Department of Life Sciences at POSTECH -

Reaching beyond the boundaries of natural science and opening a door to new possibilities for humanity.
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STRUCTURAL AND MOLECULAR BIOLOGY

Development of novel bio-molecules and the discovery of disease makers and drug target genes through structural biology, biochemistry, and bioinformatics.

X-ray crystallography and molecular biology approaches to elucidate structural interactome including protein-protein interactions and protein-ligand binding mechanisms.

Bioinformatics and systems biology approaches to discover protein localization, protein interaction and targeting mechanisms of cell signaling molecules. Systemic and quantitative analysis of molecular evolution and biological network to study cancer drug sensitivity and resistance mechanism to improve current drug developmental processes.

CELL AND DEVELOPMENTAL BIOLOGY

Establishment of a complex organism from a single cell followed by growth and ageing is a major component in the life events and understanding of underlying mechanism touches the fundamentals of biology. In the field of cell and developmental biology, we investigate the various biological phenomena at multiple levels from cell to organism using cutting-edge experimental techniques encompassing molecular, biochemical, genetic, and neurobiological approaches. Based on the outcome, we attempt to provide useful information to elucidate the pathophysiological mechanisms underlying the diseases caused by malfunction of the normal biological processes and to ultimately contribute to the advance of therapeutic approaches.

We investigate complex and elaborate regulatory processes underlying the development of an organism from a single cell including cellular differentiation, morphogenesis, and organogenesis, which will lead us to the advanced therapeutics as well as to biological understanding various diseases.

We attempt to genetically analyze major players associated with ageing, thereby understand the biological program controlling organismal ageing at the molecular level. From this, we pursue novel mechanistic insights into the pathogenesis of various age-related disorders.

We investigate the role of the intracellular communication molecules, including soluble factor and nanosome, and membrane proteins in the signal transduction among cells, which will lead us to the mechanisms underlying tumor growth, metastasis, and immune response and to the useful information for the development of novel diagnostics and therapeutics.

We investigate the information transmission process in neural circuits from the various angles to understand higher brain functions, to grasp pathological mechanisms underlying various neuropsychiatric disorders at the molecular level, and ultimately to establish the system to identify novel therapeutics.
MOLECULAR MEDICINE

New trends in life sciences are to improve the quality of life with conquering diseases based on basic science and interdisciplinary research. The Molecular Medicine group of Department of Life Sciences, POSTECH leads various biological fields in the world from identification of diseases, immunity, cell signaling, and gene transcription/translation mechanism at cellular and molecular levels to development of diagnosis and therapeutics. Our group is focusing on development of novel regulatory molecules and understanding of their function, development of vaccine and therapeutic agents for viral infection and inflammation by systematic integration of gene transcription and translation, understanding of defense mechanism and its principle. And we eventually try to apply these scientific achievement to clinical treatments for allergic disease, autoimmune disease, transplantation, and etc.

PLANT SCIENCES

The Plant Sciences Group is actively pursuing to understand fundamental biological processes involved in plant development and growth from the stage of germination to that of senescence in model organisms. We also aim to translate the basic and fundamental principles of plant systems into plant biotechnology for rebuilding crop traits and resolving environmental issues. The major research topics are as follows.

Using Arabidopsis, we are investigating the mechanisms of how eukaryotic cells produce their cellular proteins, in particular organelar proteins, and of how these cellular proteins are dynamically and spatially regulated at the molecular, biochemical, cellular, genetic levels in order to elucidate the functions and operating principles of various organelles, and ultimately to understand the operating principles of eukaryotic cells. In addition, we would like to develop cellular tools and methods to reprogram plant cells to produce a large amount of valuable proteins and secondary metabolites.

With an aim to contribute to the production of Biofuel, we are also investigating basic mechanisms of lipid production in plants and microalgae. We identified several genes that can increase lipid content of seed oil, and continue our search of genes that confer heavy metal tolerance and oil accumulation in plant and microalgae. In addition, we are developing plants for phytoremediation, which can clean up contaminated sites in an environmentally-friendly and economic manner.

As the form and function of plants is mainly determined by efficient communication among cells, tissues and organs, and cross-talks with environmental stimuli, we aim to understand how plants integrate environmental cues into intrinsic developmental programs such as phytohormone signaling networks. We are also investigating epigenetic regulations of the induced resistance against various pathogens in genome level, prompting to understand symbiotic interactions between plants and bacteria, and revealing how plants control cambial activities, vasculature development, and biomass production. To this end, we are taking ‘systems biology’ approaches with interdisciplinary researches, which provides a comprehensive research tool to understand these complex interactions viewed as the keys to understanding life.
**Research Introduction**

For normal cell proliferation and division, maintenance of genomic stability is essential. To protect the DNA from genotoxic stresses and repair their damages, it is crucial to understand the molecular network and functions of the proteins inside the cell (e.g., tumor suppressors, cell cycle regulators, and DNA damage signaling proteins). We have provided molecular insight in understanding the mechanism of maintaining genomic stability through the structural and functional studies of these proteins. We elucidated the mechanism by which eukaryotic replication licensing occurs once per cell cycle through the studies of the Geminin-Cdt1 complex (Nature, 2004), and provided the basis for inactivation mechanism of the E2F transcriptional factor by Retinoblastoma to halt the cell cycle progression for DNA repair (Genes Dev 2002). We also provided the mechanism by which eIF4A, a translation initiation factor, is regulated by a tumor suppressor PDCD4 (PNAS USA, 2009). We also determine the DNA recognition mechanism by the 9-1-1 complex (Genes Dev, 2007) and the Mre11-Rad50 complex (Genes Dev, 2011) and repair the damaged DNA by the Mus81-Eme1 complex (Genes Dev, 2008). Understanding the basis of the genomemaintenance mechanism would allow us to prevent and/or cure the accumulation of DNA damage, and in practice, reduce the side effect of Radiation or Chemotherapy in treatment of cancer.

