**Supp. Table 1:** Primers used for construction of SOEing-PCR product for mutation work.

|  |  |  |  |
| --- | --- | --- | --- |
| Construction of *sodA* SOEing product and sodA deletion screening primers. | | | |
| Primers name | Sequence 5`🡪 3` | Product size | |
| SodA-UF | F 5'-GAAGATACCGCACATTACCG-3' | 800 bp | |
| SodA-UF+ Kan1 | R 5'-**GAAGCAGCTCCAGCCTACAC**CATC  TCCATTATTGTCGAGC-3' |
| Kan1 | F 5'-GTGTAGGCTGGAGCTGCTTC-3' | 1496 bp | |
| Kan2 | R 5'-ATGGGAATTAGCCATGGTCC-3' |
| SodA-DF+ Kan2 | F 5'-**GGACCATGGCTAATTCCCAT**AAA  TAAGGTTGCATTGCGCT-3' | 834 bp | |
| sodA-DF | R 5'-ATAAACGAACCTGACGCCGA-3' |
| del-sodA/screen | F 5'-ATGATAATCACCACGCAGCC-3' |  | |
| del-sodA/screen | R 5'-GACGGTGAAAGCCAATCAGC-3' |  | |
| Construction of *sodB* SOEing product and sodB deletion screening primers. | | | |
| SodB-UF | F 5'-CATCTGTTTTTGCCATCGTCG-3' | | 793 bp |
| SodB-UF+ Kan1 | R 5'-**GAAGCAGCTCCAGCCTACAC**AAA  CGACATTGCTACTCTCC-3' | |
| SodB-DF+ Kan2 | F 5'-**GGACCATGGCTAATTCCCAT**GCGG  CATAAACGACAAACCG-3' | | 787 bp |
| sodB-DF | R 5'-CTAGGCAACTATCTGGGCGG-3' | |
| del-sodB/screen | F 5'-GCGATTTAGTCTTCTTCCGC-3' | |  |
| del-sodB/screen | R 5'-GATCAGTGCGTATGCCATCG-3' | |  |
| Construction of *sodC* SOEing product and sodC deletion screening primers. | | | |
| SodC-UF | F 5'-GCGTGCTCTACTCCGTATCC-3' | | 840 bp |
| SodC-UF+ Kan1 | R 5'-**GGACCATGGCTAATTCCCAT**GTGA  TTAAGTAGTTCCTTCG-3' | |
| SodC-DF+ Kan2 | F 5'-**GAAGCAGCTCCAGCCTACAC**TCGT  TGCATAACACCTCC-3' | | 830 bp |
| sodC-DF | R 5'-TCGATCACGCCGATATCTATG-3' | |
| del-sodC/screen | F 5'-ACCAGCGTCATCTCCAGTCTG-3' | |  |
| del-sodC/screen | R 5'-CGTGAGGAACGTTTTAACTGGC-3' | |  |

**Bold** sequence is complementary to primer Kan1/F and Kan2/R (kanamycin antibiotic cassette). All primers were designed using APE software and NCBI primer designer, then synthesized by Eurofins Company in Germany (<https://www.eurofinsgenomics.eu>).

**Supp. Table 2:** Sources of bacterial strains and plasmids used in this study.

|  |  |  |
| --- | --- | --- |
| **Plasmids & bacterial strains** | **Description** | **Reference or source** |
| **Plasmids** | | |
| pKOBEG-Apra | Ts, gam-bet-exo, ApR | ([Chaveroche *et al.*, 2000](#_ENREF_14)) |
| pFLP2with ampicillin | AmpR, encodes FLP recombinase | ([Hoang *et al.*, 1998](#_ENREF_43)) |
| **Bacterial Strains** | | |
| *Klebsiella pneumoniae* KR3167 | Clinical isolate sensitive to most antibiotics except ampicillin | Dr. Kumar Rajakumar, University of Leicester |
| Δ*sodA* | *K. pneumoniae* KR3167 with unmarked single SOD mutant | This study |
| Δ*sodB* | *K. pneumoniae* KR3167 with unmarked single SOD mutant | This study |
| Δ*sodC* | *K. pneumoniae* KR3167 with unmarked single SOD mutant | This study |
| Δ*sodA::sodB* | *K. pneumoniae* KR3167 with unmarked double SOD mutant | This study |
| Δ*sodA::sodC* | *K. pneumoniae* KR3167 with unmarked double SOD mutant | This study |
| Δ*sodB::sodC* | *K. pneumoniae* KR3167 with unmarked double SOD mutant | This study |
| Δ*sodA::sodB::sodC* | *K. pneumoniae* KR3167 with unmarked triple SOD mutant | This study |

**Supp. Table 3:** Primer list for reverse transcriptase quantitative PCR (qRT-PCR)

|  |  |  |
| --- | --- | --- |
| Primers name | Sequence 5`🡪 3` | Product size |
| *rpoD* (House keeping gene) | F 5'-TCTCCGGTACCGTTATCGAC-3' | 201 bp |
| *rpoD* (House keeping gene) | R 5'-TGTCGAGCTTCTCAGCTTCA-3' |
| *sodA*/F | F 5'-CCGCTGAAGAGCTGATTACC-3' | 184 bp |
| *sodA*/R | R 5'-TTGAAGTTCTCCACGGAACC-3' |
| *sodB*/F | F 5'-GACCTGGCTGGTCAAAAATG-3' | 202 bp |
| *sodB*/R | R 5'-GTTAGCCGCAACAAACTTCC-3' |
| *sodC*/F | F 5'-ATTACGATCCGCAGCATACC-3' | 195 bp |
| *sodC* /R | R 5'-GACTGTCGGCCATGTTATCC-3' |

