



Does *Staphylococcus aureus* use copper resistance to evade host immune responses?

¹Moyne Institute of Preventive Medicine, Department of Microbiology, Trinity College Dublin, Ireland.
²Institute for Cell and Molecular Biosciences, Newcastle University, UK.

Marta Zapotoczna¹, Gus Pelicoli-Riboldi², Kevin J. Waldron² & Joan A. Geoghegan¹

Introduction:

Copper is an essential trace element used in the cellular metabolism of Prokaryotes and Eukaryotes due to its redox potential ($\text{Cu}^+ \leftrightarrow \text{Cu}^{2+}$). This transition metal is also toxic if present beyond cellular needs resulting in copper toxicity & oxidative stress caused by Fenton chemistry.

Macrophage phagocytosis involve killing of intracellular bacteria with toxic levels of copper, [1] and several bacterial pathogens including *Streptococcus pneumoniae* and *Mycobacterium tuberculosis*, require transition metal efflux and detoxification systems to thrive inside hosts cells [2]. These pathogens have been shown to utilize copper resistance genes for full virulence in pulmonary, intraperitoneal and intravenous models of infections [3-5].

In *S. aureus* copper resistance is mediated by P-type efflux transporters; conserved CopA and unique CopB, which is found in pathogenic strains either as part of a replicating plasmid or incorporated into the chromosome (Table 1). The *copB* gene is part of the same operon as the gene encoding multicopper oxidase (*mco*).

Table 1. CsoR – controlled expression of copper resistance genes in *S. aureus*.

Strain/ copper availability	Transcriptional regulation of copper resistance by CsoR	Resistance
MRSA wt/ - Cu^{2+}	REPRESSION	LOW
MRSA wt/ + Cu^{2+}	DEREPRESSION	HIGH
MRSA CsoR CHC/ + Cu^{2+}	REPRESSION	LOW

Expression of *copA* and *copB/mco* is regulated by the CsoR repressor controlled by the availability of Cu^{2+} [6] (Table 1). In the absence of copper CsoR represses copper resistance genes. Upon copper availability CsoR-coordinates Cu^{2+} derepressing transcription of copper resistance genes, leading to an increase in metal tolerance of the bacteria. A CsoR C41A/H66A/C70A (CHC) variant defective in Cu^{2+} coordination represses copper resistance genes despite metal availability (Table 1).

Aim:

To investigate the role of copper resistance in promoting MRSA survival against phagocytic killing by macrophages & in human blood.

Determinants of hyper-resistance to Copper

MRSA isolates used in the study carry copper resistance genes, either as part of their chromosome (ch) or a replicating plasmid (p) (Table 2). A mutant of MRSA252 strain defective in CsoR-coordination of Cu^{2+} (CsoR C41A/H66A/C70A) was made by allelic exchange using a temperature sensitive plasmid pIMAY.

Table 2. Copper resistance genes & resulting levels of Cu^{2+} tolerance by MRSA strains.

Strains	<i>copA</i>	<i>copB</i>	<i>mco</i>	MIC Cu_2SO_4 (mM)
USA300 (CA-MRSA)	Yes (ch)	No	No	4
USA300 <i>copA::Tn</i>	No	No	No	4
14-2533T	Yes (ch)	No	No	5
14-2533T <i>csoR</i> CHC	Yes (ch)	No	No	5
14-2533T pSCBU	Yes (ch)	Yes (p)	Yes (p)	10
14-2533T pSCBU Δ <i>mco</i>	Yes (ch)	Yes (p)	No	10
14-2533T pSCBU Δ <i>copB</i>	Yes (ch)	No	Yes (p)	10
MRSA252	Yes (ch)	Yes (ch)	Yes (ch)	8
MRSA252 <i>csoR</i> CHC	Yes (ch)	Yes (ch)	Yes (ch)	5
MRSA252 Δ <i>mco</i>	Yes (ch)	Yes (ch)	No	5
MRSA252 Δ <i>copB</i>	Yes (ch)	No	Yes (ch)	5