**Career**

1989–1993: Ph. D., Protein Crystallography, Protein Engineering, Cornell Univ. (Ithaca, USA)

1993–1995: Post-doc, Protein Crystallography, Cancer Biology, Memorial Sloan-Kettering Cancer Center (N.Y. USA)

1995–2000: Senior Scientist, Korea Institute of Science and Technology (Seoul) Structural Biology Center

2000–2004: Associate Professor, Department of Life Sciences, POSTECH

2005–Present: Professor, Department of Life Sciences, POSTECH

**Major Awards/Honors**

- Queen Elizabeth II award, (British Government), Korea (1999)
- 2nd Young Scientist award (Presidential award), KAST, Korea (1999)
- Director, National Creative Research Center (DNA damage signaling center) (2001-2010)
- A Rising Star Fellow (POSTECH) (2011)
- Jongyeol Hong’s Chair Professor (2013-2015)

**Research Areas**

- Structural Biology of Cancer; Tumor suppressors, DNA damage signaling and repair, Cell cycle regulation
- Nucleic acid biochemistry
- Anti-cancer drug discovery

**Activities**

- Editorial Board, KSBMB (2007-2009)
- Senior member, KOSUA (2008-2012)
- Selection committee, HFSP (Human Frontier Science Program, France) (2009-2012)
- Review committee, HFSP (Human Frontier Science Program, France) (2009-2012)

**Major Publications**

Proteins play central roles in biological systems. They are not functioning as a single entity, but are frequently multifunctional while interacting with other biomolecules like proteins, lipids or carbohydrates after various post-translational modifications. We are focusing on the roles of proteins which are key effector molecules of the signaling networks from the point of systems biology. Since various biological phenomena like cancer, aging, metabolism etc. are closely related to each other at the molecular level, we are investigating mechanistic actions of key effector molecules based on the structure-function relationship and their interactions with other molecules in various mechanistic processes such as autophagy, apoptosis, metastasis, etc. in the signaling networks under specific conditions like hypoxia, starvation, or inhibition of target molecules. We also engineer protein and biofunctional nano molecules for biomedical application.

| Research Introduction |
Proteins play central roles in biological systems. They are not functioning as a single entity, but are frequently multifunctional while interacting with other biomolecules like proteins, lipids or carbohydrates after various post-translational modifications. We are focusing on the roles of proteins which are key effector molecules of the signaling networks from the point of systems biology. Since various biological phenomena like cancer, aging, metabolism etc. are closely related to each other at the molecular level, we are investigating mechanistic actions of key effector molecules based on the structure-function relationship and their interactions with other molecules in various mechanistic processes such as autophagy, apoptosis, metastasis, etc. in the signaling networks under specific conditions like hypoxia, starvation, or inhibition of target molecules. We also engineer protein and biofunctional nano molecules for biomedical application.

| Research Areas |
- Protein networks in the interactome of cancer, aging and metabolism
- Roles and interactions of key effector molecules in autophagy, apoptosis and metastasis in cancer, aging and metabolic diseases
- Engineering of recombinant proteins and nano molecules for biomedical application

| Activities |
- Metabolic reprogramming and prognostic markers for cancers in carcinogenesis
- Metabolism, immunology, and aging associated with cancer
- NAD metabolomics under hypoxia and starvation
- Application of dendron-based nanotechnology

| Major Publications |

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Education
B.S., Seoul National University, Seoul, Korea (1975)
M.S., Korea Advanced Institute of Science and Technology, Korea (1977)
Ph.D., University of California, Davis, CA, USA (1988)
Lab. of Protein Dynamics and Signaling

Prof. Cheol-Sang Hwang

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Education

Research Introduction
Research in my laboratory focuses on protein dynamics and signaling through post-translational protein modifications. N-terminal acetylation is one of the most common protein modifications. For example, more than 80% of soluble human proteins are N-terminally acetylated. However, over the past half century, the physiological roles of N-terminal acetylation largely remained a mystery. In 2010, we discovered that N-terminal acetylation of cellular proteins creates specific degradation signals for ubiquitin-mediated proteolysis. While we are interested in all aspect of protein modifications and signaling, the work in my laboratory concentrates on the machinery and functions of N-terminal acetylation-dependent proteolysis, cross-talks between ubiquitin-mediated pathways, cotranslational protein degradation, and protein quality control. We also have an interest in the development of new drugs or targets that selectively inhibit the activity of disease-specific components of N-terminal acetylation and ubiquitin-mediated proteolysis.

Career
1996~1999: Research Associate, Seoul National University, Seoul, Korea
2000~2003: Postdoctoral Fellow, Seoul, National University, Seoul, Korea
2003~2009: Postdoctoral Scholar, Caltech, Pasadena, USA
2009~2011: Senior Staff Scientist, Caltech, Pasadena, USA
2011~Present: Assistant Professor, POSTECH, Pohang, Korea

Research Areas
- Functions of N-terminal-acetylation protein degradation pathway
- The ubiquitin-proteasome system in human diseases
- The N-end rule pathway and Johanson-Blizzard syndrome (JBS)
- Cotranslational protein degradation

Major Publications

Activities
- Discovery of the major function of protein N-terminal acetylation
- Discovery of proteolytic pathways of O6-methylguanine DNA alkyltransferase
- Establishment of a new N-end rule pathway
- Elucidation of cross-talks between E3 ubiquitin ligases

JBS patients
Protein-protein interactions (PPIs) and protein subcellular localizations are crucial for many biological functions. Although advances in high-throughput proteomics enable us to construct many comprehensive PPI networks providing holistic view of biological phenomena, there are huge amount of unidentified PPIs. Furthermore, little attention is paid for the network-level understanding of diverse characteristics of PPI. We attempt to solve these problems by integrating various approaches such as modeling physical property of PPI, subcellular localization information, and high-throughput genomics data. We also focused on evolution of protein structures and sequences. While the number of sequenced genomes continues to increase, experimentally verified functional annotations and structures of whole genomes remains unknown. Because subsequence experimental investigation is costly and time-consuming, accurate computational methods for predicting protein functions and structures become attractive. We develop various computational methods for identifying functionally important residues and modeling structures by using evolutionary information.

| Research Areas |
- Computational Biology and Bioinformatics
- Structural and functional characterization of membrane proteins
- Development of prediction methods for protein structure and protein-protein interaction
- Systematic & quantitative analyses of molecular evolution and biodiversity
- Mathematical & statistical approaches to find bio-patterns from sequence and structural information

| Major Publications |
Lab. of Cancer & Vascular Biology

Prof. G-One Ahn

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Education
B.S., University of Auckland, New Zealand (1998)  
M.S., University of Auckland, New Zealand (2000)  
Ph.D., University of Auckland, New Zealand (2004)

| Research Introduction |
We aim to understand the role of myeloid cells (monocytes and macrophages) in the progression of hypoxic (low oxygen tension) inflammatory diseases including cancer and cardiovascular diseases. In particular, we are interested in determining the function of hypoxia-inducible factor-1 (HIF-1) in myeloid cells during the disease progression. Myeloid cells play a critical role in initiation, progression, and exacerbation of the diseases. Furthermore, hypoxic sensing by these cells is known to be essential for mediating inflammatory responses (such as in bacterial infection). However, it is currently unknown how HIF-1, the major transcription factor stabilized under hypoxic conditions, in myeloid cells may modulate the disease progression, in which chronic accumulation of subtle changes in hypoxia and inflammatory microenvironment may overall govern the disease progression. Hence, by using the genetically manipulated mouse model we seek to understand how myeloid cells under the control of HIF-1 may modulate the disease process. With our research, we hope to identify novel therapeutic targets to combat these diseases more effectively in patients.

