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## ENVIS CENTRE

Department of Zoology

University of Madras, Guindy Campus, Chennai - 600 025

Telefax: 91-44-22300899; E-mail: [dzum@envis.nic.in](mailto:dzum@envis.nic.in); [enviscoordinator@gmail.com](mailto:enviscoordinator@gmail.com)

Websites: [www.dzumenvis.nic.in](http://www.dzumenvis.nic.in) ; [www.envismadrasuniv.org](http://www.envismadrasuniv.org); [www.envismicrobes.in](http://www.envismicrobes.in) (Tamil version)

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**ENVIS Centre**

Department of Zoology

University of Madras

Guindy Campus, Chennai - 600 025

Tamil Nadu, INDIA

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[dzum@envis.nic.in](mailto:dzum@envis.nic.in)

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**Cover page :** Microscopic image shows the surface of the mold *Emericella nidulaus* with globular spores produced for its dispersion.

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### From the Coordinator's Desk!

Dear Readers,

Greetings!

Fungi are eukaryotic microorganisms which play an integral role in the development of the biotechnological and biomedical sectors, at the same time they also pose substantial threat to the human health. Understanding different fungal biology in diverse ecosystems and their interactions with other microorganisms, animals and plants, is essential to underpin effective and innovative technological developments. Among many applications, the fungi in the environment are utilized mainly for bioremediation, bio fertilizers and food crops development. The degradative activities of fungi and their antibiotic producing potentials have also been studied for bioremediation of contaminated land, treatment of industrial wastes and biotransformation of specific compounds. Many of the applications of fungal biotechnology rely not on identifying new activities but also in harnessing and expanding roles the fungi may undertake normally in the environment.

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# Fungal diversity of industrial sewages

N. Ashwin Karthick<sup>1</sup>, A. Balamurugan<sup>1</sup>, N. K. Udaya Prakash<sup>2</sup> and S. Bhuvaneswari<sup>3\*</sup>

<sup>1</sup>Research and Development, MARINA LABS, Plot No. 14, Kavya Gardens, N.T.Patel Road, Nerkundram, Chennai - 600 107. <sup>2</sup>Department of Biotechnology, School of Life Sciences, Vels University, Pallavaram, Chennai - 600 117. <sup>3</sup>\*Department of Botany, Bharathi Women's College, Broadway, Chennai - 600 108.

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## ABSTRACT

Fungi in sewages are known as one involved in degradation of lignin, cellulose, hemicellulose, fermentation of ammonia and also used in bio removal of heavy metals and dyes. Their diversity varies according to the composition of sewage. Any data on the diversity, prevalence and predominance of fungal species are of importance to identify the specific fungal species for the application as remediaters. In the present study, the variation of fungal diversity in sewages of three different industrial hubs of Chennai i.e., Ambattur, Chrompet and Guindy each possessing different types of industrial units were compared with Cooum River, the drainage for city's domestic sewage. A total of 1492 colonies were isolated from the samples and classified under 33 species belonging to 19 genera along with non-sporulating colonies. *Absidia corymbifera*, *Aspergillus flavus*, *A. fumigatus*, *A. nidulans*, *A. niger*, *A. tamari*, *A. terreus* and *Trichoderma viride* were commonly recorded in all the sites studied. The data obtained were subjected to statistical analysis like Jaccard co-efficient Index and Shannon diversity index. These indices imply that the fungal diversity differ according to the environment and nature of sewage.

## Introduction

Sewages are artificial ecosystems of unknown composition that varies from time to time and place to place. The nature of the sewage is defined by the condition of environment, nature of waste and traces of other substances like odour, taste, pesticides, steroids etc. (Cooke, 1970). Based on the human settlements and establishments such as industries and their function the effluent generated differs. Fungi in these sewages are important members serving in absorption of nutrients, digesting sludges and granular formation (Subramanian *et al.*, 2008). Sewages which are largely composed of organic matter (Strachan *et al.*, 1983) from diverse source (Maki, 1954) support growth of numerous fungi and act as a continuous nutrient source (Razi and Molla, 2007). However, the viability of fungi depends on the adaptation to the absurdity caused by contaminants.

The presence of fungi either as spores or vegetative cells, on synthetic or semi-synthetic substrates in sewages represent the diversity of native flora which can potentially be used in cleaning up of the environment (Vidali, 2007). These native flora are known to be involved in the degradation of lignin, cellulose, hemicellulose (Dashtban *et al.*, 2010), fermentation of ammonia (Hayatsu *et al.*, 2008), granular

formation in sewage treatment processes (Weber *et al.*, 2009), bio removal of heavy metals (Dacera and Babel, 2008) and dyes (Rani *et al.*, 2014). Fungal biomass has been successfully used as adsorbing agents for removal of heavy metals (Prasenjit and Sumathi, 2005) and degradation of hydrocarbons (Zheng and Obbard, 2002). Further, the fungal enzymes such as peroxidases, tyrosinases and laccases (Cabana *et al.*, 2007) are found to play a major role in dye removal. Thus, any data on the diversity, prevalence and predominance of fungal species are of importance to identify the specific fungal species and exploitation of the same in bioremediation.

