

**ADDITIONAL INFORMATION ON THE *B. CEPACIA* COMPLEX STRAINS INCLUDED  
IN THE UPDATED VERSION OF THE *B. CEPACIA* COMPLEX EXPERIMENTAL  
STRAIN PANEL**

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When using this information please refer to the following paper :

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*B. cepacia* genomovar VI

Four *B. cepacia* genomovar VI strains were included in the panel. Isolates AU0645 (LMG 18943) and CEP021 (LMG 21819) were isolated from CF patients in the USA, while E12 (LMG 21820) was isolated from a CF patient in the UK. AU0645 (LMG 18943) produced *N*-acyl-L-homoserine lactones and siderophores, and showed chitinase and lipase but no protease activity (6). The only quorum-sensing gene detected in isolates AU0645 was *cepR* (14). Isolate CEP021 (LMG 21819) can survive inside PU5-1.8 murine macrophages for at least 5 days without replication ; entry of CEP021 into the macrophages stimulated TNF- $\alpha$  production and primed the macrophages to release toxic oxygen radicals (22). It was also shown that CEP021 is able to survive within different isolates of the genus *Acanthamoeba* (15). STM 1441 (LMG 21443) was isolated from root nodules of the tropical legume *Alysicarpus glumaceus* in Senegal (25).

*B. ambifaria* (*B. cepacia* genomovar VII)

Three *B. ambifaria* strains were included in the panel. The type strain of *B. ambifaria*, AMMD<sup>T</sup> (LMG 19182<sup>T</sup>), was isolated from the rhizosphere of peas (*Pisum sativum* L.) grown in a *Aphanomyces* root rot nursery in Wisconsin (USA) in 1985. It is one of the most studied biocontrol isolates (2, 7, 8, 11, 18-20) and has activity against *Pythium aphanidermatum* (responsible for pre-

and post-emergence damping-off in peas) (18, 20) and *Aphanomyces euteiches* (responsible for root rot in peas) (11). Several mutants, including a rifampin-resistant mutant of *B. ambifaria* AMMD<sup>T</sup> (designated AMMDR1) and a Tn5 mutant that does not exhibit antibiosis against *Pythium* mycelial growth (designated 1324) have been constructed (7, 8). The genome of *B. ambifaria* AMMD<sup>T</sup> consists of three circular replicons of 3.4, 2.8 and 1.0 Mb (19). Isolate AMMD<sup>T</sup> contains the putative type III secretion gene cluster *bcscQ/bcscV* (21). *B. ambifaria* ATCC 53266 (LMG 17828) is another strain with possible biocontrol applications ; it was isolated from corn roots in Wisconsin (USA). ATCC 53266 is sensitive to the T-even-like phages NS1 and NS2 (17). Strain CEP0996 (LMG 19467) was isolated from the sputum of a CF patient in Australia (5). The quorum-sensing genes *cepI*, *cepR*, *bviI* and *bviR* could not be detected in strains AMMD<sup>T</sup>, ATCC 53266 and CEP0996 but *N*-octanoyl-L-homoserine lactone, *N*-hexanoyl-L-homoserine lactone and additional unidentified *N*-acyl-L-homoserine lactones are produced by these strains (14).

#### *B. anthina* (*B. cepacia* genomovar VIII)

Four *B. anthina* strains were included in the panel. The type strain W92<sup>T</sup> (LMG 20980<sup>T</sup>) was isolated from the rhizosphere of a houseplant in Nashville (USA) in 1997 (26), while strain C1765 (LMG 20983) was isolated from the respiratory tract of a CF patient in the UK. J2552 (LMG 16670) was isolated from the rhizosphere of *Carludaucas palmata* in the tropical aquatic house of a botanic garden in the UK (3). Isolate AU1293 (LMG 21821) was isolated from the respiratory tract of a CF patient in the US ; this patient has been chronically infected with this organism for over two years (JLL, unpublished data). Isolates W92<sup>T</sup> and J2552 produce *N*-acyl-L-homoserine lactones and show lipase activity ; they do not show protease or chitinase activity and do not produce siderophores (6).

