CURRICULUM VITAE

김준호

성균관대학교 생명과학과

[학력]

2009.09-2014.08 박사과정, KAIST 바이오및뇌공학과
2008.03-2009.08 석사과정, KAIST 바이오및뇌공학과
2004.03-2008.02 학사과정, KAIST 바이오및뇌공학과

[경력]

2021.09-현재 조교수, 성균관대학교 생명과학과
2017.04-2021.08 박사후연구원, Boston Children's Hospital / Harvard Medical School
2014.09-2017.03 박사후연구원, 연세대학교 의과대학

[관심분야]

생명정보학, 유전체학, 체성돌연변이 분석

[논문]

1. In Seok Yang, Insu Jang, Jin Ok Yang, Jinhyuk Choi, Min-Seo Kim, Ka-Kyung Kim, Byung-Joon Seung, Jae-Ho Cheong, Jung-Hyang Sur, Hojung Nam, Byungwook Lee§, Junho Kim§, and Sangwoo Kim§, CanISO: a database of genomic and transcriptomic variations in domestic dog (Canis lupus familiaris), BMC genomics, 2023, 24.1: 613.
2. Junho Kim, August Yue Huang, Shelby L. Johnson, Jenny Lai, Laura Isacco, Ailsa M. Jeffries, Michael B. Miller, Michael A. Lodato, Christopher A. Walsh§ and Eunjung Alice Lee§, Prevalence and mechanisms of somatic deletions in single human neurons during normal aging and in DNA repair disorders, Nature Communications, 2022, 13.1: 5918.
3. Michael B. Miller, August Yue Huang, Junho Kim, Zinan Zhou, Samantha L. Kirkham, Eduardo A. Maury, Jennifer S. Ziegenfuss, Hannah C. Reed, Jennifer E. Neil, Lariza Rento, Steven C. Ryu, Chanthia C. Ma, Lovelace J. Luquette, Heather M. Ames, Derek H. Oakley, Matthew P. Frosch, Bradley T. Hyman, Michael A. Lodato§, Eunjung Alice Lee§ and Christopher A. Walsh§, Somatic genomic changes in single Alzheimer's disease neurons, Nature, 2022, 604.7907: 714-722.
4. Junho Kim, Boxun Zhao, August Yue Huang, Michael B. Miller, Michael A. Lodato, Christopher A. Walsh§ and Eunjung Alice Lee§, APP gene copy number changes reflect exogenous contamination, Nature, 2020, 584.7821: E20-E28.
5. Junho Kim, Dachan Kim, Jae Seok Lim, Ju Heon Maeng, Hyeonju Son, Hoon-Chul Kang, Hojung Nam, Jeong Ho Lee§ and Sangwoo Kim§, The use of technical replication for detection of low-level somatic mutations in next-generation sequencing, Nature Communications, 2019, 10.1: 1047.

Exploring the role of somatic mutations in human brain diseases

Junho Kim

Department of Biological Sciences, Sungkyunkwan University, South Korea

With advances in next-generation sequencing (NGS) technologies, somatic mutation analysis has made great strides in establishing a comprehensive description of genomic changes in cancer over the past decade. International collaborative efforts such as The Cancer Genome Atlas (TCGA) and International Cancer Genome Consortium (ICGC) have been made to construct the landscape of somatic mutations in various cancer types, leading to unprecedented knowledge of the somatic mutations and their underlying mechanisms.

Recent analyses of somatic mutations have begun to be made in non-cancerous diseases, especially in brain diseases. Unlike cells in other tissues, differentiated neurons in the brain are rarely replaced and regenerated during the course of a person's life, so that somatic mutations in those cells may critically affect the function of neurons and even brain circuits. Recent studies have demonstrated that somatic mutations occurring during brain development do actually cause multiple neurodevelopmental diseases, supporting a new pathogenesis of brain disorders. However, due to the lack of specialized bioinformatic tools for detecting rare somatic mutations in tissues without clonal expansion, somatic mutations in brain have not been comprehensively explored yet.

In this talk, the speaker will discuss the difficulties associated with analyzing somatic mutations in the brain, as well as the current efforts aimed at tackling these challenges. The talk will cover different sequencing approaches and developed bioinformatic methods used to detect rare somatic mutations in low cell population or even in a single cell.