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# Linking Allele-Specific Expression and Natural selection in wild population of *Oithona similis*

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## Abstract

Allele-specific expression (ASE) is now a molecular mechanism widely studied at the cell and organism-levels. However, population-level ASE and its evolutive impacts have still never been investigated. Here, we deciphered the potential link between ASE and natural selection. As a model, we used metagenomic and metatranscriptomic data of seven wild populations of the marine copepod *Oithona similis* from Tara Consortium sampling in the Arctic Seas. We were able to (i) Study the structure between these populations, (ii) Detect variants under local adaptation, (iii) Develop a method to detect variants under ASE. We found a significant amount of variants under ASE in at least one population and under selection across all the populations, proving that a link exists between these two molecular mechanisms. The next step of this work is to determine the nature of the link between ASE and selection.

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