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GENOME REPORTS

Whole Genome Sequence of the Heterozygous Clinical Isolate *Candida krusei* 81-B-5
Christina A. Cuomo, Terrance Shea, Bo Yang, Reeta Rao, and Anja Forche

Candida krusei is an important fungal pathogen in immunocompromised patients and is innately resistant to the antifungal drug fluconazole. Cuomo *et al.* generated a high quality genome assembly of a clinical *C. krusei* isolate using PacBio sequencing technology. They report high levels of heterozygosity across most of the genome and a unique profile of transporters that could impact the species′ drug sensitivity and adaptation to different environments. This genome will serve as a reference for further genetic study of this pathogen.

The Nuclear and Mitochondrial Genomes of the Facultatively Eusocial Orchid Bee *Euglossa dilemma*
Philipp Brand, Nicholas Saleh, Hailin Pan, Cai Li, Karen M. Kapheim, and Santiago R. Ramírez

Bees provide indispensable pollination services and have become important models for the study of learning and memory, plant–insect interactions, and social behavior. Here, Brand *et al.* describe the nuclear and mitochondrial genomes of the facultatively eusocial orchid bee *Euglossa dilemma*. The *E. dilemma* genome has high conservation of gene synteny when compared to the honey bee, despite genome size difference and evolutionary divergence. This study provides valuable genomic resources for genetic analyses on the ecology, evolution, and conservation of orchid bees and the evolution of sociality in bees.

Genome-Wide Analysis of the First Sequenced *Mycoplasma capricolum* subsp. *capripneumoniae* Strain M1601
Shengli Chen, Huafang Hao, Ping Zhao, François Thiaucourt, Ying He, Pengcheng Gao, Han Guo, Wenheng Ji, Zhanhui Wang, Zhongxin Lu, Yuefeng Chu, and Yongsheng Liu

Mycoplasma capricolum subsp. *capripneumoniae* (Mccp) is a common goat pathogen that causes contagious caprine pleuropneumonia. Chen *et al.* closed the gap in the Mccp M1601 draft genome and corrected the rRNA operon sequences to yield complete genomic sequences. Comprehensive genomic analysis identified twenty-six potential virulence genes, and Chen *et al.* also performed comparative and phylogenetic analyses. Further understanding the virulence genes, genome features, and genetics of Mccp will help determine its pathogenic mechanisms and genetics.

MUTANT SCREEN REPORT

Genome-Wide Screen for Genes Involved in *Caenorhabditis elegans* Developmentally Timed Sleep
Huiyan Huang, Chen-Tseh Zhu, Lukas L. Skuja, Dustin J. Hayden, and Anne C. Hart

Huang *et al.* describe the first genome-wide, classic genetic screen focused on identifying genes required for developmentally timed sleep in *C. elegans*. In the screen, they identified causal genes for two mutant lines with decreased sleep: *goa-1* and *gpb-2*. To understand the role of GPB-2, they examined previously described regulators of G protein signaling (RGS) proteins and determined which proteins contribute to developmentally timed sleep. The work presented here highlights the importance of G protein signaling in sleep regulatory pathways.

INVESTIGATIONS