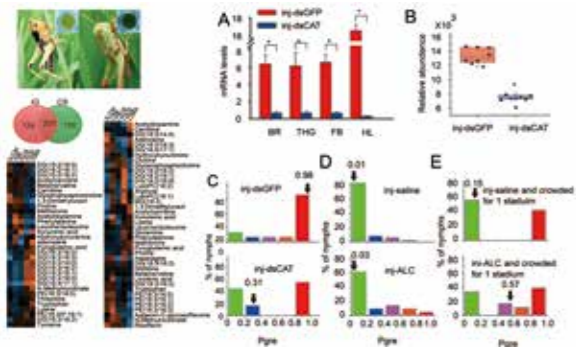


Kang Le, Institute of zoology, Chinese Academy of Sciences

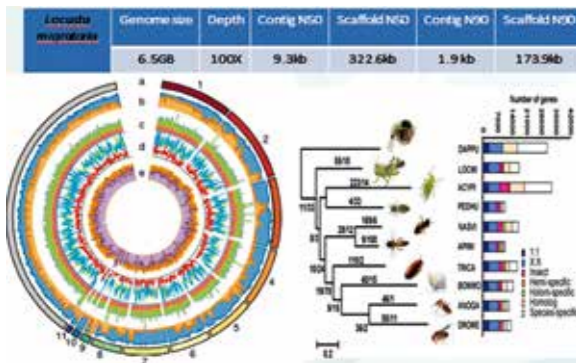


Dr. Le Kang is an internationally recognized pioneer in ecological genomics. He has been devoting himself to solve ecological and adaptive questions of insects by integrating multiple approaches from molecular, gene, genome to behavior. He has achieved outstanding accomplishments in mechanism of population 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 regulatory 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.

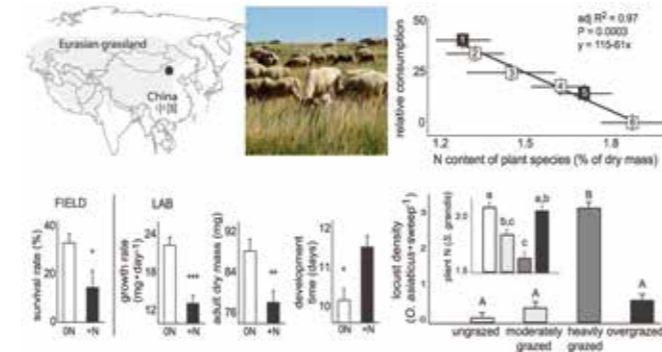
母代 miR-276 通过上调 brm 促进飞蝗后代卵一致性发育
miR-276 promotes egg hatching synchrony by upregulating brm in locusts



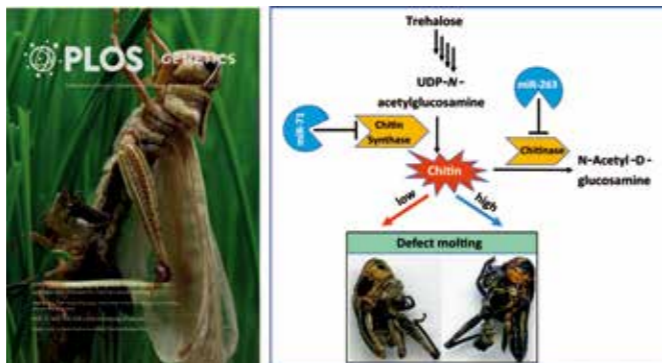
代谢组分析揭示肉碱类代谢物在飞蝗行为转变中的关键调控作用
Metabolomic analysis reveals that carnitines are key regulatory metabolites in phase transition of the locusts



飞蝗基因组揭示其食性及远距离迁飞的遗传基础
The locust genome provides insight into phytophagy and long-distance flight



重度放牧通过降低植物 N 含量促进亚洲小车蝗爆发
Heavy livestock grazing promotes locust outbreaks by lowering plant nitrogen content



MiR-71 和 miR-263 共同调控飞蝗几丁质代谢和蜕皮
mir-71 and mir-263 jointly regulate target genes chitin synthase and chitinase to control locust molting