Though the studies on the occurrence and distribution of fungi in sewage sludge were widely reported (Avasn *et al.*, 2012; Matsunaga *et al.*, 2014; Pandey *et al.*, 2014), the diversity of fungi in sewage water is scanty. It is known that sewage water induces more stress due to its low nutrient composition, agitation and flow resulting in the variation of fungal diversity. Thus, in this study, the prevalence of fungal species from the sewage water of three major industrial hubs of Chennai city with different industrial activities, i.e. leather industries (Chrompet), metal finishing and electroplating industries (Ambattur) and electronic and light engineering industries (Guindy) were studied and compared with the Cooum River, one of the major rivers comprised mostly of domestic sewage as major constituent.

\*Corresponding author.

E-Mail address: drsbhuvaneswari8@gmail.com

## **Materials and Methods**

### **Sampling site:**

The samples of sewages were collected from different industrial hubs present in Chennai which is one among the major metropolitan cities in India. The city is situated between 13.04°N and 80.17°E on the East coast of India and its altitude is around 16m above mean sea level. Ambattur Industrial Estate has more than 2000 manufacturing units working on auto components, machineries, tools and accessories, welding, moulding, dyes, etc. Chrompet solely has tannery industries (Ramesh and Thirumangai, 2014) while Guindy, with a spread over area of 404 acres, houses about 700 units of industries dealing with electronics, readymade garments and light engineering works. The Cooum River which runs through the city is highly polluted by discharge of untreated sewage, industrial and domestic effluents especially at the downstream end. The sewage generated from these sites were studied for their mycological diversity.

### **Sampling method:**

The samples were collected from running sewages of respective industrial hubs, i.e. Ambattur, Chromepet and Guindy along with Cooum River as control using 250ml volume sterile bottles (Schott Duran, Germany). Around 100ml of sewage from 10 different spots of each industrial hub totaling 40 samples were collected and brought to the laboratory. The collected samples were stored in a refrigerator and samples were processed within a day interval.

### **Isolation method:**

The fungal colonies were isolated using serial dilution method. One ml of each sample was diluted in 10ml of sterile water and serially diluted to achieve 10<sup>2</sup> concentrations. One ml from the diluted sample was directly plated to Petridishes with Potato Dextrose Agar (PDA) (Himedia, Mumbai) supplemented with Streptomycin (0.06 g/L) to arrest the bacterial growth for the isolation of fungi and maintained in triplicates at room temperature (28°C ± 2°C) (Prashanth *et al.*, 2012).

### **Identification of Fungi:**

The isolated colonies were identified after 4-5 days based on their morphological, macroscopic and microscopic features using the standard manuals up to the species level wherever possible (Udayaprakash, 2004). The fungi observed in their asexual stages in the laboratory were classified under

Mitosporic fungi. Identification through direct microscopy is adapted in this study as this is widely used in industries to reduce the time and cost expenditure (Udayaprakash *et al.*, 2014).

### **Presentation of Data:**

The average colony forming units (CFU /ml) of sewage sample was calculated as follows:

$$\text{Average (CFU/ml)} = \frac{\text{No. of colonies counted (Avg. of 3 replicates)}}{\text{Volume of sewage sample (1ml)}} * \text{dilution factor (100)}$$

The percent contribution is the ratio of individual fungal species to the total number of CFU of all species isolated which was calculated as,

$$\% \text{ Contribution} = \frac{\text{CFU of an individual fungal species}}{\text{Total No. of CFU of all species}} * 100$$

### **Jaccard Coefficient:**

To describe the taxonomic affinity of mycotic flora among the various sewages of Chennai, Jaccard's coefficient (JI) was used to measure the similarity between pairs of samples (Arnold *et al.*, 2000).

$$JI = \frac{a}{a + b + c}$$

where *a* represents the number of species occurring in both the samples, *b* represents the number of species restricted to sample 1, and *c* represents the number of species restricted to sample 2. JI ranges from 0 (no taxa shared) to 1 (all taxa shared).

### **Shannon Diversity index:**

Shannon Diversity index represents the species diversity.

Shannon index (HS) = -  $\sum_j (p_j \ln p_j)$ , j = 1..... N<sub>s</sub>, where, N<sub>i</sub> is the total number of individuals, N<sub>s</sub> is the number of species identified among these isolates, And p<sub>j</sub> is the proportion of individuals in the j<sup>th</sup> species

## **Results and Discussion**

The study on mycofloral diversity from different industrial sewage waters resulted in an isolation of 1492 colonies classified under 33 species belonging to 19 genera. Among the species isolated 4 belong to Zygomycotina, 1 to Ascomycotina and remaining 28 species belonged to Mitosporic fungi. Among the genera recorded, the genus *Aspergillus* was represented by maximum number of species (10 species) followed by *Penicillium* (5 species). All other genera are represented by single species except that of *Fusarium* where it was represented by 2 species. The list of fungi isolated, their percent contribution recorded in respective sites is presented in Table 1.

