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Project Title

Structural mapping of the *in vivo Pseudomonas aeruginosa* biofilm matrix exopolysaccharide, Psl, does it change with virulence?

Summary

Quantitative 3D mapping of Psl exopolysaccharide in 72 murine tissue samples using IHC, CLSM and automated ZEISS Intellesis segmentation to correlate biofilm structure with genotypic virulence.

My Role: Lead Researcher - designed wet-lab pipeline, imaging workflow and automated image-analysis.

Methods

Sample prep	Tissue fixation, embedding, H&E, IHC staining, PA01 antibody, HHL-TRITC, POPO1.
Imaging	Confocal Microscopy (CLSM), ZEISS Axioscan Slide scanner, fluorescent, brightfield & pol
Image Analysis	ZEISS Intellesis machine-learning segmentation pipeline; and metrics quantification
Stats and Plots	Data cleaning and statistics in R and GraphPad Prism (Two-way RM ANOVA, post-hoc tests, correlation tests).

Key Results

• Processed and analysed **72 tissue samples** with a consistent imaging pipeline. Automated segmentation reduced manual processing time by **~70%** and produced reproducible volume metrics (CV < 8%).
• Statistically significant correlation between Psl volume and virulence genotype ($p < 0.01$). Biofilm/ aggregate is not solely dependent on Psl expression levels.

Impact / Takeaway

Provided a reproducible, high-throughput imaging + analysis pipeline enabling data-driven comparisons across genotypes - directly translatable to assay validation or phenotypic screens.

Images and Plots

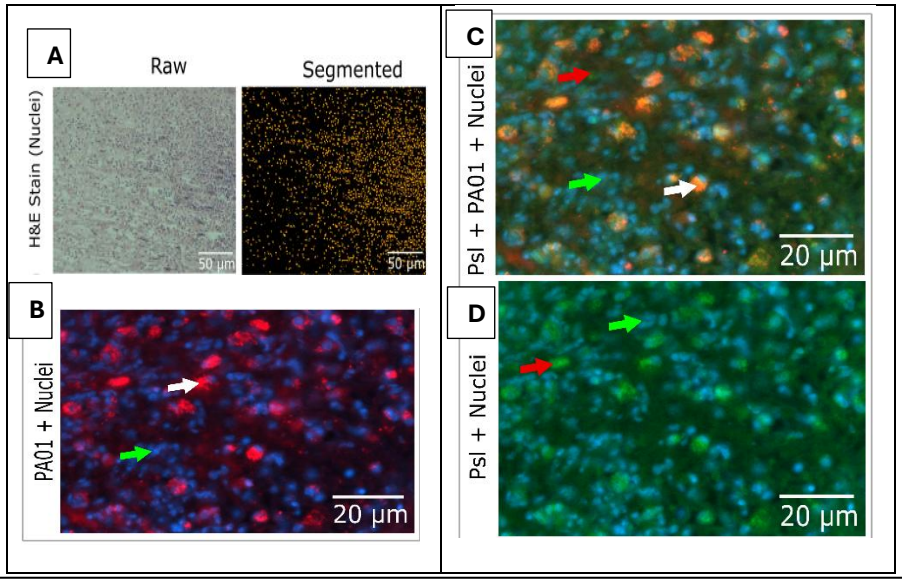

Figure X. (A) Representative ROIs stained with H&E and acquired using ZEISS Axioscan 7 slide scanner 20× objective. Raw images were segmented and analysed in ZEISS Intellesis.

(B-D) Representative image (CE group) showing bacterial aggregates (white arrows), Psl clusters (red arrows) and host nuclei (POPO-1, green arrows). Acquired on ZEISS Axioscan 7, 20×; scale bar = 20 µm.

Available for discussion. Full Psl quantitative and reproducible analysis: [GitHub link or Portfolio PDF]