UNIVERSITY OF BIRMINGHAM

Molecular Cartography of ‘Healthy’ and ‘Diseased’ Gingival Tissues

BACKGROUND INFO

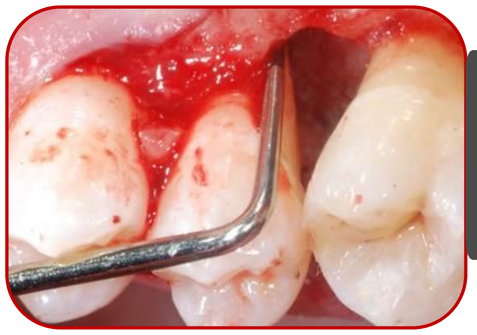
- Periodontitis: the most common non-communicable disease in humans
- Caused by a destructive interaction between dysbiotic biofilm and dysregulated host immune-inflammatory response, leads to tooth loss and associated with pre-mature mortality
- Pathophysiological mechanisms only incompletely understood

We **aim** to identify the spatial transcriptomic signatures that

(i) define the transition from ‘healthy’ to ‘diseased’ status,

(ii) help explain the potential differences of grade B (‘moderate’ progression) to grade C (‘fast progression’) periodontitis, and

(iii) can be linked to specific bacterial-host interactions



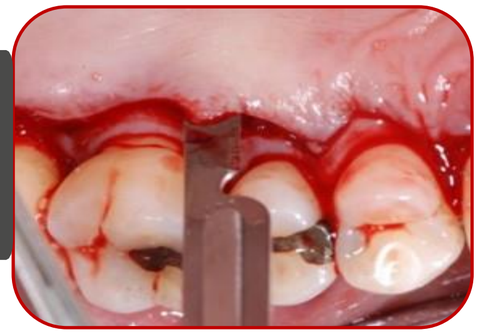


Figure 1: Sample Harvesting (right) and Intra-operative Situation (left)

