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• **Current Position:** Assistant Professor, Faculty of Food Science and Biotechnology, College of Life Science, Sejong University

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• **Educational Background:**

03/2008 - 08/2013, M.S./Ph.D.

Food Science and Biotechnology  
Department of Food and Animal Biotechnology  
Seoul National University, Seoul, Republic of Korea

03/2004 - 02/2008, B.S.

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• **Professional Experiences:**

09/2016 – Present

**Assistant Professor**  
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College of Life Science, Sejong University  
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10/2014 – 08/2016

**Postdoctoral Fellow**  
New York University School of Medicine  
New York, NY, USA

03/2014 – 09/2014

**Senior Research Scientist**  
Center for Food Safety and Toxicology  
Seoul National University, Seoul, Republic of Korea

09/2013 - 02/2014

**Senior Research Scientist**  
Research Institute for Agriculture and Life Sciences  
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• **Professional Organizations:**

Member of American Society for Microbiology  
Member of Korean Society for Microbiology and Biotechnology  
Editorial Board of Journal of Microbiology and Biotechnology

• **Main Scientific Publications** (\* = **Co-first author**):

1. Mueller, N.T. \*, **Shin, H. \***, Pizoni, A., Werlang, I.C., Matte, U., Goldani, M.Z., Goldani, H.A., Dominguez-Bello, M.G. Delivery mode and the transition of pioneering gut-microbiota structure, composition and predicted metabolic function. (2017) *Genes*. 8(12):364
2. Earth Microbiome Project Consortium (as collaborator). A communal catalogue reveals Earth's multiscale microbial diversity. (2017) *Nature*. 551(7681):457-463

3. Huazano-García, A.\* , **Shin, H.\***, López, M.G. Modulation of gut microbiota of overweight mice by agavins and their association with body weight Loss. (2017) *Nutrients*. 9(9): E821
4. Lee, H., Ku, H.J., Lee, D.H., Kim, Y.T., **Shin, H.**, Ryu, S., Lee, J.H. Characterization and genomic study of the novel bacteriophage HY01 infecting both *Escherichia coli* O157:H7 and *Shigella flexneri*: Potential as a biocontrol agent in food. (2016) *PLoS One*. 11(12):e0168985
5. Bik, H.M., Maritz, J.M., Luong, A., **Shin, H.**, Dominguez-Bello, M.G., Carlton, J.M. Microbial community patterns associated with automated teller machine keypads in New York City. (2016) *mSphere*. 1(6):e00226-16
6. Nelson, D., **Shin, H.**, Wu, J., Dominguez-Bello, M.G. The gestational vaginal microbiome and spontaneous preterm birth among nulliparous African American women. (2016) *Am J Perinatol*. 33(9):887-893
7. Mueller, N.T., **Shin, H.**, Pizoni, A., Werlang, I.C., Matte, U., Goldani, M.Z., Goldani, H.A., Dominguez-Bello, M.G. Birth mode-dependent association between pre-pregnancy maternal weight status and the neonatal intestinal microbiome. (2016) *Sci Rep*. 6:23133
8. **Shin, H.**, Price, K., Albert, L., Dodick, J., Park, L., Dominguez-Bello, M.G. Changes in the eye microbiota associated with contact lens wearing. (2016) *MBio*. 7(2):e00198-16
9. **Shin, H.**, Pei, Z., Martinez, K.A., Rivera-Vinas, J.I., Mendez, K., Cavallin, H., Dominguez-Bello, M.G. The first microbial environment of infants born by C-section: the operating room microbes. (2016) *Microbiome*. 3:59
10. Lee, J.H., Bai, J., **Shin, H.**, Kim, Y., Park, B., Heu, S., Ryu, S. A novel bacteriophage targeting *Cronobacter sakazakii* is a potential biocontrol agent in foods. (2015) *Appl Environ Microbiol*. 82(1):192-201
11. Lee, S.H., Ku, H.J., Ahn, M.J., Hong, J.S., Lee, S.H., **Shin, H.**, Lee, K.C., Lee, J.S., Ryu, S., Jeon, C.O., Lee, J.H. *Weissella jogaejeotgali* sp. nov., isolated from jogae jeotgal, a traditional Korean fermented seafood. (2015) *Int J Syst Evol Microbiol*. 65(12):4674-4681
12. Chang, Y., **Shin, H.**, Lee, J.H., Park, C.J., Paik, S.Y., Ryu, S. Isolation and genome characterization of the virulent *Staphylococcus aureus* bacteriophage SA97. (2015) *Viruses*. 7(10):5225-5242
13. Lim, S., Lee, D.H., Kwak, W., **Shin, H.**, Ku, H.J., Lee, J.E., Lee, G.E., Kim, H., Choi, S.H., Ryu, S., Lee, J.H. Comparative genomic analysis of *Staphylococcus aureus* FORC\_001 and *S. aureus* MRSA252 reveals the characteristics of antibiotic resistance and virulence factors for human infection. (2015) *J Microbiol Biotechnol*. 25(1):98-108
14. **Shin, H.**, Lee, J.H., Park, J., Heu, S., Ryu, S. Characterization and genome analysis of the *Bacillus cereus*-infecting bacteriophages BPS10C and BPS13. (2014) *Arch Virol*. 159(8):2171-2175
15. Lim, J.A., **Shin, H.**, Lee, D.H., Han, S.W., Lee, J.H., Ryu, S., Heu, S. Complete genome sequence of the *Pectobacterium carotovorum* subsp. *carotovorum* virulent bacteriophage PM1. (2014) *Arch Virol*. 159(8):2185-2187
16. **Shin, H.**, Lee, J.H., Yoon, H., Kang, D.H., Ryu, S. Genomic investigation of lysogen formation and host lysis systems of the *Salmonella* temperate bacteriophage SPN9CC. (2014) *Appl Environ Microbiol*. 80(1):374-384
17. Lee, J.H., **Shin, H.**, Ryu, S. Characterization and comparative genomic analysis of bacteriophages