**Supp. Table 4:** Fold differences in expression of *sodA, sodB* and *sodC* in mutants relative to wild type *K. pneumoniae* KR3167 strain. Total RNA was extracted at mid exponential phase for all strains grown in LB broth medium under aerobic growth condition (200 rpm).The data represent the mean, and the standard error of the mean (±) of three independent experiments in replicates.

|  |  |  |  |
| --- | --- | --- | --- |
| Strains | Fold difference relative to wild type | | |
| *sodA* | *sodB* | *sodC* |
| Δ*sodA* | 0.00±0.00 | 1.14±0.01 | 2.60±0.02 |
| Δ*sodB* | 1.93±0.02 | 0.00±0.00 | 2.08±0.02 |
| Δ*sodC* | 2.13±0.02 | 1.26±0.02 | 0.00±0.00 |
| Δ*sodA::sodB* | 0.00±0.00 | 0.00±0.00 | 3.75±0.01 |
| Δ*sodA::sodC* | 0.00±0.00 | 0.69±0.05 | 0.00±0.00 |
| Δ*sodB::sodC* | 2.16±0.02 | 0.00±0.00 | 0.00±0.00 |
| Δ*sodA::sodB::sodC* | 0.00±0.00 | 0.00±0.00 | 0.00±0.00 |



**Supp. Fig. 1:** Analysis of growth rate of *K. pneumoniae* strains under aerobic incubation (200 rpm) at 37**°**C. Growth rate μ (h-1)of the mutant and wild type strains under aerobic incubation in LB broth with without (blue column) or with paraquat (red column), and in M9-medium (green column). Values are derived from three independent experiment, and analysed using one-way ANOVA and Dunnett's multiple comparisons test \*\*\*\*p≤0.0001.

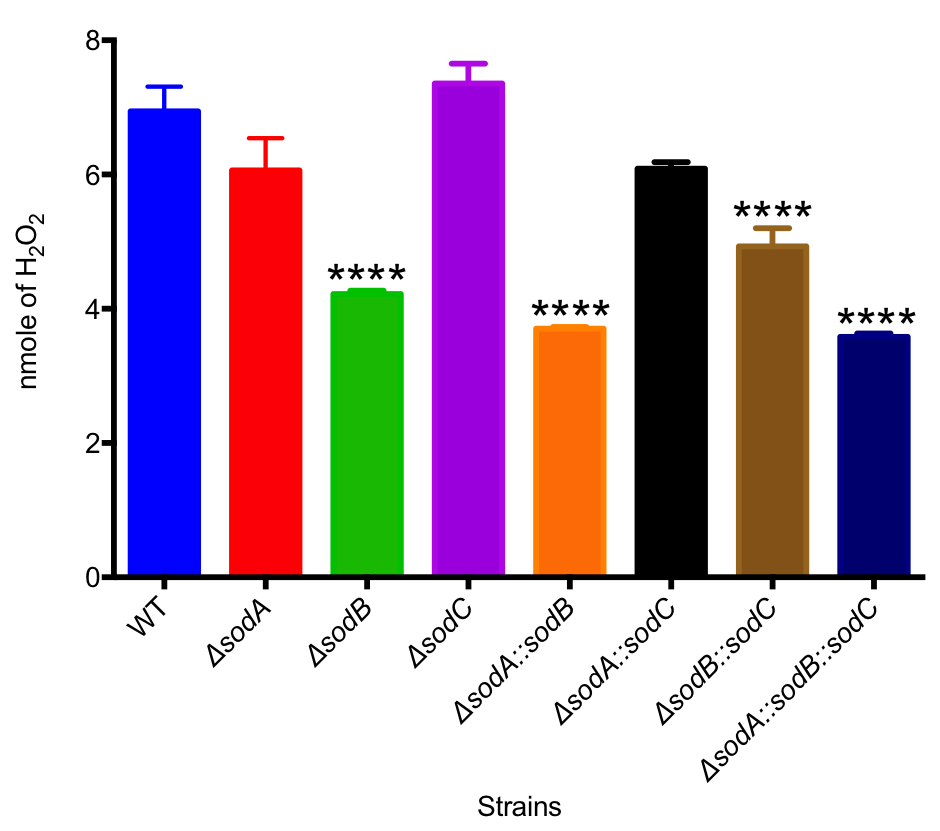
**A**



**B**



**Supp. Fig. 2:** Colony size analysis of isogenic mutant and *cis-*complemented *sod* mutants of *K. pneumoniae.* Strains were grown under aerobic incubation at 37◦C on LB agar plate **(A)** and on M9 agar plate **(B)**. Each column represents the mean of 10 well-isolated colonies. Data were analysed using ANOVA and Dunnett's multiple comparisons test \*\*\*\*p≤0.0001

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**Supp. Fig. 3:** Assessment of hydrogen peroxide formation in mutants and wild type *K. pneumoniae* KR3167 strain. Each column represents the average of tree independent experiments, each with triplicates. Error bars indicate standard error of the mean. One-way ANOVA and Dunnett's multiple tests were used for comparison. \*\*\*\*P≤0.0001.