| Career |
2003–2008: Postdoctoral Fellow, Department of Radiation Oncology, Stanford University School of Medicine  
2008–2011: Research Associate, Department of Radiation Oncology, Stanford University School of Medicine

| Research Areas |
Radiation and Cancer Biology
- Role of HIF-1 in myeloid cells affecting tumor response to radiotherapy and chemotherapy
- Investigation of mechanisms for tumor recurrence after radiotherapy
- Role of HIF-1 in myeloid cells in establishing pre-metastatic niche for tumor metastasis
- Developing strategies for overcoming normal tissue damage (including lung fibrosis, brain damage, esophagitis) induced by radiotherapy

Mouse models of human inflammatory diseases
- Cancer (various orthotopic models such as brain tumors, lung tumors, various metastasis models)
- Inflammation-associated cancer models
- Spontaneous cancer models (colon and liver cancers)
- Stroke (middle cerebral artery ligation through microsurgery)
- Hindlimb ischemia (femoral artery ligation through microsurgery)
- Hepatosteatosis
- Obesity and parabiosis
- Window chamber models (dorsal window and intracranial window chamber techniques) for real-time in vivo imaging

| Major Publications |
Prof. Sin-Hyeg Im

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Education
B.S., Korea University, Seoul, Korea (1987)
M.S., Korea University, Seoul, Korea (1989)
Ph.D., Weizmann Institute of Science, Israel (2001)

Lab. of Immune Regulation and Tolerance (IRT)

| Career |
2001~2003: Postdoctoral Fellow, Department of Pathology, Harvard Medical School
2004~2008: Assistant Professor, School of Life Sciences, Gwangju Institute of Science and Technology (GIST)
2008~2012: Associate Professor, School of Life Sciences, Gwangju Institute of Science and Technology (GIST)
2012~2013: Professor, School of Life Sciences, Gwangju Institute of Science and Technology (GIST)
2014~Present: Professor, Division of Integrative Biosciences and Biotechnology, POSTECH

| Major Awards/Honors |
- Cancer Research Institute Fellowship (USA, 2001-2004).
- Young Investigator Award by the Society of Biomedical Research, (USA, 2003)
- Top 100 Achievements of National R&D (Korean government, 2011)

| Research Area |
Immune regulation and tolerance at the cellular and molecular level
Role of transcription factors (Ets1 and NFAT1) in immune regulation and tolerance
Role of transcription factors (Ets1 and NFAT1) in immune regulation and tolerance
Molecular mechanism of IL-10 gene regulation in lymphocytes and antigen presenting cells (DCs and macrophages)
Elucidation of the signaling pathways and underlying mechanism for IL-10 generation by probiotics.
Characterization of regulatory DCs and iTreg cells induced by probiotics
Development of antigen-specific immunotherapy for autoimmune disorders (Myasthenia gravis and rheumatoid arthritis)

| Major Research Achievements |
- Studies on the role of transcription factors in cytokine gene regulation
- Discovery of the key cis- and trans-acting regulatory elements involved in IL-10 gene regulation
- Development and elucidation of probiotics-mediated immune modulation for hyper-immune disorders (autoimmunity and allergic disorders)
- Development of oral tolerogen for autoimmune disorder (myasthenia gravis as a model)

| Major Publications |
Lab. of Molecular Virology

Prof. Sung Key Jang

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Education
B.S., Seoul National University, Seoul, Korea (1982)
M.S., Seoul National University, Seoul, Korea (1984)
Ph.D., University of New York, Stony Brook, USA (1989)

| Research Introduction |
HCV is a pathogenic virus causing hepatitis, liver cirrhosis, and hepatocellular carcinoma. More than 170 million people are suffering from this virus infection worldwide. We are investigating the molecular basis of the pathogenic processes of HCV. We showed that a human protein GRP94 is required for viral proliferation and that GRP94 is involved in persistent production of HCV in the presence of a cytokine (TRAIL) triggering host cell death. Currently we are developing a cure for HCV infection based on the inhibitors of NS5A that is a viral protein essential for RNA replication.
Cap-independent translation of eukaryotic mRNAs requires a specific RNA structure, named internal ribosomal entry site (IRES), and IRES-specific cellular factors along with basic translational machinery. We are investigating the molecular mechanism of translation via IRESs by revealing the roles of cis-acting elements in various IRES [viral (encephalomyocarditis virus, poliovirus and hepatitis C virus) and cellular (BIP and c-myc) IRESs] and cellular factors (ITAFs) specifically enhancing the IRES function.
We are trying to reveal the molecular details of translational regulation of gene expression at various physiological conditions such as inflammation, heat stress, and viral infection. We also study the molecular mechanism of persistent translation of stress-resistant mRNAs such as hepatitis c virus (HCV) mRNA at stress conditions when translation of most mRNAs is repressed.

| Research Areas |
Hepatitis C Virus (HCV)
- Development of anti-HCV drugs
Translation Initiation
- Translation initiation mechanisms through cap and IRES elements
Aptamer Technology
- Utilization of aptamers in diagnostics and therapeutics

| Career |
1989–1991: Postdoctoral associate, University of New York at Stony Brook
1991–2003: Assistant and associate professor, POSTECH
2003–Present: Professor, POSTECH
2009–Present: Academic editor, PLoS ONE
2009–Present: CSO, Aptamer Sciences Inc.
2013–2014: Head, Department of Life Sciences
2014–Present: Director, POSTECH Biotech Center

| Major Awards/Honors |
- Sigma Xi award

| Major Publications |

eIF2A facilitates stress-resistant translation of HCV mRNA (Kim et al., 2011). Predicted positions of eIF5B, tRNAi, and eIF2A on the 40S ribosomal subunit.
**Research Introduction**

The current research in the lab focuses on the study of innate immunity and inflammation which provide the human body with the first line of defense mechanisms against invading pathogens. While well-orchestrated innate immune responses are essential for human health, unregulated and overactivated immune responses may cause acute or chronic inflammatory diseases as well as autoimmune diseases. The goal of our research is to elucidate the cellular and molecular mechanisms of the innate immune responses and to provide the framework for therapeutic intervention of inflammatory and autoimmune diseases.