- infesting the *Bacillus cereus* group. (2014) Arch Virol. 159(5):871-884 (**Review article**)
18. Lee, J.H.\*, **Shin, H.\***, Park, H.J., Ryu, S., Han, S.W. Draft genome sequence of *Xanthomonas axonopodis* pv. *glycines* 8ra possessing transcription activator-like effectors used for genetic engineering. (2014) J Biotechnol. 10(179):15-16
  19. **Shin, H.\***, Lee, J.H.\*, Ahn, C.S., Ryu, S., Cho, B.C. Complete genome sequence of marine bacterium *Pseudoalteromonas phenolica* bacteriophage TW1. (2014) Arch Virol. 159(1):159-162
  20. Lee, J.H.\*, **Shin, H.\***, Son, B., Heu, S., Ryu, S. Characterization and complete genome sequence of a virulent bacteriophage B4 infecting food-borne pathogenic *Bacillus cereus*. (2013) Arch Virol. 158(10):2101-2108
  21. Lee, H.S., Choi, S., **Shin, H.**, Lee, J.H., Choi, S.H. *Vibrio vulnificus* bacteriophage SSP002 as a possible biocontrol agent. (2013) Appl Environ Microbiol. 80(2):515-524
  22. Lee, J.H., **Shin, H.**, Choi, Y., Ryu, S. Complete genome sequence analysis of bacterial-flagellum-targeting bacteriophage chi. (2013) Arch Virol. 158(10):2179-2183
  23. Choi, Y., **Shin, H.**, Lee, J.H., Ryu, S. Identification and characterization of a novel flagellum-dependent *Salmonella*-infecting bacteriophage, iEPS5. (2013) Appl Environ Microbiol. 79(16):4829-4837
  24. Lim, J.A., **Shin, H.**, Heu, S., Ryu, S. Exogenous lytic activity of SPN9CC endolysin against gram-negative bacteria. (2014) J Microbiol Biotechnol. 24(6):803-811
  25. Chang, Y., Lee, J.H., **Shin, H.**, Heu, S., Ryu, S. Characterization and complete genome sequence analysis of *Staphylococcus aureus* bacteriophage SA12. (2013) Virus Genes. 47(2):389-393
  26. Kim, S.Y., Oh, C.G., Lee, Y.J., Choi, K.H., Shin, D.S., Lee, S.K., Park, K.J., **Shin, H.**, Park, M.S., Lee, J.H. Sequence analysis of a cryptic plasmid pKW2124 from *Weissella cibaria* KLC140 and construction of a surface display vector. (2013) J Microbiol Biotechnol. 23(4):545-554.
  27. Lee, D.H., Lee, J.H., **Shin, H.**, Ji, S., Roh, E., Jung, K., Ryu, S., Choi, J., Heu, S. Complete genome sequence of *Pectobacterium carotovorum* subsp. *carotovorum* bacteriophage My1. (2012) J Virol. 86(20):11410-11411
  28. **Shin, H.\***, Lee, J.H.\*, Kim, H., Choi, Y., Heu, S., Ryu, S. Receptor diversity and host interaction of bacteriophages infecting *Salmonella enterica* serovar Typhimurium. (2012) PLoS One. 7(8):e43392
  29. Jung, J.H., Holden, J.F., Seo, D.H., Park, K.H., **Shin, H.**, Ryu, S., Lee, J.H., Park, C.S. Complete genome sequence of the hyperthermophilic archaeon *Thermococcus* sp. strain CL1, isolated from a *Paralvinella* sp. polychaete worm collected from a hydrothermal vent. (2012) J Bacteriol. 194(17):4769-4770
  30. Lee, J.H., **Shin, H.**, Ji, S., Malhotra, S., Kumar, M., Ryu, S., Heu, S. Complete genome sequence of phytopathogenic *Pectobacterium carotovorum* subsp. *carotovorum* bacteriophage PP1. (2012) J Virol. 86(16):8899-8900
  31. **Shin, H.\***, Lee, J.H.\*, Choi, Y., Ryu, S. Complete genome sequence of the opportunistic food-borne pathogen *Cronobacter sakazakii* ES15. (2012) J Bacteriol. 194(16):4438-4439
  32. Jung, J.H., Lee, J.H., Holden, J.F., Seo, D.H., **Shin, H.**, Kim, H.Y., Kim, W., Ryu, S., Park, C.S. Complete genome sequence of the hyperthermophilic archaeon *Pyrococcus* sp. strain ST04,