CsoR Cys41 His66A & Cys70 are essential for Cu^{2+} dependent derepression of copper resistance, both *in vitro* & *in vivo*

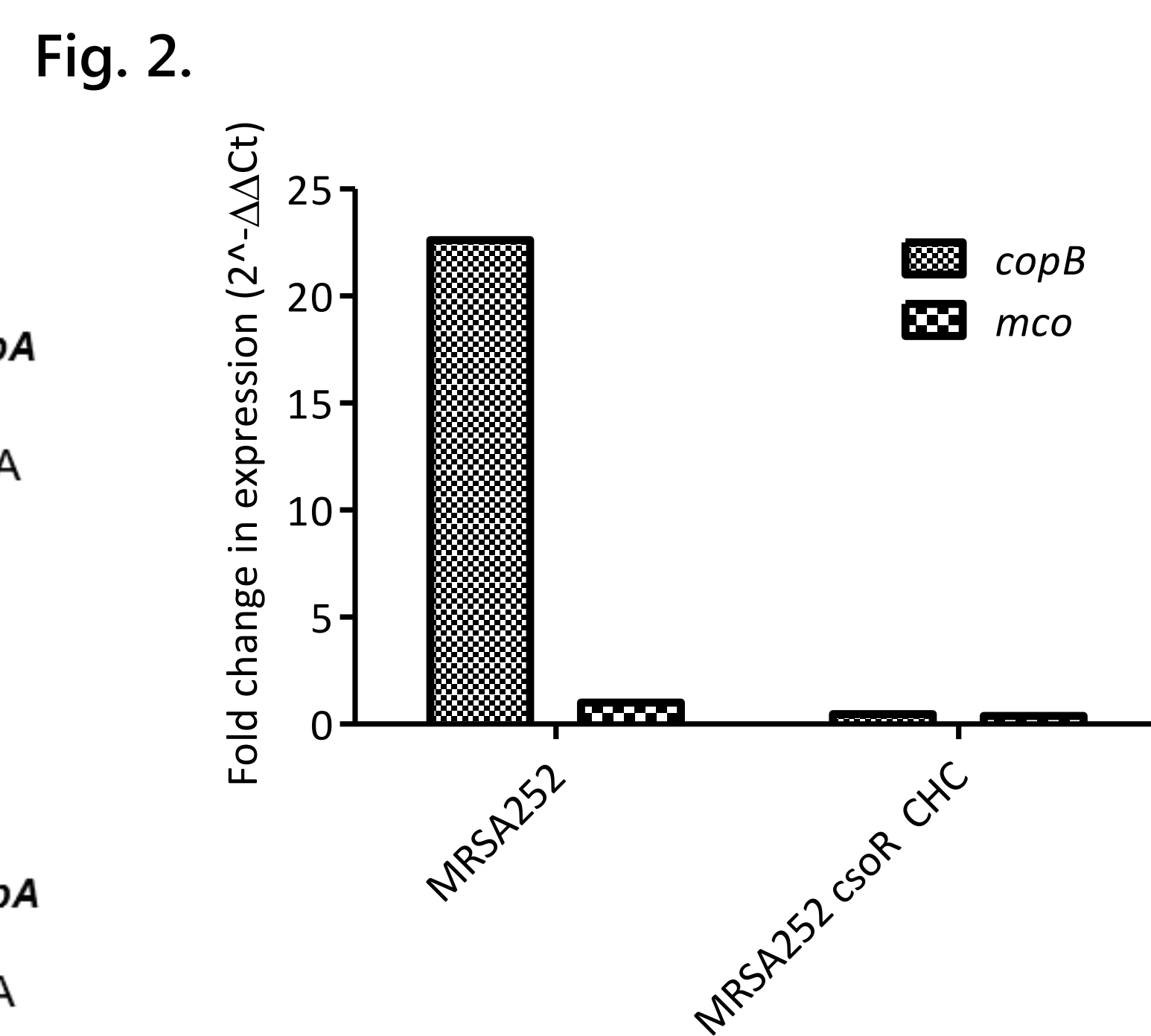
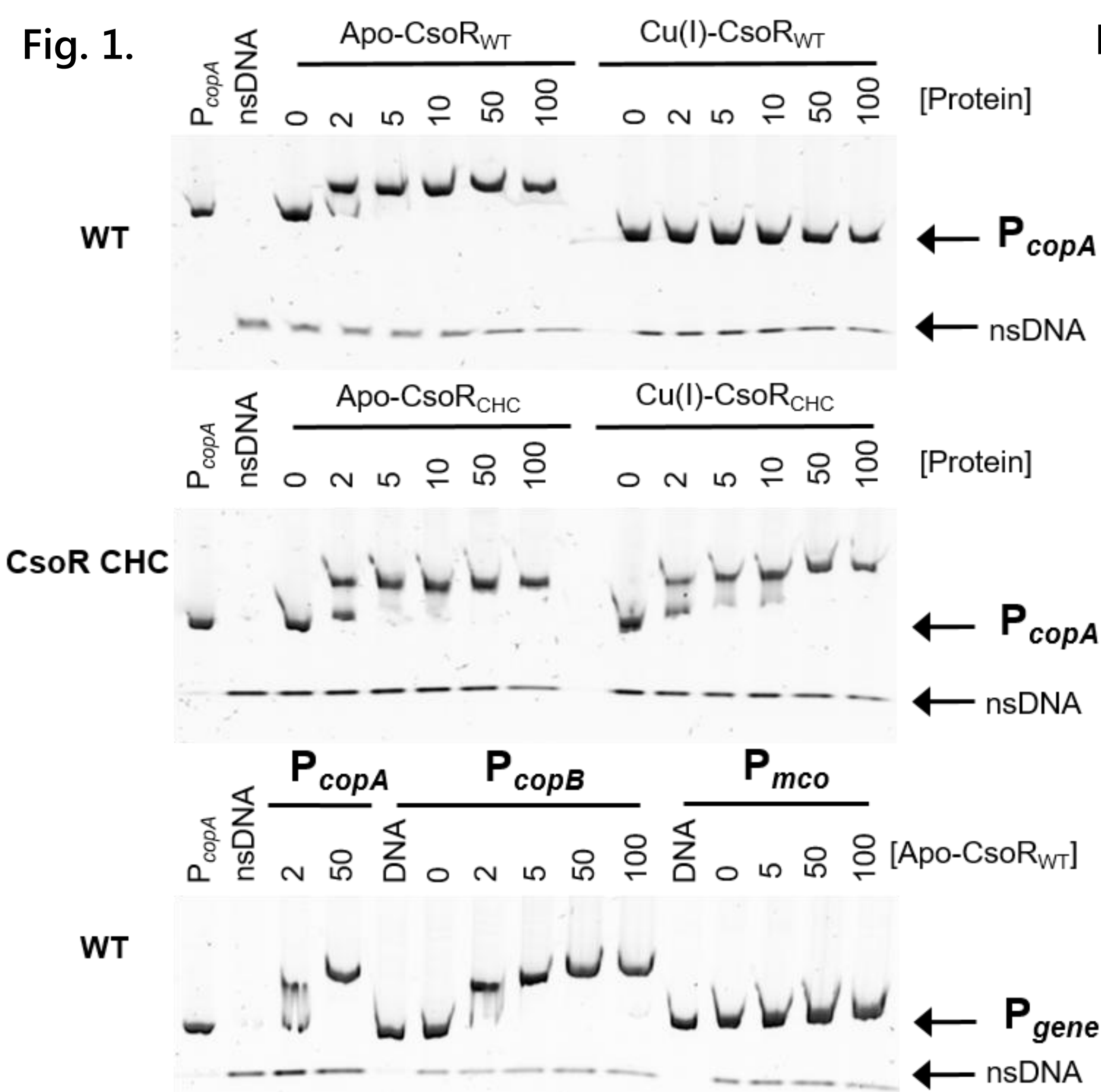


Fig. 2. CsoR Cys41 His66A & Cys70 are required for *copB* upregulation during phagocytic killing in INF γ -activated macrophages in the presence of Cu^{2+} . qRT-PCR was used to determine the transcription of *copB* and *mco* during phagocytic killing or intracellular MRSA252 or MRSA252 CHC. $\Delta\Delta\text{CT}$ method was used to determine the relative change of expression to applied housekeeping gene (*saeR*). Presented is the mean of n=2.