**Career**

2002–2007: Postdoctoral Fellow, Harvard Medical School and Whitehead Institute for Biomedical Research  
2008–2009: Visiting Scholar, Whitehead Institute for Biomedical Research  
2008–2009: Research Investigator, Novartis Institutes for Biomedical Research  
2009–Present: Assistant Professor, Department of Life Sciences, Pohang University of Science and Technology

**Major Awards/Honors**

- American Heart Association Fellowship  
- Leukemia & Lymphoma Society Career Development Grant  
- NIAID Scholar, Keystone Symposia

**Research Areas**

- Innate Immunity  
- Immune Receptor Regulation  
- Immune Cell Biology and Live Cell Microscopy  
- Inflammation and Autoimmune Diseases  
- Drug Target Identification

**Recent Projects**

- Regulatory mechanisms of innate immune receptor signaling  
- Immune receptor trafficking  
- Antigen receptor activation pathway  
- Pathogenesis of lupus  
- Regulation of interferon signaling

**Major Publications**


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| Research Introduction |
Since the mammalian host has evolved to accommodate colonization by symbiotic bacteria communities (the microbiota), host immune system must have adapted to maintain the homeostasis of the microbiota while retaining the integrity of our body. In fact, there are some connections between the microbiota and the development of our immune system, particularly the gut-associated lymphoid tissues (GALT). Furthermore, some components of gut microbiota can be circulated systemically and modulate the activities of immune cells. Our Lab is primarily investigating the immune regulation achieved by the interplay between host immune system and the microbiota in multiple immune cells, including T cells, antigen-presenting cells (APC), and hematopoietic stem & progenitor cells (HSPC). We are also studying the role of tumornecrosis factor (TNF)/TNF receptor family molecules in modulating the activities of immune cells. In particular, our Lab has an interest in exploring whether TNF/TNFR family molecules can regulate the biology of HSPC in the chronic inflammation.

| Career |
2003~2008: Postdoctoral Fellow, La Jolla Institute for Allergy and Immunology, San Diego, USA.
2009~2011: Research Scientist, La Jolla Institute for Allergy and Immunology, San Diego, USA.

| Major Awards/Honors |
- Fellowship from the Diabetes and Immune Disease National Research Institute (DIDNRI) (2008)

| Research Areas |
- Immune regulation between the host immune system and the gut “microbiota”
- Regulation of hematopoietic stem & progenitor cells and the cancer stem cells
- Development of mucosal antigen presenting cells and CD4 T helper subsets

| Activities |
- Regulation of CD4 T helper differentiation and mucosal antigen presenting cells
- Identification of the role of TNF/TNFR family molecules in hematopoiesis and development of dendritic cells
- Studies about TNFR family molecules in modulating T cell responses

| Major Publications |

Cytokinin-induced immune response
Plant developmental network analysis
We are currently investigating the roles of ATXN1 protein family and CIC transcription repressor complexes in cancer progression and metabolism using mice as a model organism. By generating tissue specific either Cic or ATXN1 protein family knock-out mice, we are investigating roles of CIC and ATXN1 protein family in cancer progression and metabolism in particular tissues. We are also interested in molecular functions of this transcription repressor complex. We are trying to identify novel CIC target genes including non-coding RNA genes and regulators for the activity of the ATXN1 protein family and CIC transcription repressor complexes. In summary, a better understanding of functions of the ATXN1 protein family and CIC transcription repressor complexes is a primary research goal in our lab.

| Career |
2007–2011: Postdoctoral Fellow, HHMI at Baylor College of Medicine, Houston, USA.
2011–Present: Assistant professor, Department of Life Sciences, POSTECH

| Major Awards/Honors |
Knowledge creation award (Korean Ministry of Science, ICT and Future Planning, 2013)
BK21 distinguished studentship, President award (Korean Ministry of Science and Technology, 2006)
Weintraub graduate student award (Fred Hutchinson Cancer Research Center at Seattle, 2006)
Best thesis award (Korean Society for Molecular and Cellular Biology, 2006)

| Research Areas |
1. Role of Capicua-Atxn1/Atxn1L transcriptional repressor complexes in tumorigenesis and cancer metastasis.
2. Role of Capicua-Atxn1/Atxn1L transcriptional repressor complexes in metabolism.
4. In vivo study on microRNA functions.

| Major Publications |
Lab. of System Genomics

Prof. Tae-Young Roh

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Education
B.S., Hanyang University, Seoul, Korea (1996)
M.S., Seoul National University, Seoul, Korea (1998)
Ph.D., Seoul National University, Seoul, Korea (2002)

Research Introduction
Dr. Roh and his group are interested in genome-wide cellular events. Using experimental and computational tools, we are seeking the basics of cell growth, differentiation, senescence, and disease as well as technical application to develop diagnostic and preventive biomarkers using stem cell and cancer models.

Career
2002~2007: Visiting Fellow, NIH
2007~2008: Research Fellow, NIH
2008~Present: POSTECH, Assistant Professor

Major Awards/Honors
- Fellows Award For Research Excellence, NIH, USA (2004, 2005)
- Lenfant Biomedical Fellowship Award, NHLBI, NIH, USA (2005)
- Young Scientist Award, Society for Biomedical Research, USA (2007)
- Excellent Scientist who has brightened Korea, MEST, Korea (2007)
- Excellent Research Award, The Korean Society for AIDS (2014)

Research Areas
- Epigenetic modification
  Comparative genomic/epigenetic information of normal/cancer cells or stem cells/differentiated cells could provide a valuable clue to identify targets for disease diagnosis and treatment.
- Genome function
  Transcriptional regulation occurs via interactions between proteins and functional elements on DNA. Novel functional elements could be found by intensive analysis of genomic data.
- Construction of database for genome and development of data analysis tool Databases for high resolution and high throughput data generated from next generation sequencing will be constructed and applied to understand the molecular basis of individual gene transcription.

