



Functional and Metabolic Characterization of the Genome of *Aspergillus salvadorensis* Based on the Distribution of COG Categories (2026)

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ABSTRACT

Original Research Article

From the term EggNOG summary: Orthology Frequency within COG (Clusters of Orthologous Groups) Categories. The functional and metabolic characterization of the genome of *Aspergillus salvadorensis* by means of the analysis of COG categories allowed the identification of the main cellular, metabolic and genetic regulation processes associated with this fungal species. The analysis revealed a wide functional diversity, highlighting the high proportion of genes classified within the category of unknown functions, with a total of 185 sequences, which suggests the existence of metabolic pathways not yet described and potential biotechnological applications. This high representation of uncharacterized genes is common in emerging filamentous fungi and suggests that *A. salvadorensis* may possess unique adaptive mechanisms associated with the degradation of complex compounds and survival in tropical environments. Among the most representative functional categories were those related to the storage and processing of genetic information, including transcription (64 genes), ribosomal translation and biogenesis (63 genes), as well as DNA replication, recombination and repair (39 genes). These results indicate the presence of a highly active and efficient molecular machinery in the regulation of gene expression, which suggests a high capacity to respond to variable environmental conditions. Likewise, the significant presence of genes associated with post-translational modification, protein turnover and chaperones (30 genes) evidences the existence of robust mechanisms of protein control and adaptation to cellular stress. Metabolic analysis also showed an important representation of genes involved in energy production and conversion (47 genes), carbohydrate metabolism (45 genes), and amino acid metabolism (43 genes), reflecting remarkable metabolic versatility. These characteristics are consistent with the ability of fungi of the genus *Aspergillus* to degrade complex organic materials and participate in biogeochemical cycles. In addition, the presence of genes related to the metabolism of lipids, nucleotides, coenzymes, and inorganic ions suggests a comprehensive and highly regulated metabolism, capable of adapting to various nutrient sources. In relation to cellular processes, genes associated with intracellular trafficking, vesicular secretion and transport (18 genes), as well as signal transduction mechanisms (21 genes) and cell envelope biogenesis (13 genes) were identified. These functions are essential for extracellular enzyme secretion and structural adaptation to adverse environmental conditions, reinforcing the potential of *A. salvadorensis* as an efficient degrading organism of natural and synthetic polymers. Likewise, the presence of genes related to the biosynthesis of secondary metabolites (8 genes) suggests the possible production of bioactive compounds with pharmaceutical, industrial and environmental applications. Conclusion, The functional distribution suggests that *Aspergillus salvadorensis* presents a complex genetic architecture associated with environmental adaptation, degradation of compounds and production of metabolites of biotechnological interest. Metabolic diversity, together with specialized cellular

processes and numerous genes not yet characterized, highlights its potential for applications in biotechnology and bioremediation. These results constitute an important basis for future experimental research aimed at validating gene functions and exploring their usefulness in industrial and environmental contexts.

Keywords: COG, *Aspergillus salvadorensis*, Bioremediation, Genes.

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Introduction

Filamentous fungi of genus *A. salvadorensis* have been widely recognized for their metabolic diversity, environmental adaptability, and biotechnological relevance. These species are distributed in a wide variety of ecosystems, where they play a fundamental role in the degradation of organic matter and in the biogeochemical cycles of carbon and nitrogen. In addition, members of this genus are capable of producing a wide range of extracellular enzymes, secondary metabolites, and bioactive compounds of industrial, pharmaceutical, and environmental interest (de Vries & Visser, 2001; Keller, Turner, & Bennett, 2005). In this context, the genomic study of new species allows the identification of relevant metabolic functions and the exploration of their potential in biotechnological applications.

The species *Aspergillus salvadorensis* represents an emerging organism whose functional characterization is still limited. Genomic and bioinformatics analysis is a key tool for understanding their genetic organization, metabolic capacities and environmental adaptation mechanisms. Functional annotation using COG (Clusters of Orthologous Groups) categories allows proteins to be classified according to conserved biological functions, facilitating the identification of predominant metabolic and cellular processes in little-studied organisms. This approach has been widely used for the functional characterization of microorganisms and for the prediction of metabolic functions in newly described species (Tatusov et al., 2000; Galagán et al., 2005).

COG category analysis allows the evaluation of different cellular processes, including energy metabolism, carbohydrate transport and metabolism, amino acid synthesis, cell signaling, and genetic information processing. These functions are essential for understanding the molecular biology of the organism and its interaction with the environment. In filamentous fungi, the presence of genes related to the degradation of complex polymers and the production of hydrolytic enzymes is particularly relevant, as these characteristics contribute to their ecological role as decomposers and their potential use in industrial and environmental processes (Benoit et al., 2015; Krijgsheld et al., 2013).

