A tale from 30 French vineyards: how shifts in bacterial and fungal species shape microbial communities from vine to wine

Marie Belair[a], Flora Pensec[a], Adeline Picot[a], Adrien Destanque[a,b], Laurence Guérin[b], Emmanuel Coton[a], Marion Hervé[b], Monika Coton[a]

a- Univ Brest, INRAE, Laboratoire Universitaire de Biodiversité et Ecologie Microbienne, F-29280 Plouzané, France
b- Centre de Recherche Robert-Jean de Vogüé Moët-Hennessy, F-51530 Oiry, France

Grape berry quality is highly influenced by the pedoclimatic conditions in vineyards and specific microbial communities colonizing the berry surface during ripening. Yet, microbial community shifts from vine to wine have not been fully explored, especially mycobiota. Fungi are well-known producers of volatile organic compounds (VOCs) that may impact wine quality. Some fungi as well as their interactions may contribute to wine defects such as fresh mushroom aroma (FMA).

To decipher the microbial succession from vine to wine, we monitored bacterial and fungal communities in 30 vineyards at five different stages from vine to wine during three successive years (2021-23). Climatic conditions, vine data and growing practices were recorded. The cultural and metabarcoding data generated were compared with sensorial analyses of still wines resulting from 30 grape must micro-vinifications to determine to what extent fungal composition and microbial interactions led to the FMA defect in wines.

We observed distinct shifts in microbial communities, mainly influenced by climatic data and berry ripening stage. In the early stages, yeasts dominated followed by a progressive increase in mold diversity. Climatic conditions not only shaped mycobiota but also played a crucial role in FMA detection in wines. Wines exhibiting FMA off odors were linked to vineyards with higher precipitation and lower temperatures during the 2021 and 2023 growing seasons. FMA was primarily linked to higher fungal counts and *Penicillium* species, especially *Penicillium crocicola* among the fifteen *Penicillium* species identified.

Overall, our results advance the understanding of how microbial communities evolve from vine to wine. We showed how specific individual and co-cultured grape-associated fungi thrived on berries and induced FMA off odors. This research provides the groundwork to put in place better vineyard and wine management practices including the possible use of the identified repressive species to control fungal populations on berries.

Effet du sexe sur la réponse cardiovasculaire au choc septique

Maikel Assaf[a*], Maël Blandin[ab*], Sylvain Gourier[ac], Thomas Castel[a], Michael Theron[a], Karine Pichavant-Rafini[a], Karelle Léon[a]

a- Univ. Brest, ORPHY EA4324, Brest, France
b- Département de Médecine d'Urgence (SAU, SAMU 29, SMUR), Centre Hospitalier Universitaire de
Brest, France
c- Service d'Anesthésie-Réanimation et Médecine Péri-Opératoire, Centre Hospitalier, France

Introduction : Le sepsis est une réponse inflammatoire systémique excessive survenant suite à une infection, menant à une défaillance multiviscérale et représentant la principale cause de mortalité en unités de soins intensifs [1]. Les atteintes cardiovasculaires sont responsables de 90 % de cette mortalité. Elles impliquent, entre autres, une altération de la contractilité myocardique et des perturbations de la circulation systémique [2]. Si des spécificités cardiovasculaires ont été observées selon le sexe, l'influence de ce dernier sur la physiopathologie du sepsis reste peu explorée et mal comprise [3]. Dans ce contexte, ce projet vise à évaluer l'impact du sexe sur les altérations de la contraction cardiaque, ainsi que sur la vasomotricité de l'aorte thoracique induites par le sepsis.

Matériel et méthodes : Un modèle murin de sepsis induit par ponction et ligature du caecum (CLP) a été utilisé (60 rats Wistar, 30 mâles et 30 femelles). Les capacités contractiles cardiaques ont été déterminées par myographie aux temps 0, 1 et 3 heures après l'induction du sepsis. Les réponses vasomotrices ont également été analysées sur des anneaux d'aorte thoracique isolés en réponse à l'acétylcholine (10^{-10} à 10^{-4} M), à la phényléphrine (10^{-9} à 10^{-4} M) et au nitroprussiate de sodium (10^{-10} à 10^{-4} M).

Résultats : À une fréquence de stimulation de 1 Hz, une augmentation significative de la force de contraction des trabécules du ventricule gauche a été observée chez les femelles septiques à 3 h, comparées aux femelles contrôles à 0 h (*p=0.046*) et à 1 h (*p=0.0367*). Cette augmentation n'est pas retrouvée chez les mâles septiques. Par ailleurs, comparativement aux femelles, l'aorte des mâles à 3 h présente une diminution de la vasorelaxation endothélium dépendante induite par l'acétylcholine aux concentrations 10^{-7} (*p=0.0076*), 10^{-6} (*p=0.0053*), 10^{-5} (*p=0.0012*) et 10^{-4}M (*p=0.0013*). Aucune différence n'a été observée concernant les réponses à la phényléphrine ou au nitroprussiate de sodium.

