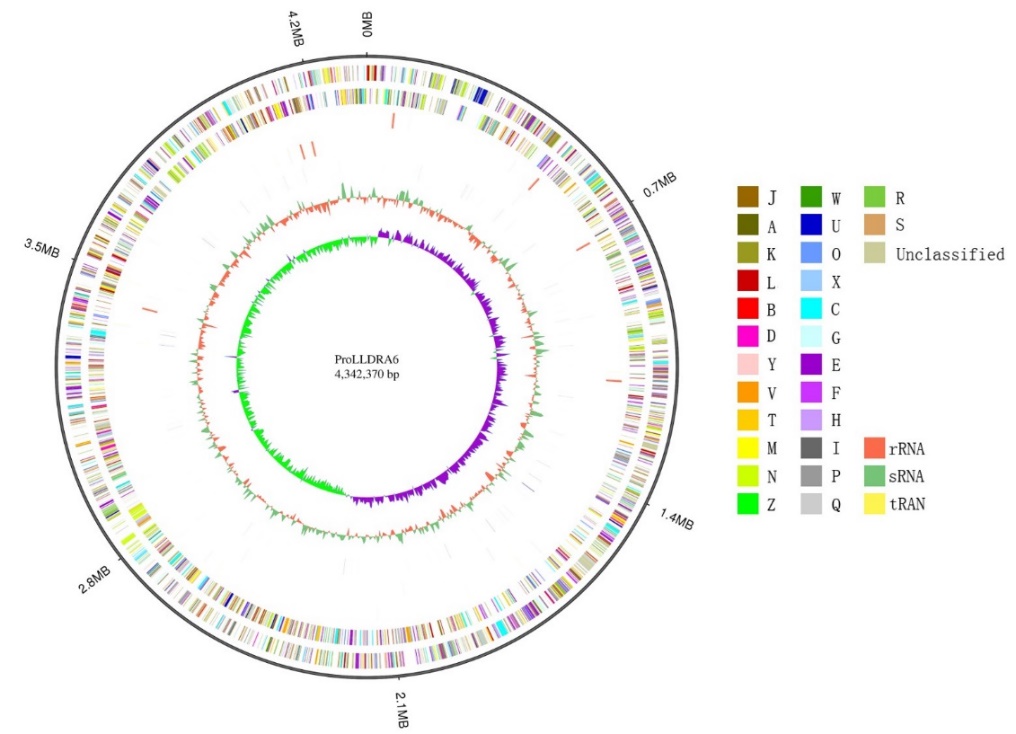
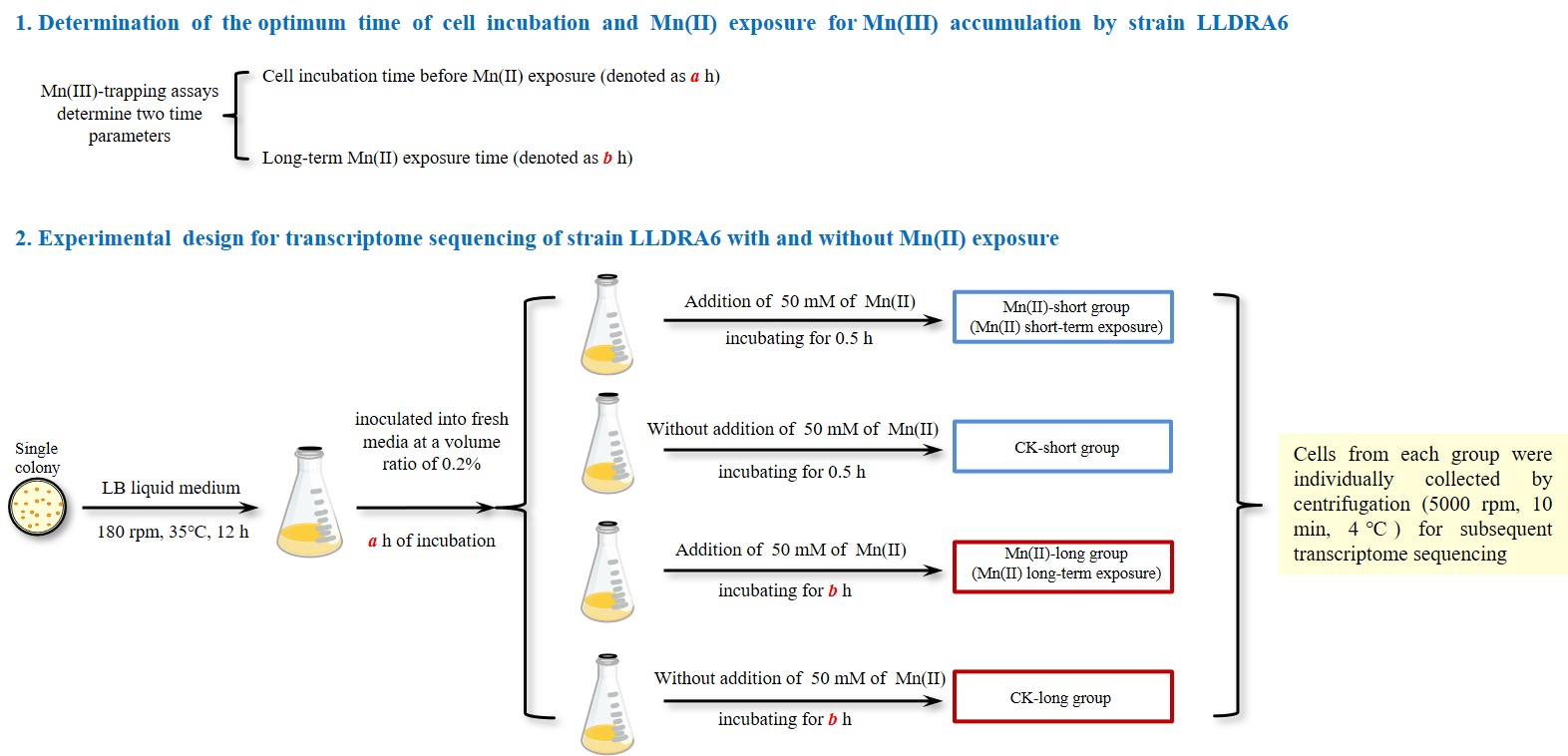
**Supplementary material**

