

Genus Ochrobactrum

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Ochrobactrum spp. are found in a wide range of environments including soils and water. They are non-enteric, Gram-negative organisms that are closely related to the genus *Brucella*. Several species of this genus have now been characterised and implicated as opportunistic pathogens in multiple outbreaks. This entry gives a brief overview of the Genus *Ochrobactrum*.

Keywords: Genus *Ochrobactrum* ; pathogens ; environmental bacteria

1. Introduction

Gram-negative, non-fermenting bacteria are an emergent worry in medical situations and are becoming a growing cause of severe infections. Pathogens of this type are opportunistic and include many different bacterial species, such as *Ralstonia* spp., *Pseudomonas aeruginosa*, *Sphingomonas paucimobilis* and *Brevundimonas* spp. [1][2][3][4][5]. Gram-negative, non-fermenting bacteria can infect both patients undergoing treatments and individuals outside of a clinical setting with various underlying conditions or diseases. Another type of these bacteria are the members of the α -proteobacterial genus *Ochrobactrum* [6].

Ochrobactrum spp. are found in a wide variety of environments including water, aircraft water, soil, plants and animals [6][7][8][9][10][11][12]. Several *Ochrobactrum* spp. have been investigated for their potential to degrade xenobiotic pollutants and for heavy metal detoxification under a variety of environmental conditions [13][14][15][16]. *Ochrobactrum* spp. are very closely related to brucellae, and even though they are considered to be of low virulence, they have increasingly been found to cause infections (some serious including endocarditis and septicaemia) in immunocompetent hosts [17][18].

Investigation of the scientific/medical literature presented a wide variety of infections resultant from *Ochrobactrum* spp. and these were resistant to wide variety of antibiotics. Our data point to the genus being a more common pathogen than previously supposed, with many of the infections/conditions caused by *Ochrobactrum* spp. being aggressive and debilitating.

2. Genus Ochrobactrum

The genus *Ochrobactrum* emerged from what was previously categorised as the CDC group VD1-2. The type species *Ochrobactrum anthropi* had previously been called *Achromobacter* VD based on the Special Bacteriology Section of the US Center for Disease Control [19]. Initial results indicate members of the group grew on MacConkey agar producing catalase, oxidase and urease; strains could be Gram-negative to variable [20]. However, the taxonomic position of *Achromobacter* became complicated and the name *Achromobacter* and related CDC group VD were no longer accepted by Bergeys Manual [19] leading to a new classification and the emergence of the genus *Ochrobactrum* [21]. *Ochrobactrum* spp. are phylogenetically related to members of the alpha-2 subdivision of *Proteobacteria*. They are catalogued on the *Brucella* rRNA branch of rRNA superfamily IV. Thus, from the previous CDC group Vd, a novel genus and a new species, *Ochrobactrum anthropi*, was proposed [21][22]. The type strain was Gram-negative, aerobic, rod shaped, non-pigmented and motile. It produced acid from a selection of carbohydrates and reduced both nitrate and nitrite and possessed a GC ratio between 56 to 59% [21]. Almost all 56 strains categorised as CDC GroupVD that were used to support the new genus *Ochrobactrum* came from various human clinical specimens. Since the initial description of *O. anthropi*, several other species have since been described (Table 1 and Figure 1). Certain *Ochrobactrum* spp. can be opportunistic pathogens especially in a hospital environment with the majority of reported cases due to hospital-acquired infections in patients with indwelling and invasive medical devices, including central venous catheters and drainage tubes [23]. In addition, the organism shows widespread resistance to penicillins and other antibiotics that cause clinical management issues with immunocompromised hosts [24][25]. The phylogenetic relationship between all described *Ochrobactrum* spp can be seen in Figure 1.

Table 1. List of current accepted *Ochrobactrum* species.