Conclusion : Ces résultats mettent en évidence des différences entre mâles et femelles dans la réponse cardiovasculaire au sepsis. Les résultats suggèrent ainsi une vulnérabilité vasculaire endothéliale accrue chez les mâles et une meilleure adaptation de la réponse cardiaque chez les femelles.

Références.

1. X. Yu, J. Gao, C. Zhang. Intensive Care Medicine Experimental, 2025, Sepsis-induced cardiac dysfunction: mitochondria and energy metabolism.

2. J.Q. Yap, et al. International Journal of Molecular Sciences, 2023, Mitochondria at the Heart of Sepsis: Mechanisms, Metabolism, and Sex Differences.
3. C.A. Shields, X. Wang, D.C. Cornelius. American Journal of Physiology, 2022, Sex differences in cardiovascular response to sepsis.

Comparative Incidence of Decompression Sickness and Microparticles Release in Heliox vs. Nitrox Simulated Dives in Rats

Jérémy Orsat[a], Michel Mandin[a], Thomas Castel[a], Géraldine Leman[a], Nathalie Guegueniat[a], Marie-Dominique Jezequel[a], Guillaume Gilbert[a], Michaël Théron[a], François Guerrero[a], Emmanuel Dugrenot[a,b,c,d]

a: Univ Brest, Laboratory ORPHY EA4324, IBSAM, F-29200 Brest, France (jeremy.orsat@univ-brest.fr)
b: Divers Alert Network, Durham, NC27707 USA
c: Lampe Joint Department of Biomedical Engineering, The University of North Carolina and North Carolina State University, Chapel Hill, NC 27599, USA
d: Subaquatic Operational Research Team (ERRSO), Military Institute of Biomedical Research (IRBA), 83000 Toulon, France

Introduction / Background: Decompression sickness (DCS) is driven by gas bubble formation after scuba diving and a subsequent thromboinflammatory response. Extracellular vesicles (EV) and especially microparticles (MPs) have emerged as potential mediators of this inflammatory cascade. While the physical properties of helium versus nitrogen, two widely used inert respiratory gases, are well-documented, the biological impact on MPs release and content remains poorly understood. This study aims to evaluate DCS outcomes and characterize MPs subtypes in a rat model using identical heliox and nitrox profiles.

Methods: Male Sprague Dawley rats (n=12/group) underwent simulated dives in a 40-L hyperbaric chamber, compressed to 700 kPa (200 kPa/min) for 90 min and decompressed at 50 kPa/min. Two gas mixtures were compared: Nitrox 21% (79% N_2, 21% O_2) and Heliox 21% (79% He, 21% O_2). After decompression, rats were monitored for 60 min for DCS signs and blood was collected for MPs isolation. Control rats were exposed to the same gases at atmospheric pressure (n=6/group). MPs were characterized by flow cytometry using thromboinflammatory markers (P-selectin, CD142, phalloidin, thrombospondin).

Results: Despite identical pressure–time profiles, DCS incidence differed significantly between gas mixtures. Severe DCS occurred in 83% of Nitrox 21% dives versus 33% with Heliox 21%. Flow cytometry revealed a significant reduction in MPs concentration in helium-diving rats without DCS compared with helium controls ($p = 0.0317$), accompanied by lower proportions of CD142 ($p = 0.02214$) and phalloidin-positive MPs ($p = 0.01502$). In nitrogen dives, DCS rats showed a trend toward increased MPs concentration ($p = 0.0992$) and a reduced proportion of thrombospondin-positive MPs ($p = 0.01931$). Further analyses, including OMICS profiling (proteins, mRNA, miRNA), are ongoing.

Summary / Conclusion: In this rat model, helium-based decompression resulted in a lower incidence of DCS associated with a decrease in pro-inflammatory/coagulant MPs.

AltraFlowSOM: A Semi-Supervised Framework for Scalable Phenotyping of Imaging Mass Cytometry Data

Akhiya Anilkumar. Rekha[1,2], Eléonore Bettacchioli[1], Christelle Le Dantec[1], Divi Cornec[1], Pierre Emmanuel Jouve[2], Sophie Hillion[1]**

1. Lymphocytes B, Autoimmunité et Immunothérapies - LBAI (UMR 1227), Université de Bretagne-Occidentale
2. AltraBio SAS, Lyon France

Background : Imaging Mass Cytometry (IMC) enables high-dimensional spatial profiling of complex tissue microenvironments, yet current analysis pipelines still rely heavily on unsupervised clustering followed by manual post-hoc annotation. While expert annotation is essential for assigning biological meaningful populations, the upstream clustering step is performed without biological priors and can be strongly influenced by technical variation, leading to clusters that are not immediately biologically interpretable. This workflow is labour-intensive, difficult to scale, and becomes increasingly challenging in large multi-sample datasets, where batch effects and data heterogeneity can obscure rare but biologically important cell populations and reduce the biological meaningfulness of clustering**.**

Objectives : Develop and evaluate a semi-supervised clustering tool that better aligns with the biological knowledge that scales with larger datasets, possibly reducing the cons of classical workflow.

