

Figure S1. Catechol-type siderophore pathway in *S. tricolor* HM10 and the related bacteria with up to 85% similarity with *Streptomyces* sp. BK340 when compared in ClusterBlast.

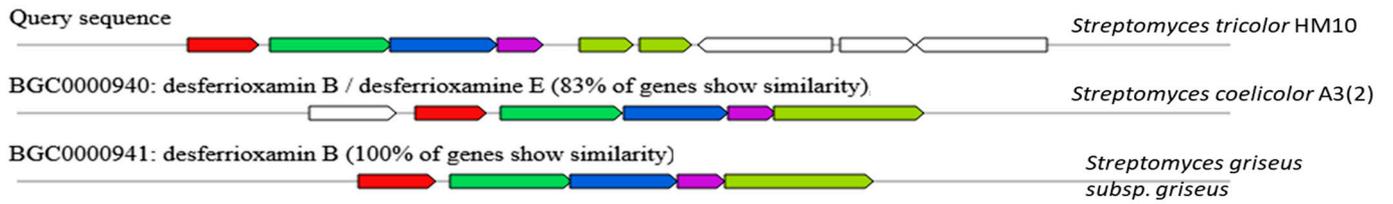


Figure S2. Hydroxamate-type siderophore pathway in *S. tricolor* HM10 and the related bacteria with up to 100 % similarity with *S. griseus* compared with KnownClusterBlast.

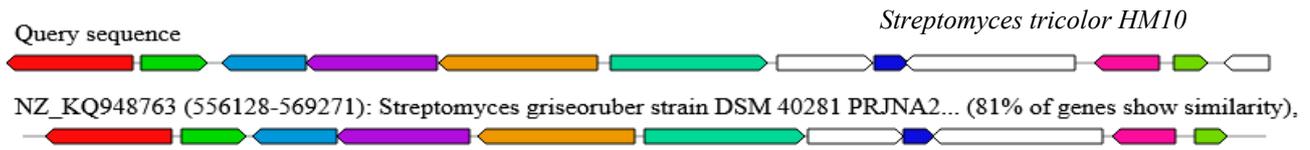


Figure S3. Carboxylate-type siderophore pathway in *S. tricolor* HM10 and the related bacteria with up to 81 % similarity with *S. griseoruber* DSM 40281 PRJNA2 when compared at ClusterBlast.

Table S1: The statistics of *S. tricolor* HM10 sequenced genome.

Isolate	Number of sequenced Bases	Number of Reads	Average	Largest read	Total genome Length	Number of contigs	GC content (%)	Shortest contig size
<i>S. tricolor</i> HM10	69891559	50197	1392.35	33582	8,392,594	62	72.75	3197
Median sequence size	Mean sequence size	Longest contig size	N50 value	L50 value	Number of Subsystems	Number of Coding Sequences	Number of RNAs	Closest neighbors
82125	135364.4	1098672	238069	9	317	12077	78	<i>Streptomyces cinerochromogenes</i> JCM 3385