Species	Isolation	Genome Sequences	Reference
<i>Ochrobactrum anthropi</i>	Clinical isolate	Strain: OAB; Size: 4.9 Mbp; Ref Genome: GCA_000742955.1 (41 genomes)	[22]
<i>Ochrobactrum ciceri</i>	Nodules of Cicer	No Genome	[26]
<i>Ochrobactrum cytisi</i>	Cystisus nodules	Strain: IPA7.2; Size: 5.96 Mbp; Ref Genome: GCA_001876955.1 (1 genome)	[27]
<i>Ochrobactrum daejeonense</i>	Sludge	Strain: JCM 16234;; Size: 4.8 Mbp, Ref Genome: GCA_012103095.1 (1 genome)	[28]
<i>Ochrobactrum endophyticum</i>	Roots of <i>Glycyrrhiza</i>	No Genome	[29]
<i>Ochrobactrum gallinifaecis</i>	Chicken faeces	Strain: ISO196; Ref Genome: GCF_006476605.1; Size: 3.74 Mbp (1 genome)	[11]
<i>Ochrobactrum grignonense</i>	Wheat Roots	Strain: OgA9a; Size: 4.84 Mbp; Ref Genome: NZ_NNRL00000000.1 (1 genome)	[9]
<i>Ochrobactrum haematophilum</i>	Clinical Isolate	Strain: LISuc1; Size: 4.91 Mbp; Ref Genome: GCA_003550135.1 (3 genomes)	[30]
<i>Ochrobactrum intermedium</i>	Human blood	Strain: NCTC12171; Size: 4.73 Mbp; Ref Genome: GCA_900454225.1 (18 genomes)	[22]
<i>Ochrobactrum lupini</i>	<u>Lupinus albus</u> rhizosphere	Strain: LUP21; Size: 5.5 Mbp; Ref Genome: GCA_002252535.1 (2 genomes)	[31][32] *
<i>Ochrobactrum oryzae</i>	Rice rhizosphere	Strain: OA447; Size: 4.47 Mbp; Ref Genome: NZ_PTRC00000000.1 (1 genome)	[33]
<i>Ochrobactrum pecoris</i>	Farm Animals	Strain: 08RB2639; Size: 5.06 Mbp; Ref Genome: GCA_006376675.1 (1 genome)	[34]
<i>Ochrobactrum pituitosum</i>	Industrial Environment	Strain: AA2 Size: 5.47 Mbp; Ref Genome: GCA_002025625.1 (4 genomes)	[35]
<i>Ochrobactrum pseudintermedium</i>	Clinical isolate	Strain: CCUG34735; Size: 4.39 Mbp; Ref Genome: GCA_008932435.1 (1 genome)	[36]
<i>Ochrobactrum pseudogrignonense</i>	Clinical isolate	Strain: K8; Size: 4.99 Mbp; Ref Genome: GCA_001652485.1 (6 genomes)	[30]
<i>Ochrobactrum quorumnogens</i>	Potato rhizosphere	Strain: A44; Size: 5.5 Mbp; Ref Genome: GCA_002278035.1 (2 genomes)	[37]

<i>Ochrobactrum rhizosphaerae</i>	Potato rhizosphere	Strain: PR17; Size: 4.9 Mbp; Ref Genome: GCF_002252475.1 (2 genomes)	[38]
<i>Ochrobactrum soli</i>	Cattle farm soil	Strain: BO-7; Size: 45 Mbp; Ref Genome: GCA_003664555.1 (3 genomes)	[39]
<i>Ochrobactrum thiophenivorans</i>	Industrial Environment	Strain: DSM 7216; Size: 4.4 Mbp; Ref Genome: GCA_002252445.1 (2 genomes)	[38]
<i>Ochrobactrum teleogrylli</i>	insect <i>Teleogryllus occipitalis</i>	No Genome	[40]
<i>Ochrobactrum tritici</i>	wheat rhizosphere root soil	Strain: DSM 13340; Size: 5.5 Mbp; Ref Genome: GCA_012395245.1 (6 genomes)	[9]

* First described as *Ochrobactrum lupini* by Trujillo et al. [31] and later reclassified as *Ochrobactrum anthropi* by Volpiano et al. [32] following whole-genome sequence analysis.

