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L.V. POLISHCHUK

Zabolotny Institute of Microbiology and Virology, NAS of Ukraine,
154 Akademika Zabolotnoho Str., Kyiv, 03143, Ukraine
Author for correspondence; e-mail: LVPolishchuk@ukr.net

GENES OF *STREPTOMYCES GLOBISPORUS* 1912-4Crt ENCODING CHITIN CATABOLISM ENZYMES

Polysaccharide chitin is one of the most common biopolymers in nature. Chitin (when used as the sole source of energy, carbon, and nitrogen) has been shown to be a substrate sufficient to enable the growth and synthesis of secondary metabolites by the S. griseus NCIMB 8136 strain and some other streptomycetes. The species Streptomyces globisporus and S. griseus belong to the same lower hierarchical taxon (S. griseus clade). The ***aim*** *was to find in the S. globisporus 1912-4Crt genome genes encoding proteins that are necessary for chitin fermentation and transmembrane transport of resulting products.* ***Methods****. The object of the study was a sequence of the S. globisporus 1912-4Crt genome (reference NZ_QWFA01000000.1, GenBank) on the server of NCBI (The National Center for Biotechnology Information). Streptomycete S. globisporus 1912 and its variants are producers of antibiotic landomycin E and carotenoids. Search for and analysis of nucleotide and amino acid sequences were performed using programs BLAST (Basic Local Alignment Search Tool) on the aforementioned server.* ***Results****. A set of genes that determine enzymes of chitin catabolism and Ngc-transporter proteins were identified in the S. globisporus 1912-4Crt genome. Genes encoding 10 endo-acting chitinases (from the GH18 and GH19 families) and 2 exo-acting hydrolases (GH20) were identified in the S. globisporus 1912-4Crt sequence. Several genes determining deacetylases that deacetylate both chitin and oligosaccharides were found in the genome of the strain. One gene that determines endo-acting chitosanase from the GH75 family was discovered there. The ability of the wild-type strain S. globisporus 1912 and a number of its variants (including S. globisporus 1912-4Crt) to ferment chitin was proven in vitro.* ***Conclusions.*** *A set of genes sufficient for chitin assimilation was established in the S. globisporus 1912-4Crt genome sequence. Streptomycetes from different clades (for example, strains of S. coelicolor (S. albidoflavus group) and S. griseus, S. globisporus (S. griseus group)) containing different complexes of chitinolytic enzymes could be suggested.*

Keywords: *hydrolase, chitin, streptomycete, nucleotide and amino acid sequences.*

Chitin is a linear, insoluble natural homopolymer with a β-1,4N-acetylglucosamine (GlcNAc) structural unit. In addition to the fact that chitin is the main component of the external skeleton of arthropods and the internal organs of enterocytes, it performs protective and supporting functions in the cell walls of fungi and algae (Veliz et al., 2017). Chitin monomer β-1,4N-

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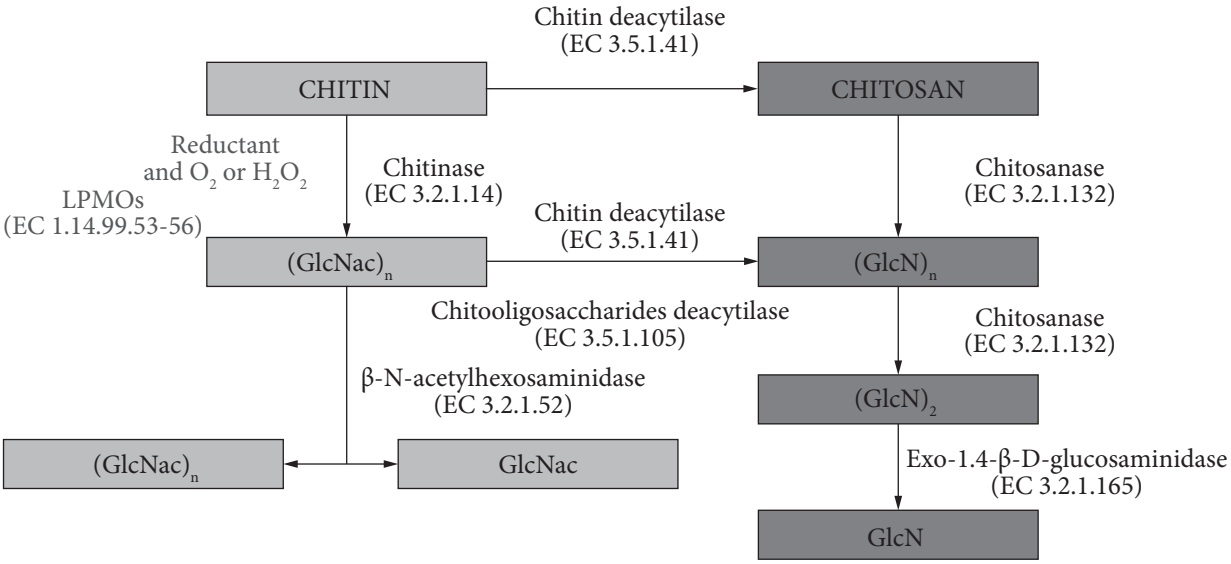

