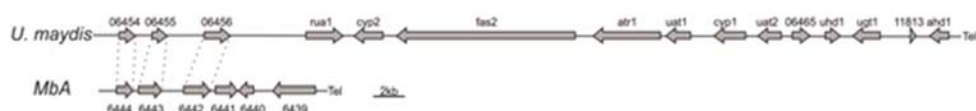


A

Cluster	Contig	Gene cluster type	Present in <i>U. maydis</i>
1	1	other	✓
2	2	Terpene cluster	X
3	3	other	✓
4	3	other	✓
5	4	other	✓
6	5	other	✓
7	13	Terpene cluster	✓
8	17	other	X
9	20	Nonribosomal peptide synthetase cluster	✓
10	21	Nonribosomal peptide synthetase cluster	X
11	22	Nonribosomal peptide synthetase cluster	✓
12	24	Type I PKS cluster	✓
13	25	Terpene cluster	✓

B



C

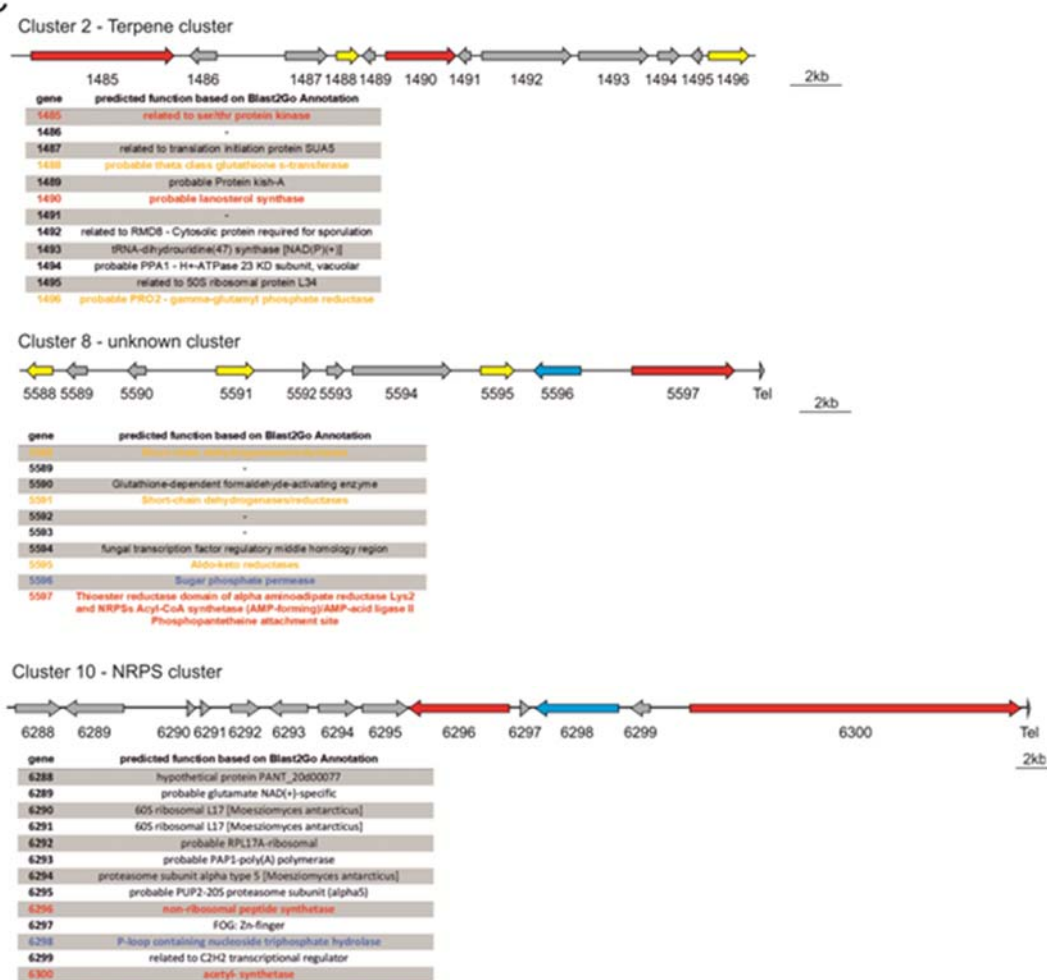


Figure 3 – figure supplement 1: (A) Predicted secondary metabolite clusters in the genome of *MbA*. Most clusters are having unpredictable functions, three are each belonging to the type of terpene or non-ribosomal peptide synthetase types and one is a polyketide synthetase cluster type I. (B) The gene cluster encoding for production of ustilagic acid, a well-studied secondary metabolite of smut fungi [2], is not present in the genome of *MbA*. (C) Out of the 13 predicted secondary metabolite clusters, three are unique to *MbA*. Cluster 2 is predicted to encode a terpene, cluster 8 is a cluster of unknown function and cluster 10 is predicted as NRPS cluster. Core biosynthetic genes are highlighted in red, additional biosynthetic genes in yellow and transport related genes in blue, based on AntiSMASH predictions.