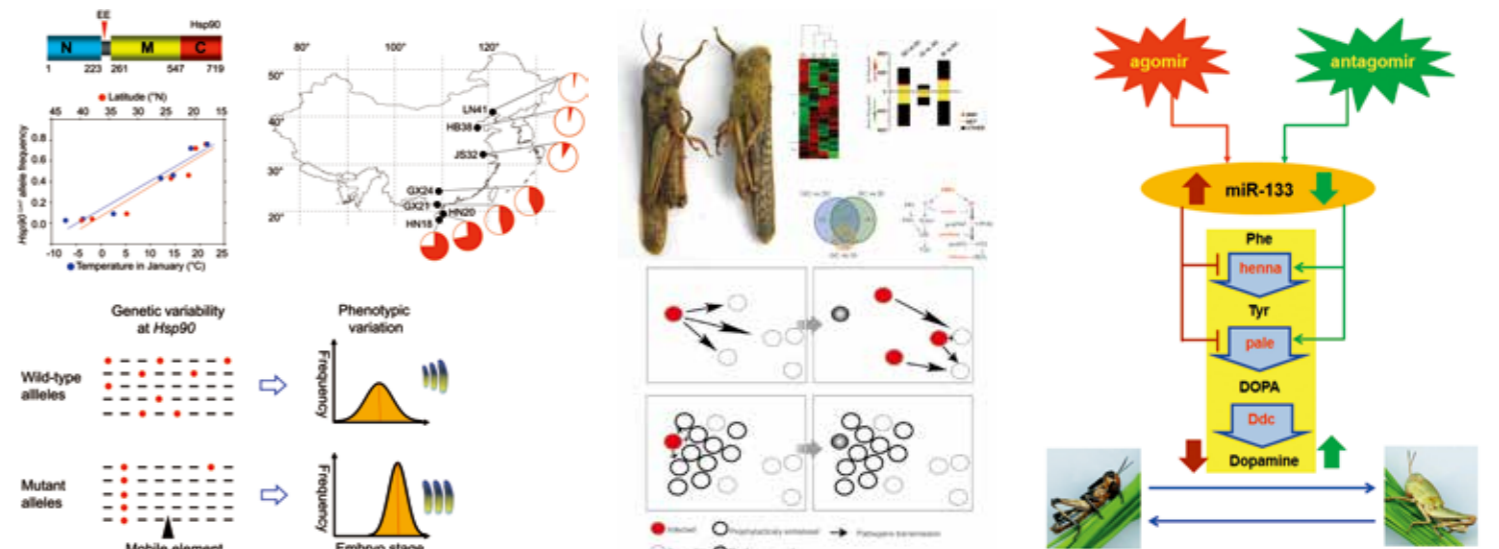
康乐
Kang Le

康乐

推荐单位：中国科学院动物研究所

主要科技贡献：

康乐院士将基因组学研究和生态学问题有机结合，以飞蝗为研究模式，围绕种群暴发成灾机制等世界难题，取得系列重大突破性进展，并成为国际上生态基因组学研究的主要开拓者。破译了飞蝗基因组（已测序的最大动物基因组），并揭示大基因组形成的原因和飞蝗长距离飞行、食性和大规模聚群的遗传基础。确定了嗅觉感受基因和多巴胺代谢途径参与飞蝗聚群行为调控的功能，以及表型可塑性的表观遗传调控机制。阐明了飞蝗在世界范围内的起源、扩散、种群遗传和适应性分化机制。揭示了植物营养等生态因子在种群暴发成灾中的作用机制，改变了传统认识。为我国绿色农业战略实施做出了基础性贡献。



转座因子介导的平衡选择作用于 Hsp90 控制飞蝗胚胎发育变异
Transposable element-mediated balancing selection at Hsp90 underlies embryo developmental variation.

飞蝗生态免疫分子机制研究
Molecular mechanisms of locust ecological immunology

miR-133 通过控制飞蝗多巴胺合成而抑制群聚行为
miR-133 inhibits behavioral aggregation by controlling dopamine synthesis in locusts