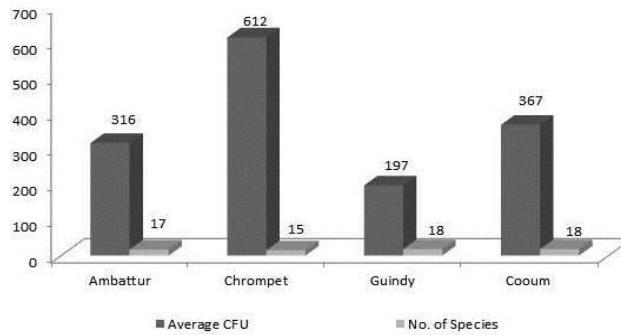
**Table1:** Average CFU/ml and Percent contribution of fungal species isolated from sewages of different industrial hubs in Chennai

No.	Species	Cooum River (Control)		Chrompet		Guindy		Ambattur	
		Average CFU (x 10 <sup>2</sup> )	%	Average CFU (x 10 <sup>2</sup> )	%	Average CFU (x 10 <sup>2</sup> )	%	Average CFU (x 10 <sup>2</sup> )	%
1	<i>Absidia corymbifera</i>	0.06	0.540	2.30	11.18	0.2	2.96	0.03	0.28
2	<i>Alternaria alternata</i>	-	-	0.1	0.48	-	-	-	-
3	<i>Aspergillus flavipes</i>	-	-	-	-	0.03	0.44	-	-
4	<i>A. flavus</i>	0.23	1.91	1.26	6.16	0.4	5.93	0.9	8.41
5	<i>A. fumigatus</i>	0.4	3.26	3.66	17.83	0.33	4.89	2.16	20.1
6	<i>A. glaucus</i>	-	-	0.43	2.10	-	-	-	-
7	<i>A. japonicas</i>	-	-	2.1	10.21	-	-	-	-
8	<i>A. nidulans</i>	0.2	1.63	0.33	1.58	0.23	3.41	0.3	2.80
9	<i>A. niger</i>	5.03	41.14	4.03	19.61	1.1	16.32	3.03	28.3
10	<i>A. ochraceus</i>	0.03	0.27	-	-	-	-	0.03	0.28
11	<i>A. tamari</i>	0.03	0.27	-	-	0.03	0.44	0.26	2.42
12	<i>A. terreus</i>	0.93	7.62	1.03	5.02	0.13	1.92	1.76	16.44
13	<i>Aureobasidium pullulans</i>	-	-	-	-	0.46	6.82	-	-
14	<i>Chrysosporium sp.</i>	-	-	0.13	0.64	-	-	-	-
15	<i>Curvularia lunata</i>	0.03	0.27	0.13	0.64	-	-	0.23	2.14
16	<i>Emericella nidulans</i>	-	-	-	-	0.16	2.37	-	-
17	<i>Fusarium oxysporum</i>	-	-	-	-	0.03	0.44	-	-
18	<i>F. moniliforme</i>	0.06	0.54	-	-	-	-	-	-
19	<i>Geotrichum candidum</i>	0.36	2.99	-	-	-	-	-	-
20	<i>Humicola grisea</i>	0.26	2.17	-	-	-	-	-	-
21	<i>Lasiodiplodia theobromae</i>	-	-	-	-	0.06	0.89	-	-
22	<i>Monilia sitophila</i>	-	-	-	-	0.06	0.89	0.03	0.28
23	<i>Mucor racemosus</i>	0.1	0.81			-	-	0.06	0.56
24	<i>Paecilomyces variotti</i>	-	-	0.1	0.48	0.4	5.93	0.3	2.80
25	<i>Penicillium citrinum</i>	-	-	-	-	-	-	0.26	2.42
26	<i>P. corylophilum</i>	0.03	0.27	-	-	-	-	-	-
27	<i>P. frequentans</i>	0.03	0.27			0.16	2.37	0.13	1.21
28	<i>P. funiculosum</i>	-	-	0.06	0.32	0.03	0.44	-	-
29	<i>P. oxalicum</i>	0.03	0.27	-	-	-	-	-	-
30	<i>Phialophora sp.</i>	-	-	-	-	0.1	1.48	-	-
31	<i>Rhizopus stolonifer</i>	0.06	0.54	-	-	0.2	2.96	0.06	0.56
32	<i>Syncephalastrum racemosum</i>	-	-	0.4	1.94	-	-	0.03	0.28
33	<i>Trichoderma viride</i>	3.83	31.06	4.23	20.58	2.23	33.08	0.83	7.75
	Non sporulating colonies	0.5	4.08	0.16	0.81	0.4	5.93	0.3	0.28

Of the sewage samples collected from three different industrial hubs, Chrompet recorded with highest colony forming units (612 CFU/ml), followed by Ambattur (316 CFU/ml) and Guindy (197 CFU/ml) as the least. On contrary, diversity richness was found maximum at Guindy (18), followed by Ambattur (17) and least at Chrompet (15) (Fig 1). The pollutants present in the sewage are known to reduce the diversity of sensitive fungi,

while increasing the diversity of less sensitive organisms (Cooke, 1970). The presence of organic pollutants generated from leather tanneries in Chrompet might have selected and made the adapted fungal species to thrive and proliferate when compared with other two industrial hubs. The samples of Cooum River showed 367 CFU/ml with 18 different species with high diversity richness as of Guindy and Ambattur.

**Fig. 1. The average CFU and number of species recorded in sewages of different industrial hubs.**



The most dominant species isolated was *Aspergillus niger* (26.55%) followed by *Trichoderma viride* (22.26%), while *Aspergillus fumigatus* (13.21%), *Aspergillus terreus* (7.73%), *Aspergillus flavus* (5.63%) and *Absidia corymbifera* (5.23%) were the other notable contributors. Difference in dominance of species was observed among the sites. The following species, *Trichoderma viride* and *Aspergillus niger* were recorded as dominant species from the sewages of Chrompet and Guindy. However third dominant species found to differ, it was *Aspergillus fumigatus* in Chrompet and *Aureobasidium pullulans* in Guindy. Similarly, in Ambattur and Cooum, it was *Aspergillus niger* recorded as most dominant species and the second dominant species found to differ. The difference between the dominant species is evident due to different nature of sewages emanating from different industrial hubs. Shannon diversity index and Shannon evenness index provided the difference between the species at different sites (Table 2).