Major Research Achievements
- Functional regulation during cancer development
- Epigenetics on genome replication
- Epigenetics of Stem cell

Major Publications
We are working on the machinery and principles of cell signaling from receptor to cell growth and metabolism to understand the processes of diseases such as cancer and diabetes. Signaling proteomics, ligand discovery, aptamer development and disease mouse models are the major strategy for the research in the lab. Molecular imaging, network modeling and discovery of drug and diagnostics are also included in the interdisciplinary collaborative projects. EGF Receptor and Insulin Receptor signalings are major targets in current projects. Phospholipase D, C1-Ten and mTOR are core signaling hubs we have been working on. Tens of modulators including peptides, chemicals and aptamers are now in the process of development as candidates for drugs. Members of Signal Transduction Lab have contributed in cell signaling area as experts for the discovery of new signaling machineries and pathways in cancer, diabetes, stem cells and inflammations.

| Activities |
- Signaling proteome for phospholipase mediated network
- Peptide ligands for control immune responses, sepsis and cancer
- Process in mTOR signaling station in metabolic diseases
- Aptamer platform technology

| Major Publications |

| Research Areas |
- Signal transduction for cell growth and metabolism
- Proteomics and system biology
- Aptamer technology for detection and modulation of diseases
- Principles of signaling networks in cancer and diabetes
Lab. of Cellular Immunology

Prof. Young Chul Sung

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Education
B.S., Yonsei University, Seoul, Korea (1981)
Ph.D., University of Minnesota, Minnesota, USA (1988)

| Research Introduction |
Since 1989, Prof. Sung has conducted extensive research in the field of vaccine and immunotherapy. His specialty has been developing therapeutic DNA vaccines for treating incurable diseases, including chronic hepatitis B, CIN/VIN, and tuberculosis, and he managed to expand his vaccine research from mouse model to non-primate, and ultimately to human patients (from bench to clinic). Many of these vaccines are currently being evaluated in clinical trials in collaboration with various pharmaceutical and biotech companies. Recently, he has been focusing on mesenchymal stem cell (MSC)-based gene therapies and antibody-fusion proteins. Based on the positive results obtained from preclinical studies, he plans to apply genetically engineered MSCs for cancer therapy and utilize hyFc-fusion technology for treating various types of infectious diseases as well as non-infectious diseases in clinic. Through many years of experiences in academia and industry, he has been establishing a global collaboration network among universities, institutions, hospitals, and companies to build a foundation for improving biotechnology in Korea and pioneering next generation therapeutics to save the lives of patients.

| Career |
1988~1989: Postdoctoral fellow, Harvard Medical School
1989~Present: Professor, Dept. of Life Sciences, POSTECH
2005~2011: Director, POSTECH-Catholic Biomedical Institute
2005~Present: CEO, Genexine, Ltd
2006~2008: President/vice-president, Korean Association of Immunologist
2009~2013: Director, POSTECH Biotech Center
2010~2012: Chairman, Dept. of Life Sciences, POSTECH

| Major Awards/Honors |
- 7th Hantaan Prize from Hantaan Life Science Foundation (2003)
- The 2nd Mystery of life award (2008)

| Research Areas |
- Vaccine & Immunotherapy
- Stem cell-based cancer gene therapy

| Activities |
- Development of naked DNA immunotherapeutics for chronic hepatitis B & tuberculosis
- Evaluation of therapeutic efficacy of mesenchymal stem cell based cancer gene therapy.
- Clinical trials and commercialization of various hyFc-fused long-acting protein/peptide drugs

| Major Publications |
Prof. Charles D. Surh

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Education
B.A., University of California at San Diego, USA (1983)
Ph.D., University of California at Davis, USA (1989)

Career
1989~1993: Postdoctoral Fellow, Department of Immunology, The Scripps Research Institute
1993~1998: Assistant Professor, Department of Immunology, The Scripps Research Institute
1998~2005: Associate Professor, Department of Immunology, The Scripps Research Institute
2005~2008: Associate Professor with Tenure, Department of Immunology, The Scripps Research Institute, La Jolla, California
2008~2012: Professor, Department of Immunology, The Scripps Research Institute, La Jolla, California
2009~2012: WCU Professor, Division of Integrative Bioscience and Biotechnology, POSTECH
2012~Present: Adjunct Professor, Department of Immunology, The Scripps Research Institute
2012~Present: Adjunct Professor, Division of Development Immunology, La Jolla Institute of Allergy and Immunology
2012~Present: Professor, Division of Integrative Bioscience and Biotechnology, POSTECH
2012~Present: Director, Academy of Immunology and Microbiology (AIM), Institute for Basic Science (IBS)

Major Awards/Honors
- Special Fellow, Leukemia Society of America, July 1993 - June 1996
- Scholar, The Leukemia and Lymphoma Society, July 1999 - June 2004
- Ho-Am Prize in Medicine, 2007
- 100 Distinguished minds who will shine Korea in 2020, 2010

Research Areas
- Development, homeostasis and function of naïve and memory T cells
- Modulating T cell populations for treatment of cancer and autoimmune diseases
- Regulation of homeostasis between the immune system and the commensal microbiota

Major Research Achievements
- Studies on mechanisms of T cell selection in the thymus
- Discovery of the factors that regulate homeostasis of naïve and memory T cells
- Study on how mature T cells can be manipulated with cytokines

Major Publications
| Research Introduction |
Our research aims on the characterization, utilization, and engineering of defense signaling machinery against pathogenic infection, and to contribute humankind by discovery of therapeutic targets in the area of biomedical research on infectious diseases. In particular, research goal lies in the discovery of fundamentals that govern the recognition of non-self and interplay between the host and the pathogen, utilizing the strategic cope planning against pathogen that Metazoans have developed, and to provide innovative ways to treat and cure disease related to infection.

| Career |
1997~2002: Postdoctoral Fellow, Howard Hughes Medical Institute, The Johns Hopkins Univ., Baltimore, USA
2003~2004: Research Associate, The Johns Hopkins Univ., Baltimore, USA
2011~present: Associate professor, Dept. of life sciences, POSTECH, Pohang, Korea.

| Research Areas |
- Host defense against intracellular virus or bacteria
- Mitochondria in the regulation of infection
- Cellular signaling network of innate immune response
- Transcriptional control of inflammation and cancer

| Activities |
- Identify host factors with anti-HCV activity
- Understand genetic & epigenetic regulation of inflammation by PAF complex
- Development of the RIG-I aptamer with anti-viral therapeutic potential
- Construction of the computational framework for investigation of the transcriptional regulatory network of inflammation

| Major Publications |
In multicellular organisms, including humans and bacteria, intercellular communication is an essential process. Cells release a variety of intercellular communication molecules into their surroundings that execute intracellular and intercellular communication via binding to their cognate receptors.

