Investigation of plasma resistance-mediating genes in *Escherichia coli*

T. Dirks¹, M. Krewing¹, K. Weisgerber¹, F. Jarzina¹, J.W. Lackmann^{1,2}, J. Benedikt³, J. E. Bandow¹

¹Applied Microbiology, Faculty of Biology and Biotechnology, Ruhr University Bochum, Germany ²Current address: Leibniz Institute for Plasma Science and Technology, Greifswald, Germany ³Experimental Plasma Physics, Institute for Experimental and Applied Physics, Christian-Albrechts-Universität zu Kiel, Germany

Abstract: Since cold atmospheric pressure plasmas can inactivate even multidrug-resistant bacteria, there is a special interest in understanding the mechanism underlying bacterial inactivation by plasma and in investigating possible resistance development. In this study, we showed that an upregulation of a single protein increases plasma resistance. Moreover, our findings regarding [Fe-S]-cluster containing proteins suggest that they limit survival and could present the bottleneck of surviving plasma-mediated stress.

Keywords: COST plasma jet, bacterial inactivation, plasma resistance, [Fe-S]-cluster, superoxide, hydrogen peroxide

The increasing number of multidrug-resistant bacteria leads to a growing interest in finding additive therapies that can be combined with antibiotics [1, 2]. For some applications, plasma can present such an additive, since it can inactivate even multidrug-resistant bacteria. In this study, the COST jet was used [3] to investigate potential intrinsic mechanisms of plasma resistance. We have screened a library of single-gene knockout Escherichia coli mutants for strains exhibiting increased plasma sensitivity. The collection constructed at KEIO university includes approximately 4000 strains, each missing one nonessential gene [4]. 87 mutants with increased plasma sensitivity were identified, indicating a potential function of these genes in mediating plasma resistance [5]. The increased plasma sensitivity of four strains ($\Delta iscS$, $\Delta mntH$, $\Delta rep, \Delta cysB$) was verified with an independent CFU-based assay and complementation experiments. The gene iscS encodes a cysteine desulfurase, which is involved in synthesis of [Fe-S]-clusters [6, 7]. CysB is the regulator of the cysteine regulon and activates the expression of cysteine-related genes in the absence of sulfur [8]. Rep is a DNA helicase [9, 10] and mntH encodes a protondependent transporter for divalent cations (mainly Mn²⁺) [11]. Overexpression of iscS, rep, or cysB has led to survival rates higher than those of the wild type, indicating that plasma resistance can indeed increase, resulting in less sensitive strains (Fig. 1).

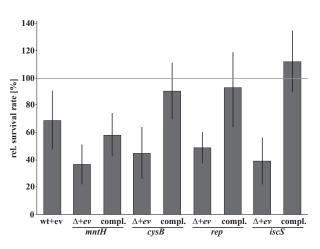


Fig. 1: Relative survival rates of *E. coli* wild type, $\Delta mntH$, $\Delta cysB$, Δrep , and $\Delta iscS$ containing the empty vector or a plasmid for complementation after 30 s of plasma treatment. A low-density cell suspension of approximately 1600 CFU x ml⁻¹ µl was exposed to the effluent of the COST jet. The survival rate of the wild type without plasmid was set to 100%. wt: wild type, ev: empty vector, compl.: complemented strain.

The overall data of the screening suggested [Fe-S]-clusters to be major targets of plasma, since 17 of the 87 strains initially identified as plasma-sensitive lacked a gene related to iron, sulfur, or [Fe-S]-cluster metabolism. In *E. coli* there are two systems for maturation of [Fe-S]clusters: *isc* and *suf*. The *isc* system has a housekeeping function, while the *suf* system is active under stress conditions [12, 13]. Since [Fe-S]-proteins play a role in diverse biological processes (*e.g.* DNA repair or gene regulation) [12], an inactivation of [Fe-S]-clusters in the course of plasma treatment could lead to bacterial inactivation. Due to this fact, the plasma sensitivity of deletion mutants defective in the *isc* and *suf* operon was determined. An increased plasma sensitivity for most of the deletion mutants was observed (Fig. 2).

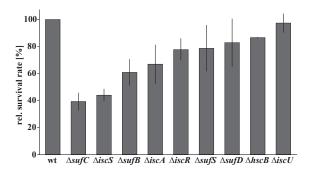


Fig. 2: Relative survival rates of the wild type and deletion mutants of the *isc* and *suf* operon after 30 s of plasma treatment. wt: wild type.

In vitro analysis of enzyme activities of the [Fe-S]-cluster free enzyme malate dehydrogenase and the [Fe-S]enzymes aconitase, succinate dehydrogenase, and fumarase revealed that [Fe-S]-enzymes are more susceptible to plasma-induced inactivation than other enzymes. An incubation of the cells for 20 min after plasma treatment led to higher enzyme activities of the [Fe-S]cluster containing enzymes, indicating a repair of damaged [Fe-S]-clusters. It is known that [Fe-S]-clusters are likely susceptible to O_2^- and H_2O_2 . Therefore, we investigated whether SodA or KatE provide any benefit for [Fe-S]clusters under plasma exposure. Overexpression of sodA, which protects against superoxide-induced damage, showed a positive effect on enzyme activities of succinate dehydrogenase and fumarase. Overexpression of katE, which protects against hydrogen peroxide, had a positive effect on enzyme activities of all [Fe-S]-cluster containing enzymes. Although many different radicals act on the cells during plasma treatment, the protection against hydrogen peroxide and superoxide seems to be critical for [Fe-S]enzymes for surviving plasma since an overexpression of a combination of *sodA* and *katE* completely protected the [Fe-S]-enzymes from plasma-induced damage (Fig.3).

