microbiota structure of farm-raised and wild-caught dotted gizzard shad, and to develop sustainable strategy to control potential foodborne pathogen on dotted gizzard shads.

Food Science & Technology

Transglycosylation mechanism of an engineered 4,6-α-glucanotranferase with pure maltodextrin

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Abstract

The recombinant 4,6-α-glucanotransferase (4,6-α-GT) that acts on starch-derived maltooligosaccharides to produce long chain polysaccharides with high anhydroglucosyl α1→6 bonds was obtained as the fused protein with *Escherichia coli* maltose binding protein. In this study, transglycosylation mechanism of 4,6-α-GT on the different concentrations of different degrees of polymerization (DP) 4,6,8 and 10 as substrates were investigated for determinations of linkage ratio and DP distributions. As the DP of substrate increased, the ratio of α1→6 bonds increased by up to 84% of the reaction with DP 10. In addition, the longer the DP of substrate, the more products with DP>10 were synthesized. Final glucose content generated by hydrolysis also decreased significantly as the substrate DP increased. In the reaction with DP 4 and 10, the ratio of DP>10 oligosaccharides increased from 51% to 79%, and the glucose contents lowered from 20% to 6%, respectively. All the products were excessively water-soluble, and showed little digestion by intestinal amylases. Consequently, this 4,6-α-GT synthesized fibers that may applicable in the food and pharmaceutical industries.

Food Science & Technology

Tailor-made Noble Lipids

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Abstract

Structured lipids are tailor-made noble functional lipids to change the fatty acid composition and positional distribution to improve the physico-chemical functionality and the nutritional properties of lipids. Nutritional good effect of functional fatty acids such as medium chain fatty acid, conjugated linoleic acid, and omega-3 fatty acids (EPA and DHA) can be expected when they exist as a triacylglycerol (TAG) molecule in lipid foods. Synthesis technique of structured lipid can be used for the production of low-trans fat substitutes, cocoa butter substitutes, human milk fat substitutes and whipping cream fat substitutes. Because dairy whipping cream fat contain a lot of cholesterol and saturated fats related to cardiovascular disease, non-dairy whipping cream fat using vegetable fats (hydrogenated coconut oil, HCO; palm oil; palm kernel oil) has been widely used in food industry. These vegetable fats have a high oxidative stability owing to 99% saturated fats and a desirable melting point similar to human body temperature (about 35-37℃). Tailor-made noble functional lipids can be produced by several synthetic techniques such as Interesterification, acylmigration, fractionation, and blending. These techniques were used for production of alternative fat blends with low saturated fat as a whipping cream fat substitute. First, palm mid fraction (PMF) fat was acylmigrated under enzymatic reaction. Second, the reactant was purified for production of the enriched TAG molecules and then solvent fractionation at 25℃ was carried out to obtain the liquid part of acyl migrated PMF. Finally, the alternative fat blend product was prepared by the blending of the liquid fraction and HCO (1:1, w/w). The prepared alternative fat blend shows an about 18% reduction in saturated fat content compared to HCO (100% saturated fat content). The atherogenicity index (AI) of Alternative fat blend was 5.36 and its atherogenic fatty acids (lauric, myristic, and palmitic acids) were reduced by 40%. In addition, physical melting characteristic and solid fat index of alternative fat blend prepared was similar to those of HCO. Therefore, this alternative fat blend can be expected to be used as a non-dairy cream fat substitute with a low saturated fat content.

Key words: Structured lipid, enzymatic modification, whipping cream fat substitute, alternative fat, acylmigration

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Food Science & Technology

Analysis of Microbial Community on Kale cultivated in South Korea to Detect the Potential Risk of Food-borne Illness

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Abstract

Kale (*Brassica oleracea* L.) is one of the some popular leafy vegetables, and can be consumed immediately without further cooking. The bacterial communities of kale include potential pathogens, but the presence of pathogens on kale has not been evaluated. The gDNA on kale were extracted and 16S rRNA genes were sequenced on an Illumina Miseq. The alpha diversity (Observed OTUs and simpson's) indices were significantly different between the 2 sites (gwangju and yeoju city in gyeonggi province). The microbiota were composed mainly by Firmicutes (59.52±26.21%) and Proteobacteria (39.80±26.51%) phyla. At the order level, Bacillales (57.60±27.61%), Enterobacteriales (31.51±29.77%), and Pseudomonadales (7.08±7.95%) were found dominantly. The predominant genera were *Bacillus* (15.05±20.75%), *Acinetobacter* (5.05±7.48%), *Pantoea* (4.93±7.69%), *Escherichia* (4.09±14.36%), and *Pseudomonas* (1.95±2.26%). The food-borne pathogens such as *B. cereus*, *A. lwoffii*, *P. agglomerans*, *E. coli* (EAEC, EHEC, ETEC, EPEC), and *P. aeruginosa* were detected and quantified by qRT-PCR. To analyze the changes of endogenous microbiota, the non-wash samples were stored at different temperatures (4 or 30℃). The relative abundance of *Klebsiella* were the highest at 30℃ after washing (8.50 to 59.95%). These results provide a better understanding of the kale microbiota and insights into the role of washing and storage conditions in fresh produces.