Methods : We developed AltraFlowSOM, a semi-supervised extension of the FlowSOM framework. AltraFlowSOM extends the FlowSOM framework by incorporating Supervised Self Organizing Maps (SSOM's) an existing supervised extension of SOM to integrate partial expert annotations directly into the clustering process, thereby guiding the formation of clusters toward biologically meaningful populations. The framework merges raw marker expression with biological knowledge layers (e.g., manual gating labels) using a multi-layer SSOM architecture. This guides cluster formation toward biologically relevant phenotypes while preserving the ability to discover previously unrecognized populations.

We benchmarked the performances across major analytical strategies, including:

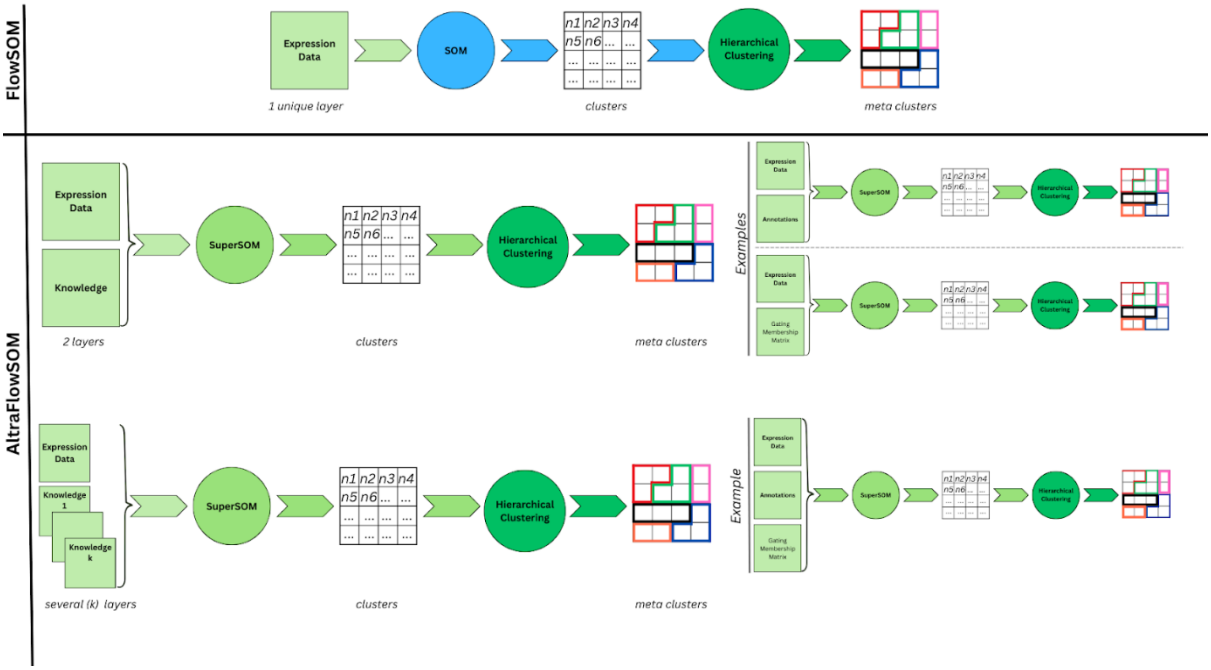
- Unsupervised (FlowSOM & Phenograph, with and without batch-effect correction)
- Supervised learning (Random Forest)
- AltraFlowSOM (semi-supervised)

Two independent IMC datasets were used for evaluation; Lupus Nephritis (n=22) and Sjögren's Disease (n=10).

Results : AltraFlowSOM achieved the highest concordance with manually gated ground truth, outperforming FlowSOM, Phenograph (with and without batch correction), and Random Forest across Adjusted Rand Index (ARI), purity and F1-score metrics. High performance persisted even under full supervision and when only partial annotations were available; models trained on only a subset of samples performed comparably to those trained on fully annotated datasets. Using a leave-one-out strategy, training on (n-

1) samples and testing on the remaining held-out sample, AltraFlowSOM demonstrated strong generalizability across unseen patient samples and across disease indications. The method improved resolution of rare and biologically meaningful cell populations, and produced phenotypes that aligned more closely with known immunobiology.

Conclusion : AltraFlowSOM integrates expert knowledge directly into cluster formation, bridging the gap between manual gating and automated phenotyping. It enhances biological interpretability, increases sensitivity to rare populations, and provides a scalable, generalizable tool for high-dimensional IMC data. This framework supports reproducible, biologically informed cellular phenotyping in autoimmune disease research and is broadly applicable across spatial and single-cell cytometry platforms.



Références.

1- Jackson, H. W., Fischer, J. R., Zanotelli, V. R. T., Ali, H. R., Mechera, R., Soysal, S. D., … & Bodenmiller, B. (2020). The single-cell pathology landscape of breast cancer. Nature, 578(7796), 615–620. https://doi.org/10.1038/s41586-019-1876-x

2- Van Gassen, S., Callebaut, B., Van Helden, M. J., Lambrecht, B. N., Demeester, P., Dhaene, T., & Saeys, Y. (2015). FlowSOM: Using self-organizing maps for visualization and interpretation of cytometry data. Cytometry Part A, 87(7), 636–645.