Fig. 1. Chitin cleavage scheme of microorganisms (Kaczmare et al., 2019)

acetylglucosamine is no less important as it is a necessary component for the formation of peptidoglycan of the cell wall of bacteria, a factor for the initiation of gene transcription under stressful conditions, and a Nod factor that induces bubble formation (Chen et al., 2010). The volume of accumulation of chitin in nature is inferior only to the volume of accumulation of cellulose. More than 10 gigatons of chitin are synthesized per year (Gooday, 1990). However, there is no catastrophic accumulation of chitin in nature due to its effective degradation by chitinases and chitosanases in organisms from various taxa (Gooday, 1990; Kielak et al., 2013; Wang et al., 2002a).

All organisms that synthesize chitin (crustaceans, jellyfish, worms, spiders, insects, algae, fungi, and others) necessarily produce chitinolytic enzymes required for the morphogenesis of the cell wall or exoskeleton (Schrempf, 2001; Štrojsová & Vrba, 2005; Štrojsová & Dyhrman, 2008). At the same time, other organisms such as bacteria, higher plants, and vertebrates do not synthesize chitin but are able to hydrolyze it (Gooday, 1990; Paoletti et al., 2007; Chen et al., 2010; Kielak et al., 2013). However, it is believed that the main destructors of the polymer in nature are microorganisms from various taxa *Bacillus, Pseudomonas, Streptomyces,* and many others (Xiao et al., 2005; Hunt et al., 2008; Kielak et al., 2013; Wang et al., 2020). It was established that due to the presence of chitin and chitosanolytic activity, a number of organisms are able to use chitin and chitosan as the only source of energy, carbon, and nitrogen (Meanwell & Shama, 2005; Meanwell & Shama, 2007; Duhsaki et al., 2023).

In addition, the production of chitinases and chitosanases by many organisms is an important protective factor against various pathogens (Gupta et al., 1995; Wang et al., 2020; Kawase et al., 2006).

The destruction of chitin in microorganisms takes place in two currently known ways (Fig. 1).

The first way — direct depolymerization — is carried out by endo- and exo-chitinases, which belong to the O-glycoside hydrolases. Endo-acting chitinases (from the families of glycoside hydrolases GH18 and GH19) destroy the glycosidic bonds of insoluble chitin with the formation of water-soluble oligomers of various molecular sizes, followed by their cleavage to the GlcNAc monomer (Chen et al., 2010; Kaczmare et al., 2019). In addition, β-N-acetylhexosaminidase enzymes (hydrolase families GH20, GH89) are exo-active and

hydrolyze chitin oligomers, as well as chitin, with the formation of monomers, cleaving them from the non-reducing end (Valiz et al., 2017).

Along with this, polysaccharide monooxidase (LPMO) enzymes take part in the destruction of chitin, which, by oxidizing polymer, accelerate its hydrolysis monomer (Kaczmare et al., 2019).

