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Mining the Human Microbiome for Bioactive Small Molecules

Bacteria use small molecule chemicals to interact with each other and with their eukaryotic host. We use a combination of activity-driven and genomics-driven approaches to mine the human commensal microbiota for bioactive molecules, as well as the genes that encode their production. The ClusterFinder algorithm was developed to scan bacterial DNA for biosynthetic gene clusters (BGCs), identifying new classes of chemical compounds. Genetic and biochemical characterization of identified BGCs from skin bacteria revealed molecules with antibacterial, biofilm inducing and immunomodulatory functions. The identification of small molecule interactors produced by human commensals contributes to a better understanding of the complex interplay that is taking place in the communities from our microbiome. This will facilitate the development of therapeutic strategies to influence community structures with the aim to eliminate already established pathogens or inhibit their colonization prior to hospitalization.

Vendredi 10 mars 2017 à 11 h 30
Pavillon Roger-Gaudry, salle P-217

EN VISIOCONFÉRENCE :
Campus de Saint-Hyacinthe, salle 2115
Campus de la Mauricie, salle U4-418, 4e Étage du Pavillon d’Enseignement
Hôpital Maisonneuve-Rosemont, salle 11, 1er étage du Pavillon J-A Desève
Hôpital du Sacré-Cœur de Montréal, salle G4115
Hôpital Notre-Dame du CHUM, salle K6202
Hôtel-Dieu du CHUM, salle 2-423

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