Fig. 1. CsoR & CsoR CHC binds to the *copA* & *copB* but not the *mco* promoter sequence *in vitro*. EMSA analysis was performed to test for Cu^{2+} dependent binding of purified recombinant CsoR and CsoR C41A/H66A/C70A (CHC) variant protein to the promoter sequences of the *copB/mco* locus. PCR products (~200 bp) containing the sequences upstream of either promoter were mixed with a PCR product of non-specific DNA sequence (nsDNA), and probed for binding of purified recombinant CsoR variants.

CsoR-mediated hyper-resistance to copper promotes MRSA survival inside the macrophages & in whole human blood

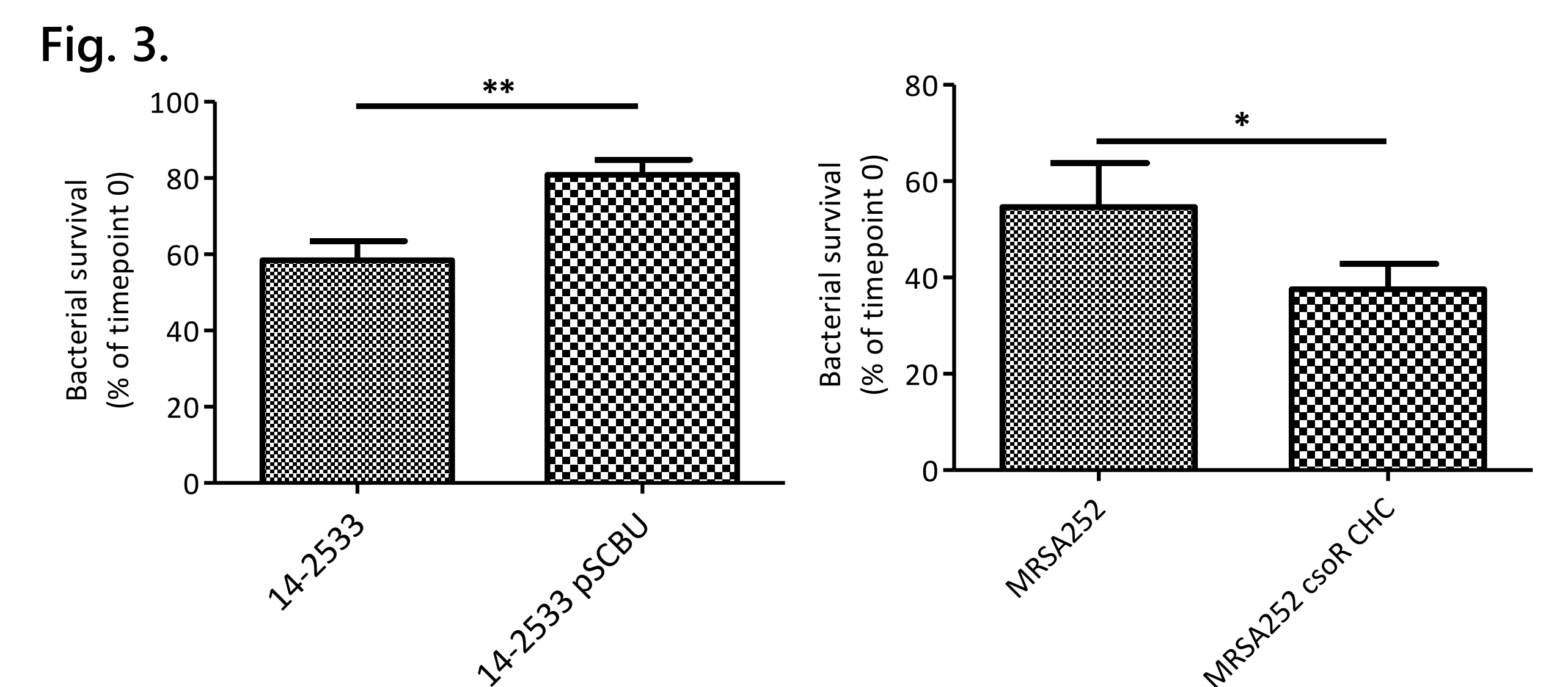


Fig. 3. Increased survival of macrophage killing by copper resistant *S. aureus* variants. Mouse macrophage RAW264.7 were seeded at 2×10^6 per mL in DMEM into 24-well plates and activated with mouse INF γ (40ng/mL) and Cu_2SO_4 (40 μM) for 18h. *S. aureus* variants (as indicated) were inoculated into the wells at an MOI of 10 in DMEM only allowing phagocytosis for 30min following killing of extracellular bacteria with gentamycin/lysostaphin for 30 min. Macrophage was lysed at this time (T0) and after 3h incubation (T3h) and intracellular bacteria were subjected to viable count to determine the levels of survival. The CsoR C41A/H66A/C70A expressing variant of the MRSA252 isolate is indicated as *csoR* CHC. Presented are means \pm SD of three independent experiments. Statistical significance is indicated, ** $P < 0.005$ * $P < 0.05$.