Another way of destroying chitin is depolymerization with preliminary deacetylation. Deacetylation of acetylated compounds occurs thanks to the enzyme activity of chitindeacetylases and chitooligodeacetylases of the hydrolase families GH5, GH7, and GH8. Partially or completely deacetylated chitin and oligosaccharides, in turn, are cleaved into monomers by chitosanase enzymes (hydrolase families GH46, GH75, and GH80) and exochitosanase monomers (Jung & Park, 2014; Kaczmare et al., 2019).

The destruction of chitin occurs in the extracellular space by secreted enzymes, but the formed monomers and dimers are absorbed by the cell in the cytoplasm. In the cells of streptomycetes, the existence of several transmembrane formations that transport them into the cell was found, in particular ABC transporters (ATP-binding cassette transporters) and PTS (Phosphoenolpyruvate-dependent phosphotransferase system). Such structures usually have a complex organization and are formed by several proteins with different functions, for example, the Ngs transporter (N-acetylglucosamine transport system) from CUT-1 of the ABC transporter family. As reported, the Ngs transporter of *S. olivaceoviridis* is the first to be found to transport N-acetylglucosamine and chitobiose. The three-component transporter system is encoded by the *ngc*EFG operon (Wang et al., 2002b; Xiao et al., 2002).

Exported into the cell, the degradation products of chitin and chitosan undergo additional changes in it, including hydrolysis of acetyl and amino groups. It is reported that chitin biodegradation products (monomers and dimers of N-acetylglucosamine and N-glucosamine) are good substrates for the growth and development of microorganisms *S. flavopersicus, S. coelicolor, S. clavuligerus, S. collinus, S. griseus, S. hygroscopicus,* and *S. venezuelae* (Rigali et al., 2008; van Wezel & McDowall, 2011). In particular, it has been proven that chitin is a sufficient single source of nutrients for the growth of strain *S. griseus* NCIMB 8136 and its synthesis of the antibiotic streptomycin nitrogen (Meanwell & Shama, 2005; Meanwell & Shama, 2007; Duhsaki et al., 2023).

It has been established that chitinases of microorganisms are a safe alternative to pesticides in the fight against pests and pathogens. The resulting soluble chitin hydrolysis products can be used to increase soil fertility (Veliz et al., 2017). In addition, low-molecular-weight derivatives of chitin and chitosan are used in medicine as immunomodulators, antitumor agents, and radio protectors (Wang et al., 2020).

The **aim** of the work was to establish the presence in the genome of *Streptomyces globisporus* 1912-4Crt of genes encoding enzymes that perform chitin fermentation and transmembrane transfer of the resulting products.

Materials and Methods. The object of the study was the nucleotide sequence of the genome of the variant 1912-4Crt wild type of the *S. globisporus* 1912 strain (Matselyukh et al., 2016). Information on the nucleotide sequence of the total DNA of *S. globisporus* 1912-4Crt is deposited in the GenBank database of the NCBI server (The National Center for Biotechnology Information) under the number NZ_QWFA00000000.1 (7.4 Mbp) in the form of 466 contigs.

Analysis of the primary structures of streptomycete DNA and proteins was performed using BLAST (Basic Local Alignment Search Tool) programs on the NCBI server.

Results. *Streptomyces globisporus* 1912 and some of its variants (for example, 3-1, 1912-2) are producers of the antitumor antibiotic landomycin E, and regulators of antibiotics biosynthesis and morphogenesis of streptomycetes. Its other derivatives (for example, 1912-4Crt, 1912-7Crt, 16.2Lcp, and Hp7Lcp) are producers of

carotenoids (beta-carotene and lycopene) (Matselyukh et al., 2016). As reported above, chitin catabolism by streptomycetes is carried out in 2 ways: 1) direct depolymerization of chitin and 2) depolymerization of the polymer after its deacetylation (Kaczmare et al., 2019).

