



**HAL**  
open science

## Draft Genome Sequences of Three Airborne *Aspergilli* Series Versicolores

Antoine Géry, Virginie Séguin, Julie Bonhomme, David Garon

► **To cite this version:**

Antoine Géry, Virginie Séguin, Julie Bonhomme, David Garon. Draft Genome Sequences of Three Airborne *Aspergilli* Series Versicolores. *Mycobiology*, 2022, pp.1-3. 10.1080/12298093.2022.2028437 . hal-03589051

**HAL Id: hal-03589051**

**<https://hal.science/hal-03589051v1>**

Submitted on 4 Sep 2024

**HAL** is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.

## Draft Genome Sequences of Three Airborne *Aspergilli* Series *Versicolores*

Antoine Géry<sup>a</sup>, Virginie Séguin<sup>a</sup>, Julie Bonhomme<sup>b</sup> and David Garon<sup>a</sup> 

<sup>a</sup>Normandie Univ, Unicaen & Unirouen, ToxEMAC-ABTE, Centre F. Baclesse, Caen, France; <sup>b</sup>Microbiology Department, Caen University Hospital, Caen, France

### ABSTRACT

The *Aspergilli* of the section *Nidulantes* series *Versicolores* are among the most recurrent molds in indoor environments. These species cause damage to the quality of air. Indeed, they are responsible for allergies, aggravation of asthma and can even cause infections in immunocompromised patients. Molds belonging to the *Versicolores* series also produce sterigmatocystin, a mycotoxin classified as potential human carcinogen by the International Agency for Research on Cancer (group 2B). Here, we provide for the first time the genome of three species of the series *Versicolores*: *Aspergillus creber*, *Aspergillus jensenii* and *Aspergillus protuberus* which are the most abundant species of this series in bioaerosols. The genomes of these three species could be assembled with a percentage of completeness of 97.02%, 96.21% and 95.35% for *Aspergillus creber*, *A. jensenii* and *A. protuberus* respectively. These data will allow to study the genes and gene clusters responsible for the expression of virulence factors, the biosynthesis of mycotoxins and the proliferation of these ubiquitous and recurrent molds.

### ARTICLE HISTORY

Received 12 October 2021  
Revised 7 January 2022  
Accepted 9 January 2022

### KEYWORDS

*Aspergillus*; series  
*Versicolores*; genome

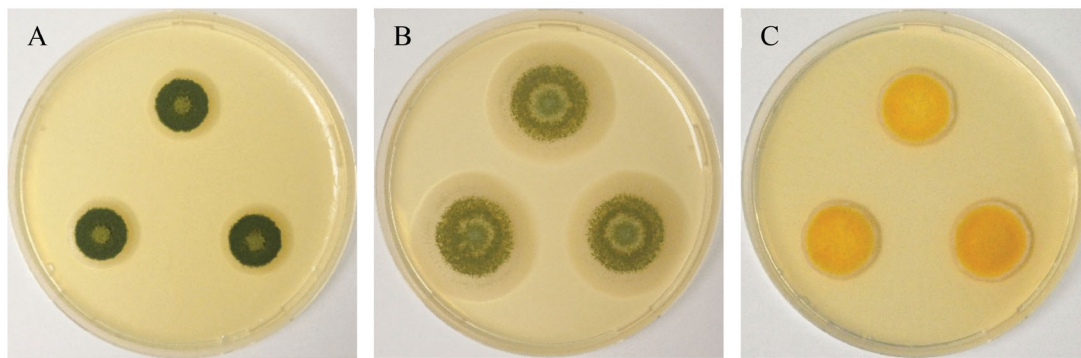
*Aspergillus creber* (Jurjević, S.W. Peterson & B.W. Horn), *A. jensenii* (Jurjević, S.W. Peterson & B.W. Horn) and *A. protuberus* (Munt.-Cvetk) are three airborne *Aspergilli* belonging to the section *Nidulantes* series *Versicolores* [1,2].

*Aspergillus creber* is considered to be the most abundant mold of the series *Versicolores* especially in damp indoor environments [3]. It is recurrently found in indoor air [4,5] but it has also been isolated from dust, soil, food (grape, cocoa powder, etc) and animal hair [1,6]. *A. jensenii* is also commonly found in indoor environment even though it is less recurrent than *A. creber* [3,5]. It has been isolated from indoor air samples, dust and food (pilled millet) [5,6]. *A. protuberus* is less recurrent than *A. creber* and *A. jensenii* [5] but remains quite frequently found in dust, indoor air and food (brined meat) [1,6]. These three species were also found in clinical samples (arm skin, bronchoalveolar lavage fluid, eye, nail, skin mucosa, sputum and in vaginal discharge) [7–9]. They are considered as cryptic species [10] that can be found in cases of onychomycosis (both *A. creber*, *A. jensenii* and *A. protuberus*) [8] and in endophthalmitis, keratitis, scalp mycosis and in vaginitis (*A. protuberus*) [9,11,12]. Although these species are opportunistic pathogens, they are also known to be involved in allergies [13], asthma aggravations [14] and may cause infections in

immunocompromised patients [15,16]. *A. creber*, *A. jensenii* and *A. protuberus* produce sterigmatocystin [3], a mycotoxin classified as a group 2B (potential human carcinogen) by IARC [17]. This is the first genome report for these three species.