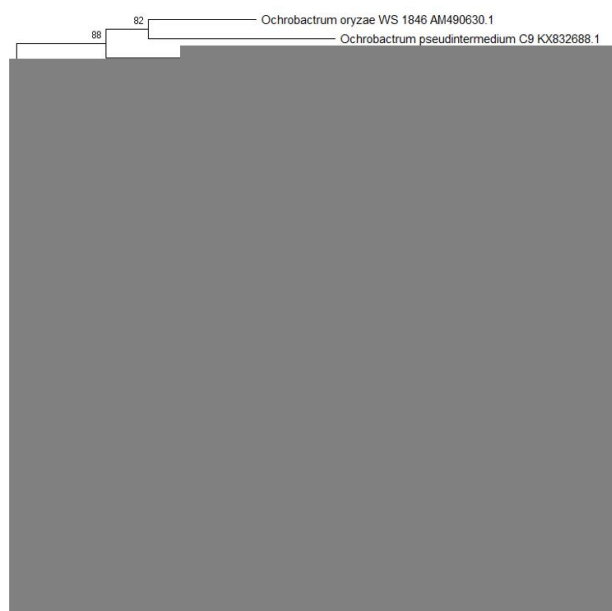


Figure 1. Phylogenetic structure of the genus *Ochrobactrum* along with the genus *Brucella*. (a) The tree based on partial 16S rRNA gene sequences obtained using neighbour joining with Maximum Composite Likelihood method (MEGA package). GenBank accession numbers are given with the species name. Numbers at nodes are bootstrap values based on 1000 resamplings. Bar, 0.0050 substitutions per site [41][42].

References

1. Ryan, M.P.; Adley, C.C. *Ralstonia*: Emerging global opportunistic pathogens. *Eur. J. Clin. Microbiol. Infect. Dis.* 2014, 33, 291–304.
2. Ryan, M.P.; Pembroke, J.T.; Adley, C.C. *Ralstonia pickettii*: A persistent Gram-negative nosocomial infectious organism. *J. Hosp. Infect.* 2006, 62, 278–284.
3. Ryan, M.P.; Adley, C.C. *Sphingomonas paucimobilis*: A persistent Gram-negative nosocomial infectious organism. *Hosp. Infect.* 2010, 75, 153–157.
4. Coughlan, A.; Ryan, M.P.; Cummins, N.M.; Towler, M.R. The response of *Pseudomonas aeruginosa* biofilm to the presence of a glass polyalkenoate cement formulated from a silver containing glass. *Mater. Sci.* 2011, 46, 285–287.
5. Ryan, M.P.; Pembroke, J.T. *Brevundimonas* spp: Emerging global opportunistic pathogens. *Virulence* 2018, 9, 480–493.
6. Jelveh, N.; Cunha, B.A. *Ochrobactrum anthropi* Hear. *Lung J. Acute Crit. Care* 1999, 28, 145–146.