Food Science & Technology

Emerging Food Safety Issues from the Perspective of One Health

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Abstract

The magnitude of food safety impact on public health is closely affected by a variety of factors, including pathogens, humans, and the environment. New foodborne pathogens may emerge by acquiring virulence factors, stress tolerance, and antibiotic resistance, which makes it more difficult to control food safety and treat patients with foodborne illnesses. Environmental changes such as global warming may expand habitats for foodborne pathogens and their natural hosts. Also, the aging population facilitated by the development of medical technology makes significant changes in the host's susceptibility to foodborne infection. Since major foodborne pathogens of food safety concern are transmitted zoonotically from livestock, animals are also another important factor affecting food safety. For instance, the use of antibiotics in livestock production results in the emergence of antibiotic-resistant pathogens, threatening food safety and public health. In this presentation, emerging food safety issues will be discussed from the perspective of One Health to provide a holistic insight into how the interaction of pathogens, humans, animals, and the environment impact food safety and public health.

Food Science & Technology

Chemo-enzymatic Depolymerization of Food Packaging Plastic

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Abstract

Polyethylene terephthalate(PET), a commonly used beverage container has continuously appeared in the plastic waste endangering the environment. PET recycling methods have been reported but due to the high cost and poor quality of recycled PET, the recycle rate is still low. Discovery and use of engineered microorganisms has been reported in various studies however PET depolymerisation is still costly as it involves use of a dual enzyme system: PETase and MHETase. This research aims to develop an efficient chemo-enzymatic depolymerisation pathway with a single enzyme system using *Bacillus subtilis* esterase (Bs2EST). In the previous study, PET depolymerisation faced a problem of long time due to slow hydrolysis of one of the PET oligomers, mono (2-hyroxyethyl terephthalate(MHET). The formation of non-productive location in MHET towards the enzyme active site caused reduced catalysis, requiring further structure based protein engineering of enzyme to improve the MHET binding ability. Applying the mutated enzyme system to the chemoenzymatic depolymerization process of PET, we expect the depolymerization will be efficient. Details will be presented in the presentation.

Key words: Chemoenzymatic depolymerization, PET, MHET, Bacillus subtilis esterase(Bs2Est), Structure Based Protein Engineering

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Bio-Environmental Chemistry

Adsorption characteristics of NH4-N by biochar derived from pine needles

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Abstract

Nitrogen applied to soil is highly prone to leaching and volatilization leading to gaseous emissions of nitrous oxide (N2O) and ammonia (NH3) which are of great environmental concern. Usage of biochar to reduce the discharge of nitrogen to the environment has attracted much interest in the recent past. Biochar is produced by pyrolyzing various biomasses under oxygen-limited conditions. Biochar is a carbonized material with high adsorptive powers for not only plant nutrients but also heavy metals. The objective of this study was to investigate the adsorption characteristics of NH4-N onto biochar made from pine needles. The biochar was produced at various pyrolysis temperatures including 300, 400 and 500℃ and holding times of 30 and 120 minutes. The Langmuir isotherm was used to evaluate the adsorption test results. The chemical properties of the biochar varied with the pyrolysis conditions. In particular, the pH, EC and total carbon content increased with the increasing pyrolysis conditions. The rate of adsorption of NH4-N by the biochar decreased with the increasing pyrolysis conditions. Of these conditions, biochar that was pyrolyzed at 300℃ for 30 minutes showed the highest adsorption rate of approximately 0.071 mg·g-1. Thus, the use of biochar pyrolyzed at low temperatures with a short holding time can most efficiently reduce ammonia emissions from agricultural land.