#### *B. pyrrocinia* (*B. cepacia* genomovar IX)

Four *B. pyrrocinia* isolates were included in this panel. The type strain ATCC 15958<sup>T</sup> (LMG 14191<sup>T</sup>) was isolated from soil and produces the antifungal antibiotic pyrrolnitrin (9). Several enzymes have been isolated from this strain, including a 154 kDa bromoperoxidase with a ferriprotoporphyrin IX prosthetic group (showing brominating as well as peroxidase and catalase activity) (27) and a 64 kDa non-heme chloroperoxidase requiring the presence of H<sub>2</sub>O<sub>2</sub> and involved in pyrrolnitrin biosynthesis (28, 29). *B. pyrrocinia* ATCC 39277 (LMG 21822) was isolated from cornfield soil in New Jersey (USA). This strain produces a complex of antifungal peptides, referred to as xylocandin, some of which displayed potent anticandidal and antidermatophytic activities in vitro (1, 16). Isolate BC011 (LMG 21823) was isolated from a blackwater stream (water system with a low content of suspended sediments but high concentration of dissolved organic matter) in South-Carolina (USA) (12, 31). Isolate C1469 (LMG 21824) was isolated from a CF patient attending a treatment center in Manchester (UK).

*Additional information on B. cepacia complex strains included in the first experimental strain panel*

The first experimental strain panel was published in February 2000 and has widely been used to investigate various aspects of the biology of *B. cepacia* complex organisms. Due to its wide use, considerable additional information on strains belonging to this panel is now available. All members of the previously described panel, except the *B. cepacia* genomovar I strains and *B. multivorans* 249-2 contain the putative type III secretion gene cluster *bcscQ/bcscV* (21). All *B. cepacia* genomovar III strains included in the first panel (except C5424 which was not investigated) and the two *B. vietnamiensis* isolates investigated (FC441 and LMG 16232) were sensitive to the T-even like phage NS2 ; isolates PC184, CEP511 and LMG 16232 were also sensitive to the T-even like phage NS1 (17). Interspecies biofilms with *P. aeruginosa* were observed for all strains studied (*B. cepacia* genomovar I CEP0509, *B. multivorans* ATCC 17616, *B. cepacia* genomovar III K56-2, *B. stabilis* LMG 14086 and *B. vietnamiensis* LMG 16232) (24). *B. cepacia* genomovar III isolates CEP0511, C5424, J2315, C6433, PC184, J415 and BC7 expressed a 96 to 100 kDa heme-binding

protein located in the outer membrane (23). The genome size for several members of the first panel have also been published (13, 19), including *B. cepacia* genomovar I ATCC 25416<sup>T</sup> (7.7 Mb) and ATCC 17759 (7.9 Mb), *B. multivorans* C5393 (5.7 Mb) and LMG 13010<sup>T</sup> (6.9 Mb), *B. cepacia* genomovar III J2315 (7.6 Mb), C5424 (7.4 Mb), C6433 (7.8 Mb) and J415 (7.3 Mb), *B. stabilis* LMG 14294<sup>T</sup> (8.2 Mb), and *B. vietnamiensis* PC259 (6.7 Mb), FC441 (6.0 Mb) and LMG 10929<sup>T</sup> (7.6 Mb). Additional characteristics investigated for most or all of the strains included in the first panel include the presence of quorum-sensing genes (14), production of protease, chitinase, lipase and siderophores (6), presence of type I or type II flagellin genes (30) and the level of epithelial cell invasion in an in vitro assay using A549 cells (4, 10).

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**Tom Coenye\***

**Peter Vandamme**

Laboratorium voor Microbiologie, Ghent University, K. L. Ledganckstraat 35, B-9000 Ghent,  
Belgium

**John J. LiPuma**

Department of Pediatrics and Communicable Diseases, University of Michigan, Ann Arbor, MI,  
USA

**John R.W. Govan**

Department of Medical Microbiology, University of Edinburgh, Edinburgh, UK

**Eshwar Mahenthiralingam**

School of Biosciences, Cardiff University, Cardiff, UK

\* Phone : +32 9 264 51 14

Fax : +32 9 264 50 92

E-mail : Tom.Coenye@rug.ac.be