7. Handschuh, H.; Ryan, M.P.; O'Dwyer, J.; Adley, C.C. Assessment of the bacterial diversity of aircraft water: Identification of the frequent fliers. *PLoS ONE* 2017, 12, e0170567.
8. Möller, L.V.M.; Arends, J.P.; Harmsen, H.J.M.; Talens, A.; Terpstra, P.; Slooff, M.J.H. *Ochrobactrum intermedium* infection after liver transplantation. *Clin. Microbiol.* 1999, 37, 241–244.
9. Lebuhn, M.; Achouak, W.; Schlöter, M.; Berge, O.; Meier, H.; Barakat, M.; Hartmann, A.; Heulin, T. Taxonomic characterization of *Ochrobactrum* isolates from soil samples and wheat roots, and description of *Ochrobactrum tritici* sp. nov. and *Ochrobactrum grignonense* sp. nov. *Int. J. Syst. Evol. Microbiol.* 2000, 50, 2207–2223.
10. Goris, J.; Boon, N.; Lebbe, L.; Verstraete, W.; De Vos, P. Diversity of activated sludge bacteria receiving the 3-chloroaniline-degradative plasmid pC1gfp. *FEMS Microbiol. Ecol.* 2003, 46, 221–230.
11. Kämpfer, P.; Buczolits, S.; Albrecht, A.; Busse, H.J.; Stackebrandt, E. Towards a standardized format for the description of a novel species (of an established genus): *Ochrobactrum gallinifaecis* nov. *Int. J. Syst. Evol. Microbiol.* 2003, 53, 893–896.
12. Bathe, S.; Achouak, W.; Hartmann, A.; Heulin, T.; Schlöter, M.; Lebuhn, M. Genetic and phenotypic microdiversity of *Ochrobactrum* FEMS Microbiol. Ecol. 2006, 56, 272–280.
13. El-Sayed, W.S.; Ibrahim, M.K.; Abu-Shady, M.; El-Beih, F.; Ohmura, N.; Saiki, H.; Ando, A. Isolation and Identification of a Novel Strain of the Genus *Ochrobactrum* with Phenol-Degrading Activity. *J. Biosci. Bioeng.* 2003, 96, 310–312.
14. Sultan, S.; Hasnain, S. Reduction of toxic hexavalent chromium by *Ochrobactrum intermedium* strain SDCr-5 stimulated by heavy metals. *Technol.* 2007, 98, 340–344.
15. Wu, Y.; He, T.; Zhong, M.; Zhang, Y.; Li, E.; Huang, T.; Hu, Z. Isolation of marine benzo[a]pyrene-degrading *Ochrobactrum* BAP5 and proteins characterization. *J. Environ. Sci.* 2009, 21, 1446–1451.
16. Zhang, X.H.; Zhang, G.S.; Zhang, Z.H.; Xu, J.H.; Li, S.P. Isolation and characterization of a dichlorvos-degrading strain DDV-1 of *Ochrobactrum* Pedosphere 2006, 16, 64–71.
17. Kettaneh, A.; Weill, F.X.; Poilane, I.; Fain, O.; Thomas, M.; Herrmann, J.L.; Hocqueloux, L. Septic shock caused by *Ochrobactrum anthropi* in an otherwise healthy host. *Clin. Microbiol.* 2003, 41, 1339–1341.
18. Ozdemir, D.; Soypacaci, Z.; Sahin, I.; Bicik, Z.; Sencan, I. *Ochrobactrum anthropi* endocarditis and septic shock in a patient with no prosthetic valve or rheumatic heart disease: Case report and review of the literature. *J. Infect. Dis.* 2006, 59, 264–265.
19. Chester, B.; Cooper, L.H. *Achromobacter* species (CDC group Vd): Morphological and biochemical characterization. *Clin. Microbiol.* 1979, 9, 425–436.
20. Barson, W.J.; Cromer, B.A.; Marcon, M.J. Puncture wound osteochondritis of the foot caused by CDC group Vd. *Clin. Microbiol.* 1987, 25, 2014–2016.
21. Holmes, B.; Popoff, M.; Kiredjian, M.; Kersters, K. *Ochrobactrum anthropi* nov., sp. nov. from human clinical specimens and previously known as group Vd. *Int. J. Syst. Bacteriol.* 1988, 38, 406–416.
22. Velasco, J.; Romero, C.; López-Goñi, I.; Leiva, J.; Díaz, R.; Moriyón, I. Evaluation of the relatedness of *Brucella* spp. and *Ochrobactrum anthropi* and description of *Ochrobactrum intermedium* nov., a new species with a closer relationship to *Brucella* spp. *Int. J. Syst. Bacteriol.* 1998, 48, 759–768.
23. Rastogi, N.; Mathur, P. *Ochrobactrum anthropi*: An emerging pathogen causing meningitis with sepsis in a neurotrauma patient. *Infect. Dev. Ctries.* 2017, 11, 733–735.
24. Nadjar, D.; Labia, R.; Cerceau, C.; Bizet, C.; Philippon, A.; Arlet, G. Molecular characterization of chromosomal class C β -lactamase and its regulatory gene in *Ochrobactrum anthropi*. *Agents Chemother.* 2001, 45, 2324–2330.
25. Soloaga, R.; Carrion, N.; Pidone, J.; Guelfand, L.; Margari, A.; Altieri, R. Bacteremia relacionada a cateter por *Ochrobactrum anthropi*. *Medicina (Buenos Aires)* 2009, 69, 655–657.
26. Imran, A.; Hafeez, F.Y.; Frühling, A.; Schumann, P.; Malik, K.A.; Stackebrandt, E. *Ochrobactrum ciceri* nov., isolated from nodules of *Cicer arietinum*. *Int. J. Syst. Evol. Microbiol.* 2010, 60, 1548–1553.
27. Zurdo-Piñeiro, J.L.; Rivas, R.; Trujillo, M.E.; Vizcaíno, N.; Carrasco, J.A.; Chamber, M.; Palomares, A.; Mateos, P.F.; Martínez-Molina, E.; Velázquez, E. *Ochrobactrum cytisi* nov., isolated from nodules of *Cytisus scoparius* in Spain. *Int. J. Syst. Evol. Microbiol.* 2007, 57, 784–788.
28. Woo, S.G.; Ten, L.N.; Park, J.; Lee, M. *Ochrobactrum daejeonense* nov., a nitrate-reducing bacterium isolated from sludge of a leachate treatment plant. *Int. J. Syst. Evol. Microbiol.* 2011, 61, 690–696.
29. Li, L.; Li, Y.Q.; Jiang, Z.; Gao, R.; Nimaichand, S.; Duan, Y.Q.; Egamberdieva, D.; Chen, W.; Li, W.J. *Ochrobactrum endophyticum* nov., isolated from roots of *Glycyrrhiza uralensis*. *Arch. Microbiol.* 2016, 198, 171–179.

