
Lignocellulose degradation at the holobiont level: teamwork in a keystone soil invertebrate

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Abstract

Lignocellulose is the main component of plants and is composed of cellulose, lignin and hemicellulose. Its degradation requires the collective action of diverse Carbohydrate-Active enZymes (called CAZymes). Many invertebrates express few lignocellulose-degrading enzymes, but in most of them efficient degradation of lignocellulose is only possible thanks to mutualistic associations with endosymbionts.

Due to their important role in the decomposition of organic matter, terrestrial isopods are recognised as keystone species in terrestrial ecosystems. Past studies have shown that they can digest cellulose and are able to produce some endogenous cellulases (Kostanjsek et al. 2010). Although marine isopods like *Limnoria quadripunctata* secrete all the enzymes necessary for cellulose digestion in the absence of gut microbes (King et al. 2010), terrestrial isopods would not be able to digest cellulose without the help of their microbiota (Bouchon et al. 2016). Similar to termites, it has been suspected that several hepatopancreatic symbionts may be involved in the lignocellulose degradation in terrestrial isopods completing the CAZyme repertoire of their hosts (Zimmer et al. 2002).

To test this hypothesis, transcriptomic and metagenomic approaches have been used in the pill bug *Armadillidium vulgare*. We identified the CAZyme repertoire from both the microbiome and the isopod host. Depending on CAZyme families, complementary as well as redundancy between host and microbiome repertoires were recorded. Tissue specific expression of some representative of the host CAZymes were shown. Experimental diet manipulations showed that the expression of these CAZymes was modified in correlation with the modification of the microbiote. Our results provide an insight into the role of the microbiome in the evolution of terrestrial isopods and their adaptive radiation in terrestrial habitat.

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