genomeA
Journals.ASM.org

# Draft Genome Sequence of *Pasteurella multocida* subsp. *multocida* B:2 Strain VTCCBAA264 Isolated from *Bubalus bubalis* in North India

**R. K. Vaid,[a] K. Shanmugasundaram,[a] Ashok Boora,[b] B. C. Bera,[a] B. N. Shukla,[a] Taruna Anand,[a] Harisankar Singha,[c] Thachamvally Riyesh,[a] N. Virmani,[c] S. Barua,[a] V. B. Ahir,[d] P. G. Koringa,[d] M. R. Sajnani,[d] Vaibhav D. Bhat,[d] N. Rana,[b] K. P. Singh,[b] P. Malik,[a] R. K. Singh,[a,c] C. G. Joshi[d]**

Veterinary Type Culture Collection, National Research Centre on Equines, Hisar, Haryana, India[a]; Central Institute for Research on Buffalo, Hisar, Haryana, India[b]; National Research Centre on Equines, Hisar, Haryana, India[c]; Department of Animal Biotechnology, College of Veterinary Science and Animal Husbandry, Anand Agricultural University, Anand, Gujarat, India[d]

**The *Pasteurella multocida* subsp. *multocida* B:2 serotype causes hemorrhagic septicemia in bubalines with high morbidity and mortality in the Indian subcontinent. We report the draft genome sequence of *Pasteurella multocida* strain VTCCBAA264 isolated from the small-intestine of a buffalo calf that died of high fever.**

**Received** 7 July 2014 **Accepted** 16 July 2014 **Published** 31 July 2014

**Citation** Vaid RK, Shanmugasundaram K, Boora A, Bera BC, Shukla BN, Anand T, Singha H, Riyesh T, Virmani N, Barua S, Ahir VB, Koringa PG, Sajnani MR, Bhat VD, Rana N, Singh KP, Malik P, Singh RK, Joshi CG. 2014. Draft genome sequence of *Pasteurella multocida* subsp. *multocida* B:2 strain VTCCBAA264 isolated from *Bubalus bubalis* in north India. Genome Announc. 2(4):e00755-14. doi:10.1128/genomeA.00755-14.



Address correspondence to R. K. Vaid, rk_vaid@yahoo.com.

North India is the cradle of high milk-yielding buffalo breeds which routinely suffer from haemorhhagic septicemia (HS), which has been estimated to cause huge economic losses (1). *Pasteurella multocida* subsp. *multocida*, normally an upper respiratory tract commensal, is responsible for HS outbreaks, which mostly occur in hot humid weather, indicating failure of immunity after vaccination or otherwise. The Asian serotype B:2 is mainly responsible for the disease in domestic ruminants (2). Although many of the molecular determinants for virulence of *P. multocida* are now identified, the pathogenesis of HS is still not well understood (3). The sequencing of this *P. multocida* strain VTCCBAA264, isolated from a buffalo calf, will be useful because of the wealth of its molecular clues.

This is the first whole-genome sequence of *Pasteurella multocida* isolate from north India. Strain VTCCBAA264, a B:2 serotype, was isolated from the morbid intestinal content of a buffalo (*Bubalus bubalis*) calf which died of high fever and respiratory distress on an organized buffalo dairy farm (4).

The genome sequencing was achieved by 454 pyrosequencing of a shotgun library. The sequence was assembled *de novo* using Newbler v2.6. A total of 123,415 reads were generated using the GS FLX Titanium system, giving ~23× coverage of the genome. The data generated 78 contigs ranging in size from 710 to 319,560 bp, with a total size of 2,280,332 bp, an $N_{50}$ of 65,447 bp, and a Q40 of 99.65%. Annotation was carried out against strain Pm70 using the RAST server (5). The VTCCBAA264 strain showed a G+C content of 40.4% with 2,176 predicted genes, out of which there were 2,127 protein-encoding genes, 4 coded rRNAs, and 45 encoded tRNAs. Among the 2,127 coding sequences (CDSs), 2,074 (97.5%) were assigned to functional clusters of orthologous groups (COGs), 1,863 (87.6%) were assigned to FIGfams (fellowship for interpretation of genome families) and 1,527 (71.8%) to KEGG (Kyoto encyclopedia of genes and genomes). One clustered regularly interspaced short palindromic repeats (CRISPRs) array was also detected.