**A soil-borne Mn(II)-oxidizing bacterium of *Providencia* sp. exploits a strategy of superoxide production coupled to hydrogen peroxide consumption to generate Mn oxides**

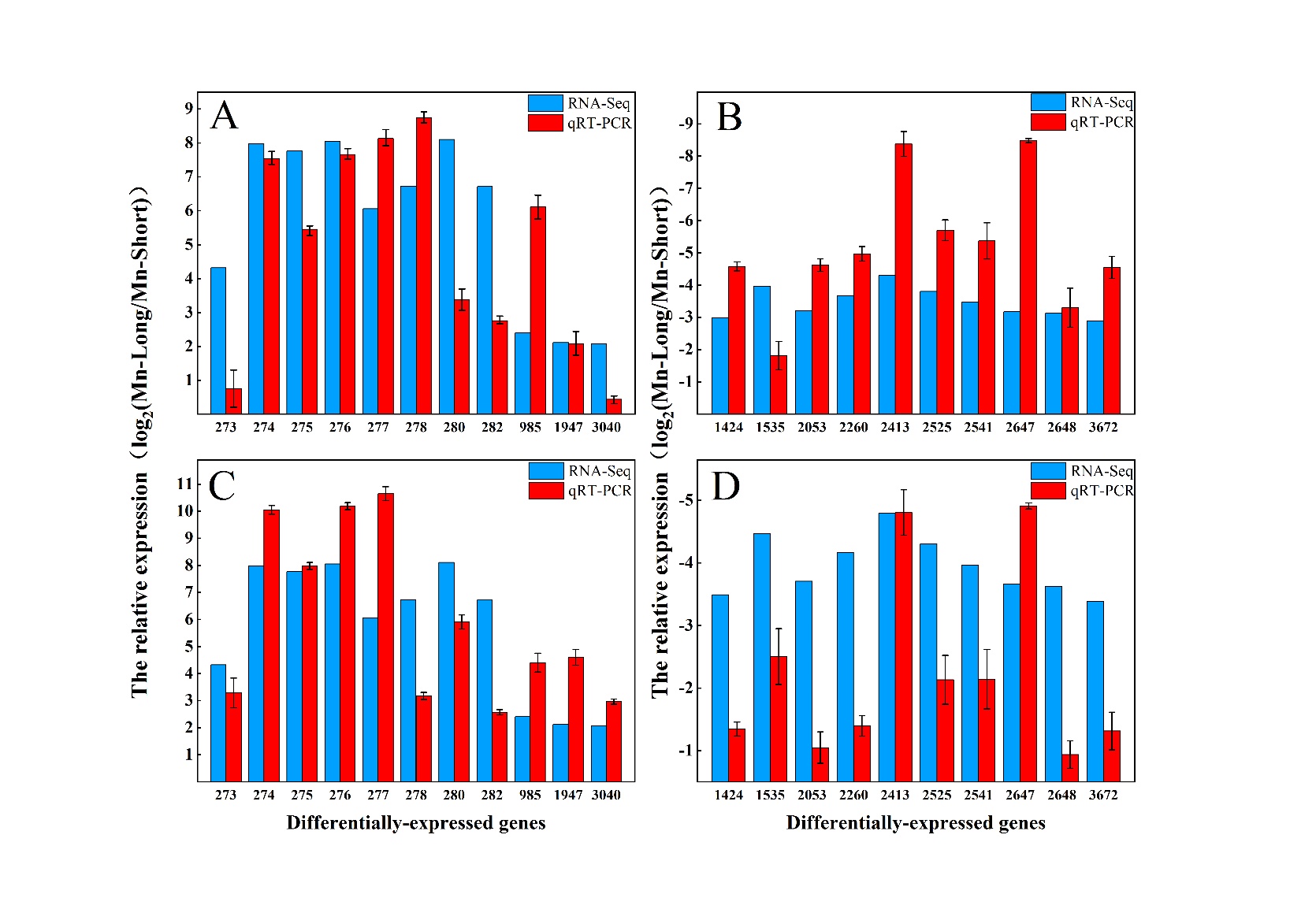
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**Fig. S1.** Circular representation of the chromosome genome for *Providencia* sp. LLDRA6. The distribution of the circle from outer to inner indicates forward/reverse strand genes (colored according to cluster of orthologous groups of proteins, COG), forward/reverse strand ncRNAs, repeat sequences, GC-skew, and genome size, respectively. According to COG analysis, uppercases on the right denote as follows. A: RNA processing and modification; B: Chromatin structure and dynamics; C: Energy production and conversion; D: Cell division; E: Amino acid metabolism; F: Nucleotide metabolism; G: Carbohydrate metabolism; H: Coenzyme metabolism; I: Lipid metabolism; J: Translation; K: Transcription; L: DNA replication, recombination and repair; M: Cell wall/membrane biogenesis; N: Cell motility; O: Posttranslational modification; P: Inorganic ion metabolism; Q: Secondary metabolites biosynthesis and catabolism; R: General function; S: Function unknown; T: Signal transduction mechanisms; U: Intracellular secretion; V: Defense mechanisms; W: Extracellular structures; X: Mobilome: prophages, transposons; Z: Cytoskeleton.