**Table 2: Shannon diversity and evenness index recorded among the fungal species from sewages of different industrial hubs.**

	Cooum River	Chrompet	Guindy	Ambattur
Shannon Diversity index	4.185603	4.236164	3.018438	3.664098
Shannon's Evenness index	0.232533	0.282411	0.167691	0.215535

Out of 33 species isolated, nearly 16 species were reported as common inhabitants of sewage (Kacprzak *et al.*, 2005; Fleury, 2007). *Absidia corymbifera*, *Aspergillus flavus*, *A. fumigatus*, *A. nidulans*, *A. niger*, *A. tamari*, *A. terreus* and *Trichoderma viride* were commonly recorded in all the sites studied. The most dominant genera recorded was *Aspergillus* (10 species) followed by *Penicillium* (5 species), and *Fusarium* (2 species) which were in accordance with Zubeiry (2005) from Yemen. However, this

was found to differ in sewage sludges where *Penicillium* was reported as dominant genus (Cooke and Pipes, 1970).

Jaccard similarity index showed chrompet had the least similarity index than the other industrial hubs. As inferred from similarity index, Chrompet had 38.46% and 45.45% species in common with species isolated from Guindy and Ambattur respectively, while Ambattur and Guindy shared 52% of their total species diversity (Table 3). However, compared with control Cooum River, Chrompet had 34.61% similarity, Guindy with 40.74% and Ambattur had 68.18% species similarity.

**Table 3: Jaccard's Similarity Coefficient among the fungal species recorded from sewages of different industrial hubs.**

	Cooum River	Chrompet	Guindy	Ambattur
Cooum River	1			
Chrompet	0.3461	1		
Guindy	0.4074	0.3846	1	
Ambattur	0.6818	0.4545	0.52	1

Few species reported in this study are widely identified as a potential fungal species for bioremediation. This includes, *Aspergillus niger* (Jamal *et al.*, 2005), *Penicillium* sp. and *Paecilomyces* sp. (Subramanian *et al.*, 2006), *Trichoderma* sp. (Verma *et al.*, 2007). Among these, *Aspergillus niger* and *Trichoderma viride* were found to be one of the dominant species in all industrial sewage types studied. Therefore, data on the diversity, prevalence and predominance of fungal species are of importance and further studies from different geographical zones with different sewage types are highly recommended.

## Conclusion

The present study has revealed the diversity of fungi in sewages of different industrial hubs, i.e. Ambattur, Chrompet and Guindy of Chennai. The fungal diversity was found to differ according to the environment and nature of sewage when compared with Cooum River as control. A total of 33 species belonging to 19 genera were recorded from the sewages among which *Aspergillus niger*, *Trichoderma viride* and *Aspergillus terreus* are found to be the dominant species. The isolated fungal species from sewage water can be potentially used in bioremediation for the removal of heavy metals, toxic compounds and dyes after monitoring their epidemiology.

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## RESEARCH REPORTS

### Bacterial protein structure could aid development of new antibiotics

Bacterial cells have an added layer of protection, called the cell wall, which animal cells don't. Assembling this tough armor entails multiple steps, some of which are targeted by antibiotics like penicillin and vancomycin. Yet one step in the process has remained a mystery because the molecular structures of the proteins involved were not known. Duke University researchers have now provided the first close-up glimpse of a protein, called MurJ, which is crucial for building the bacterial cell wall and protecting it from outside attack. They published MurJ's molecular structure on Dec. 26, 2016 in *Nature Structural and Molecular Biology*.

Antibiotic researchers feel an urgent need to gain a deeper understanding of cell wall construction to develop new antibiotics in the face of mounting antibacterial resistance. In the

U.S. alone, an antibiotic-resistant infection called MRSA causes nearly 12,000 deaths per year.

"Until now, MurJ's mechanisms have been somewhat of a 'black box' in the bacterial cell wall synthesis because of technical difficulties studying the protein," said senior author Seok-Yong Lee, Ph.D., Associate professor of biochemistry at Duke University School of Medicine. "Our study could provide insight into the development of broad spectrum antibiotics, because nearly every type of bacteria needs this protein's action."

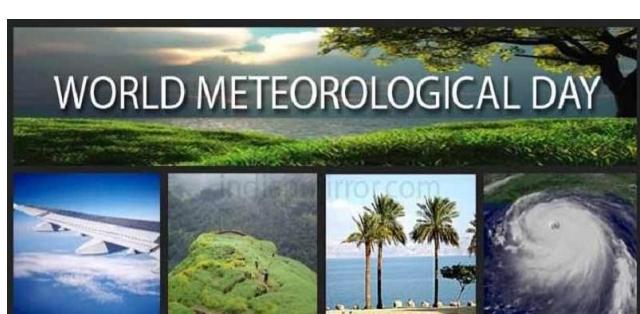
### KNOW A SCIENTIST

#### Dr. Luc Montagnier



**Born on** 18<sup>th</sup> August 1932 at Chabris, France.

He was awarded noble prize for the discovery of human immunodeficiency virus. Retroviruses are viruses whose genomes consist of RNA and whose genes can be incorporated into host cell's DNA. In 1983, Luc Montaigner and Françoise Barré-Sinoussi discovered a retrovirus in patients with swollen lymph glands that attacked lymphocytes - a kind of blood cell that is very important to the body's immune system. The retrovirus, later named as Human Immunodeficiency Virus (HIV), proved to be the cause of the immunodeficiency disease AIDS. This discovery has been crucial in radically improving treatment methods for AIDS sufferers.