- isolated from a deep-sea hydrothermal sulfide chimney on the Juan de Fuca Ridge. (2012) J Bacteriol. 194(16):4434-4435
33. Choi, Y., Kim, K.P., Kim, K., Choi, J., **Shin, H.**, Kang, D.H., Ryu, S. Possible roles of LysR-type transcriptional regulator (LTTR) homolog as a global regulator in *Cronobacter sakazakii* ATCC 29544. (2012) Int J Med Microbiol. 302(6):270-275
  34. Lee, J.H., Choi, Y., **Shin, H.**, Lee, J., Ryu, S. Complete genome sequence of *Cronobacter sakazakii* temperate bacteriophage phiES15. (2012) J Virol. 86(14):7713-7714
  35. **Shin, H.\***, Lee, J.H.\*, Kim, Y., Ryu, S. Complete genome sequence of *Cronobacter sakazakii* bacteriophage CR3. (2012) J Virol. 86(11):6367-6368
  36. Son, B., Yun, J., Lim, J.A., **Shin, H.**, Heu, S., Ryu, S. Characterization of LysB4, an endolysin from the *Bacillus cereus*-infecting bacteriophage B4. (2012) BMC Microbiol. 12(1):33
  37. Lee, J.H., **Shin, H.**, Ryu, S. Complete genome sequence of *Salmonella enterica* serovar Typhimurium bacteriophage SPN3UB. (2012) J Virol. 86(6):3404-3405
  38. Lim, J.A., **Shin, H.**, Kang, D.H., Ryu, S. Characterization of endolysin from a *Salmonella* Typhimurium-infecting bacteriophage SPN1S. (2012) Res Microbiol. 163(3):233-241
  39. **Shin, H.\***, Lee, J.H.\*, Lim, J.A., Kim, H., Ryu, S. Complete genome sequence of *Salmonella enterica* serovar typhimurium bacteriophage SPN1S. (2012) J Virol. 86(2):1284-1285
  40. Lee, J.H., **Shin, H.**, Son, B., Ryu, S. Complete genome sequence of *Bacillus cereus* bacteriophage BCP78. (2012) J Virol. 86(1):637-638
  41. Lee, J.H., **Shin, H.**, Kim, H., Ryu, S. Complete genome sequence of *Salmonella* bacteriophage SPN3US. (2011) J Virol. 85(24):13470-13471
  42. Park, M., Lee, J.H., **Shin, H.**, Kim, M., Choi, J., Kang, D.H., Heu, S., Ryu, S. (2012) Characterization and comparative genomic analysis of a novel bacteriophage, SFP10, simultaneously inhibiting both *Salmonella enterica* and *Escherichia coli* O157:H7. Appl Environ Microbiol. 78(1):58-69
  43. **Shin, H.\***, Bandara, N.\*, Shin, E., Ryu, S., Kim, K.P. Prevalence of *Bacillus cereus* bacteriophages in fermented foods and characterization of phage JBP901. (2011) Res Microbiol. 162(8):791-797