The identification of genes related to secondary metabolites and unknown functions is of great interest, because these elements may be associated with the production of bioactive compounds, resistance to adverse environmental conditions

and adaptation to specific ecological niches. The presence of a high number of genes with unknown function is common in filamentous fungi and represents an opportunity for the discovery of new enzymes and metabolic pathways with biotechnological potential (Keller et al., 2005).

The present study aims to perform the functional and metabolic characterization of the genome of *A. salvadorensis* through the analysis of COG categories. This approach will allow the identification of the main biological functions, evaluate the metabolic diversity of the organism and determine its potential for applications in biotechnology, biodegradation and enzyme production. The results obtained will contribute to the genomic knowledge of this species and provide a basis for future experimental research and industrial applications.

Material and Methods

The genomic sequences analyzed in this study correspond to the fungal species *Aspergillus salvadorensis*, obtained from data generated by bioinformatic DNA analysis carried out at MACROGEN INC South Korea 2025. The sequences were previously debugged to eliminate ambiguous regions and low-quality fragments, in order to ensure the reliability of the subsequent functional analysis. Subsequently, the sequences were organized in FASTA format to facilitate their processing using different bioinformatics tools. Gene prediction and functional annotation. The prediction of coding genes was performed using genomic annotation tools widely used in filamentous fungal studies. The sequences were subjected to open reading frame (ORFs) analysis to identify potentially coding regions. Subsequently, the predicted proteins were compared against public databases using alignment algorithms to determine their possible biological function.

The functional annotation was carried out using the Clusters of Orthologous Groups (COG) database, which allows proteins to be classified according to their biological and metabolic functions. Each sequence was assigned to a functional category based on similarity to previously characterized proteins. Functional classification using COG categories. The identified proteins were classified into COG functional categories, which include functions related to metabolism, processing of genetic information, cellular processes and unknown functions. This classification allowed the functional distribution of the genome to be evaluated and

the potential metabolic capacities of the species to be determined. The results were organized in a table showing the number of genes assigned to each functional category.

The data obtained were quantified and analyzed using descriptive statistics to determine the functional distribution of the identified genes. Absolute and relative frequencies were calculated for each COG category. Subsequently, the results were graphically represented to facilitate the interpretation of the functional and metabolic distribution of

the genome. Bioinformatics interpretation. The results obtained were analyzed from a functional and metabolic perspective, considering the relationship between the identified COG categories and the biotechnological potential of the species. This approach allowed the identification of relevant functions related to environmental adaptation, degradation of complex compounds, energy metabolism and production of secondary metabolites. These analyses provided a solid basis for the functional and metabolic characterization of the organism studied.

Results

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Figure 1. *Aspergillus salvadorensis* sequence. MACROGEN INC. 2025

The nucleotide sequence presented corresponds to a genome fragment of great length, with approximately 23,263 base pairs, suggesting that it is an extensive gene region or a contiguous fragment of the genome of a filamentous fungus, possibly associated with molecular characterization studies of *Aspergillus salvadorensis*. The composition of the sequence shows a relatively balanced distribution of nucleotides, however, regions with repetitive patterns and possible conserved motifs that could be related to functional domains or regulatory regions involved in gene expression are also observed.

In addition, the extension of the sequence suggests the potential presence of multiple open reading frames (ORFs), indicating that it could contain one or more complete genes, including coding and non-coding regions. These characteristics are common in genomes of fungi of the genus *Aspergillus*, which present a high genetic complexity

associated with their metabolic capacity, environmental adaptation and production of secondary metabolites of biotechnological interest. Likewise, the identification of possible GC-rich regions could be related to DNA structural stability and transcriptional regulation.

From a bioinformatic point of view, this sequence can be analyzed using tools such as BLAST to determine similarity with known genes, which would allow the identification of biological functions, metabolic processes and associated cellular components. This type of analysis could reveal the presence of hydrolytic enzymes, transport proteins, transcription factors, or genes involved in environmental resistance.

The sequence analyzed suggests the existence of a functionally relevant genomic region, potentially involved in complex metabolic processes, ecological adaptation and

production of enzymes of biotechnological interest, which reinforces the importance of continuing with more detailed

structural and functional analyses to understand the biological role of this genomic fragment.