Enzymes for direct depolymerization of chitin (chitinases) and the genes (*chi*-genes) that determine them have been best studied in strain *S. coelicolor* A3(2) (NC_003888.3). In general, according to the literature, 14 *chi*-genes were found in the genome of the strain, which encode

Table 1. **Genes of *S. globisporus* 1912-4Crt and the proteins they determine**

Chi-genes	Contigs of accession NZ_QWFA00000000.1	Determined enzymes
D3105_RS00035.1 D3105_RS28195.1	NZ_QWFA01000001.1	WP_118898962.1
D3105_RS02530.1	NZ_QWFA01000200.1	WP_118905792.1
D3105_RS32610.1	NZ_QWFA01000007.1	WP_118899561.1
D3105_RS11115.1	NZ_QWFA01000311.1	WP_118906440.1
D3105_RS02885.1	NZ_QWFA01000045.1	WP_118902827.1
D3105_RS30570.1	NZ_QWFA01000008.1	WP_240646782.1
D3105_RS07300.1	NZ_QWFA01000245.1	WP_118906157.1
D3105_RS11020.1	NZ_QWFA01000028.1	WP_118901153.1
D3105_RS34170.1 *	NZ_QWFA01000045.1	WP_118902782.1
D3105_RS04445.1	NZ_QWFA01000433.1	WP_133305757.1
	NZ_QWFA01000013.1	WP_118900192.1

*contig NZ_QWFA01000433 contains a fragment of the *chi* gene sequence.

Table 2. **Domains of chitinolytic enzymes of *S. globisporus* 1912-4Crt**

Chitinases of *S. globisporus* 1912-4Crt	Identification of chitinase domains		Families of glycoside hydrolases
	catalytic domains	Substrate-binding domains	
WP_118898962.1	cl00222[1], 381595[2]	cl00046, 444668	Family GH19
WP_118905792.1	cl00222, 381595	cl00046, 213175	
WP_118899561.1	cl10447, 119350	—	Family GH18
WP_240646782.1	cl10447, 119365	cl21579, 425748	
WP_118902782.1	cl34587, 225862 cl05806, 368936	cl00046, 213178	
WP_118906157.1	cl10447, 119350	cl19911, 396553	
WP_118901153.1	cl10447, 119350	cl19911, 396553	
WP_118906440.1	cl10447, 119365	—	
WP_118902827.1	cl10447, 119365	—	
WP_133305757.1	cl10447, 119365		
WP_118900192.1	cl03741, 446174 cl02948, 119333	—	Family GH20

[1] the superfamily of the domain, [2] the domain identifier.

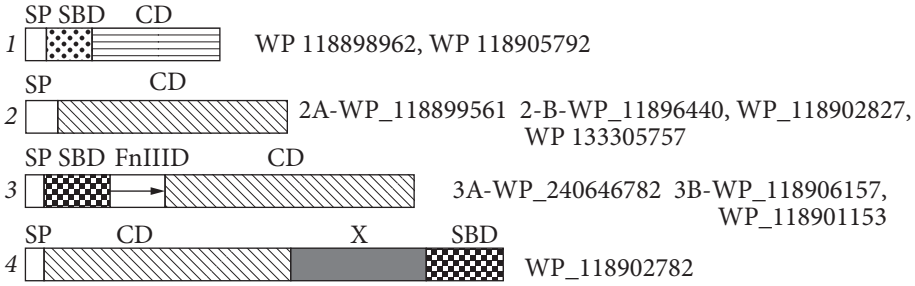

Fig. 2. Organization schemes of *S. globisporus* 1912 4Crt chitinases. Designation: SP — signal peptide, CD — catalytic domain, X — fragment of another domain or with an unknown function, SBD — substrate binding domain, FnIIID — fibronectin type III.

enzymes that destroy chitin into dimers and monomers (Kawase et al., 2006).

When examining the genomic DNA of *S. globisporus* 1912-4Crt strain, it was established that its sequence contains 12 genes determining chitinolytic hydrolases (Table 1). We believe that only 90—95% of the real size of the strain's genome has been determined, so we assume that there is a possibility in the future, after determining the complete sequence of the strain's chromosome, to identify other chi-genes. The sequence of strain *S. globisporus* 1912-4Crt with a size of 7.365 Mb was determined, while the sequence of the related strain S. globisporus C-1027 (NZ_CP013738.1) was 7.608 Mb.

As established, chitinases from both families (GH18 and GH19), in addition to essential structures (signal peptides and catalytic domains), may also contain assisting domains, such as substrate binding domains and type III fibronectins.