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**Fig. S2**. The flowchart of experimental design for transcriptome sequencing of strain LLDRA6 with and without Mn(II) exposure.



**Fig. S3**. A total of 21 genes upregulated or downregulated between long-term Mn(II) exposure and short-term Mn(II) exposure were chosen to validate the RNA-seq data by qRT-PCR. The red column represents log2-transformed mean value obtained from three independent biological replicates of qRT-PCR data. The error bar shows standard deviation (SD). The blue column represents log2(fold change) value based on RNA-seq data. The16s rRNA gene was used as an internal control for 11 upregulated genes **(A)** and10 downregulated genes **(B)**,respectively. The *gyrA* gene was used as an internal control for 11 upregulated genes **(C)** and 10 downregulated genes **(D)**, respectively. The numbers on the bottom of figures represent selected genes as described in Table S2.

**Table S1**. Principle features of the genome of *Providencia* sp. LLDRA6.

|  |  |
| --- | --- |
| Feature | Chromosome |
| Genome size (bp) | 4,342,370 |
| Illumina Data (Mb) | 1,131 (260X) |
| PacBio Data (Mb) | 1,497 (344X) |
| GC content (%) | 40.18 |
| Total number of genes | 3,956 |
| Genes with predicted functions | 3,818 (96.51%) |
| Total number of ncRNAs | 116 |
| Repeat number | 185 |
| CRISPR number | 5 |
| Prophage number | 4 |

Note: "X" stands for sequencing depth, the amount of sequenced reads divided by genome size.