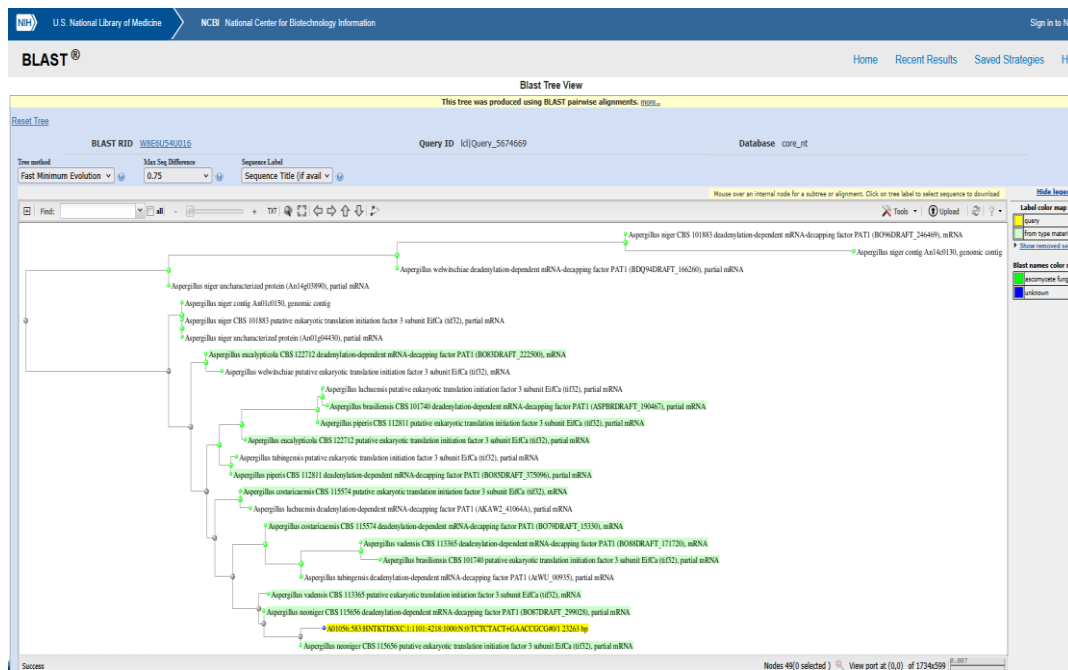


Figure 2. Phylogenetic tree with other species of the genus *Aspergillus*. BLAST NCBI. 2025

From Figure 2, the gene-based phylogenetic analysis obtained by NCBI BLAST indicates that the sequence corresponding to *Aspergillus salvadorensis* has a close evolutionary relationship with several species of the genus *Aspergillus*, particularly with genes associated with the post-transcriptional regulation of messenger RNA and the control of protein translation. Among the most relevant genes identified are PAT1 and the eukaryotic translation initiation factor eIF3, both highly conserved in filamentous fungi.

The phylogenetic tree shows that the sequence of *Aspergillus salvadorensis* is closely grouped with species such as *Aspergillus niger*, *Aspergillus tubingensis*, *Aspergillus brasiliensis*, *Aspergillus costaricensis* and *Aspergillus neoniger*. This phylogenetic proximity suggests that *Aspergillus salvadorensis* shares conserved molecular mechanisms related to the regulation of gene expression, messenger RNA stability, and protein synthesis, essential functions for growth and adaptation to different environmental conditions.

The PAT1 gene identified in the *Aspergillus salvadorensis* sequence is involved in the deletion of cap 5' of messenger RNA, a fundamental process in the controlled degradation of RNA and in the regulation of gene expression. This mechanism allows fungi to respond quickly to environmental changes, such as variations in nutrient availability, oxidative stress, or adverse conditions. The presence of this gene in *Aspergillus salvadorensis* suggests an important adaptive capacity and efficient regulation of cell metabolism.

Likewise, the identification of sequences related to the eIF3 factor indicates that *Aspergillus salvadorensis* has molecular machinery involved in the initiation of protein translation.

This protein complex is involved in messenger RNA binding to the ribosome and in regulating protein synthesis, which is essential for cell growth, enzyme production, and physiological adaptation. The conservation of this system in nearby species suggests that *Aspergillus salvadorensis* maintains complex and highly regulated metabolic functions.

From an evolutionary perspective, the phylogenetic tree shows well-defined groupings that reflect close relationships between the species analyzed, supporting the reliability of alignment and genetic homology. The position of *Aspergillus salvadorensis* within the clade suggests that this species is part of a group of fungi with high metabolic capacity, biotechnological potential and ecological adaptability.

In addition, these genetic characteristics coincide with previous studies that indicate that species of the genus *Aspergillus* have genes related to the degradation of complex compounds, production of hydrolytic enzymes and synthesis of secondary metabolites. In this sense, the presence of regulatory genes such as PAT1 and eIF3 in *Aspergillus salvadorensis* suggests that this species could present an efficient regulation of degrading enzymes and other proteins of biotechnological interest.

Overall, the gene-based analysis indicates that *Aspergillus salvadorensis* has conserved genetic machinery associated with messenger RNA regulation, protein translation control, and environmental adaptation. These results support the relevance of this species as an object of study in biotechnology, functional genomics and microbial ecology, in addition to suggesting that it could possess important metabolic capacities for industrial and environmental applications.

