

Impact of continuous Topical Oxygen Therapy on biofilm gene expression in a porcine tissue model

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Introduction

Up to 80% of chronic non-healing wounds contain a biofilm.¹

Oxygen and nutritional limitations in bacterial biofilms, particularly pronounced towards the centre,² can result in slow bacterial growth & metabolism.^{3,4} This reduced metabolism can lead to reduced efficacy of antibiotics against these communities.⁵

Supplemental oxygen has been shown to increase oxygen penetration into a biofilm with increased metabolism linked to subsequent increased susceptibility of biofilm bacteria to antibiotics demonstrated *in vitro*.^{6,7}

The aim of this *ex vivo* study was to determine the effect of continuous Topical Oxygen Therapy (cTOT) on *Pseudomonas aeruginosa* biofilm gene transcription profiles following inoculation onto porcine skin, using a customised molecular assay.

Methods

Sterilized porcine skin explants were inoculated with *P. aeruginosa* in triplicate (0h negative control, 24h cTOT on, 24h cTOT off). The oxygen delivery system (ODS) of the cTOT device was applied to the inoculated tissue and covered with a semi-occlusive dressing. All samples were incubated at 37°C ± 2°C for 24h with the 0h negative control inoculated porcine skin samples recovered immediately.

Planktonic suspensions and porcine skin biopsy samples were taken at 0 and 24h. Samples were processed and quantifiably assessed using gene specific RT-qPCR assays for a panel of eight *P. aeruginosa* genes (16S, *pelA*, *pslA*, *rsaL*, *pcrV*, *pscQ*, *acpP*, *cbrA*) associated with biofilm formation, quorum sensing, protein secretion/translocation and metabolism.

*cTOT device tested was NATROX® O₂ Wound Therapy

Results



Figure 1. A) cTOT device placed onto inoculated porcine skin, B) skin & cTOT device covered with 10 cm x 10 cm semi-permeable dressing, C) Final assay result following 24 hour humidified incubation at 37 °C ± 2 °C.



Transcriptional **up-regulation** of genes linked to increased metabolism (*pelA*, *pcrV* and *acpP*)

Transcriptional **down-regulation** of genes linked to biofilm formation (*cbrA*, *pscQ*, *pslA*)

Suggests **increased** metabolic activity within bacterial cells and **less** requirement to form biofilm following cTOT treatment

Gene	Function	SAMPLE		
		0 hour negative control	24 h cTOT device off	24 h cTOT device on
<i>pelA</i>	Intracellular adhesin			
<i>pslA</i>	AMR & Biofilm structure (exopolysaccharide synthesis)			
<i>rsaL</i>	Transcription regulator for transition to biofilm			
<i>pcrV</i>	Needle-tip protein, secretion			
<i>pscQ</i>	Quorum sensing system translocation protein			
<i>acpP</i>	Fatty acid synthesis			
<i>cbrA</i>	Regulator biofilm genes, carbon and nitrogen utilization			

AMR = Antimicrobial Resistance

Figure 2. Heat map representation of the gene transcription profiles for the seven genes investigated following 24 hours incubation with cTOT device on or off.

Red = significant up-regulation, Blue = significant down-regulation, white = no significant change in gene expression

Discussion

cTOT is an adjunctive therapy that supports faster healing⁸⁻¹⁰ and pain reduction¹¹ in non-healing hypoxic wounds. Data in this study suggests increased metabolic activity within bacterial cells following cTOT treatment. Oxygen has previously been shown to increase susceptibility of biofilms to antibiotics⁷ through enhancing metabolism.

Observed gene expression changes here highlight the impact of cTOT on biofilms potentially influencing antimicrobial treatment success in wounds warranting further *in vitro* and clinical investigations.

References

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