The domain organization of the identified 12 hydrolases of *S. globisporus* 1912 4Crt, which was determined by the analysis of enzyme annotations in the Protein Database (NCBI), is presented in Table 2.

According to the results of our analysis of the domain organization of the detected hydrolases from the GH18 and GH19 families of *S. globisporus* 1912 4Crt, 4 schemes of their organization were determined (Fig. 2). However, a number of chitinases with the same scheme of molecular organization differ in the structure of amino acids of similar domains. Thus, chitinases organized by schemes 2 and 3 can be divided into 2 variants, taking into account the differences in the sequences of the catalytic domain (variants of scheme 2) or the domain of binding to the substrate (variants of scheme 3) (Table 2).

An alternative pathway of chitin catabolism begins with deacetylation of chitin by deacetylases. This direction includes reactions catalyzed by a number of enzymes — chitosanase, esterase, exo-beta-glucosaminidase, and other chitinolytic enzymes. A number of enzymes that catalyze various reactions of this chitin biodegradation pathway were identified in the genome of *S. globisporus* 1912-4Crt (Table 3).

As reported, three chitosanases from the GH75 and GH46 families can function in streptomycetes (Dubeau et al., 2011; Viens et al., 2015). In the genome of the *S. globisporus* 1912-4Crt variant, only one gene determining chitosanase WP_016327920.1, which belongs to the GH75 family, was detected.

To include the products of extracellular catabolism of chitin into the cell metabolism, the activity of transmembrane mechanisms that will deliver N-acetylglucosamine and chitobioses into the cytoplasm is necessary. The genome of the *S. globisporus* 1912-4Crt was searched for genes that encode proteins of Ngc-transporter from the family of ABC transporters (Table 4) as an example to determine the presence of such a possibility. The table also shows the enzymes of the strain that modify substances after their

transfer to the cytoplasm: N-acetylglucosamine-6-phosphate deacetylase (NagA) and N-acetylglucosamine-6-phosphate deaminase (NagB).

S. globisporus 1912 and a number of its variants have significant industrial potential as producers of biologically active compounds. The ability to synthesize carotenoids (carotene and lycopene), antibiotics (landomycin E), and enzymes (beta-galactosidase) was found in them (Matselyukh et al., 2016).

The possibility of using chitin by *S. globisporus* 1912 and its variants (including the 1912-4Crt

Table 3. ***S. globisporus*** **1912-4Crt enzymes of the alternative pathway of chitin biodegradation and the genes that determine them**

Enzymes	Catalytic domains	Genes that determine the enzymes	Contigs of accession NZ_QWFA00000000.1
Chitin deacetylases (EC 3.5.1.41)			
WP_118905243.1	cl15692 [1]	D3105_RS24725	NZ_QWFA01000153
WP_118905649.1	213023 [2]	D3105_RS27320	NZ_QWFA01000187
WP_206272674.1	cl15692	D3105_RS07075	NZ_QWFA01000027
WP_118902871.1	213022	D3105_RS11220	NZ_QWFA01000046
WP_118901993.1	cl15692 426305	D3105_RS09240	NZ_QWFA01000036
WP_240647088.1	cl15692 449579	D3105_RS30960	NZ_QWFA01000256
Chitosanase (EC 3.2.1.132)			
WP_016327920.1	cl06393 429415	D3105_RS24725	NZ_QWFA01000015
Exo-chitosanase (EC 3.2.1.165)			
WP_118905314.1	cl43822 225789	D3105_RS25195	NZ_QWFA01000158

[1] the superfamily of the domain; [2] the domain identifier.

Table 4. ***S. globisporus*** **1912-4Crt proteins of the Ngc-transporter, enzymes of monomers modification, and the genes that determine them**

Proteins	Genes that determine enzymes	Contigs of accession NZ_QWFA00000000.1
N-acetylglucosamine transport system permease protein (EC 7.5.2.2)		
WP_093813274	D3105_RS31215 (*ngc*G)	NZ_QWFA01000264
WP_118906254	D3105_RS31220 (*ngc*F)	NZ_QWFA01000264
N-acetylglucosamine transport system substrate-binding protein (EC 7.5.2.11)		
WP_008745947	D3105_RS31225 (*ngc*E)	NZ_QWFA01000264
N-acetylglucosamine-6-phosphate deacetylase (EC 3.5.1.25)		
WP_1189901216	D3105_RS07470 (*nag*A)	NZ_QWFA01000029
Glucosamine-6-phosphate deaminase (EC 3.5.99.6)		
WP_118905330	D3105_RS25290 (*nag*B)	NZ_QWFA01000160

variant) as the sole source of carbon, nitrogen, and energy for growth, cytodifferentiation, and synthesis of secondary metabolites has been experimentally proven (report by PhD S.L. Golembivovskaya).

