# LATTECO

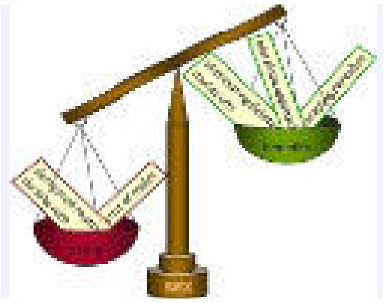
## Lateral gene transfer as a radically novel mechanism for ecological adaptations

| DURATION | BUDGET |
|---|---|
| **15/12/2014 - 10/09/2018** | **149 601 €** |

### PROJECT DESCRIPTION

**Context**

Novel gene combinations provide the evolutionary arena on which natural selection will act. In most higher animals, this is achieved by meiotic recombination as part of sexual reproduction. Bacteria do not have germ lines and thus do not have sex. Nevertheless, they can effectively and rapidly exchange genetic material horizontally through lateral gene transfer (LGT). Evolutionary patterns in the tree of life have long been regarded to be fundamentally different between bacteria and higher organisms, with LGT being limited to the prokaryotic world. New, high-throughput sequencing techniques have meanwhile demonstrated that also higher organisms can have LGT including algae, invertebrates and higher plants. Genes coming from bacteria have provided novel adaptations to extreme environments, such as ice (Raymond & Kim 2012) or heat (Schönknecht et al. 2013).



*LATTECO - paradox of sex. (D. Lamatsch).*

However, the frequency of foreign genes in most host genomes is with 0.001 and 0.01% very low (Schönknecht et al. 2014). In two noticeable exceptions, foreign genes comprise several % of host genomes and originate from bacteria, fungi or plants. The root knot nematode Meloidogyne incognita has a global distribution and parasitizes a wide range of plant hosts, including many agricultural important crops. Its genome contains around 3% of foreign genes (Paganini et al. 2012). It has even been postulated that this nematode and related species could only develop a parasitic lifestyle because of the horizontal acquisition of these genes (Danchin et al. 2010). Two species of bdelloid rotifers, Adineta ricciae (Boschetti et al. 2012) and A. vaga (Gladyshev et al. 2008; Flot et al. 2013), contain up to 8-9% of foreign genes. Interestingly, the nematode M. incognita as well as these two bdelloids reproduce asexually, thus having lost the possibility to acquire novel gene combinations through sexual recombination.

**General objectives and underlying research questions**

LATTECO will investigate whether novel genes have also been acquired by LGT in the ostracod Darwinula stevensoni. We chose this micro-crustacean as model species because it is of old age (several million years), is a putative ancient asexual and has a wide ecological tolerance. We will estimate the frequency of possible LGT events in these ostracods, what the functions of these foreign genes are and who the potential donors could have been.

*LATTECO - Darwinula stevensoni, model organism (K. Martens 1998. Sex and parthenogenesis)*

**Methodology**

We will conduct metagenomics studies on D. stevensoni, because bacteria could have potentially have acted as donors for LGT. We will also culture ostracods to test for any possible ecological effects of bacteria which they might host. We will obtain large scale transcriptome (RNA) data from D. stevensoni and identify candidate genes for LGT within these transcriptomes, using automated bioinformatic pipelines. We will localize any possible foreign genes in an existing genomic cosmid library of D. stevensoni and sequence those among their genomic DNA background (thus eliminating contaminations). We will apply bioinformatics analyses on the obtained sequence data to confirm candidate cases of LGT and to predict the putative functions of these foreign genes.

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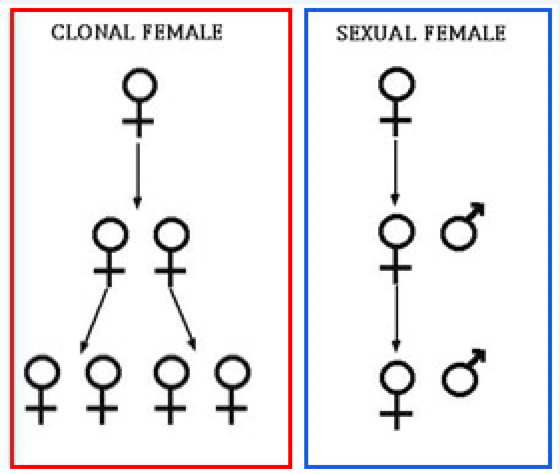
## Potential impact of the research on science, society and/or on decision-making

The question how organisms adapt to changing environments is becoming increasingly important in view of climate change. Mutations and the creation of novel gene combinations through sexual recombination have long been regarded as the main instruments of eukaryotes for adaptive evolution. LGT across the different domains of life could offer another, equally important but so far mainly overlooked mechanism. Higher rates of LGT in metazoans to date have been observed in asexually-reproducing species. For our understanding of how organisms adapt and change, it is essential to assess how frequent LGT is in various eukaryotic groups from different habitats and which categories of genes are preferentially transferred (if any). This has important applications for evolution and science in general, challenging the metaphor of the tree of life with strictly separated domains for eubacteria, archaea, animals, fungi, higher plants etc. LGT will also have important implications for society, especially for pest management, medicine and agriculture. Many agriculturally used crops or aquacultures consist of monocultures and/or clonal lineages with very little or no genetic variation and high risk for insufficient adaptive potentials. But the frequency of LGT in these organisms is as good as unknown. The impact of LGT for medicine and human health has also been recently proposed by the group of JC Dunning Hotopp (Robinson et al. 2013; Riley et al. 2013). They showed that the rate of LGT with bacterial origin was higher in human cancer samples compared to controls. The proposed research has also important implications in biotechnological decision making, including biosafety of genetically engineered bacteria and eukaryotes.

## Description of finished products of research

We will produce publications in scientific journals, presentations at conferences and press releases to inform public and decision makers of the most relevant results.



*LATTECO - cost of males. (D. Lamatsch)*

## CONTACT INFORMATION

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