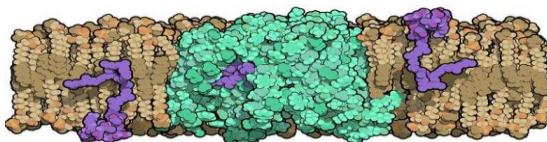
WORLD METEOROLOGICAL DAY 23<sup>rd</sup> March 2017

A bacterium's cell wall is composed of a rigid mesh-like material called peptidoglycan. Molecules to make peptidoglycan are manufactured inside the cell and then need to be transported across the cell membrane to build the outer wall. In 2014, another group of scientists discovered that MurJ is the transporter protein located in the cell membrane that is responsible for flipping these wall building blocks across the membrane. Without MurJ, peptidoglycan precursors build up inside the cell and the bacterium falls apart. Many groups have attempted to solve MurJ's structure without success, partly because membrane proteins are notoriously difficult to work with.

In the new study, Lee's team was able to crystallize MurJ and determine its molecular structure to 2-angstrom resolution by an established method called X-ray crystallography which is difficult to achieve in a membrane protein. The structure, combined with follow-up experiments in which the scientists mutated specific residues of MurJ, allowed them to propose a model for how it flips peptidoglycan precursors across the membrane. After determining the first structure of MurJ, Lee's team is now working to capture MurJ in action, possibly by crystallizing the protein while it is bound to a peptidoglycan precursor.

"Getting the structure of MurJ linked to its substrate will be key. It will really help us understand how this transporter works and how to develop an inhibitor targeting this transporter," Lee said.

Lee's group is continuing structure and function studies of other key players in bacterial cell wall biosynthesis as well. Last year, they published the structure of another important enzyme, MraY, bound to the antibacterial muraymycin.



**Fig.** Structure of MurJ enzyme. Researchers at Duke University solved the structure of an enzyme that is crucial for helping bacteria to build their cell walls. The molecule, called MurJ (shown in green), must flip cell wall precursors (purple) across the bacteria's cell membrane before these molecules can be linked together to form the cell wall. This new structure could be important to

**help develop new broad-spectrum antibiotics.**

(Image credit: Alvin Kuk, Duke University).

Source: [www.phys.org](http://www.phys.org).

## Revealing *Aspergillus* diversity for industrial applications

In the world of fungi, *Aspergillus* is an industrial superstar. *Aspergillus niger*, for example, has been used for decades to produce citric acid, a compound frequently added to foods and pharmaceuticals through fermentation at an industrial scale. Other species in this genus play critical roles in biofuel production, and plant and human health. Since the majority of its 350 species have yet to be sequenced and analyzed, researchers are still at the tip of the iceberg when it comes to understanding *Aspergillus* full potential and the spectrum of useful compounds they may generate.

In a study published in the journal Genome Biology, an international team including researchers at the U.S. Department of Energy Joint Genome Institute (DOE JGI), a DOE Office of Science User Facility, report sequencing the genomes of 10 novel *Aspergillus* species, more than doubling the number of *Aspergillus* species sequenced to date. The newly sequenced genomes were compared with the eight other sequenced *Aspergillus* species. With this first ever genus-wide view, the international consortium found that *Aspergillus* has a greater genomic and functional diversity than previously understood, broadening the range of potential applications for the fungi it is considered as one of the most important workhorses in the biotechnology.

"Several *Aspergillus* species have already established status as cell factories for enzymes and metabolites. However, little is known about the diversity in the species at the genomic level and this paper demonstrates how diverse the species of this genus are," said study lead author Ronald de Vries of the Westerdijk Fungal Biodiversity Institute in the Netherlands. "One can't assume that an *Aspergillus* species will have the same physiology as a better studied species of the genus."

The study, conducted through the DOE JGI's Community Science Program, also demonstrates the importance of evaluating biodiversity within a genus to understand how fungi can be greater utilized to solve a variety of problems. Sequencing a diverse set of *Aspergillus* genomes allows researchers to build a more comprehensive catalog of enzymes

for biotechnological applications, added DOE JGI Fungal Genomics Program Head Igor Grigoriev and senior author of the paper. Those applications include harnessing *Aspergillus* to help protect crops and ward off agents that can cause diseases in plants.

Comparing the newly sequenced genomes to those already available, researchers found a huge variety of carbohydrate-active enzymes (CAZymes) among the *Aspergillus* species, suggesting distinct strategies to break down plant biomass. CAZymes are responsible for breaking down plant cell walls, useful for industrially processing plants the DOE considers candidate bioenergy crops. The sugars that are part of these cell walls can't be accessed and fermented to make biofuels unless the walls are broken down by agents like CAZymes.

"Each of these 10 genomes encodes for a unique composition of CAZymes and the wider assortment helps formulate enzyme cocktails better suited for different types of plant biomass to efficiently convert them into biofuels," Grigoriev said.

In addition to biofuels, CAZymes can also help to facilitate the production of paper, textiles, food, feed and pharmaceuticals. The comparative analysis between the genomes also enabled researchers to uncover a high diversity of genes that: 1) allow the fungi to produce secondary metabolites, compounds that may be useful for applications such as crop protection; and 2) enable the fungi to tolerate stress. The knowledge gained in secondary metabolism and stress response will help to provide more insight in the mechanisms underlying these functions.