The cumulative sequence length of our genome compares favorably with the 2 other draft genome sequences of buffalo isolates of *P. multocida* B:2 serotype strains currently available, those for Anand1_buffalo (GenBank accession no. ALBY0100000000) and PMTB (AWTD01000000).

SEED subsystem analysis revealed various genes involved in a number of pathways (6). Noteworthy are the genes for antimicrobial resistance including translation elongation factor, DNA gyrase subunit A, topoisomerse IV subunit B, and DNA directed RNA polymerase $\beta$-subunit, among others. Genes for resistance to flouroquinolones and negative regulators of beta-lactamase expression were reported.

Copper is critical in the pathogenesis of bacterial pathogens (7). Analysis revealed copper-translocating chaperone, and copper homeostasis protein genes. The iron acquisition and hemin-transport system genes in this strain underlines its virulence potential. The genome also contained 45 phage related proteins. This whole-genome sequence and its functional analyses will be useful for realizing a universal vaccine for the prevention of HS.

**Nucleotide sequence accession numbers.** This whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession no. ALYC00000000. The version described in this paper is version ALYC02000000.

## ACKNOWLEDGMENT

This work was supported by Veterinary Type Culture Collection grant IXX00269, from the Indian Council of Agricultural Research, National Research Centre on Equines, Hisar.

## REFERENCES

1. **Venkataramanan R, Bandyopadhyay SK, Oberoi MS.** 2005. Present status and strategies for the control of transboundary and other economically

important animal diseases in India: a review. Indian J. Anim. Sci. **75:** 456–464.
2. **Ataei S, Burchmore R, Hodgson JC, Finucane A, Parton R, Coote JG.** 2009. Identification of immunogenic proteins associated with protection against haemorrhagic septicaemia after vaccination of calves with a live-attenuated *aro*A derivative of *Pasteurella multocida* B:2. Res. Vet. Sci. **87:** 207–210. http://dx.doi.org/10.1016/j.rvsc.2009.01.007.
3. **Wilkie IW, Harper M, Boyce JD, Adler B.** 2012. *Pasteurella multocida*: diseases and pathogenesis. Curr. Top. Microbiol. Immunol. **361:** 1–22.
4. **Vaid RK, Shanamugasundaram K, Boora A, Riyesh T, Bera BC, Shukla BN, Anand T, Virmani N, Barua S, Rana N, Singh KP, Malik P, Singh RK.** 2012. Sporadic outbreak of haemorrhagic septicaemia in buffalo calves in an organized farm. Vet. Pract. **13:**326–329.
5. **Aziz RK, Bartels D, Best AA, DeJongh M, Disz T, Edwards RA, Formsma K, Gerdes S, Glass EM, Kubal M, Meyer F, Olsen GJ, Olson R, Osterman AL, Overbeek RA, McNeil LK, Paarmann D, Paczian T, Parrello B, Pusch GD, Reich C, Stevens R, Vassieva O, Vonstein V, Wilke A, Zagnitko O.** 2008. The RAST server: Rapid Annotations using Subsystems Technology. BMC Genomics **9:**75. http://dx.doi.org/10.1186/1471-2164-9-75.
6. **Overbeek R, Olson R, Pusch GD, Olsen GJ, Davis JJ, Disz T, Edwards RA, Gerdes S, Parrello B, Shukla M, Vonstein V, Wattam AR, Xia F, Stevens R.** 2014. The SEED and the Rapid Annotation of microbial genomes using Subsystems Technology (RAST). Nucl. Acids Res. **42:** D206–D214. http://dx.doi.org/10.1093/nar/gkt1226.
7. **Samanovic MI, Ding C, Thiele DJ, Darwin KH.** 2012. Copper in microbial pathogenesis: meddling with the metal. Cell Host Microbe **11:**106–115. http://dx.doi.org/10.1016/j.chom.2012.01.009.