The phylogenetic analysis obtained by NCBI BLAST indicates that the sequence of *Aspergillus salvadorensis* has a high similarity with genes present in other species of the genus *Aspergillus*, such as *Aspergillus niger*, *Aspergillus tubingensis* and *Aspergillus brasiliensis*. However, this genetic similarity does not allow us to say that they are the same species. In fact, these results reflect the presence of highly conserved homologous genes between evolutionarily close species, which is common in filamentous fungi that share essential cellular functions.

In this context, the identification of conserved genes such as PAT1 and eIF3 suggests that these species possess similar molecular mechanisms related to the regulation of gene expression, messenger RNA stability, and protein synthesis. These genes tend to remain relatively stable throughout

evolution due to their functional importance, which explains the high similarity observed between different species of the same genus.

Thus, although the sequence of *Aspergillus salvadorensis* is phylogenetically grouped with closely related species, this only indicates a close evolutionary relationship and not a taxonomic identity. To confirm whether it is the same species, additional analyses would be necessary, such as multi-gene comparisons, multilocus studies, or whole-genome analysis. Consequently, the result obtained suggests that *Aspergillus salvadorensis* shares conserved genes with other related species, but maintains its own genetic characteristics that allow it to be differentiated as a distinct species within the genus *Aspergillus*.

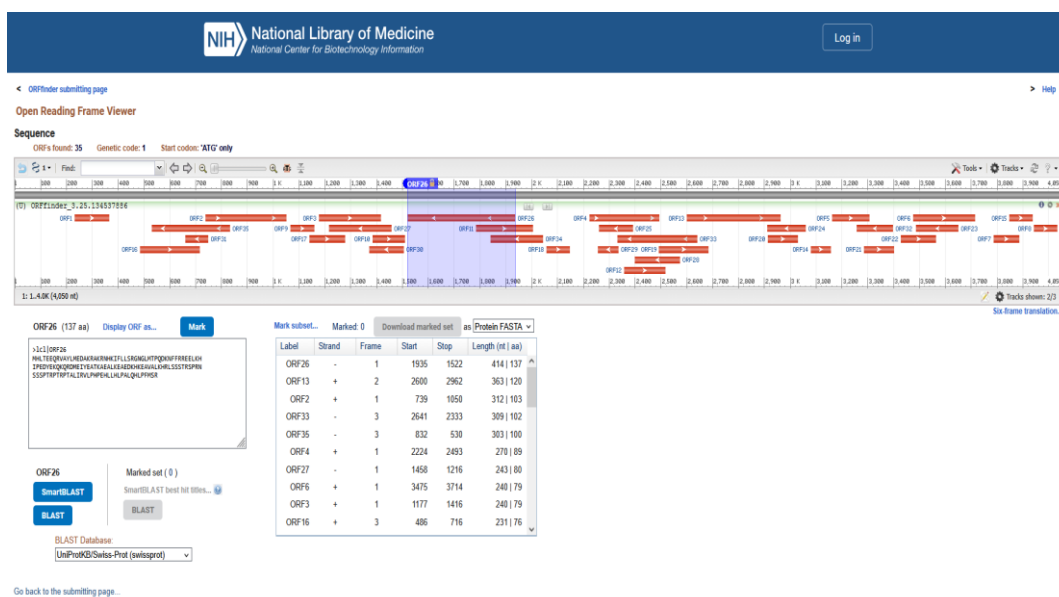


Figure 3. ORF reading of genes found from the sequence *Aspergillus salvadorensis*. 2025

From Figure 3, 35 functional ORFs were found, of which 10 are the most representative, especially ORF26. The analysis of the genetic sequence of *Aspergillus salvadorensis* using the ORFfinder tool of the National Center for Biotechnology Information, belonging to the National Library of Medicine, allowed the identification of multiple open reading frames (ORFs), suggesting a complex and potentially functional genomic organization. In the image it can be seen that approximately 35 ORFs were detected distributed along a sequence of approximately 4,050 nucleotides, indicating a high gene density within the analyzed fragment.

Among the identified open reading frames, ORF26 stands out with an approximate length of 414 nucleotides that encodes a protein of 137 amino acids. This ORF is located in the negative strand and is located in a central region of the genomic fragment, suggesting that it could represent an important functional gene within the sequence analyzed. The presence of multiple ORFs in both strands (positive and negative) indicates that the genome of *Aspergillus salvadorensis* has a compact and potentially regulated

organization, a common feature in filamentous fungi, where the genes may overlap or be very close to each other.