Key words: adsorption, biochar, NH4-N, Langmuir isotherm

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Bio-Environmental Chemistry

Comparing Heavy Metal Pollution in Agricultural Field Locatedat the Industrial Complex with Calculation of Pollution Index

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Abstract

Heavy metal pollution in agricultural field has been concerned because of crop safety. The main purpose ofthis study was to evaluate heavy metal pollution in agricultural field by comparing two groups. The first group(A) was agricultural field where no industrial complex is located within 2 km radius and the second group (B)was that industrial complex is located within 2 km radius. A total of 330 soil samples in Chungbok provincesof Korea. Heavy metal concentration was measured in both groups and pollution index was calculated basedon measured heavy metal concentration and threshold value. Result showed that chemical properties of bothgroups were within optimum range of agricultural field set by national institute of agricultural science inKorea. Heavy metal concentration such as Cd and Pb was generally higher in group B compared to group Adue to impact of industrial complex. However, concentration of As and Cu was higher in group A compared toB and we could assumed that abandoned mine located near at the sampling site in group A and over use ofcompost might be the source of higher heavy metal concentration in group A. Soil pollution index calculationshowed that group B (0.21) was higher than group A (0.19) although no heavy metal species were exceededthreshold value in Korea. Among other chemical properties, soil organic matter and available phosphorusconcentration were highly correlated with soil pollution index indicating that management of compost couldbe utilized to decrease heavy metal concentration in soil.

Key words: Arable field, Compost, Heavy metals, Pollution index, Soil organic matter

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Bio-Environmental Chemistry

A review of the potentiality of biochar technology to abate emissionsof particulate matter originating from agriculture

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Abstract

Agricultural operations and processes generate copious quantities of particulate matter (PM) both directly and indirectlythrough emissions of PM precursor gases with dire consequences for human health, environment and climate. PM emissionsfrom agricultural activities are projected to continually rise in the light of soaring food demand driven by a ballooning globalpopulation, and thus, plausible measures are needed to combat them. Recently, interest in using biochar to attenuate PM emissions of agricultural origin, especially the secondary PM precursors, has gained traction and this review study is purposedto examine the capacity of the technology to curb the agricultural-related PM emissions basing on observations made in thepreviously concluded studies. The study gives a brief overview of the efects of PM and delineates its weighty agriculturalsources plus detailing whether and how the pyrolysis technology and biochar as its product can help to alleviate the emissions. Additional discussions address the looming dilemma of biochar applications becoming a PM emission problem andthe techniques that should be applied to ensure its sustainable usage. It is overwhelmingly clear from the studies reviewedthat pyrolysis and resultant biochar have an enormous potential to attenuate PM from agriculture if adequately utilised.

Key words: Agriculture · Biochar · Particulate matter emissions · Pyrolysis

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Bio-Environmental Chemistry

Nutrient Dynamics in Sandy Soil and Leaf Lettuce Following the Application of Urea and Urea-Hydrogen Peroxide Impregnated Co-Pyrolyzed Animal Manure and Bone Meal

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Abstract

There is a paucity of data regarding the effect of nutrient-enriched biochar amendmentson nutrient dynamics in both soil and crops. This is important because unlike pristine biochar,nutrient-enriched biochar is applied to the soil in minute quantities as large amounts may ledto over application of the nutrients loaded in it. The current study examined the effects of bothphosphorus- and nitrogen-enriched biochars on the dynamics of both macro and micronutrients inthe sandy soil and leaf lettuce grown thereon. The phosphorus enrichment followed co-pyrolysisof animal manure (cow dung) with 25% and 50% bone meal (w/w), while the nitrogen enrichmentwas achieved by soaking the co-pyrolyzed biochar into urea and urea-hydrogen peroxide. Theperformances of the nutrient-enriched biochar were compared with the conventional amendment ofurea and triple superphosphate (TSP) in the production of leaf lettuce over a period of two seasonsin a pot experiment. The nutrient-enriched biochar amendments resulted into higher microbialbiomass carbon and carbon to nitrogen ratios than the conventional amendment. The conventionalamendment caused more phosphorus, potassium, and magnesium accumulations in the leaf lettucethan the nutrient-enriched biochar amendments. The nutrient-enriched biochar amendments ledto more accumulations of nitrogen, calcium, and micronutrient elements in the leaf lettuce andavailabilities of all the nutrient elements in the soil and thus, nutrient-enriched biochar acted as areservoir that could provide nutrients to the growing lettuce beyond a single growing season.

Key words: leaf lettuce; nutrient availability; nutrient dynamics; nutrient-enriched biochar

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> **Bio-Environmental Chemistry**

Efects of brewer's spent grain biocharon the growth and quality of leaf lettuce(Lactuca sativa L. var. crispa.