30. Kämpfer, P.; Scholz, H.C.; Huber, B.; Falsen, E.; Busse, H.J. *Ochrobactrum haematophilum* nov. and *Ochrobactrum pseudogrignonense* sp. nov., isolated from human clinical specimens. *Int. J. Syst. Evol. Microbiol.* 2007, 57, 2513–2518.
31. Trujillo, M.E.; Willems, A.; Abril, A.; Planchuelo, A.M.; Rivas, R.; Ludeña, D.; Mateos, P.F.; Martínez-Molina, E.; Velázquez, E. Nodulation of *Lupinus albus* by Strains of *Ochrobactrum lupini* nov. *Appl. Environ. Microbiol.* 2005, 71, 1318–1327.
32. Volpiano, C.G.; Sant'anna, F.H.; Ambrosini, A.; Lisboa, B.B.; Vargas, L.K.; Passaglia, L.M.P. Reclassification of *Ochrobactrum lupini* as a later heterotypic synonym of *Ochrobactrum anthropi* based on whole-genome sequence analysis. *J. Syst. Evol. Microbiol.* 2019, 69, 2312–2314.
33. Tripathi, A.K.; Verma, S.C.; Chowdhury, S.P.; Lebuhn, M.; Gättinger, A.; Schlöter, M. *Ochrobactrum oryzae* nov., an endophytic bacterial species isolated from deep-water rice in India. *Int. J. Syst. Evol. Microbiol.* 2006, 56, 1677–1680.
34. Kämpfer, P.; Huber, B.; Busse, H.J.; Scholz, H.C.; Tomaso, H.; Hotzel, H.; Melzer, F. *Ochrobactrum pecoris* nov., isolated from farm animals. *Int. J. Syst. Evol. Microbiol.* 2011, 61, 2278–2283.
35. Huber, B.; Scholz, H.C.; Kämpfer, P.; Falsen, E.; Langer, S.; Busse, H.J. *Ochrobactrum pituitosum* nov., isolated from an industrial environment. *Int. J. Syst. Evol. Microbiol.* 2010, 60, 321–326.
36. Teyssier, C.; Marchandin, H.; Jean-Pierre, H.; Masnou, A.; Dusart, G.; Jumas-Bilak, E. *Ochrobactrum pseudintermedium* nov., a novel member of the family Brucellaceae, isolated from human clinical samples. *Int. J. Syst. Evol. Microbiol.* 2007, 57, 1007–1013.
37. Krzyżanowska, D.M.; Maciąg, T.; Ossowicki, A.; Rajewska, M.; Kaczyński, Z.; Czerwicka, M.; Rąbalski, Ł.; Czaplewska, P.; Jafra, S. *Ochrobactrum quorumnocens* Nov., a quorum quenching bacterium from the potato rhizosphere, and comparative genome analysis with related type strains. *PLoS ONE* 2019, 14, e0210874.
38. Kämpfer, P.; Sessitsch, A.; Schlöter, M.; Huber, B.; Busse, H.J.; Scholz, H.C. *Ochrobactrum rhizosphaerae* nov. and *Ochrobactrum thiophenivorans* sp. nov., isolated from the environment. *Int. J. Syst. Evol. Microbiol.* 2008, 58, 1426–1431.
39. Choi, G.M.; Kim, K.M.; Yun, C.S.; Lee, S.Y.; Kim, S.Y.; Wee, J.H.; Im, W.T. *Ochrobactrum soli* nov., Isolated from a Korean cattle farm. *Curr. Microbiol.* 2020, 77, 1104–1110.
40. Hu, M.; Li, X.; Li, Z.; Liu, B.; Yang, Z.; Tian, Y. *Ochrobactrum teleogrylli* nov., a pesticide-degrading bacterium isolated from the insect *Teleogryllus occipitalis* living in deserted cropland. *Int. J. Syst. Evol. Microbiol.* 2020, 70, 2217–2225.
41. Kumar, S.; Stecher, G.; Li, M.; Knyaz, C.; Tamura, K. MEGA X: Molecular Evolutionary Genetics Analysis across computing platforms. *Biol. Evol.* 2018, 35, 1547–1549.
42. Ryan, M.P.; Adley, C.C.; Pembroke, J.T. The use of MEGA as an educational tool for examining the phylogeny of antibiotic resistance genes. In *Microbial Pathogens and Strategies for Combating Them: Science, Technology and Education*, Méndez-Vilas, A., Ed.; Formatex: Badajoz, Spain, 2013; Volume 4 pp. 736–743.

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