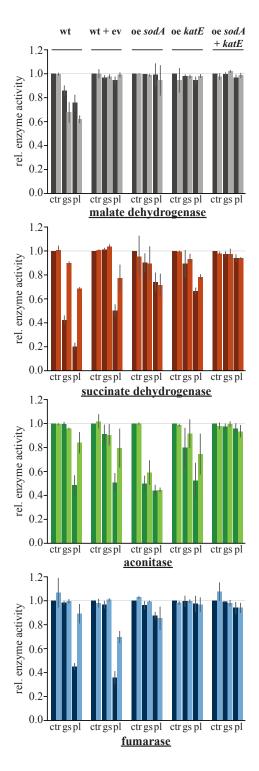


Fig. 3: Enzyme activities of the [Fe-S]-cluster-free enzyme malate dehydrogenase and [Fe-S]-enzymes aconitase, succinate dehydrogenase, and fumarase. Measurements were carried out without plasma treatment (ctr), after an exposure to helium/oxygen gas flow (gs) and after 1 min of plasma treatment (pl). Determination of enzyme activities was performed either directly after treatment (dark bars) or after incubation at 37°C for 20 min (light bars). wt: wild type, ev: empty vector, oe: overexpressing.

Conclusion

The KEIO collection, in which each non-essential gene of *E. coli* has been knocked out, was used to identify 87 plasma-sensitive deletion mutants. The increased plasma sensitivity of four deletion mutants was analysed in detail using a CFU-based assay. An overexpression of *iscS*, *rep*, and *cysB*, led to higher survival rates than observed for the wild type. Plasma resistance can thus be increased by elevated levels of a single protein. An upregulation of gene expression can emerge in bacteria, even at a higher rate due to the mutagenic effect of plasmas [14]. Our results indicate that plasma resistance can increase resulting in less sensitive strains. This may limit the clinical application of plasmas as antibacterial strategy.

Furthermore, the role of [Fe-S]-clusters in the course of bacterial inactivation by plasma was investigated. A comparison of enzyme activities after plasma treatment of [Fe-S]-enzymes and [Fe-S]-cluster free enzymes showed that [Fe-S]-enzymes are more susceptible to plasma than other enzymes. Moreover, an overexpression of *sodA* and *katE* completely protected the enzymes from plasma-induced damage, indicating that superoxide and hydrogen peroxide are presumably most important for [Fe-S]-cluster inactivation. Overall, our findings suggest that [Fe-S]-clusters could be the bottleneck in surviving plasma and that protective mechanisms (like overexpression of *sodA* and *katE*) mediate plasma resistance.

References

[1] A.A. Adegoke, A.C. Faleye, G. Singh and T.A. Stenström, Molecules, **22**, 29, (2017).

[2] J.W. Lackmann and J.E. Bandow, Applied Microbiology and Biotechnology, **98**, 6205, (2014).

[3] J. Golda, J. Held, B. Redeker, M. Konkowski, P. Beijer, A. Sobota, G. Kroesen, N.St.J. Braithwaite, S. Reuter and M.M. Turner, Journal of Physics D: Applied Physics. **49**, 084003, (2016).

[4] T. Baba, T. Ara, M. Hasegawa, Y. Takai, Y. Okumura, M. Baba, K.A. Datsenko, M. Tomita, B.L. Wanner and H. Mori, Molecular Systems Biology, **2**, 2006, (2006).

[5] M. Krewing, F. Jarzina, T. Dirks, B. Schubert, J. Benedikt, J.W. Lackmann and J.E. Bandow, Journal of the Royal Society Interface, **16**, 20180846, (2019).

[6] D.H. Flint, The Journal of Biological Chemistry, **271**, 16068, (1996).

[7] B. Py and F. Barras, Nature Reviews Microbiology, **8**, 436, (2010).

[8] G. Jagura-Burdzy and D. Hulanicka, Journal of Bacteriology, **147**, 744, (1981).

[9] T.M. Lohman, K. Chao, J.M. Green, S. Sage and G.T. Runyon, Journal of Biological Chemistry, **264**, 10139, (1989).

[10] K.P. Bjornson, I. Wong and T.M. Lohman, Journal of Molecular Biology, **263**: 411, (1996).

[11] H. Makui, E. Roig, S.T. Cole, J.D. Helmann, P. Gros and M.F. Cellier, Molecular Microbiology, **35**, 1065, (2000).

[12] B. Roche, L. Aussel, B. Ezraty, P. Mandin, B. Py and F. Barras, Biochimica et Biophysica Acta, **1827**, 455, (2013).

[13] W.S. Yeo, J.H. Lee, K.C. Lee and J.H. Roe, Molecular Microbiology, **61**, 206, (2006).

[14] X. Zhang, C. Zhang, Q.Q. Zhou, X.F. Zhang, L.Y. Wang, H.B. Chang, H.P. Li, Y. Oda and X.H. Xing, Applied Microbiology and Biotechnology, **99**, 5639, (2015).