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Abstract

The need for organic soil amendments is increasing in the Republic of Korea against the backdrop of increased soilacidifcation and nutrient losses. The pyrolysis of biomass produces biochar which not only increases soil productivitybut also provides environmental benefts through carbon sequestration. The portion of the brewer's spent grain (BSG)recycled is by far less than the amount generated, but pyrolysis can help to reverse this trend by turning BSG wasteinto a valuable soil amendment. The current study, therefore, evaluated the efects of brewer's spent grain biochar(BBXXX) produced at three diferent temperatures of 300 ℃, 500 ℃ and 700 ℃ on the yield and quality characteristicsof the leaf lettuce as well as the efects on soil chemical properties through a pot experiment. Each of the BBXXX andBSG were added to the soil at two rates of 2% and 5% by weight. The pH and carbon content of the BBxxx increasedwith increasing pyrolysis temperatures and the trend was replicated in the soil upon biochar application i.e. the soilpH and carbon content increased alongside temperatures at which biochar was pyrolyzed. On the other hand, how-ever, the soil electrical conductivity (EC) diminished with the increasing pyrolysis temperatures of the biochar applied.With regards to crop growth, the BB500 5% amendment produced the highest marketable yield of the leaf lettuce andwhile the lettuce grown on the control produced leaf lettuce with the lowest content of nitrate nitrogen, BB500 5%amendment generally produced the highest quality lettuce. The results indicate that BB500 performed agronomicallybetter than the rest of the amendments and is thus recommended as an efective BSG recycling measure

Key words: Biochar, Brewer's spent grain, Leaf lettuce, Pyrolysis, Soil amendment

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Bio-Environmental Chemistry

Heavy Metal Remediation in Agricultural Field Based on Soil Pollution Index Calculation

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Abstract

Pollution of potentially toxic chemicals in agricultural fields is a critical problem due to crop safety in Korea. Heavy metal pollution in arable fields near industrial areas can cause adverse effects not only on crop safety but also on human health. Consequently, a national wide soil survey for heavy metal pollution in agricultural fields near industrial fields has been conducted from 1999 in Korea and these polluted agricultural fields have been remediated. However, the Korean government has found it difficult to determine the levels of heavy metal pollution in soil and has tried to rank heavy metal pollution with a pollution index (PI). Therefore, the main objective of this research was to select the critical threshold PI for determining heavy metal pollution in arable soil in Korea. A total of 40 industrial areas with over 400 agricultural fields were monitored for heavy metal pollution and two different PIs (Kloke's and Nemerow's method) were examined for determining the critical PI in soil. Mean heavy metal pollution in agricultural fields was as follows: Cd-0.23±0.07, Pb-10.18±3.32, Cu-9.35±6.48, Zn-52.9±17018, As-2.99±2.63. Based on the measured heavy metal pollution, the PI was calculated. When applying Kloke's and Nemerow's methods, PI values rangedfrom 0.03 to 0.27 and from 0.32 to 11.21 respectively. Comparing both PI methods, Kloke's method estimated no heavy metal pollution in soil while Nemerow's method estimated 2 heavy metal polluted soil where is exceed the criteria of heavy metal pollution in Korea. Overall, heavy metal pollution in arable soil was estimated more precisely when using Nemerow's method than Kloke's method and more sampling is necessary to verify the critical PI in soil.

Key words: heavy metal, soil, pollution index, remediation

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Bio-Environmental Chemistry

Identically Repeated Sequence Structures Containing Carbapenemase Resistant *bla*OXA-72 in a Single Plasmid of *Acinetobacter baumannii* Isolate from Wastewater Treatment Plant, South Korea

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Abstract

The emergence and dissemination of carbapenem-resistant *Acinetobacter baumannii* grows attention as one of the leading hazardous pathogens and hospital borne *A. baumannii* isolates are keep disseminating in the environment via wastewater treatment plants (WWTPs). Total of two *A. baumannii* islolates and one *Acinetobacter* species was isolated from 1ˢᵗ, 2ⁿᵈ Gwangju WWTPs (Yeongsan River) and Yeongcheon WWTP (Nakdong River). The clinical isolates for control were provided by the National Culture Collection for Pathogens (NCCP). Both clinical and environmental isolates were determined as *A. baumannii* by 16S rRNA sequencing, *gyrB* and *rpoB* gene alignment and biochemical test. Also, every isolate was confirmed as multi-drug resistant including carbapenems. Although environmental isolates have lower minimum inhibition concentrations (MICs) of other antibiotics excluding carbapenems compared to clinical isolates, Gwangju WWTP influent isolate, strain 17GI, had the highest MICs of carbapenems. Moreover, detection of carbapenemase encoding genes resulted that the strain 17GI possesses bla_{OXA-72} gene. This was the first report of blaOXA-72 gene found in A. baumannii isolated in Korea. Furthermore, whole genome sequencing of strain 17GI showed three identically repeated sequence structure of blaOXA-72 genes encoded in three same genomic islands (GI) located in a plasmid and qPCR results indicated that this gene was expressed even in carbapenem-free conditions. In conclusion, these results indicate that multi-drug resistant *A. baumannii* can be spread not only from hospital environments, but also from WWTPs and environment sources.