Pure cultures of *Aspergillus creber* isolate HOSP050413\_5\_135 and *A. protuberus* isolate HOSP050413\_4\_129 were recovered from bioaerosols collected in April 2013 from the fifth and fourth floors of a cancer treatment center (Center François Baclesse, Caen), respectively (Figure 1(A,B)). Bioaerosols were collected using a cyclonic biocollector (Bertin Technologies, Montigny-le-Bretonneux, France) during 40 min at 300 L.min<sup>-1</sup>. Samples were cultured on Malt Extract Agar (MEA) medium supplemented with 0.02% chloramphenicol (Cooper, Melun, France). Plates were incubated at 25 °C and checked daily. Each isolate was purified on the same medium. Pure culture of *Aspergillus jensenii* isolate C4\_18042019 was recovered from the scalp of a patient at Caen University Hospital in April 2019 (Figure 1(C)) for which a mycological examination was prescribed. After inoculation on sabouraud dextrose agar with chloramphenicol and gentamicin (Bio-Rad, Marnes-la-Coquette, France), this isolate was also purified on MEA.

All isolates were molecularly characterized by the primer set Bt2a/b (Bt2a: 5' GGT AAC CAA ATC



**Figure 1.** Two weeks-old colonies on Malt Extract Agar, from left to right (A) *Aspergillus creber* (HOSP050413\_5\_135), (B) *Aspergillus protuberus* (HOSP050413\_4\_129) and (C) *Aspergillus jensenii* (C4\_18042019).

**Table 1.** Summary of the genome assembly and annotation of *Aspergillus creber* (HOSP050413\_5\_135), *Aspergillus jensenii* (20190418\_C4) and *A. protuberus* (HOSP050413\_4\_129).

	<i>Aspergillus creber</i>	<i>Aspergillus jensenii</i>	<i>Aspergillus protuberus</i>
150-bp reads	9.03 M	10.86 M	11.65 M
Total data	2.71 Gb	3.26 Gb	3.50 Gb
Total length (bp)	34,897,705	35,429,369	34,621,709
Scaffolds	142	318	94
≥ 1,000 bp in length			
Largest scaffold (bp)	2,910,608	2,727,923	1,977,967
Genome completeness	97.02%	96.21%	95.35%
Complete Universal Single-Copy Orthologs	1,661 out of 1,712	1,650 out of 1,715	1,641 out of 1,721
GC content	49.50%	49.78%	49.82%
Scaffold N50	973,106	1,102,984	1,006,248
Scaffold N90	425,640	400,436	364,644
Scaffold L50	12	11	12
Scaffold L90	32	38	35
Protein-encoding genes	12,066	12,258	12,090

GGT GCT GCT TTC 3' and Bt2b: 5' ACC CTC AGT GTA GTG ACC CTT GGC 3' (Eurogentec, Liège, Belgique)). Genomic DNA extracted using the Nucleospin™ Plant II kit (Macherey-Nagel, Duren, Germany) was then sequenced on an Illumina NovaSeq 6000 platform using 2 × 150 bp sequence mode. The raw reads were trimmed using Trimmomatic (version 0.38.0) [18]. Quality-passed reads were assembled using SPAdes pipeline (version 3.12.0) [19] de novo genome assembler with default options. Using BUSCO (Benchmarking Universal Single-Copy Orthologs) pipeline (version 5.2.2) with the Ascomycota odb10 lineage dataset, we estimated the completeness of our genomes [20]. Gene prediction was performed using Augustus (version 3.2.3) [21] using default options. Bandage Info (version 0.8.1) [22] and Quast (version 5.0.2) [23] were used to determine the statistics of de novo assembly graphs and to provide information on the quality of genome assembly, respectively. All data on the assembled genomes are shown in Table 1.

These genomic resources will allow comparative genomic analysis to be made among these three recurrent environmental molds and will increase the data available to study the molecular basis of pathogenicity and metabolites production in these organisms. The draft genome sequences of *A. creber*

HOSP050413\_5\_135, *A. jensenii* C4\_18042019 and *A. protuberus* HOSP050413\_4\_129 have been deposited in GenBank under the accession number JAJAEB000000000, JAJAED000000000 and JAJAEC000000000, BioProject number PRJNA768996, PRJNA769000 and PRJNA768998, BioSample number SAMN22074031, SAMN22074134 and SAMN22074035 respectively.

### Acknowledgments

ABTE-ToxEMAC is a member of the FHU (University Hospital Federation) RESPIRE: “Pathogènes, ENvironnement et Hôte: une approche intégrative en santé respiratoire”.

### Disclosure statement

No potential conflict of interest was reported by the authors.

