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Symbiotic associations are widespread in nature, and constitute a driving force in the evolution of organisms. However, the interactions between partners that lead to the establishment, the specificity and the evolution of the association are oftentimes difficult to study. We used the binary mutualistic association between the squid *Euprymna scolopes* and the luminescent bacterium *Vibrio fischeri* as a natural model to study the dialogue between partners that facilitates the selection and colonization of the symbiont into host tissues, but also its maintenance over a strong diel rhythm. We coupled comparative transcriptomics analyses and functional characterizations to better understand how the initial molecular conversation between the two partners plays a role in determining the specificity of the association. We also studied the influence of the presence of a persistent luminous bacterium on the gene expression and physiology of its host. These studies reveal that a very limited number of symbionts is sufficient to reprogram host gene expression, leading to the specific establishment of the interaction and the building of its extended phenotype.

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Résumé: On s'accorde généralement à dire qu'il faut améliorer la sélectivité des engins de pêche, et réduire le gaspillage dû au rejet des captures non désirées prises dans les engins non sélectifs comme les chaluts. C'est même un sujet brûlant de la réforme en cours de la Politique Commune des Pêches de l'Union Européenne. D'un autre côté, l'approche écosystémique des pêches requiert que l'on préserve la structure et la fonction des écosystèmes exploités. Cela est-il compatible avec le prélèvement par la pêche de catégories restreintes d'animaux, par exemple les plus grands, ou quelques espèces d'intérêt commercial dans une communauté qui en compte plusieurs dizaines ? Je présenterai des résultats de modèles qui confirment cette intuition, et les premières tentatives d'analyses empiriques de cette question.

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## "Quand la demographie part a la rencontre de la biologie evolutive"

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One of the most fundamental issues in biology is the nature of evolutionary transitions from single cell organisms to multicellular ones. Not surprisingly for microscopic life in a fluid environment, many of the processes involved are related to transport and locomotion, for efficient exchange of chemical species with the environment is one of the most basic features of life. This is particularly so in the case of flagellated eukaryotes such as green algae, whose members serve as model organisms for the study of transitions to multicellularity. In this talk I will summarize recent theoretical and experimental work addressing a number of interrelated aspects of evolutionary transitions in the Volvocine green algae, which range from unicellular *Chlamydomonas* to *Volvox*, with thousands of cells. Phenomena to be discussed include allometry of nutrient uptake, phenotypic plasticity, flagellar synchronization, hydrodynamic bound states, and the dynamics of adaptive phototaxis. For more details, see <http://www.cgmc.univ-lyon1.fr/Semovi/13octobre2010.php>

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One of the principal questions in the study of animal-bacterial interactions is: What are the cellular and molecular differences between beneficial and pathogenic associations? The study of several invertebrate symbioses has demonstrated that, although the outcomes are different, beneficial and pathogenic associations share much of the same molecular language. This presentation will focus upon contributions to the field made by the study of the relationship between the Hawaiian bobtail squid *Euprymna scolopes* and its luminous bacterial partner *Vibrio fischeri*. In this symbiosis, the bacteria are acquired anew each generation and form persistent interactions along the apical surfaces of host epithelia, a pattern of symbiosis that is perhaps the most widespread among animals. The mechanisms underlying the processes of host-symbiont recognition, induction of partner development, and the maintenance of a balanced relationship will be highlighted.

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### **“ArthropodaCyc”: a BioCyc database powered by CycADS to study and compare the metabolism of arthropods (<https://hal.inrae.fr/hal-02749029>)**

Patrice Baa-Puyoulet, Augusto Vellozo, Jaime Huerta-Cepas, Gérard Febvay, Toni Gabaldon, Marie-France Sagot, Hubert Charles, Stefano Colella

20/08/2022

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### **“False heat,” big testes, and the onset of natal dispersal in European pine Martens (*Martes martes*) (<https://hal.science/hal-02025587>)**

Jeremy Larroque, Sandrine Ruet, Jean-Michel Vandel, Sébastien Devillard

12/06/2022

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### **“One code to find them all”: a perl tool to conveniently parse RepeatMasker output files (<https://hal.sorbonne-universite.fr/hal-01332104>)**

Marc Bailly-Bechet, Annabelle Haudry, Emmanuelle Lerat

12/06/2022

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### **« ArthropodaCyc » : une collection de bases de données enrichies à l’aide de CycADS pour étudier et comparer le métabolisme des arthropodes. (<https://hal.inrae.fr/hal-03506713>)**

Patrice Baa-Puyoulet, Stefano Colella, Augusto Vellozo, Jaime Huerta-Cepas, Gérard Febvay, Federica Calevro, Toni Gabaldon, Marie-France Sagot, Hubert Charles

29/07/2022

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#### NEWS

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Clémence Beslay, Mary Bouix, Henri Fauroux, Amandine Gautier, Francesco Luposella, Jean-Marie Pillon, Thibaud Porphyre, Marilynne Schell, Nathan Soleau

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01/07/2022

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