But despite the new insights gained, the authors emphasized that there is much remaining unknown about the full spectrum of what *Aspergillus* can do. They also added that the potential application of the genus has been barely touched. Encouraged by results of their study they now pursue a deeper exploration of the *Aspergillus* genus, sequencing the remaining 300 species, each carrying a unique composition genes, enzymes, and pathways.

**Source:** [www.sciencedaily.com](http://www.sciencedaily.com).

## ONLINE REPORTS

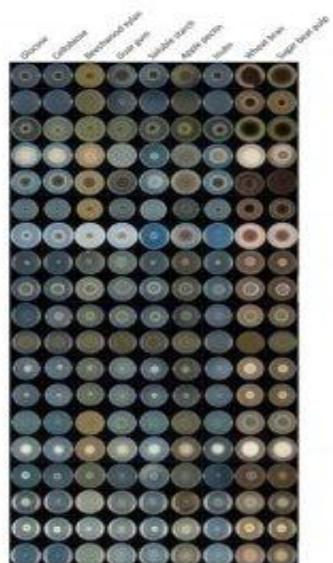
### Fungi have enormous potential for new antibiotics

Fungi are a potential goldmine for the production of pharmaceuticals. This is shown by researchers at Chalmers University of Technology, who have developed a method for finding new antibiotics from nature's own resources. The findings which could prove very useful in the battle against antibiotic resistance were published in the journal, *Nature Microbiology*.

Antibiotics have saved millions of lives since they were discovered in the 1940s. But recently we've had to learn a new term: antibiotic resistance. More and more bacteria are developing their own protection against antibiotics, thereby becoming resistant to treatment. This will lead to simple infections becoming lethal once again. Our need for new antibiotics is urgent.

The first antibiotic to be mass-produced was penicillin, derived from *Penicillium* fungi. In their quest for new antibiotics, Chalmers researchers sequenced the genomes of nine different types of *Penicillium* species. And the findings are amazing: In the study, the research group scanned the genomes of 24 different kinds of fungi to find genes responsible for the production of various bioactive compounds, like antibiotics. More than 1000 pathways were discovered, showing immense potential for fungi to produce a large variety of natural and bioactive chemicals that could be used as pharmaceuticals.

In about 90 cases, the researchers were able to predict the chemical products of the pathways. As evidence of this, they followed the production of the antibiotic, yanuthone, and identified new fungi able to produce the compound, but also that some species could produce a new version of the drug. All



Showed vast potential for fungi, not only in producing new antibiotics but also in enabling more efficient production of existing ones and may be also more effective versions of the existing ones.

"It's important to find new antibiotics in order to give physicians a broad palette of antibiotics, existing ones as well as new ones, to use in treatment. This will make it harder for bacteria to develop resistance. Previous efforts to find new antibiotics have mainly focused on bacteria. Fungi have been hard to study we know very little of what they can do but we do know that they develop bioactive substances naturally, as a way to protect themselves and survive in a competitive environment. This made it logical to apply our research tools to fungi" explains Jens Christian Nielsen.

Researchers now have various paths to follow. One way of moving forward could be to look further at the production of the new yanuthone compound. The Chalmers researchers have also drawn up a map that makes it possible to compare hundreds of genes in the continuous evaluation of bioactive products with potent drugs in sight. How long it would take to launch new antibiotics on the market is impossible to say.

"Governments need to act. The pharmaceutical industry doesn't want to spend money on new antibiotics, it's not lucrative. This is why our governments have to step in and, for instance, support clinical studies. Their support would make it easier to reach the market, especially for smaller companies. This could fuel production," says Jens Christian Nielsen.



**Fig. Penicillia.** While Penicillia are already industrially used in the production of antibiotics, other pharmaceuticals, industrial enzymes and in the manufacturing of food products, new research reveals that their potential for production of novel antibiotics is far from exhausted. Penicillia are naturally found in temperate climates growing on organic matter, including soil, plant material, dung and food products. The isolation of novel bioactive compounds from these species might encompass a source of new antibiotics to fight infectious microorganisms.

(**Image Credit:** Jens Christian Nielsen)

**Source:** [www.sciencedaily.com](http://www.sciencedaily.com)

## 200-year-old banyan tree near Ambattur gets new lease of life

A team of horticulturists and a group of residents have successfully transplanted a 200-plus-year-old banyan tree uprooted by cyclone Vardah on December 12 at Ayanambakkam near Ambattur.



**SECOND CHANCE:** Replanting the tree began on Saturday and ended on Monday night

Horticulturist and landscape expert B Ilango, who was part of the operation, told Times of India that residents of the area had approached him to take up the transplantation work. He visited the spot and agreed to help in the work.

On the first the residents used a bulldozer to push the tree, and this damaged a few portions. The second day, branches were pruned, fungicide applied on the branches and rooting enzymes applied on the roots. On the third day, the tree was transplanted in a 6 foot-deep pit. A 40-tonne crane was used to lift the tree. Will the tree survive the transplant operation? Ilango said his team had successfully transplanted banyan trees in a few other places and they survived.

Water has to be sprayed on the branches for the next 45 days. After that, the roots need to be watered. Once that is done, the tree will get back its life, he said.