Key words: *Acinetobacter baumannii*, carbapenem-resistance, OXA type carbapenemase

Bottom Ash Modification via Sintering Process for Its Use as a Potential Heavy Metal Adsorbent: Sorption Kinetics and Mechanism

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Abstract

Heavy metal pollution in the environment is a critical issue, engendering ecosystem deterioration and adverse effects on human health. The main objective of this study was to evaluate heavy metal adsorbents by modifying industrial byproducts. The bottom ash was sintered and evaluated for Cd and Pb sorption. Three adsorbents (bottom ash, sintered bottom ash (SBA), and SBA mixed with microorganisms (SBMA)) were tested to evaluate the sorption kinetics and mechanism using a lab-scale batch experiment. The results showed that the highest sorption efficiency was observed for Cd (98.16%) and Pb (98.41%) with 10% SBA. The pseudo-second-order kinetic model ($R^2 > 0.99$) represented the sorption kinetics better than the pseudo-first-order kinetic model for the SBA and SBMA, indicating that chemical precipitation could be the dominant sorption mechanism.

This result is supported by X-ray photoelectron spectroscopy analysis, demonstrating that -OH, -CO3, -O, and -S complexation was formed at the surface of the sintered materials as $Cd(OH)_2$ and $CdCO_3$ for Cd and PbO, and PbS for Pb. Overall, SBA could be utilized for heavy metal sorption. Further research is necessary to enhance the sorption capacity and longevity of modified industrial byproducts.

Key words: bottom ash; modification; heavy metal; sorption; kinetics; precipitation

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> **Bio-Environmental Chemistry**

Characteristics of food waste: water andsalinity contents

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Abstract

The high intrinsic water content and salinity of food waste prevent a smooth compostingprocess and consequently cause social, economic and environmental problems. In this study,we investigated the distribution of the water content and salinity in food wastes to obtainuseful primary data to ensure adequate and quality recycling. A total of 300 food waste (FW)samples were collected from residential apartments (home generated FW), a wide rangeof restaurants, i.e., restaurant generated FW that included Korean, Chinese, Japanese andwestern FWs, and several places that included food waste processing facilities (dehydrated FWcakes). The collected food wastes were oven dried for 48 hours at 80°C after which the waterand salinity contents were analyzed. The results show that the average water content of theFWs was $72.45 \pm 10.51\%$, and the average salinity content was $2.03 \pm 0.57\%$. Furthermore,the salinity of the collected FWs was characterized by where the FW was generated. Bylocation, the salinity concentration of home generated FW was 2.30% while western foodhad the lowest salinity concentration of 1.18%. However, dehydrated cakes had the highestsalinity concentration of 2.84%. Especially, the distribution of the salinity content in foodwastes can form the basis for improving the compost quality in food waste recycling.

Key words: food waste, salinity, water content

Low-Income Household Food Consumption Consequences of Rice Policy and Pandemic Impacts on Income and Price in Thailand

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Abstract

Using Thai household data, we estimate a demand system and analyze the impacts of changes in rice prices and household income on food consumption, then use these results in four experiments. First, the impacts of the Thai government's 2011 rice policy are estimated taking into account rice farm income effects as well as rice price effects. Results suggest that the net effect of the Thai rice policy on food security was mixed, with potentially positive impact on food security of poor rice-producing households, but negative effects for others, including all poor households not engaged in rice production. Second, the latest data on the likely effects of the COVID-19 pandemic on food prices and income overall are used to estimate the impacts on household food consumption. We also test the impact of a hypothetical trade policy response to mitigate COVID-19 rice price effects. We find that a trade policy that attempts to reduce domestic prices benefits households in the higher income ranks while negatively affecting low-income, rice-producing households' food security. Results suggest that an agricultural policy with a view to support food security might have different, if not opposite, distributional impacts on targeted groups. It is important to understand these dynamics in designing agricultural, trade and food security policies for this or other countries that rely on commodity trade policy to achieve a variety of domestic policy goals.

Key words: Food Security, COVID-19, Household Survey, Demand Estimation, Rice Policy, Food Policy, Censored Model, Consumer Economics

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