Discussion. As previously reported, the best-studied chitinolytic complex of 14 chitinases of the *S. coelicolor* A3(2) strain is involved in chitin catabolism by direct depolymerization (Kawase et al., 2006). Of them, 11 belong to 3 subfamilies (GH18A, GH18B, GH18C) of the GH18 family, two chitinolytic enzymes belong to the GH19 family, and 2 enzymes to the GH20 family. In the defined sequence of *S. globisporus* 1912 4Crt DNA, we found 12 loci of *chi*-genes, which encode 2 enzymes from the GH19 family, 8 enzymes from the GH18 family, and 1 chitinase from the GH20 family (Table 2). Interestingly, the genome of the *S. griseus* NBRC 13350 strain also contains 12 loci of chi genes encoding chitinases: 2 chitinases from the GH19 family, 1 chitinase from the GH20 family, and 8 chitinases from the GH18 family. *S. globisporus* C-1027 and *S. globisporus* TFH56 have 12 chitinases in their genomes, including 3 genes from the GH19 subfamily (Polishchuk, 2023a). It is possible that when determining the complete sequence of the chromosome of *S. globisporus* 1912, 3 genes for chitinase GH19 will be found.

In the genome of *S. globisporus* 1912-4Crt, no genes were found that determine chitinases from the GH18C subfamily, the catalytic domain of which belongs to the superfamily of domains cl10447 and has the domain identifier CDD119360. There were also no genes in the genomes of strains *S. griseus* NBRC 13350 and *S. globisporus* C-1027, which determine hydrolases from the GH18C subfamily.

Streptomycete chitinases are polydomain structures: in addition to the catalytic domain, they may include chitin-binding domains, signal sequences, and sequences whose functions have not yet been determined (Kawase et al., 2006). As it was established, *S. globisporus* 1912-4Crt chitinases of both families, in addition to essential structures (signal peptide and catalytic domain), may also contain assisting domains that ensure the passage of auxiliary reactions, for example, domains of substrate binding and type III fibronectin. According to the literature, the functioning of these additional domains improves the passage of enzymatic reactions by optimizing the chitinase orientation relative to the substrate (Kawase et al., 2006).

By the results of our analysis of the organization of the detected hydrolases from the GH18 and GH19 families of *S. globisporus* 1912 4Crt, four schemes of their organization were determined (Fig. 2). However, a number of chitinases organized by schemes 2 and 3 can be divided into 2 variants based on the differences in the sequences of the catalytic domain (variants of scheme N2) or the domain of binding to the substrate (variants of scheme N3) (Table 2).

By comparing the domain organization of chitinases from the GH18 family of the *S. globisporus* 1912-4Crt strain with the organization of enzymes from the GH18 (GH18A, GH18B, GH18C) subfamilies of *S.coelicolor* A3(2) was found, chitinases WP_118899561.1, WP_118906157.1, and WP_118901153.1 can be assigned to the GH18B subfamily, enzymes WP_118902782.1, WP_133305757.1, WP_240646782.1, WP_118906440.1, and WP_118902827.1 can be assigned to the GH18A subfamily.