### Funding

This work was supported by the EREM (Equipe de Recherche et d'Études en Mycologie), UFR Santé, Normandie Université, 14000 Caen - France.

### ORCID

David Garon  <http://orcid.org/0000-0003-3545-6641>

## References

- [1] Jurjevic Z, Peterson SW, Horn BW. *Aspergillus* section *versicolores*: nine new species and multilocus DNA sequence based phylogeny. *IMA Fungus*. 2012;3(1):59–79.
- [2] Houbraeken J, Kocsubé S, Visagie CM, et al. Classification of *Aspergillus*, *Penicillium*, *Talaromyces* and related genera (Eurotiales): an overview of families, genera, subgenera, sections, series and species. *Stud Mycol*. 2020;95:5–169.
- [3] Jakšić D, Sertić M, Kifer D, et al. Fungi and their secondary metabolites in water-damaged indoors after a major flood event in eastern Croatia. *Indoor Air*. 2021;31(3):730–744.
- [4] Jakšić Despot D, Šegvić Klarić M. A year-round investigation of indoor airborne fungi in Croatia. *Arh Hig Rada Toksikol*. 2014;65(2):209–218.
- [5] Géry A, Rioult J-P, Heutte N, et al. First characterization and description of *Aspergillus* series *versicolores* in French bioaerosols. *JoF*. 2021;7(8):676.
- [6] Kobayashi N, Kubosaki A, Takahashi Y, et al. Distribution of sterigmatocystin-producing *Aspergilli* in Japan. *Food Saf (Tokyo)*. 2018;6(2):67–73.
- [7] Tsang C-C, Hui TWS, Lee K-C, et al. Genetic diversity of *Aspergillus* species isolated from onychomycosis and *Aspergillus hongkongensis* sp. nov., with implications to antifungal susceptibility testing. *Diagn Microbiol Infect Dis*. 2016;84(2):125–134.
- [8] Siqueira JPZ, Sutton DA, García D, et al. Species diversity of *Aspergillus* section *Versicolores* in clinical samples and antifungal susceptibility. *Fungal Biol*. 2016;120(11):1458–1467.
- [9] Borsa BA, Özgün G, Houbraeken J, et al. The first case of persistent vaginitis due to *Aspergillus protuberus* in an immunocompetent patient. *Mikrobiyol Bul*. 2015;49(1):130–134.
- [10] Vidal-Acuña MR, Ruiz M, Torres MJ, et al. Prevalence and in vitro antifungal susceptibility of cryptic species of the genus *Aspergillus* isolated in clinical samples. *Enferm Infecc Microbiol Clin (Engl Ed)*. 2019;37(5):296–300.
- [11] Jia J, Chen M, Mo X, et al. The first case report of kerion-type scalp mycosis caused by *Aspergillus protuberus*. *BMC Infect Dis*. 2019;19(1):506.
- [12] Al-Hatmi AMS, Castro MA, de Hoog GS, et al. Epidemiology of *Aspergillus* species causing keratitis in Mexico. *Mycoses*. 2019;62(2):144–151.
- [13] Rick E, Woolnough K, Pashley C, et al. Allergic fungal airway disease. *J Investig Allergol Clin Immunol*. 2016;26(6):344–354.
- [14] Tiotiu AI, Novakova P, Nedeva D, et al. Impact of air pollution on asthma outcomes. *IJERPH*. 2020;17(17):6212.
- [15] Spellberg B, Edwards J, Ibrahim A. Novel perspectives on mucormycosis: pathophysiology, presentation, and management. *Clin Microbiol Rev*. 2005;18(3):556–569.
- [16] Gletsou E, Ioannou M, Liakopoulos V, et al. *Aspergillosis* in immunocompromised patients with haematological malignancies. *J BUON off J Balk Union Oncol*. 2018;23:7–10.
- [17] IARC monographs on the identification of carcinogenic hazards to humans. Available online: <https://monographs.iarc.who.int/>. (accessed on 10 September 2021).
- [18] Bolger AM, Lohse M, Usadel B. Trimmomatic: a flexible trimmer for illumina sequence data. *Bioinformatics*. 2014;30(15):2114–2120.
- [19] Bankevich A, Nurk S, Antipov D, et al. SPADIS: a new genome assembly algorithm and its applications to single-cell sequencing. *J Comput Biol*. 2012;19(5):455–477.
- [20] Seppey M, Manni M, Zdobnov EM. BUSCO: assessing genome assembly and annotation completeness. *Methods Mol Biol Clifton NJ*. 2019;1962:227–245.
- [21] Nachtweide S, Stanke M. Multi-genome annotation with AUGUSTUS. *Methods Mol Biol Clifton NJ*. 2019;1962:139–160.
- [22] Wick RR, Schultz MB, Zobel J, et al. Bandage: interactive visualization of de novo genome assemblies. *Bioinformatics*. 2015;31(20):3350–3352.
- [23] Mikheenko A, Prjibelski A, Saveliev V, et al. Versatile genome assembly evaluation with QUAST-LG. *Bioinformatics*. 2018;34(13):i142–50.