**Source:** The Times of India. January 04, 2017.

## Research altered the scientific understanding of the transmission routes of fungal viruses by revealing them to be unfaithful to their host

According to a research conducted at the Natural Resources Institute Finland (Luke), some fungal viruses (mycoviruses) that infect fungi associated with forest trees are able to cross the barriers between distantly related fungal species. This overturns the former theory that mycoviruses are host specific, and will create new perspectives on their possible roles in regulating forest biodiversity.

The wood decay fungus *Heterobasidion parviporum* causes root rot in spruce and is a serious pathogen. Its viruses have been intensively investigated in order to discover a method of controlling root rot in spruce. *Heterobasidion* root rot fungi host to more than 20 species of mycoviruses, which are known to survive for years in infected mycelium and can transfer from one fungal species to another, both in the laboratory and under natural conditions.

The new study investigated whether the mycoviruses of *Heterobasidion* root rot fungi are capable of being transmitted to more distant fungal species or not and had found that it could be possible.

"We found two species of *Heterobasidion* viruses in the ectomycorrhizal fungus *Lactarius tabidus*, commonly known as the Birch Milkcap, and *Rhodocollybia butyracea*, the Butter Cap, which is known to be a saprotrophic fungus. In addition, *Heterobasidion* viruses were detected in the mycelium of mycorrhizal fungi that grow underground" says, Professor Jarkko Hantula of Luke.

Mycoviruses are not distributed by air like the viruses of many other organisms, but along the mycelial bridges formed between fungal mycelia. They were thought to be strongly tied to their host species, but Luke's research results call into question this idea of mycoviruses being host specific.

"A few similar observations have been made elsewhere in recent years, but the evidence we found poses a serious challenge to the former theory. Even if the transmission of viruses between species seems rare, it will nevertheless be necessary to investigate whether, for instance, the viral prevention of root rot that would pose a risk to other fungal species," says Hantula.

Forest trees support a diverse fungal community, which includes many highly beneficial or harmless fungi. Symbiotic mycorrhizae in the root system boost the growth of green mold, endophytic fungi that live in tissues, many epiphytes that cover the surfaces of trees and saprotrophic fungi which recycle the nutrients of dead trees.

"An example from the 1960s illustrates the economic benefits of mycoviruses: viruses helped to save the European chestnut from a dangerous pathogen of non-native origin. This incentivised our research of root rot viruses," says Hantula.



**Fig.** Forest tree stumps support a diverse fungal community coexisting with the root rot fungus *Heterobasidion*.  
**(Image Credit:** Tuula Piri, Luke)

**Source:** [www.sciencedaily.com](http://www.sciencedaily.com)

## NEWS

### Petrol, jet fuel alternatives are produced by yeast cell factories

We are in great need of sustainable and clean alternatives to oil-derived products. One of the choices at hand is to produce chemicals and biofuels from sustainable biomass.

To do this, a research team at Chalmers University of Technology is hard at work trying to design yeast cell factories that can actually produce the chemicals we need in a sustainable way. The group has now had a major breakthrough, having developed a novel method of modifying the fatty acid synthase (FAS) enzyme so that it can create new products.

The enzyme normally synthesizes long chain fatty acids that had been modified to synthesize medium chain fatty acids and methyl ketones which are chemicals that are components in currently used transportation fuels said Zhiwei Zhu, post-doc and first author of the study. According to the study they are now able to produce petrol and jet fuel alternatives in yeast cell factories, and this has never been done before.

The important enzyme was first described by Nobel Prize winner Feodor Lynen, and many researchers have tried to modify it in recent years. But it seemed very hard, or close to

impossible until now. "We did not expect this. Actually, it was thought by the scientific community that this rigid enzyme was not readily amenable to manipulation," says Zhiwei Zhu.

The findings are in fact a result of a lucky break. A few years ago, the researchers occasionally found a fatty acid synthase which had two acyl carrier protein domains. They first tried to change this fatty acid synthase by replacing one of its acyl carrier protein domains with a foreign enzyme to modify its properties and, surprisingly, it worked. Then they implemented such modification in other fungal fatty acid synthesis and found this approach versatile.

The researchers are now focusing on using the modified enzyme to build yeast cell factories for production of chemicals and fuels from glucose. An invention patent has been applied for, and the company Biopetrolia, a spin-off from Chalmers University of Technology is closely involved in trying to further develop the technique to make it economically viable. But as a scientist, Zhiwei Zhu also has a long-term goal of his own that he is interested in deeply revealing the biochemical and structural basis of this novel modification in fungal fatty acid synthase.

**Source:** [www.sciencedaily.com](http://www.sciencedaily.com)

### Abstract of Recent Publications

**01. Food Science and Technology, 2017, Vol. 79, Pages: 52 – 59.**

**Compositional analysis of Scottish honeys with antimicrobial activity against antibiotic-resistant bacteria reveals novel antimicrobial components.**

Lorna Fyfe, Paulina Okoro, Euan Paterson, Shirley Coyle and Gordon J. McDougall.

*Dietetics, Nutrition and Biological Sciences, Queen Margaret University, Musselburgh, East Lothian, Scotland, EH21 6UU, United Kingdom.*

Antibiotic-resistant bacteria are a major health concern and honey may provide an alternative to antibiotic use under certain conditions. The antimicrobial action of six Scottish honeys and Manuka Medihoney® was compared against antibiotic-resistant *Acinetobacter calcoaceticus*, *Staphylococcus aureus*, *Pseudomonas aeruginosa* and *Escherichia coli*. Certain Scottish honeys, such as Highland and Portobello honey 2011, were comparable in effectiveness

to the established antimicrobial Medihoney®, inhibiting growth to <1 compared to 10 log<sub>10</sub> CFU/ml in the control. Heather honey was the next most active while Blossom honeys were less active. Bacteria were inhibited by a sugar-matched control, but to a lesser extent, indicating that antimicrobial activity was associated with non-sugar components, such as polyphenols. However, total phenol content or antioxidant capacity did not correlate with antimicrobial activity. Liquid chromatography-mass spectrometric analysis revealed that the composition of polyphenol and non-polyphenol components differed between honeys. In addition, candidate components that could be associated with antimicrobial activity were noted including novel fatty diacid glycoside derivatives not previously identified in honeys.