As is known, a number of *Streptomyces chi*-genes were formed as a result of duplication (Saito et al., 1999). Thus, it was proved that the gene pairs of *chi*A and *chi*B, as well as *chi*C and *chi*D of the strain *S. coelicolor* A3(2) had common ancestors (Saito et al., 1999). Pairs of chitinase strains *S. coelicolor* A3(2) (*chi*A and *chi*B) and *S globisporus* 1912-4Crt (WP_118906157.1 and WP_118901153.1) are organized according to the same scheme. It was reported that the amino acid sequences of the *chi*A and *chi*B enzyme domains of *S. coelicolor* A3(2) are 62% (binding domains), 50% (FnIIID), and 38% (catalytic

domains) similar (Saito et al., 1999). BLASTN analysis showed that the sequences of chitinases WP_118906157.1 and WP_118901153.1 are 66% (binding domains), 67% (FnIIID), and 36% (catalytic domains) similar. Thus, these chitinases of *S. globisporus* 1912 4Crt can be considered to have a common origination.

As reported in the literature, chitin hydrolysis in streptomycete cells can proceed in another way — by depolymerization after deacetylation of the polymer. It was established that the deacetylation reaction is carried out by several hydrolases belonging to the family of carbohydrate esterases (CE4), which includes chitin deacetylases and chitooligosaccharide deacetylases (Jung & Park, 2014). In the genome of the *S. globisporus* 1912-4Crt strain, 6 deacetylases were identified, the catalytic domains of which belong to the same superfamily, but differ in the amino acid sequence and tertiary organization (Table 3).

Hydrolysis of partially or completely deacetylated chitin can be carried out in streptomycetes by 3 chitosanases — 2 hydrolases from the GH46 family and one from the GH75 family (Dubeau et al., 2011; Viens et al., 2015). For example, according to the data of the KEGG database, 3 chitinases, namely WP_011028103 (GH46), WP_011027289 (GH46), and WP_011031415 (GH75), were presented in strain *S. coelicolor* A3(2), but in strains *S. griseus* NBRC 13350 (NC_010572.1), *S. globisporus* C-1027 (NZ_CP013738.1), and *S. globisporus* TFH56 (NZ_CP029361.1), only one glycosidase was found from the GH75 family, respectively WP_012378405, WP_010064061, and WP_044374039. Our studies for the defined sequence of strain *S. globisporus* 1912-4Crt showed the presence of only one gene that determines the chitosanase from the GH75 family (Table 3). No genes that determine hydrolases from the GH46 family were detected.

According to the base date KEGG, in the genomes of strains of *S. coelicolor* A3(2) and *S. globisporus* C-1027, one exo-chitosanase-determining gene, SCO6232 and WQO_RS02075, respectively, was revealed while no such gene was detected in the *S. griseus* NBRC13350 strain. The gene D3105-RS24200, which determines exo-chitosanase, is present in the genomic sequence of the studied strain.

So, streptomycetes from different clades (for example, strains of *S. coelicolor, S. griseus,* and *S. globisporus*) can contain different complexes of chitinolytic enzymes. Thus, the S. *coelicolor* A3(2) strain from the *S. albidoflavus* group contains 2 chitinases from the GH19 family (ChiG and ChiF), which differ in the presence of a substrate binding domain in the ChiF enzyme. At the same time, strains from the *S. griseus* clade have 2 (*S. griseus* strains) or 3 (*S. globisporus* strains) enzymes that do not contain a binding domain (Polishchuk, 2023b). While working, it was found that strains of *S. coelicolor* A3(2), *S. griseus* NBRC13350, *S. globisporus* C-1027, and *S. globisporus* TFH56 differ in the amount of chitosanase (EC 3.2.1.132): strain *S. coelicolor* A3(2) contains 3 enzymes (2 chitosanases from the GH46 family and 1 from the GH75 family), while strains of *S. griseus* NBRC13350, *S. globisporus* C-1027, and *S. globisporus* TFH56 have one enzyme from the GH75 family.

Typically, streptomycetes ferment chitin and chitosan outside the cell, and the resulting monomers and dimers are transported into the cell by the action of several different transmembrane mechanisms (Wang et al., 2002b; Xiao et al., 2002). We determined, as an example, the presence in the sequence of *S.globisporus* 1912-4Crt genes that determine proteins of the transmembrane complex Ngc (N-acetylglucosamine transport system), which is a specific transporter of chitin and chitosan monomers (Wang et al., 2002b; Xiao et al., 2002). The genes determining Ngc-transporter proteins in the genome of *S. globisporus* strain 1912-4Crt form a cluster of 3 *ngc*-genes (Table 4). In the cytoplasm, the deacetylation and deamination of transferred N-acetylglucosamine-6-phosphate monomers take place, followed by the inclusion of the obtained

compounds in cell metabolism. We have shown the presence of relevant genes in the genome of the studied strain (Table 4).