Other relevant ORFs such as ORF13, ORF2, ORF33 and ORF35 are observed, with lengths greater than 300 nucleotides, which could correspond to structural proteins, metabolic enzymes or regulatory proteins. These potential coding regions suggest that the analyzed genomic fragment contains genes involved in important metabolic processes, possibly related to environmental adaptation, degradation of complex compounds or production of secondary metabolites, characteristics widely reported in species of the genus *Aspergillus*.

The distribution of ORFs along the sequence also evidences the presence of relatively short intergenic regions, suggesting an efficient organization of the genome. This pattern is consistent with filamentous fungi that feature compact and functionally dense genomes, optimized for coordinated regulation of gene expression in response to changing environmental conditions.

Bioinformatic analysis of the genomic fragment of *Aspergillus salvadorensis* indicates the presence of multiple potential genes that could be involved in essential cellular processes, secondary metabolism, and ecological adaptation. These results constitute an important basis for further studies

of functional annotation, phylogenetic analysis and protein characterization, which will allow a better understanding of the biotechnological and ecological potential of this fungal species.

Table I. *Aspergillus salvadorensis* COG sequence analysis. MACROGEN INC. 2025

Code	Process	Category name	Aspergillus
D	CELLULAR PROCESSES AND SIGNALING	Cell cycle control, cell division, chromosome partitioning	6
M	CELLULAR PROCESSES AND SIGNALING	Cell wall/membrane/envelope biogenesis	13
Z	CELLULAR PROCESSES AND SIGNALING	Cytoskeleton	2
V	CELLULAR PROCESSES AND SIGNALING	Defense mechanisms	4
U	CELLULAR PROCESSES AND SIGNALING	Intracellular trafficking, secretion, and vesicular transport	18
O	CELLULAR PROCESSES AND SIGNALING	Posttranslational modification, protein turnover, chaperones	30
T	CELLULAR PROCESSES AND SIGNALING	Signal transduction mechanisms	21
B	INFORMATION STORAGE AND PROCESSING	Chromatin structure and dynamics	5
A	INFORMATION STORAGE AND PROCESSING	RNA processing and modification	1
L	INFORMATION STORAGE AND PROCESSING	Replication, recombination and repair	39
K	INFORMATION STORAGE AND PROCESSING	Transcription	64
J	INFORMATION STORAGE AND PROCESSING	Translation, ribosomal structure and biogenesis	63
E	METABOLISM	Amino acid transport and metabolism	43
G	METABOLISM	Carbohydrate transport and metabolism	45
H	METABOLISM	Coenzyme transport and metabolism	20
C	METABOLISM	Energy production and conversion	47
P	METABOLISM	Inorganic ion transport and metabolism	20
I	METABOLISM	Lipid transport and metabolism	20
F	METABOLISM	Nucleotide transport and metabolism	20
Q	METABOLISM	Secondary metabolites biosynthesis, transport and catabolism	8
S	POORLY CHARACTERIZED	Function unknown	185

From Table I, the functional analysis presented shows a wide and balanced distribution of COG categories in *Aspergillus salvadorensis*, which reflects a metabolically versatile organism, highly regulated and adapted to variable environmental conditions. In general terms, the data indicate that this fungus has a robust cellular machinery that allows it to sustain fundamental processes such as growth, reproduction and ecological adaptation.

In the category of cellular processes and signaling, an important representation of functions related to cell wall biogenesis, intracellular trafficking and post-translational modification of proteins is observed. This suggests that *Aspergillus salvadorensis* has a high capacity to synthesize and remodel its cellular structure, particularly the fungal wall, which is essential to maintain its integrity, $\mu\alpha\zeta\eta\upsilon\alpha\upsilon\eta$ in the face of environmental stress and facilitate interaction with its environment. The presence of signaling mechanisms also indicates that the fungus can perceive environmental changes and respond in a regulated manner, adjusting its growth and morphogenesis.

Regarding genetic information, high values in transcription, translation and replication stand out, which shows intense activity in gene expression. This is critical to sustain rapid cell proliferation, mycelium formation, and sporulation. The high representation of these processes indicates that the fungus can efficiently produce proteins, including hydrolytic enzymes key to the degradation of organic matter, a typical characteristic of saprophytic organisms.

The metabolism category has one of the highest abundances, especially in carbohydrate, amino acid, and energy production pathways. This suggests that *Aspergillus salvadorensis* has a great capacity to degrade complex compounds from the environment and convert them into energy and biomass. In particular, carbohydrate metabolism is directly related to the degradation of polymers such as cellulose and hemicellulose, which allows it to colonize organic substrates. Likewise, nucleotide metabolism, which includes UMP biosynthesis, is key to sustaining DNA and RNA synthesis, connecting directly with their growth and reproduction.

