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**Individual registration form**

To send via email to mailto:frederic.bringaud@u-bordeaux.fr; lkohl@mnhn.fr; rotureau@pasteur.fr

Before November 10th 2017

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This free registration includes a full access to all the conference sessions, two coffee breaks, two lunches and one cocktail.

The conference diner will be organized in a Parisian restaurant and directly paid by the attendees, however registration is mandatory.

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**Last name: Peylhard**

**First name: Moana**

**Position** (PI, engineer, post-doc, PhD or Student): PhD

**Affiliation: CIRAD BIOS UMR INTERTRYP**

**Tel: 04 67 69 39 91**

**Email: moana.peylhard@cirad.fr**

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I will attend the Conference Diner on Tuesday 5th (price between 30 and 40 euros, to be paid on site):

⌧ yes □ no

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I’m willing to present my recent work as a **TALK** (15 min. + 5 min.):

⌧ yes □ no

I’m willing to present my recent work as a **POSTER**:

□ yes ⌧ no

**Talk / Poster title**: **Biological Pathways Discriminating African Trypanotolerant and Trypanosusceptible Cattle Breeds?**

**Authors**:

Moana Peylhard1,2, David Berthier1,2, Laurence Flori3,4, Guiguigbaza-Kossigan Dayo5, Isabelle Chantal12,, Sophie Thévenon1,2

**Affiliations**:

1 CIRAD, UMR INTERTRYP, F-34398 Montpellier, France.

2 INTERTRYP, Univ Montpellier, CIRAD, IRD, France

3 CIRAD, UMR SELMET, F-34398 Montpellier, France

4 SELMET, Univ Montpellier, CIRAD, INRA, SupAgro, Montpellier, France

5 CIRDES unité URBIO Bobo-Dioulasso

**Key words** (5 maximum):

Animal African Trypanosomosis, trypanotolerance, RNA-seq, pathways analysis, host\*parasite interactions

**Abstract** (250 words maximum):

Animal African Trypanosomosis (AAT) is a vector-borne disease caused by blood protozoan parasites of the Trypanosoma genus. It represents a major constraint to the development of cattle breeding in the humid and sub-humid zones of Africa because of the high morbidity and mortality it causes. Zebu breeds and European taurine breeds are very susceptible to AAT and they usually die in the absence treatment. On the contrary, some taurine breeds in West Africa have the capacity to tolerate the disease and are called trypanotolerant.

The trypanotolerant phenotype is known to be polygenic and multifactorial, but up to now, its mechanisms remain unknown. In order to decipher the molecular bases of trypanotolerance, we chose to analyse the genes expression of blood cells of susceptible and tolerant cattle during an experimental infection, performed in Burkina Faso, in 40 cattle from five West African breeds with T. congolense. mRNA were extracted from blood, comprising bovine leukocytes and parasites, before and during the infection and were sequenced using a Illumina highSeq2000. We mapped the reads on the bovine and trypanosome genomes, counted the reads on the annotated genes and performed a differential expression analysis. The genes identified as differentially expressed during the infection were then analysed using the Ingenuity Pathway Analysis software in order to identify enriched functional patterns. The functional analyses highlighted upstream regulators and canonical pathways associated with the immune response, the cell proliferation and signaling. Very fine differences in the modulation of the response between trypanotolerant and susceptible cattle were observed.