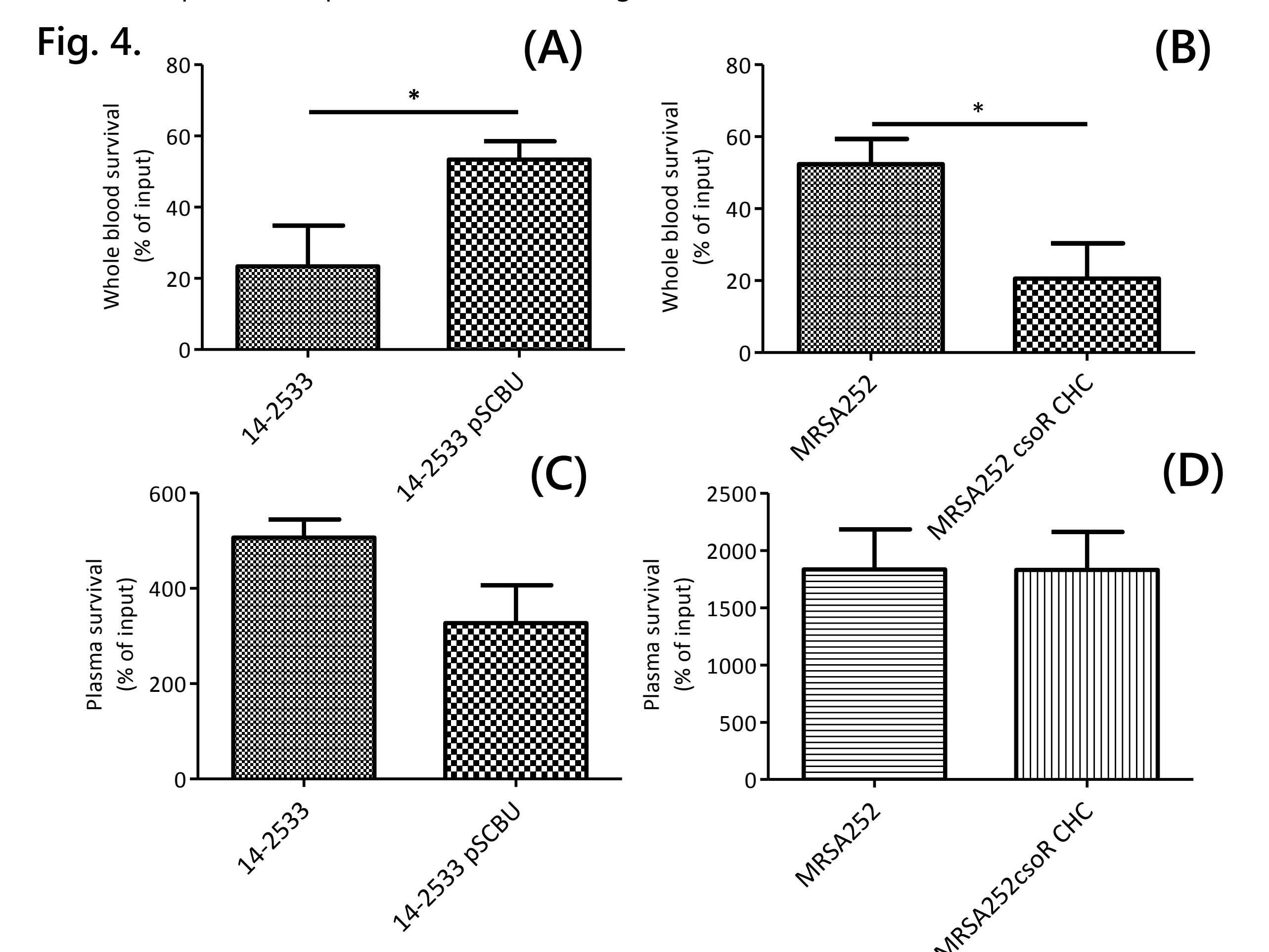


Fig. 4. Increased survival of copper-resistant *S. aureus* in human blood. *S. aureus* variants (ca. 1×10^4 CFU/mL) were inoculated into freshly drawn human blood (A-B) or plasma fraction of the blood (C-D). Following 3h incubation at 37°C with shaking blood and plasma were subjected to viable count to determine the levels of bacteria. Bacteria were grown in plasma as a control to determine that observed differences in whole blood survival are due to phagocytic killing. The CsoR C41A/H66A/C70A expressing variant of the MRSA252 isolate is indicated as *csoR** (BD). Presented data are means \pm SD of three independent experiments. Statistical significance is indicated, * $P < 0.05$.

References:

- White C, Lee J, Kambe T, Fritsche K, Petris MJ. A role for the ATP7A copper-transporting ATPase in macrophage bactericidal activity. *The Journal of Biological Chemistry* 2009; 284:33949-56.
- Neyrolles O, Mintz E, Catty P. Zinc and copper toxicity in host defense against pathogens: *Mycobacterium tuberculosis* as a model example of an emerging paradigm. *Frontiers in cellular and infection microbiology* 2013; 3:89.
- Johnson MD, Kehl-Fie TE, Rosch JW. Copper intoxication inhibits aerobic nucleotide synthesis in *Streptococcus pneumoniae*. *Metallomics* 2015; 7:786-94.
- Johnson MD, Kehl-Fie TE, Klein R, et al. Role of copper efflux in pneumococcal pathogenesis and resistance to macrophage-mediated immune clearance. *Infection and immunity* 2015; 83:1684-94.
- Ward SK, Abomoelek B, Hoye EA, Steinberg H, Talaat AM. CtpV: a putative copper exporter required for full virulence of *Mycobacterium tuberculosis*. *Mol Microbiol* 2010; 77:1096-110.
- Baker J, Sengupta M, Jayaswal RK, Morrissey JA. The *Staphylococcus aureus* CsoR regulates both chromosomal and plasmid-encoded copper resistance mechanisms. *Environ Microbiol* 2011; 13:2495-507.