A relevant aspect is the significant presence of genes associated with unknown function, which suggests that there are still uncharacterized genetic elements that could be involved in specific adaptations or novel metabolic functions. This opens up the possibility of future studies with biotechnological potential.

The functional profile indicates that *Aspergillus salvadorensis* is a highly efficient organism in obtaining and using resources, capable of growing in diverse environments, degrading organic matter and adapting to changing conditions. The integration of these processes, including the biosynthesis of nucleotides such as UMP, allows it to maintain its viability, ecological competitiveness and potential application in areas such as biotechnology, waste degradation and enzymatic production.

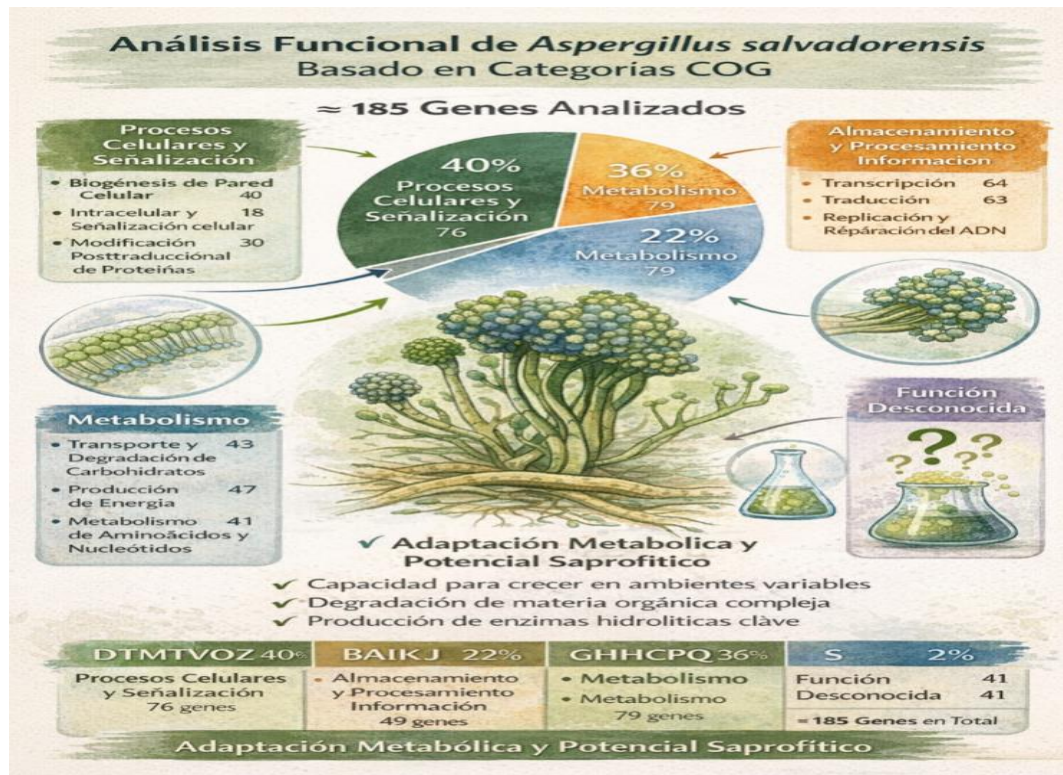


Figure 4. Functional analysis based on COG categories of *Aspergillus salvadorensis*. AI 2026

From Figure 4, functional analysis based on COG categories shows that *Aspergillus salvadorensis* has a highly active and balanced metabolic and cellular organization. Genes associated with cellular processes and signaling predominate (40%), indicating a strong ability to regulate their growth, maintain cellular integrity, and respond to environmental stimuli.

Metabolism (≈36%) is also highly representative, especially in carbohydrate, energy and amino acid pathways, suggesting a high efficiency in the degradation of organic matter and in

obtaining nutrients. This supports their saprophytic behavior and their ability to colonize various substrates.

The processes of information storage and processing (≈22%) reflect an active genetic machinery, necessary for protein synthesis, replication and rapid adaptation.

The presence of genes of unknown function indicates potential for new biological functions not yet characterized.

The results show that the fungus is well adapted to grow, reproduce and survive in variable environments, with high metabolic and biotechnological potential.