**Keywords:** Honeys; Antimicrobial; LC-MS; Polyphenols; Novel compounds.



**MARCH 03, 2017**



**World  
Forestry  
Day**  
**21<sup>st</sup> March**

**Plant More Trees! Save Wild Life!**

**WORLD FORESTRY DAY 21<sup>ST</sup> MARCH 2017**

**NATIONAL**

Microbial Genetic Resource Portal  
<http://www.mgrportal.org.in/microbialconservation.html>

Indian Institute of Horticultural Research  
<http://www.iihr.ernet.in/division-of-plant-pathology>

The National Culture Collection of Pathogenic Fungi  
<http://nccpf.com/main.php?id=5>

National Collection of Industrial Food and Marine Bacteria  
<http://www.ncimb.com/defaultinfo.aspx?page=about-ncimb>

**INTERNATIONAL**

Agricultural Biotechnology Research Institute of Iran Culture collection  
<http://www.abrii.ac.ir>

Culture Collection of Antimicrobial Resistant Microorganisms  
<http://www.knrrc.or.kr/english/rrc/rrc.jsp>

Iranian Research Institute of Plant Protection  
<http://web.iripp.ir/index.php/english/>

University of Santo Tomas Collection of Microbial Strains)  
<http://ustcms.webs.com>

**EVENTS**  
**Conferences / Seminars / Meetings 2017**

**Research Advances in Science & Technology.** May 26 - 27, 2017. **Venue:** Coimbatore, Tamil Nadu, **India.**  
**Website:** [http://www.hillgrovresearch.com/1\\_5\\_our-events.html](http://www.hillgrovresearch.com/1_5_our-events.html)

**ASM Microbe 2017.** June 01 - 05, 2017. **Venue:** New Orleans, **USA.** **Website:** <https://www.asm.org/index.php/asm-microbe-2017>

**Bioinformatics for Core Facility Managers.** June 06 - 08. **Venue:** Hinxton, Cambridge, **UK.**  
**Website:** <http://www.ebi.ac.uk/training/events/2017/bioinformatics-core-facility-managers>

**Plant Genome Editing and Genome Engineering.** July 03 - 04, 2017. **Venue:** Vienna, **Austria.**  
**Website:** <http://www.innovationsinagriculture.com/>

**Molecular Genetics of Bacteria and Phages Meeting.** August 07 - 11, 2017. **Venue:** Madison, **USA.**  
**Website:** <http://conferences.union.wisc.edu/phages/>

**Chennai: Sembakkam lake, a de facto dumping ground, to be restored**

Residents of Chitlapakkam have reason to cheer in the New Year. The Sembakkam lake, a source of water for the neighbourhood that is witnessing a real estate boom, will be restored soon.



Volunteers of Pratiks Enviro Solutions, who restored the Madipakkam lake after thousands of fish died in it, plan to restore the Sembakkam lake. "We will approach the government with a proposal. We are planning to treat the water and ensure that fish do not die due to the inflow of sewage," said Dakshayani S Dalavai, managing trustee of the organisation. "The municipality must stop dumping garbage into the lake. Green algae and water hyacinth have to be removed permanently from the water body," she said.

**Source:** The Times of India, January 04, 2017.

## Chennai Oil Spill - 2017



## World Environment Day Calendar - 2017

**Happy New Year**

**Environmental Information System  
India**

**GOVERNMENT OF TAMIL NADU**

**International Year of Sustainable Tourism For Development. 2017 Environment Calendar**

<b>World Wetlands Day</b>	<b>2 February</b>	<b>World Population Day</b>	<b>11 July</b>
<b>World Wildlife Day</b>	<b>3 March</b>	<b>International Tiger Day</b>	<b>29 July</b>
<b>World Forestry Day &amp; World Planting Day</b>	<b>21 March</b>	<b>World Elephant Day</b>	<b>12 August</b>
<b>World Water Day</b>	<b>22 March</b>	<b>International Day for preserving Ozone Layer</b>	<b>16 September</b>
<b>World Meteorological Day</b>	<b>23 March</b>	<b>World Rivers Day</b>	<b>24 September</b>
<b>World Health Day</b>	<b>7 April</b>	<b>World Animal Day</b>	<b>4 October</b>
<b>Earth Day</b>	<b>22 April</b>	<b>International Day for Natural Disaster Reduction</b>	<b>13 October</b>
<b>International Day of Biodiversity</b>	<b>22 May</b>	<b>International Day of Climate Action</b>	<b>10 October</b>
<b>World Environment Day</b>	<b>5 June</b>	<b>World Fisheries Day</b>	<b>21 November</b>
<b>World Oceans Day</b>	<b>8 June</b>	<b>World Soil Day</b>	<b>5 December</b>
<b>Global Wind Day</b>	<b>15 June</b>	<b>International Mountain Day</b>	<b>11 December</b>