To communicate with each other, cells secrete not only variable kinds of soluble intercellular communication molecules, such as growth factors and cytokines, but also extracellular vesicles (EVs), composed of various kinds of proteins, lipids, and genetic materials. EVs are extracellular organelles that modulate immune response as well as promote tumor invasion. These observations suggest that EVs could be regulators of intercellular communication, playing diverse roles compared with those of soluble intercellular communication molecules. However, the biological functions of EVs are generally unclear. We discovered that EVs from tumor cells promote angiogenesis via sphingomyelin and modulate VEGF action on endothelial cells. We will demonstrate that EVs act as multifunctional intercellular communicators through systemic research on the diversity and multiple roles of EVs as well as on the mechanisms of EV biogenesis. Furthermore, our researches will help us to develop novel cancer diagnostics and to identify novel targets that are involved in pathogenesis of diseases.

Aged humans experience higher rates of cancer, Alzheimer’s disease and atherosclerosis. The pathogenesis of these diseases is not known at the molecular level. Because disregulation in the biogenesis of intercellular communication molecules and/or dysfunction in the intercellular/intracellular communication networks could lead to progression of several diseases, many groups have studied this field. However, worldwide studies have only focused on soluble intercellular communication molecules and intracellular communication. Therefore, the systemic studies on EVs are critical for understanding the intercellular communication network that is essential for decoding the secrets of life and elucidating the exact causes of many diseases.

| Research Areas |
- Host- and bacteria-derived extracellular vesicles: Exosomes, microvesicles, and outer membrane vesicles
- Host-pathogen interaction
- Drug delivery system
- Vaccine

| Major Publications |
Research Introduction

Our lab focuses on the understanding of various signaling pathways during vertebrate development. Specifically, we are trying to elucidate molecular mechanisms of signaling pathways important for early embryogenesis, including pattern formation and germ layer differentiation using Xenopus model system. Wnt, FGF, BMP, and TGF-β pathways are key signaling govern various developmental process and serious human diseases. Wnt signaling serves as core signal for proper body axis formation and morphogenesis and related with cancer. FGF and BMP signaling is important for brain development and TGF-β pathway is crucial for germ layer formation and tumor progression. Our aim is to reveal the details of those pathways in the molecular level by vertebrate model and cell-line based approach.

Career

1991–1992: Post-Doctor, Program in Developmental Biology, University of California-San Francisco, School of Medicine
2002–2003: Visiting professor, University of California-Irvine, Department of Developmental and Cell Biology
2004–Present: Editorial Board of Developmental Dynamics
2010–2011: Visiting professor, University of California-Irvine, Department of Developmental and Cell Biology

Research Areas

- Wnt/β-catenin signaling pathway in vertebrate axis formation
- Wnt/PCP signaling pathway for regulation of cell morphogenesis during gastrulation
- BMP and FGF signaling for proper neural development
- TGF-β signaling pathway and mesoderm formation

Activities

- Finding mechanisms of Dishevelled regulation via ubiquitination, deubiquitination, and dephosphorylation in Wnt/β-catenin signaling pathway
- Elucidation of regulating mechanisms of cell polarity, cell shape, and cell adhesion during gastrulation
- Functional analysis of various Wnt-related genes during vertebrate development

Major Publications


Lab. of Developmental Biology

Prof. Jin-Kwan Han

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Education
B.S., Yeungnam University, Daegu, Korea (1982)
Ph.D., University of California, Davis, CA, USA (1991)
We are interested in elucidating how neurons are interconnected and affect each other, and how synapses are modified at the cellular and molecular level. Synapses, the points of contact and communication between neurons, can vary in their size, strength, and the number. These differences contribute to learning and memory, beyond the plasticity of neural networks and synapses.

First, we study synaptic plasticity and alteration by means of changes in the level of gene expression using viral vectors and transgenic animals. Using genetically modified materials, we can reveal mechanism of spike time dependent plasticity (STDP), dopamine’s role in synaptic plasticity or involvement of cell adhesion molecules such as Neuroligin-1. Whole-cell recording is a critical method for observing neural activity in living neurons, and we also use this technique to observe changes of synaptic plasticity. Moreover we apply behavior experiment using rodents, to find the physiological meaning of alteration in synaptic plasticity caused by genetic modification.

Second, early symptoms of neurodegenerative diseases appear apparent with failures in synaptic functions. So we pursue the pathophysiology of neurodegenerative diseases such as Alzheimer’s disease (AD). Toward this end, we employ variety methodologies, inducing LTP in vivo or acute slice, time-lapse imaging of synaptic structures, and optical determination of bimolecular interaction as well as standard biochemical assays.

We collect evidences about the regulating machinery of Abeta oligomer by naturally-secreted extracellular vesicles and find out their effects on AD model using in vivo electrophysiology or AFM methods. Third, chronic exposure to drugs of abuse (e.g. cocaine) makes long-lasting addictive memory. We investigate electro-physiological, structural and behavioral changes to study long-term changes of reward circuit. Because dopamine D1 and D2 receptor show opposite direction of response in the nucleus accumbens, and they are separately expressed in specific cell type, we are eager to distinguish the functional properties of each type of neurons. BAC transgenic mice (Drd1a-EGFP, Drd2-EGFP) enable us to study drug addiction in a cell-type specific manner.

Finally, we also conduct systemic approach to study neuronal circuits for functional understanding of various brain areas. For this, we employ a cutting-edge method, optogenetics, which enables us to control the activity of distinct type or group of neurons by optical stimuli. Thus, we can accurately see the role of only optically stimulated neural population in vivo or in vitro. Currently we are applying this technique on drug addiction and fear memory research.

**Career**
- 2000~2005: Postdoctoral Fellow, Columbia Univ., NY, USA.
- 2001~2004: Research associate, HHMI, NY, USA.
- 2005~2009: Assistant Professor, POSTECH
- 2010~Present: Associate professor, POSTECH

**Research Areas**
- Molecular mechanisms of synaptic plasticity
- Mechanistic study of cell adhesion molecules
- Pathophysiology of neurodegenerative and psychiatric diseases
- Cell-type specific alteration of neuronal circuitry occurred by drug addiction

**Activities**
- Functional roles of Neuroligin-1 in mature neural circuits
- Elucidation of small GTPase mechanism to long-term memory
- Structural changes of individual synapses in synaptic plasticity
- Identification of pathway-specific alteration of synaptic plasticity
- Drug addiction mechanism in the basal ganglia circuit

**Major Publications**
**Research Introduction**

Molecular Neurophysiology (MNP) is currently interested in molecular and cellular signaling mechanism in neuronal system. We are particularly focusing on novel protein kinase network, dendritic mRNAs, biological clock genes, cell cycle and cell apoptosis. We are currently studying functional roles of vaccinia related kinases (VRKs) family involved in cell cycle progression and neurodegenerative diseases mediated by protein aggregation. The molecular mechanisms of mRNA oscillation controlled by regulated transcription and mRNA decay are also main topics in my laboratory. In addition, transport, translational control and decay process of mRNAs in the dendritic spines of neuronal cells are also investigated to reveal the mechanism of dynamic synaptogenesis and synaptic plasticity. For more comprehensive research, we are conducting interdisciplinary research with other expertise including X-ray microscopy, computational modeling and drug delivery system. We are elucidating the images of brain and other organs which have defects during development. In addition, cell death process induced by VRK inhibitors is being investigated to possibly apply the technology to treat tumors or neurodegenerative diseases.