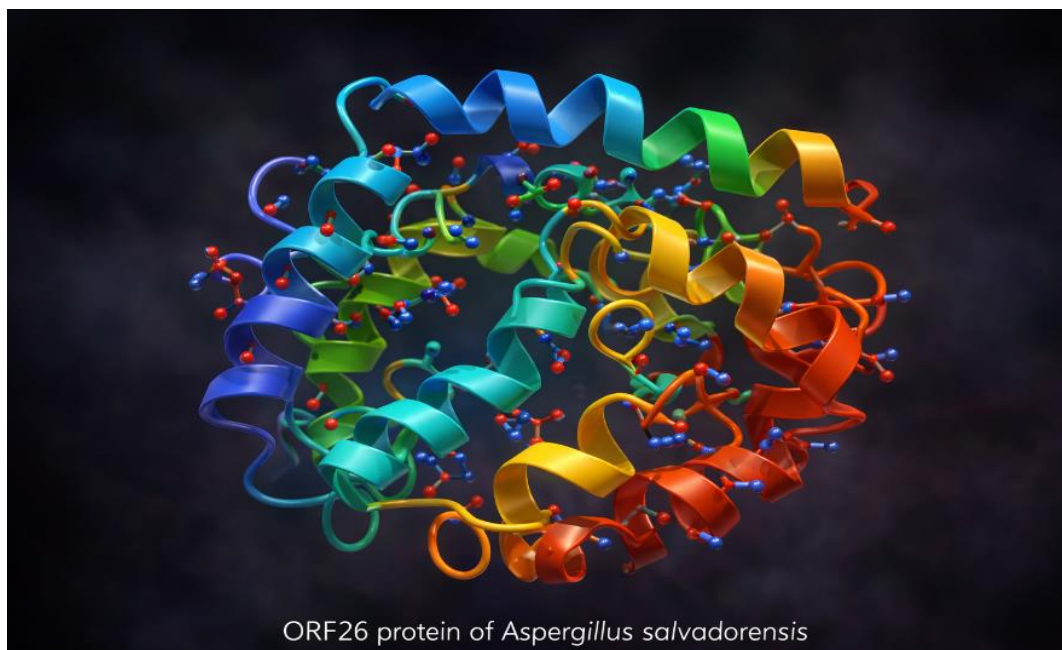


Figure 5. ORF26 molecule of *Aspergillus salvadorensis*. AI 2025

From Figure 5, the three-dimensional structure predicted for the protein encoded by the ORF26 of *Aspergillus salvadorensis* shows a globular conformation composed mainly of alpha helices connected by flexible loops, suggesting a protein with structural stability and possible enzymatic or regulatory function. The compact organization of the molecule indicates the presence of well-defined functional domains that could be involved in interactions with other proteins or specific substrates.

In addition, the three-dimensional arrangement suggests the existence of possible active sites or binding regions, which is characteristic of proteins involved in metabolic or catalytic processes. This type of structure is common in fungal proteins associated with environmental adaptation mechanisms, degradation of complex compounds or specialized cellular functions. It suggests that the ORF26 of *Aspergillus salvadorensis* could play a relevant functional role within the metabolism and physiology of this fungus.

Discussion

The functional characterization based on COG categories of the *Aspergillus salvadorensis* genome shows a wide metabolic and functional diversity, which suggests a high capacity to adapt to different environmental conditions. A relevant finding is the high proportion of genes classified as unknown functions, with 185 sequences identified, indicating that a considerable part of the genome has not yet been fully described. This pattern is frequent in little-studied filamentous fungi and suggests the possible existence of new metabolic pathways, specialized enzymes or adaptive mechanisms related to the degradation of complex compounds and survival in tropical environments. This uncharacterized gene repertoire also highlights the biotechnological potential of the species and the need for further functional studies (Tatusov, Roman L. et al., 2000; Galagan, James E. et al., 2005).

Within the known functional categories, a high representation of genes associated with the storage and processing of genetic information is observed, including transcription processes (64 genes), ribosomal translation and biogenesis (63 genes), as well as DNA replication, recombination and repair (39 genes). This distribution suggests an active and efficient cellular machinery, capable of responding quickly to environmental variations. In species of the genus *Aspergillus*, this ability has been related to the dynamic regulation of gene expression in the face of nutritional changes, oxidative stress and other environmental conditions, facilitating the production of degrading enzymes and secondary metabolites (de Vries, Ronald P. & Visser, Jaap, 2001; Krijgsheld, Pauline et al., 2013). In addition, the presence of genes related to post-translational modification, protein turnover and chaperones (30 genes) indicates robust mechanisms of protein quality control and adaptation to cellular stress.

In relation to metabolism, a significant abundance of genes involved in energy production and conversion (47 genes), carbohydrate metabolism (45 genes) and amino acid metabolism (43 genes) was identified, suggesting a high metabolic versatility. This characteristic is common in filamentous fungi capable of degrading complex organic matter through the secretion of hydrolytic enzymes, such as cellulases, hemicellulases and amylases, which allow the use of various environmental substrates (Benoit, Isabelle et al., 2015; de Vries & Visser, 2001). Likewise, the presence of genes related to lipid and amino acid metabolism suggests the body's ability to adapt to different nutritional sources.