**Table S2**. List of primers used for quantitative real time PCR (qRT-PCR).

|  |  |  |
| --- | --- | --- |
| Gene ID | Orthology | Primer sequences (5′-3′)  Forward primer/Reverse primer |
| ProLLDRA6GL000273 | *paaX* | GCAGCTCCTAGCAGTGCTCAAG |
| TGGTGGTAGTGCTCTGCAACTTG |
| ProLLDRA6GL000274 | *paaK* | GTGGACACTCACTCACGCTTACG |
| AGGAACCGCGAAGGTATTGAAGG |
| ProLLDRA6GL000275 | *paaJ* | GCCGTTATGGTGGTGCTCTGTC |
| GCCATTCTTGCGACATTACGGTTG |
| ProLLDRA6GL000276 | *paaI* | TGCTGCTGTTGCATCCAGTT |
| ACGTCCGGAGAACCAAGCTA |
| ProLLDRA6GL000277 | *paaH* | ACCGACAACGCCATGTGTTACG |
| TGATGACCTGCCGCCAATTGC |
| ProLLDRA6GL000278 | *paaG* | AATGTGACGGCCAGTGACCAAG |
| CCAGCTAATGCAATGGCAGCAC |
| ProLLDRA6GL000280 | *paaE* | ATTGCGTCAAGGAGCTGATCTGC |
| AATCGAGCACGACACCATCGC |
| ProLLDRA6GL000282 | *paaC* | TTACTGGCGAGCTGTTCCATGC |
| ACCTAGATGCTCAGTGTGATTGCC |
| ProLLDRA6GL000985 | *aroF, aroG, aroH* | GCTCGTGGTATGTGGTCCTTGTTC |
| CCATCGCAGGATCGCTGATTAGTC |
| ProLLDRA6GL001947 | *oppA, mppA* | AGGCGTTGCTACTGGCTTAATGG |
| GCCAGCGCAGATTCAGGAACC |
| ProLLDRA6GL003040 | *sucD* | CGTGAAGCCGTAGAAGCGACTG |
| AACCGTCAGCATATCCAGTGTTGG |
| ProLLDRA6GL001424 | *grcA* | GCCGACTGTACGTGTTGAAGGTG |
| CGTTGCTGCTCTGGTGTCAGTG |
| ProLLDRA6GL001535 | *hutU, UROC1* | GGTTCCGATGCGGTATCAGATTGG |
| TGCGATACGTTCAGCAGCTTCATC |
| ProLLDRA6GL002053 | *Unknown* | TCAGGGCTCCCTTTTCGTTCA |
| TAGACCCAAGCGGGTGGAAC |
| ProLLDRA6GL002260 | *ipdC* | GCCTCATACGCCGCAGATGG |
| TTGTACTCCACTTGCTGGCATCC |
| ProLLDRA6GL002413 | *Unknown* | GCGTCACTCAACAAACCACC |
| GGCGGAGTAACAGCATTGGT |
| ProLLDRA6GL002525 | *fliC* | AACAACCTGAGTGCTGCACGTAG |
| AACGCAACAGGCTCAGAACACC |
| ProLLDRA6GL002541 | *Unknown* | TGCGGCATCTGTTGTTCCATT |
| CGCCGCTTTACCACTTTCCA |
| ProLLDRA6GL002647 | *mgtA, mgtB* | ACCTTGTTTTCCCTTGCCGT |
| TGCACAGAACATCCATCGCC |
| ProLLDRA6GL002648 | *mgtC* | ATGGCTGGTCTTCGCACTAATGC |
| ACCACAGTGTTGCCGCTGTATTC |
| ProLLDRA6GL003672 | *Unknown* | TAATGGCCCGAATAGCGGTG |
| GTCACATTGAGGCCGTTCCA |
|  | *16s rRNA* | CTACACATGCAGTCGAGCGG |
| CATCCGATAGCGCAAGGACC |
|  | *gyrA* | ATCCTGGACATGCAGTTGCG |
| GTCCACGATTTCGGCGAGTT |

**Table S3**. A total of 547 DEGs were identified between Mn(II)-short group and Mn(II)-long group.

**Table S4**. 300 DEGs were identified as the ones that were only caused by Mn(II) exposure.

**Table S5.** Transcriptional profiles of putative Mn(II)-oxidizing proteins.

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Gene ID | Annotation | CK-short\_mean  TPM | CK-long\_mean  TPM | Mn(II)-short\_mean  TPM | Mn(II)-long\_mean  TPM | log2(CK-long/CK-short) | log2(Mn(II)-long/Mn(II)-short) |
| ProLLDRA6GL001078 | MCOs (CotA) | 115.37 | 106.99 | 540.3 | 78.32 | -0.10 | -2.78 |
| ProLLDRA6GL003204 | MCOs (CotA) | 255.14 | 336.62 | 394.59 | 378.71 | 0.39 | -0.06 |
| ProLLDRA6GL000992 | Laccase | 52.24 | 92.60 | 145.56 | 181.85 | 0.82 | 0.32 |

**Table S6.** Transcriptional profile of catalase gene.

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Gene ID | Annotation | CK-short\_mean  TPM | CK-long\_mean  TPM | Mn(II)-short\_mean  TPM | Mn(II)-long\_mean  TPM | log2(Mn(II)-short/CK-short) | log2(Mn(II)-long/CK-long) |
| ProLLDRA6GL001630 | Catalase | 2519.53 | 2129.90 | 3327.57 | 4505.28 | 0.40 | 1.08 |