## Common versus noble- *Bacillus subtilis* differentially responds to air and argon gas plasma

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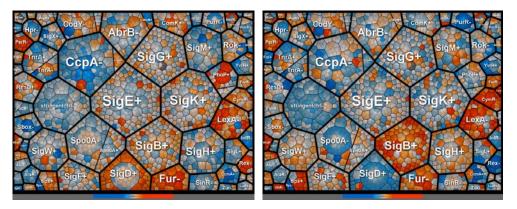
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The study of low temperature gas plasmas is not only a physicist's specific topic anymore. Especially since low temperature plasma is not only applied for decontamination and sterilization but also in the medical field in terms of wound and skin treatment.

In an initial study, the interaction between growing *Bacillus subtilis* and argon plasma was already investigated by using a growth chamber system suitable for low temperature gas plasma treatment of bacteria in liquid medium [1]. The gained results of this initial study are the basis of this now presented follow up investigation. Here, a second kind of plasma treatment- namely air plasma was applied [2]. With combined proteomic and transcriptomic analyses we are now able to investigate the plasma specific stress response of *B. subtilis* cells toward not only argon but also air plasma.

Besides an overlap of cellular responses due to both- argon and air plasma treatment (DNA damage and oxidative stress), a variety of gas dependent cellular responses such as growth retardation and morphological changes were observed. Only argon plasma treatments lead to a phosphate starvation response whereas air plasma induced the tryptophan operon implying damage by photo oxidation. Biological findings such as oxidative stress responses were supported by the detection of reactive plasma species by OES and FTIR measurements.



**Figure 1**: (*left*) Gene expression of argon plasma and (right) air plasma treated B. subtilis compared with untreated cells. Treemap design is based on hierarchically structured regulatory data (black borders: regulon/thin black borders within the regulons: operon/smallest cells: gene). To visualize differences in expression level compared with the average, level colour coding was applied as following: blue—decreased level, yellow—same level as average, orange—increased level.

[1] Winter, T., Winter, J., Polak, M., Kusch, K., *et al.*, Proteomics (2011), **11**, 3518-3530.
[2] Winter, T., Bernhardt, J., Winter, J., Mäder, U., *et al.*, PLoS One (2012), *in revision*.