Members of MNP have been successfully developing scientific careers in molecular neurophysiology field since 1991.

**Career**

1997–1998: Visiting Scientist, Dept. of Physiology and Biophysics, Univ. of Washington, Seattle, USA.
2001–Present: Professor, Dept. of Life Sciences, Div. of Integrative Biosciences & Biotechnology (IBB), Pohang Univ. of Science and Technology (POSTECH)
2006–2007: Visiting Professor, Nanyang Technological Univ., Singapore
2013–Present: Editorial member, Scientific Reports
2007–Present: Fellow, Korean Academy of Science and Technology
2010–2012: Director, Pohang Center for Evaluation of Biomaterials (POCEB)
2013–Present: Head, Div. of Integrative Biosciences & Biotechnology (IBB), Pohang Univ. of Science and Technology (POSTECH)

**Major Awards/Honors**

- Seoam Fellowship, Seoam Scholarship Foundation (1996)
- One of 50 outstanding R&D achievements in Korea (2008)

**Research Areas**

- Molecular & cellular physiology of Vaccinia Related Kinases (VRKs)
- Regulatory mechanism of bioclock gene expression
- Development of drug targets for neurodegenerative diseases
- Synaptic plasticity mediated by translational control of mRNAs in dendritic spines

**Activities**

- Posttranscriptional regulation and mathematical modeling in expressions of bioclock genes and dendritic mRNAs of neuron
- Functional analyses of VRK3 in autism spectrum disorders
- Elucidation of VRK2 function in neuronal cell death by misfolded protein aggregation
- Development of anticancer or neurodegenerative diseases drugs by regulating VRK1 and 2

**Major Publications**

Aging is a fundamental mystery in biology. Although a number of genetic and environmental factors that affect aging have been discovered, the mechanisms by which these factors influence aging are poorly understood. This is mainly due to the difficulty in studying complex aging processes at the organismal level. The roundworm C. elegans is an excellent model animal to overcome these complications because of its genetic tractability, ease of culture in controlled environments and very short lifespan. In our laboratory we plan to elucidate the molecular mechanisms by which these genetic and environmental factors regulate lifespan using C. elegans as a main model organism. Since many findings on the regulation of aging in C. elegans have already been shown to be amazingly well conserved during evolution, we believe our research may eventually help us understand the secrets of human aging and improve the quality of old age.

| Research Introduction |
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| Career |
2003–2004: Postdoctoral Fellow, The Johns Hopkins University, School of Medicine
2004–2008: Postdoctoral Fellow, University of California, San Francisco
2009–2013: Assistant Professor, POSTECH
2013–Present: Associate Professor, POSTECH

| Major Awards/Honors |
- Cheongam Fellowship, TJ Park Foundation (2010-2012)
- Postdoctoral fellowship, Life Sciences Research Foundation (2005-2008)
- Mette Strand Award, Johns Hopkins University Young Investigators’ Day (2003)

| Research Areas |
- Genetic dissection of aging using C. elegans as a model organism
- Identification and characterization of genes those are important for glucose metabolism

| Activities |
- Course lecturer for: Biology of Aging, Advanced Developmental Biology, Advanced Molecular Genetics, Undergraduate Genetics

| Major Publications |
Lab. of Molecular NeuroPsychiatry

Prof. Sang Ki Park

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Education
B.S., Seoul National University, Seoul, Korea (1991)
M.S., Seoul National University, Seoul, Korea (1993)
Ph.D., University of Virginia, USA (2001)

Research Introduction
Mental illness such as mood disorders, schizophrenia and drug addiction is one of the most prevalent diseases in modern human society. However, the molecular mechanisms underlying pathogenesis of these diseases are largely unknown. Recently, the Molecular Psychiatry - molecular neurobiological study of psychiatric disorders - has emerged as a promising research domain of the modern neuroscience, rendering a unique approach to understanding the pathogenesis of various psychiatric disorders. To this end, we pursue in depth understanding of the molecular basis of major psychiatric disorders, utilizing contemporary biochemical, molecular biological, cell biological, pharmacological, genetic and behavioral biological techniques. We believe that the research will not only unravel novel molecular targets for therapies for major psychiatric disorders but also expand our knowledge on higher brain functions.

Career
2001~2006: Postdoctoral Research Fellow, Harvard Medical School/Howard Hughes Medical Institute
2006~2006: Postdoctoral Associate, MIT/Picower Institute of Learning and Memory
2004~2008: NARSAD Young Investigator
2006~2012: Assistant Professor, Dept. of Life Sciences, POSTECH
2013~Present: Associate professor, Dept. of Life Sciences, POSTECH

Major Awards/Honors
2004 & 2006: National Alliance for Research on Schizophrenia and Depression (NARSAD, USA) Young Investigator Awards
2011: Selected, 2011 MEST Excellent Research Achievements 50 and National R&D Achievements 100

Research Areas
• Modulation of dopamine receptor-mediated signaling
  Dopamine is one of the most functionally prevalent neurotransmitters in the vertebrate brain. Its role in higher brain functions is mediated by five subtypes of dopamine receptors. Among them, dopamine D2 receptor (D2DR) has been implicated in major psychiatric diseases including mood disorders, schizophrenia and drug addiction. We are attempting to identify modulatory components in D2DR-mediated signaling in the context of higher brain functions and the pathogenesis of associated disorders.
  • Molecular modeling of schizophrenia
    Schizophrenia is a complex psychiatric disorder that is thought to have both neurochemical and neurodevelopmental causes in its pathogenesis. The complexity of the pathogenesis has been interfering establishment of the genuine molecular model. Recent advances in human genetics provided reliable candidate genes causative in the expression of schizophrenia. We attempt to understand their physiological function to elucidate the molecular basis of schizophrenia.

