



Figure 1. Analysis of *Chryseobacterium* genomes. (a) The whole-genome sequence-based phylogenetic tree of *Chryseobacterium* species, based on the merge reference alignments of all genomes. Branch length represents divergence, and stars show the keratinolytic *Chryseobacterium* species. (b) Overall orthologous average nucleotide identity (ANI) among pairwise *Chryseobacterium* genomes. Values in heatmap indicate the similarity percentage.

Remarkably, each genome had more than 200 genes assigned into the “amino acid metabolism” sub-category. Keratin is mainly composed of amino acids [3], which is ultimately the operational nutrient source exploited for microbial growth. Numerous amino acid metabolism-related enzymes were annotated, revealing the genetic potential of these *Chryseobacterium* strains for using keratin materials as carbon source.

Of particular interest, several biosynthesis genes of secondary metabolites were detected from the genomes, of which more than 20 genes were assigned to “metabolism of terpenoids and polyketides” and around 40 genes were assigned to “biosynthesis of other secondary metabolites” sub-category (Figure 2). Terpenoids are a group of natural products with diverse commercial applications, which have been produced from microbial cell factories [51]. Many polyketides are considered as significant natural products with broad applications in the agriculture and pharmaceutical industry [52]. The metabolic pathways related to polyketides biosynthesis are well understood in some microorganisms like *Streptomyces* which play a crucial role in industrial bioproduction [53]. This result indicates that these *Chryseobacterium* strains could have the potential to synthesize high-value secondary metabolites such as terpenoids and polyketides from keratinous materials.