Plasmid-expressed *mco* promotes growth of *S. aureus* in sub-inhibitory concentrations of Cu^{2+}

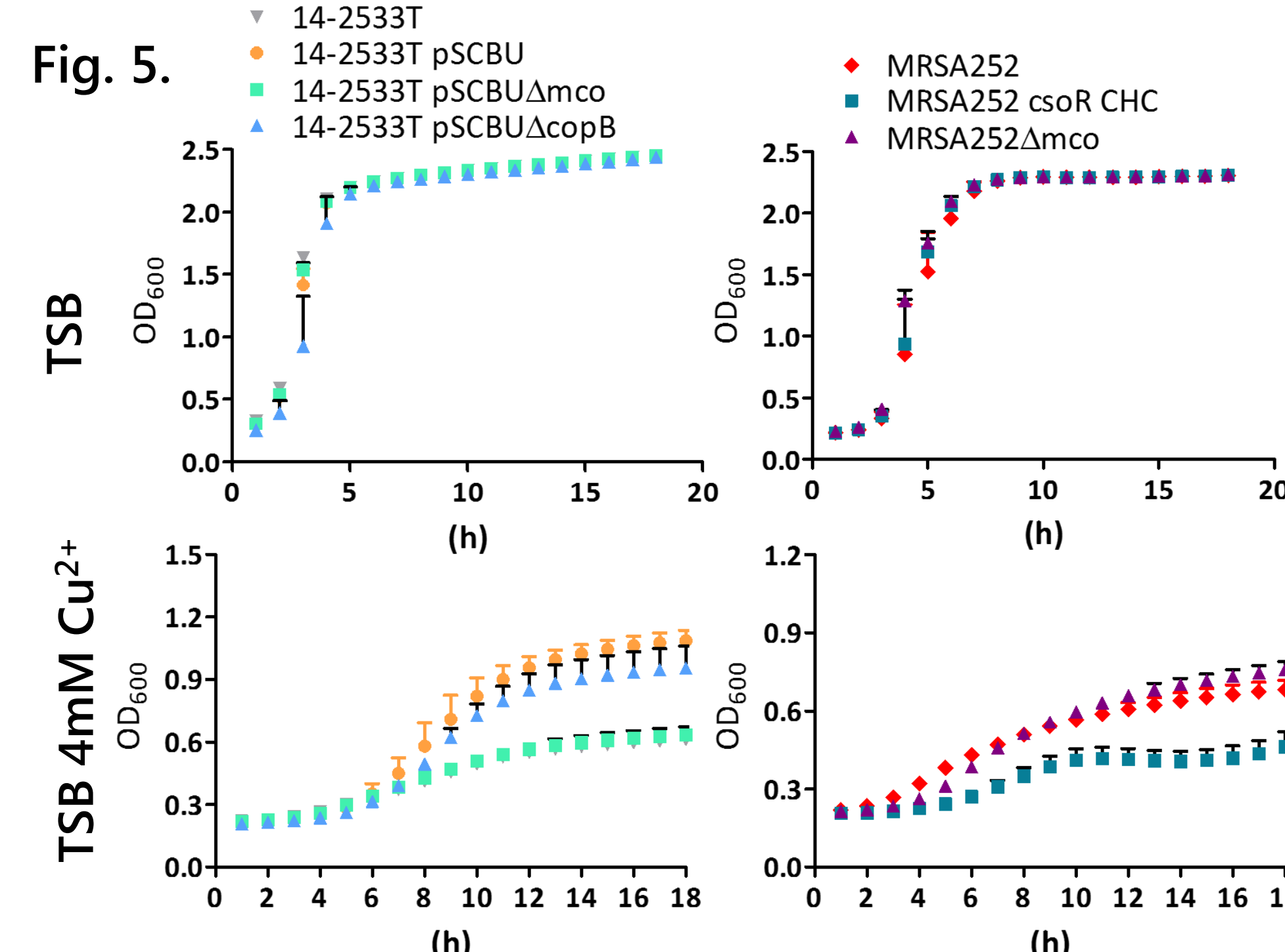


Fig. 5. *S. aureus* growth in tryptic soy broth (TSA). *S. aureus* strains (as indicated) were inoculated into 96-well plates containing either TSA alone (top) or supplemented with 4mM of Cu_2SO_4 (bottom). Presented data are representative of three independent experiments