According to the literature, N-acetylglucosamine in a number of strains - for example *S. coelicolor, S. verticillus* — is part of the regulatory cascade, at the same time N-acetylglucosamine and chitobiose are a good substrate for the synthesis of secondary metabolites, for example, in *S. griseus* (Meanwell & Shama, 2005; Meanwell & Shama, 2007; Duhsaki et al., 2023). The possibility of using chitin by *S. globisporus* 1912 strain and its variants as the sole source of carbon, nitrogen, and energy for growth, cytodifferentiation, and synthesis of secondary metabolites has been experimentally proven. Thus, we identified a set of genes of the *S. globisporus* 1912-4Crt variant, which ensure the biodegradation of chitin and chitosan and the use of polysaccharides as the only source of carbon, nitrogen, and energy.

In addition, it has been shown that streptomycetes from different clades (using the example of strains of the species *S. coelicolor* (*S. albidoflavus* group) and *S. griseus, S. globisporus* (*S. griseus* clade) contain different complexes of chitinolytic enzymes. We believe that the study of the complex of chitin catabolism enzymes can be used to determine the genetic kinship of strains, in addition to traditional morphological, tinctorial, physiological, antigenic, and molecular biological features.

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Л.В. Поліщук

Інститут мікробіології і вірусології ім. Д. К. Заболотного НАН України,
вул. Академіка Заболотного, 154, Київ, 03143, Україна

ІДЕНТИФІКАЦІЯ ГЕНІВ *STREPTOMYCES GLOBISPORUS* 1912-4Crt,
ЩО КОДУЮТЬ ФЕРМЕНТИ КАТАБОЛІЗМУ ХІТИНУ

Полісахарид хітин є одним з найпоширеніших у природі біополімерів. Встановлено, що він (якщо використовується як єдине джерело енергії, вуглецю та азоту) є субстратом, достатнім для забезпечення росту та синтезу вторинних метаболітів штамом *S. griseus* NCIMB 8136 та деякими іншими стрептоміцетами. Види *S. globisporus* і *S. griseus* належать до одного нижчого ієрархічного таксону (*S. griseus* clade). **Метою** роботи було визначити в геномі *S. globisporus* 1912-4Crt гени, що кодують білки, необхідні для ферментації хітину та трансмембранного транспорту отриманих продуктів. **Методи**. Об'єктом дослідження була послідовність генома *S. globisporus* 1912 4Crt (референс NZ_QWFA01000000.1, GenBank) на сервері NCBI (The National Center for Biotechnology Information). Стрептоміцет *S. globisporus* 1912 та його різновиди є продуцентами антибіотика ландоміцину Е та каротиноїдів. Пошук та аналіз генних і білкових послідовностей проводили за допомогою програм BLAST (Basic Local Alignment Search Tool) на вищезгаданому сервері. **Результати.** У геномі *S. globisporus* 1912-4Crt ідентифіковано комплект генів, що кодують ферменти катаболізму хітину та білки трансмембранного транспортеру Ngc. У послідовності *S. globisporus* 1912-4Crt ідентифіковано гени, що кодують 10 ендо-діючих хітиназ (із родин GH18 і GH19) і 2 екзо-діючі гідролази (GH20). У геномі штаму виявлено кілька генів, що визначають деацетилази, які деацетилюють як хітин, так і олігосахариди. Також був виявлений один ген, що визначає ендодіючу хітозаназу з родини GH75. **Висновки.** Виявлено в послідовності геному *S. globisporus* 1912-4Crt комплект генів, достатній для асиміляції хітину. Зроблено припущення, що стрептоміцети з різних клад, наприклад, штами *S. coelicolor* (група *S. albidoflavus*) і *S. griseus, S. globisporus* (група *S. griseus*) містять різні набори хітинолітичних ферментів.

Ключові слова: *гідролаза, хітин, стрептоміцет, нуклеотидні та амінокислотні послідовності.*