Genes associated with intracellular transport, vesicular secretion and transport (18 genes), as well as signal transduction mechanisms (21 genes), which are fundamental for extracellular enzyme secretion and cell communication, were also identified. These processes allow the degradation of complex polymers such as cellulose and lignin, facilitating the absorption of nutrients and the colonization of new ecological niches (Krijgsheld et al., 2013). The presence of genes related to the biogenesis of the cell envelope (13 genes) also suggests the capacity for structural adaptation to adverse environmental conditions.

On the other hand, the identification of genes related to the production of secondary metabolites (8 genes) is particularly relevant, since species of the genus *Aspergillus* are recognized for synthesizing bioactive compounds such as antibiotics, pigments, toxins and enzymes of industrial interest. Although the number identified is relatively low, these genes could play an important role in ecological competition and biotechnology applications (Keller, Nancy P., Turner, Geoffrey, & Bennett, Joan W., 2005).

Overall, the functional distribution of the genome suggests that *Aspergillus salvadorensis* has a complex genetic machinery aimed at environmental adaptation, the degradation of complex compounds and the production of metabolites of biotechnological interest. The combination of a high proportion of unknown genes and a wide metabolic diversity indicates significant potential for industrial applications, polymer biodegradation and organic waste utilization, providing a solid basis for future experimental research.

Conclusion

Genomic and structural analysis of ORF26 of *Aspergillus salvadorensis* reveals the presence of a potentially functional gene with a stable and well-organized three-dimensional protein structure. The identification of multiple ORFs, together with the structural prediction of the protein, suggests that this fungus has a complex genetic machinery associated with metabolic processes, environmental adaptation and possible biotechnological interest, highlighting the importance of continuing with more detailed functional and phylogenetic studies.

Gratitude and Recognition

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Conflicts of Interest

The author declares that he has no conflict of interest.

References

1. Benoit, I., Coutinho, P. M., Schols, H. A., Gerlach, J. P., Henrissat, B., & de Vries, R. P. (2015). Degradation of different pectins by fungi: correlations and contrasts between the pectinolytic enzyme sets identified in genomes and the growth on pectins of different origin. *BMC Genomics*, 16, 176. [https://pubmed.ncbi.nlm.nih.gov/25887408]
2. de Vries, R. P., & Visser, J. (2001). *Aspergillus* enzymes involved in degradation of plant cell wall polysaccharides. *A. Salvadorensis Microbiology and Molecular Biology Reviews A. Salvadorensis*, 65(4), 497–522. [https://doi.org/10.1128/MMBR.65.4.497-522.2001] (https://doi.org/10.1128/MMBR.65.4.497-522.2001)
3. de Vries, Ronald P., & Visser, Jaap (2001). *Aspergillus* enzymes involved in degradation of plant cell wall polysaccharides. *Microbiology and Molecular Biology Reviews*, 65(4), 497–522. https://pmc.ncbi.nlm.nih.gov/articles/PMC99039/
4. Galagan, J. E., Calvo, S. E., Borkovich, K. A., et al. (2005). The genome sequence of the filamentous fungus *Neurospora crassa*. *Nature*, 422, 859–868. https://www.nature.com/articles/nature01554
5. Galagan, James E., et al. (2005). Sequencing of *Aspergillus nidulans* and comparative analysis with *A. fumigates* and *A. oryzae*. *Nature*, 438(7071), 1105–1115. [https://doi.org/10.1038/nature04341] (https://doi.org/10.1038/nature04341)
6. Keller, N. P., Turner, G., & Bennett, J. W. (2005). Fungal secondary metabolism — from biochemistry to genomics. *A. salvadorensis Nature Reviews Microbiology A. salvadorensis*, 3(12), 937–947. [https://doi.org/10.1038/nrmicro1286] (https://doi.org/10.1038/nrmicro1286)
7. Keller, Nancy P., Turner, Geoffrey, & Bennett, Joan W. (2005). Fungal secondary metabolism—from biochemistry to genomics. *Nature Reviews Microbiology*, 3(12), 937–947.
8. Krijgheld, P., Bleichrodt, R., van Veluw, G. J., et al. (2013). Development in *Aspergillus*. *A. Salvadorensis Studies in Mycology A. Salvadorensis*, 74, 1–29. [https://doi.org/10.3114/sim0006] (https://doi.org/10.3114/sim0006)
9. Krijgheld, Pauline, et al. (2013). Development in *Aspergillus*. *Studies in Mycology*, 74, 1–29. [https://doi.org/10.3114/sim0006] (https://doi.org/10.3114/sim0006)
10. Tatusov, R. L., Galperin, M. Y., Natale, D. A., & Koonin, E. V. (2000). The COG database: a tool for genome-scale analysis of protein functions and evolution. 28(1), 33–36. https://pmc.ncbi.nlm.nih.gov/articles/PMC102395/