Chinese mitten crab (Eriocheir sinensis) belongs to the phylum Arthropoda, class Crustacea, order Decapoda, family Grapsidae, and genus Eriocheir. It is an important economic crab in China (Fu et al. 2017). In 2018, the total production of E. sinensis reached 692,723 tonnes in China, with an output value of 9,386,536 thousand dollars (http://www.fao.org/fishery/statistics, 2018). At present, the breeding areas of E. sinensis in China are mainly concentrated in Jiangsu, Hubei, Anhui, and Liaoning provinces. However, with the continuous expansion of the scale and density of crab farming, the disease has been one of the most important limitations of the sustainable development of the industry (Sui et al. 2012; Ding et al. 2015, 2016; Bao et al. 2021). In 2019, a pathogenic yeast was isolated from diseased Chinese mitten crab in many farms of Panjin City, Liaoning Province, China (121°25′–122°31′E, 40°39′–41°27′N), which was identified as Metschnikowia bicuspidata (Metschnikoff, 1884) belongs to family Metschnikowiaceae, genus Metschnikowia (Ma et al. 2020, 2022; Bao et al. 2021). However, the mitochondrial genome sequence of M. bicuspidata was still in the blank.

The specimen of M. bicuspidata (Number: 2EJM001) was stored in the Aquatic Animal Hospital of Dalian Ocean University, Dalian Ocean University, Dalian, China. We constructed the library with an average length of 350 bp using the NexteraXT DNA Libraries Preparation Kit (Illumina, San Diego, CA, USA) after the libraries were sequenced on Illumina Novaseq 6000 platform. The raw data totaled 2.84 G, and the clean data totaled 2.83 G after quality control processing and yielding a 1231-fold depth of coverage of the mitochondrial genome. The GC content of the clean data was 46.5%, the Q20 value was 97.90%, and the Q30 value was 93.96% which indicated that the quality of the mitochondrial genome sequencing and assembly results was very high. High-quality reads were assembled into the mitochondrial genome using de novo assembler SPAdes v.3.11.0 software (Bankevich et al. 2012). Finally, we annotated the assembled complete mitochondria genome by MITOS (Bernt et al. 2013). The sequence of M. bicuspidata mitochondrial genome was deposited in GenBank (accession number OK514652). Phylogenetic relationships between M. bicuspidata and other 12 yeasts were analyzed according to the mitochondrial genome using Maximum Likelihood methods by MEGA 7.0. All analytical results indicated that the complete mitochondrial genome of M. bicuspidata was 75,095 bp. Its nucleotide composition was as follows: A, 39.1%; C, 11.8%; G, 13.5%; T, 35.6%, with a high AT content of 74.7% which was higher than other kinds of yeast, such as Sporobolomyces sp and Cystobasidium sp (Huang et al. 2020; Liu and Wang 2020). The circular mitogenome of this yeast includes two rRNAs (16S rRNA and 12S rRNA), 23 tRNAs (tRNA-Ser, tRNA-Thr, tRNA-Val, tRNA-Cys, tRNA-Leu, tRNA-Glu, tRNA-His, tRNA-Met, tRNA-Tyr, tRNA-Asp, tRNA-Arg, tRNA-Gly, tRNA-Asn, tRNA-Pro, tRNA-Lys, tRNA-Ile, tRNA-Gln, tRNA-Ala, and tRNA-Sec) and 13 protein-coding genes (PCGs). From the 13 PCGs of M. bicuspidata mitogenome, nine PCGs (nad1, nad4, nad6, atp6, atp9, cob, cox1, cox2, and cox3) were located on the heavy strand and four PCGs (nad2, nad3, nad4L, and nad5) on the light strand. Among these PCGs, three genes (nad3, nad4L, and nad2) used the start codon
ATT, 4 genes (nad2, atp6, atp9, and cox2) used the start codon ATA, and the other genes (cob, cox1, cox3, nad1, nad4, and nad6) used the start codon ATG. Besides, except that the stop codon of nad2 was TAG, the stop codon of other PCGs (cob, cox1, cox2, cox3, nad1, nad3, nad4, nad4L, nad5, nad6, atp6, and atp9) was TAA.

The resulting phylogenetic tree showed that there were two main clades, Metschnikowiaceae and Sporidiobolaceae. Twelve yeasts species were clustered together within Metschnikowiaceae; Metschnikowia bicuspidata (accession number OK514652) and Metschnikowia bicuspidata (accession number MW147605.1) were clustered in a clade (Figure 1). In conclusion, the mitochondria of M. bicuspidata reported in this study provided more essential information about the yeast, which will help our understanding of M. bicuspidata better. Further, the information will do good to develop the rapid detection methods which will favor the control of the ‘milky disease’ in Chinese mitten crab.

### Storage location of the specimen or its DNA

The specimen of M. bicuspidata (Number: 2EJM001) was stored in the Aquatic Animal Hospital of Dalian Ocean University, Dalian Ocean University, Dalian, China. And the e-mail of Shigen Ye, the person in charge of the collection, is shgye@dlou.edu.cn.

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### Author contributions

Shigen Ye: conception and design. Jiannan Liu, Jieying Yu, Yihao Li, Xinran Shi, Senting Pu, and Xiaoran Zhao: analysis and interpretation of the data. Jiannan Liu: draft the paper. Shigen Ye: revising it critically for intellectual content. Shigen Ye: the final approval of the version to be published. And all authors to agree to be accountable for all aspects of the work.

### Disclosure statement

No potential conflict of interest was reported by the author(s).

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### Data availability statement

The genome sequence data that support the findings of this study are openly available in GenBank of NCBI at [https://www.ncbi.nlm.nih.gov/nuccore/OK514652](https://www.ncbi.nlm.nih.gov/nuccore/OK514652) under the accession no. OK514652. The associated BioProject accession number of the genome is PRJNA771255 [https://www.ncbi.nlm.nih.gov/bioproject/PRJNA771255](https://www.ncbi.nlm.nih.gov/bioproject/PRJNA771255). The associated BioSample accession number of the genome is SAMN22266430 [https://www.ncbi.nlm.nih.gov/biosample/?term=SAMN22266430](https://www.ncbi.nlm.nih.gov/biosample/?term=SAMN22266430). The associated SRA is SRR16328191 [https://www.ncbi.nlm.nih.gov/sra/SRR16328191](https://www.ncbi.nlm.nih.gov/sra/SRR16328191).

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Figure 1. The phylogenetic tree was inferred using the maximum-likelihood method based on the complete mitochondrial genome of 13 yeasts. A total of 1000 bootstrap replicates were computed, and the bootstrap support values are shown at the branches.
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