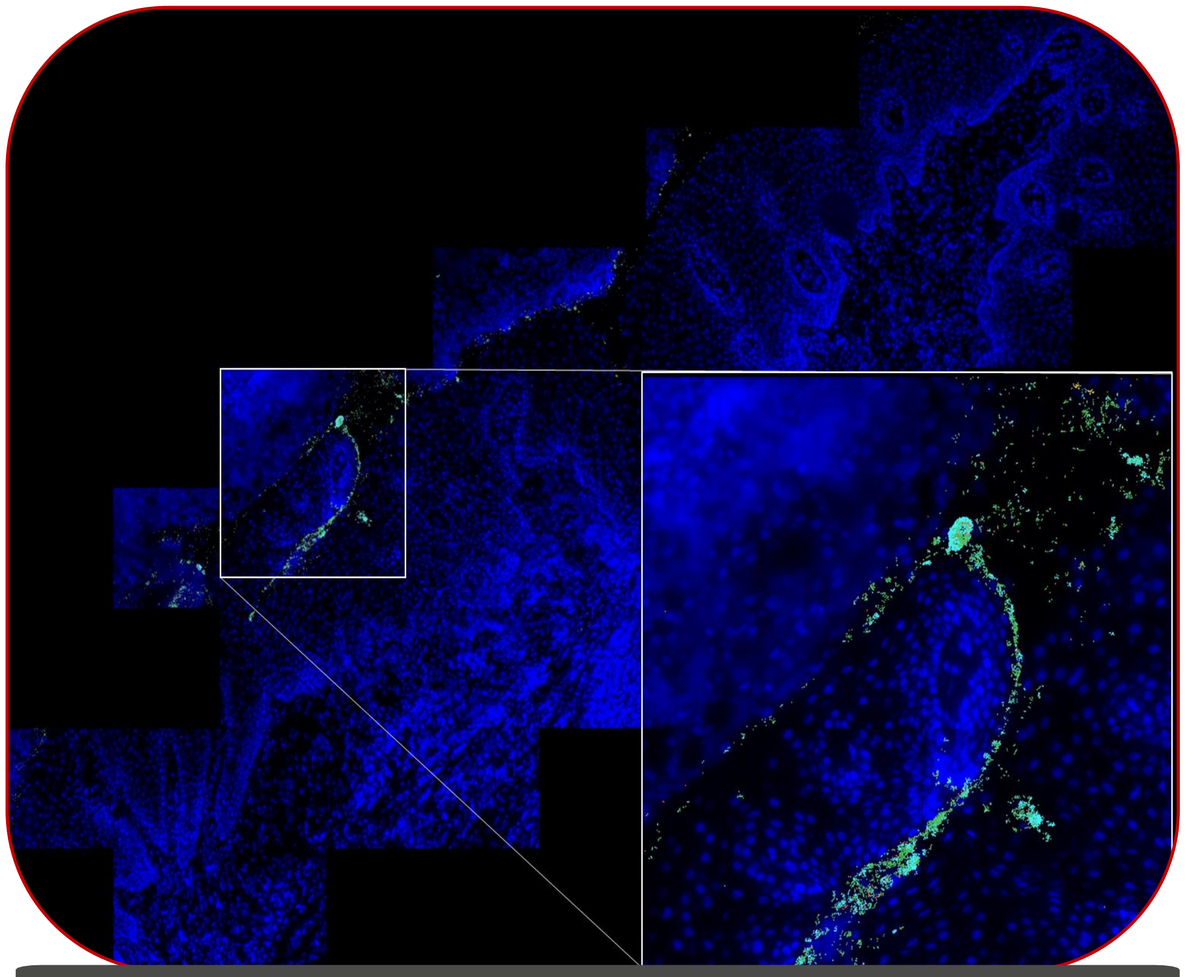


Figure 3: Bacterial Signals (green) in Diseased Tissue Sample

METHODS

- Assessment of gingival tissue samples using Resolve Molecular Cartography technology **(Figure 2)** coupled to meta-genomic sequencing of associated subgingival biofilms using Illumina technology
- Systemically healthy non-smokers contributed (**Figure 1**)

  (i) ‘diseased’ gingival papilla (bleeding-on-probing, probing depth ≥4mm, clinical attachment loss ≥3mm)

  (ii) ’healthy’ papilla (no bleeding-on-probing, probing depth ≤4mm, and clinical attachment loss ≤4mm)
- Mixed model regression utilized for assessment of specific differences between disease groups, clusters of characteristic signatures identified using mixture model-based clustering whilst accounting for covariates

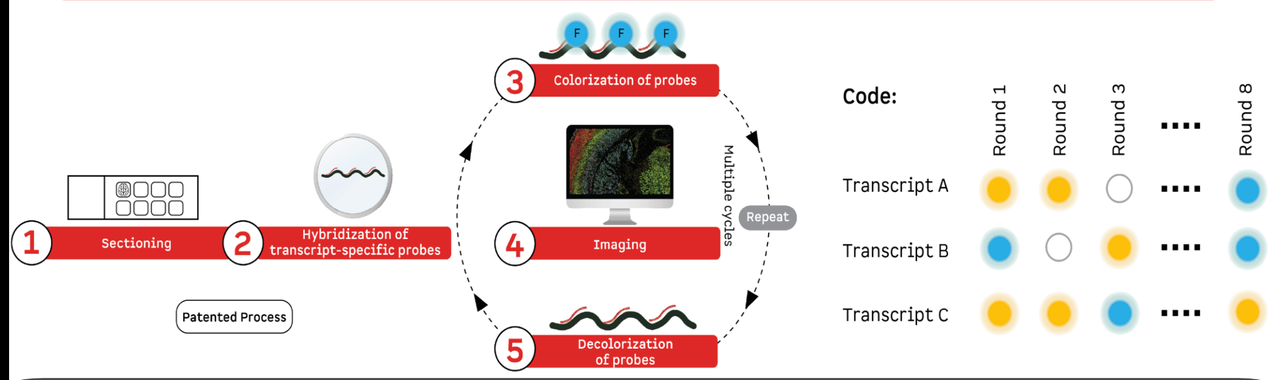


Figure 2: Workflow Diagram of the Resolve Molecular Cartography Technology

RESULTS

- Specific spatial transcriptomic signatures exist, that

  (i) help differentiate ‘healthy’ and ‘diseased’ status

  (ii) different progression rates
- These signatures can be contributed to defined cell populations and locations within tissues
- Driven by specific microbial complexes (**Figure 3**)

CONCLUSION

These findings could help to improve early diagnostics of progressive disease, as well as inform targeted therapeutic approaches.

REFERENCES

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