Activities
• Elucidation of modulatory pathways for dopamine receptor signaling
• Understanding of the cellular function of schizophrenia susceptibility factors
• Analysis of functional relationships among the risk components of psychiatric diseases

Major Publications

Figure 1. Examples of psychiatric disease-related behavioral tests. Imaging showing that the deficiency of DISC1 causes mitochondrial calcium forced swim test, novelty suppressed feeding test, tail suspension test, elevated plus maze test.
Research Introduction
The form and function of plants is mainly determined by efficient communication among cells, tissues and organs, and cross-talks with environmental stimuli. In higher plants, regulation and coordination of growth and morphogenesis utilizes phytohormone signals for efficient distribution of carbon source. We are interested in elucidating signaling networks of various phytohormones such as cytokinin, auxin, brassinosteroid, abscisic acid, and salicylic acid. We have constructed our own "interactome" database and molecular networks as a platform to explore the cross-talks among different phytohormones and environmental conditions. We are also investigating epigenetic regulations of the induced resistance (e.g. priming) against various pathogen attacks in genome level. In addition, we are prompting to understand how legume plants develop the nodules for nitrogen fixation. Recently, we have extended our research areas to address fundamental questions on how plants control cambial activities, vasculature development, and biomass production. To this end, we are taking 'systems biology' approaches with interdisciplinary researches, which provides a comprehensive research tool to elucidate these complex interactions viewed as the keys to understanding life.

Career
1999~2002: Postdoctoral Fellow, Harvard Medical Institute, Massachusetts General Hospital
2002~Present: Faculty, Pohang University of Science and Technology

Major Awards/Honors
- 2012, Minister’s award, Ministry of Agriculture, Food and Rural Affairs
- 2012, Selected as Top 100 national R&D performances, KISTEP
- 2013, Macrogen Scientist Award, KSMCB(Korean Society for Molecular and Cellular Biology)

Activities
- 2012~Present: Delegate, Global Plant Council

Major Publications
1. Ryu et al., 2014, Nature Communications 5, Article number 4138
3. Choi et al., Molecular Plant 7 : 792-813
Lab. of Cellular Systems Biology

Prof. Inhwan Hwang

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Education
B.S., Seoul National University, Seoul, Korea (1981)  
M.S., Seoul National University, Seoul, Korea (1983)  
Ph.D., University of North Carolina-Chapel Hill (1988)

Research Introduction
The plant cell is composed of various subcellular compartments. To coordinate and regulate all these subcellular compartments to function as a single unit, a large number of molecules must be involved in these complex processes. Therefore, we are trying to isolate and characterize important molecular players of these processes by molecular, biochemical, and cellular approaches. We have discovered and characterized many important proteins in various steps of intracellular trafficking pathways and elucidated the molecular mechanisms of protein trafficking. Endocytosis is another important area of our research. Now, we are trying to understand how abiotic and biotic stress responses are regulated by protein trafficking and endocytosis. In addition, we are also actively studying molecular mechanisms of protein targeting to chloroplasts and mitochondria. We started to elucidate the cytosolic events involved in protein targeting to chloroplasts and mitochondria. Furthermore, by deciphering the protein targeting mechanisms to these endosymbiotic organelles, we are trying to understand the evolution of these organelles. Another important research topic is to develop molecular and cellular tools to develop the plant cells as a protein production system for valuable proteins.

Activities
- Organizer of ICAR-2016 (Korea)
- Plenary lecture at ICAR in Japan (2010)
- Keynote speaker at ENPER in Germany (2010)

Major Awards/Honors
- Ilmac award (Science area) (2005)
- Postechian award (research area) (2007)
- Inchon award (Science area) (2008)
- Postech fellow (2011)

Research Areas
- Organelle biogenesis and evolution
- Abiotic stress responses and its application in biomass production
- Reprogramming of plant cells as a protein production system

Major Publications
We have three major goals. First is to identify genes for bioenergy production. Second is to develop trees for phytoremediation, a technique to clean up environment using plants. Our third goal is to understand functions and regulations of ABC transporters of plants.
To achieve these goals, we 1) investigate which genes increase oil accumulation and biomass increase in plants and algae, 2) identify which genes can contribute to plants’ resistance to heavy metals, environmental pollutants, and other stresses, and 3) identify the substrates and physiological roles of the many ABC transporters of plants. For the candidate genes, we investigate their action mechanisms, using many state of the art technologies. Then we generate transgenic poplar trees and algae by expressing the candidate genes, and finally, test whether these transgenic plants effectively remediate the pollutants, or produce bio-energy materials, in green house and in the field.

**Major Publications**

2. H. Choi, Y.-Y. Kim, K. Ohyama, S.-B. Lee, T. Muranaka, M.-C. Suh, S. Fujioka and Y. Lee, 2014 Two Arabidopsis ATP-binding cassette transporters that deposit steryl glycoside on the pollen coat are important for pollen fitness. The Plant Cell, 26: 310-324
5. Transgenic poplar trees expressing yeast cadmium factor 1 exhibit the characteristics necessary for the phytoremediation of mine tailing soil. Chemosphere, 90; 1478-1486 (2013)
Lab. of **Plant-Microbe Interactions**

**Prof. Kee Hoon Sohn**

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**Education**

B.S., Korea University, Seoul, Korea (2001)  
M.S., Korea University, Seoul, Korea (2003)  
Ph.D., University of East Anglia, Norwich, United Kingdom (2009)

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**Research Introduction**

Plants and microbial pathogens co-evolve their mechanisms of detection and evasion, respectively. Pathogen effectors attenuate plant immunity by interfering with the function of their host target proteins. In turn, plants evolved disease resistance (R) proteins, often carry NB-LRR domains that are also found in mammalian immune receptors, that can recognize corresponding effectors and activate a strong defence system known as effector-triggered immunity. Our research focus is to identify effectors from economically important pathogens and their corresponding R genes in order to investigate their functions in detail. In addition, we aim to use these resources to develop future crop breeding strategies for enhanced disease resistance and biomass production.

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**Career**

2013~2015: Research Fellow, Bio-protection Research Centre, Institute of Agriculture and Environment, Massey University, New Zealand.  
2009~2012: Postdoctoral Fellow, The Sainsbury Laboratory, United Kingdom.

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**Major Awards/Honors**

- Massey University College Research Award (2015)

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**Research Areas**

- Molecular basis of intracellular immune receptor functions in plants  
- Role of pathogen effectors in plant disease susceptibility  
- Developing strategies for disease resistant crop breeding

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**Activities**

- Paired immune receptor function in Arabidopsis thaliana  
- Functional investigation of the nuclear-localized pathogen effectors in transcriptional regulation of defence genes in plants  
- Identification of disease resistance resources to control important pathogens in Brassica, Capsicum and Solanum species.

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**Major Publications**

Beyond Future, Beyond Thinking