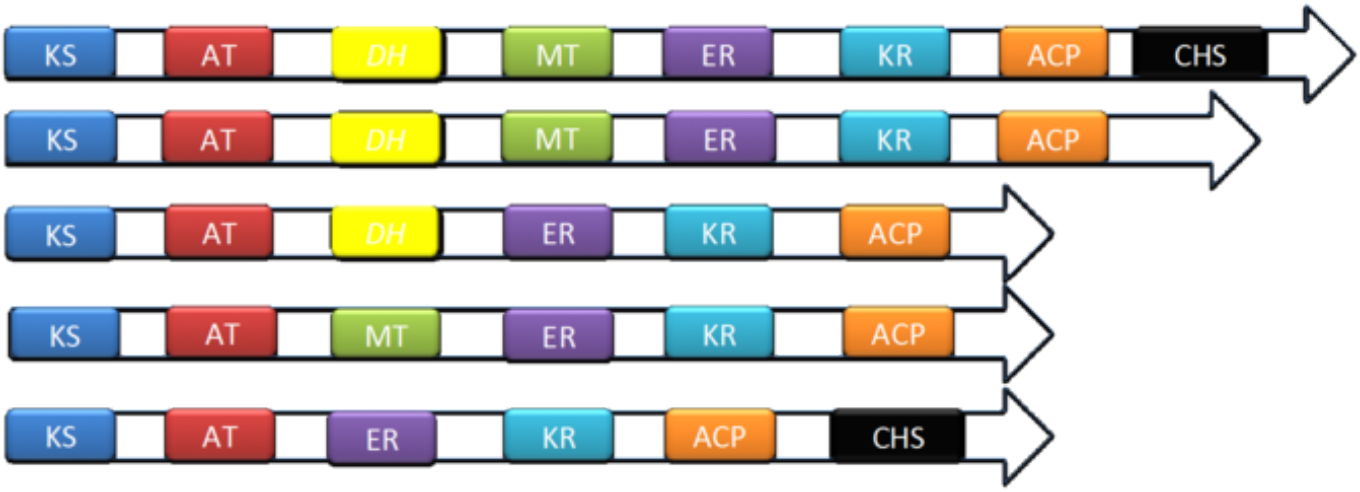
Polyketides in *Dictyostelium discoideum*



The genome of the social amoeba *Dictyostelium discoideum* contains over 40 putative polyketide synthase (pks) genes and their biosynthetic products as well as their functions are largely unknown. To identify and investigate these polyketides, we use a combination of molecular biology and analytical chemistry tools. Knockout mutants of selected pks genes are generated and the resulting secondary metabolome is compared with the wildtype strain. However, the pks genes of *D. discoideum* are a class of genes with high nucleotide sequence similarity. For this reason, well-established methods to edit the social amoeba's genome show little success.

Targeted genome editing in *D. discoideum* using the clustered, regularly interspaced repeated short palindromic repeat (CRISPR) RNA-guided Cas9 nuclease is a valuable molecular tool to address these problems. This tool is very specific, even for genes with high similarity to others. We are currently establishing this technology in *D. discoideum*, thus generating a mutant library of pks genes in *D. discoideum* to elucidate the structure and function of the so far unknown secondary metabolites.