Kang Le, Institute of zoology, Chinese Academy of Sciences

Dr. Le Kang is an internationally recognized pioneer in ecological genomics. He has been devoting himself to solve ecological and adaptive questions of insects by integrating multiple approaches from molecular, gene, genome to behavior. He has achieved outstanding accomplishments in mechanism of population outbreaks and regulation using the migratory locust as a model system. He and his colleagues decoded a 6.5 Gb whole genome sequence of the migratory locust, which is the largest animal genome sequenced so far, and revealed genetic myth of genome expansion, long-distance flight, phytophagy and swarming. In locust polyphenism, he discovered the key roles of olfactory genes and dopamine pathway in the initiation and maintenance of locust phase change, and revealed epigenetic regualtory mechanisms of locust phenotypic plasticity. He uncovered the origin and dispersal route of the migratory locust in the world, and revealed population genetics and adaptive differentiation linked with environmental changes. Moreover, Dr. Kang and his collaborators also revealed the secret of outbreaks of grasshoppers due to steppe degradation under heavy livestock grazing, which can significantly the nitrogen content of plants. These finding offers new insight into the biology and sustainable management of insect pests.

m iR-276 b rm

miR-276 promotes egg hatching synchrony by upregulating brm in locusts

> Molecular mechani immunology

康乐

主要科技贡献:

The locust genome provides insight into phytophagy and long-distance fight

mir-71 and mir-263 jointly regulate target genes chitin synthase and chitinase to control locust molting

MiR-71 miR-263

Molecular mechanisms of locust ecological

m iR-133

miR-133 inhibits behavioral aggregation by controlling dopamine synthesis in locusts