Table 1. Key genomic features of *Streptomyces* sp. ZE1316R2A^T and *Streptomyces albidoflavus* DSM 40455^T. Listed attributes include total genome size (bp), GC content (%), predicted number of coding sequences (CDS), proportion of the genome coding for proteins (%), average CDS length (bp), numbers of tRNA genes and 16S rRNA gene copies. The number of rRNA genes differed depending on the annotation system. As the absence of 23S rRNA genes is biologically unlikely in *Streptomyces*, we retained the Bakta annotation, which predicts complete operons (16S–23S–5S). Quality metrics of genome assemblies comprise completeness and contamination. CheckM assignation indicates the taxonomic classification based on genomic data.

Genomes features	***Streptomyces* sp. ZE1316R2A^T**	***S. albidoflavus* DSM 40455^T**
Size (bp)	7,407,648	6,975,571
GC-content (%)	73.26	73.43
Contigs number	3	66
Predicted CDS	6,464	6,230
Genome coding (%)	87.9	88.4
Average CDS size (bp)	1,021.01	1,003.23
Number of tRNA	66	65
Number of 16S rRNA	7	1
Number of 23S rRNA	7	2
Number of 5S rRNA	7	4
CheckM2 Completeness (%)	100	100
CheckM2 Contamination (%)	0	0.04
CheckM Assignation	*Streptomycetaceae*	*Streptomycetaceae*

Table 2. Core, unique, and pan-genome components of *Streptomyces* sp. ZE1316R2A^{T} and *Streptomyces albidoflavus* DSM 40455^{T}. The pan-genome encompasses all gene families found in either strain. The core genome consists of genes shared between *Streptomyces* sp. ZE1316R2A^{T} and *S. albidoflavus* DSM 40455^{T}, while strain-specific CDS are coding sequences unique to one strain only. Percentages reflect how much of each genome is composed of core or strain-specific CDS. (MICFAM parameter: 80% aa identity/ 80% alignment coverage).

Organism	**Total CDS per genome**	**Core -genome (CDS, %)**	**Strain specific CDS**
***S. albidoflavus* DSM 40455^{T}**	6,230	5,109 (82.06 %)	1,117 (17.94%)
***Streptomyces* sp. ZE1316R2A^{T}**	6,464	5,123 (79.25%)	1,341 (20.75%)

Table 3. Comparative table of cultural characteristics between *Streptomyces* sp. ZE1316R2A^T and *Streptomyces albidoflavus* DSM 40455^{T}on ISP Media.

ISP Medium	Strain	Growth [a]	Aerial mycelium [b]	Substrate mycelium [c]	Diffusible pigment [d]
Tryptone-Yeast Extract agar (ISP 1)	*S. albidoflavus* DSM 40455^T	Poor	Absent	Light yellow	**Deep orange yellow**
	Streptomyces sp. ZE1316R2A^T	Poor	Absent	Light yellow	**Light orange yellow**
Yeast extract-malt extract agar (ISP 2)	*S. albidoflavus* DSM 40455^T	Moderate	White	**Dark orange yellow**	**Deep brown**
	Streptomyces sp. ZE1316R2A ^{T}	Moderate	White	**Strong yellowish brown**	**Strong orange**
Oatmeal agar (ISP 3)	*S. albidoflavus* DSM 40455^T	**Abundant**	White	**Strong yellowish brown**	**Strong yellowish brown**
	Streptomyces sp. ZE1316R2A ^{T}	**Moderate**	White	**Light yellowish brown**	**Moderate orange yellow**
Inorganic salt-starch agar (ISP 4)	*S. albidoflavus* DSM 40455^T	**Moderate**	**White**	**Dark yellow**	**Moderate orange yellow**
	Streptomyces sp. ZE1316R2A ^{T}	**Poor**	**Absent**	**Moderate yellow**	**Pale orange yellow**
Glycerol-asparagine agar (ISP 5)	*S. albidoflavus* DSM 40455^T	**Moderate**	**Absent**	**Dark yellow**	Light yellow
	Streptomyces sp. ZE1316R2A ^{T}	**Abundant**	**White**	**Moderate yellow**	Light yellow
Peptone-yeast extract agar (ISP 6)	*S. albidoflavus* DSM 40455^T	Moderate	**Absent**	Light orange yellow	**Strong brown**
	Streptomyces sp. ZE1316R2A ^{T}	Moderate	**White**	Light orange yellow	**Strong orange**
Tyrosine agar (ISP7)	*S. albidoflavus* DSM 40455^T	**Abundant**	White	**Moderate orange yellow**	**Light yellow**
	Streptomyces sp. ZE1316R2A ^{T}	**Good**	White	**Dark orange yellow**	**Moderate orange yellow**

ISP: International *Streptomyces* Project **(Shirling and Gottlieb 1966).**

[a] **No growth:** No visible colonies or mycelium; **Poor growth:** Limited colony formation and colonies underdeveloped; **Moderate growth:** Colonies with typical actinobacterial features, less dense than optimal; **Good growth:** Distinct colonies with sporulation; **Abundant growth: Extensive** colony formation with dense sporulation.

[b, c, d] Colours of both substrate and aerial mycelia and any soluble pigments produced were determined by comparison with chips from the colour charts of the Inter-Society Color Council National Bureau of Standards **(Kelly ,1964).**

In bold: Differences between strain ZE1316R2A^T and strain DSM 40455^T.

Table 4. Different Major cellular fatty acid, phospholipids, menaquinones profiles (%) of strain *Streptomyces* sp. ZE1316R2A^T and its closely related type strain *Streptomyces albidoflavus* DSM 40455^T.

Characteristics	***Streptomyces* sp. ZE1316R2A^T**	***S. albidoflavus* DSM 40455^T**
Major fatty acids: (%)		
anteiso-$C_{15:0}$	**23.3**	17.6
iso-$C_{16:0}$	22	**27.7**
anteiso-$C_{17:0}$	**18.4**	15.6
Major phospholipids	DPG, PE, PI, APL, GPL, GL, PL, L	DPG, PE, PI, APL, GPL, GL, PL, L
Major menaquinones (%)	MK-9(H_2, H_4, H_6)	MK-9(H_2, H_4, H_6)
MK-8 H_2	5.3	5.4
MK-8 H_4	9.8	10.1
MK-8 H_6	5.7	6.7
MK-9 H_2	**15.2**	**19.3**
MK-9 H_4	**31.0**	**33.2**
MK-9 H_6	**33.0**	**25.4**

In bold: Differences between strain ZE1316R2A^T and strain DSM 40455^T.