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Transcriptional profiling of midguts prepared from *Trypanosoma/T. congolense*-Positive *Glossina palpalis palpalis* collected from two distinct cameroonian Foci: Coordinated signatures of the Midguts' remodeling as *T. congolense*-supportive niches

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Our previous transcriptomic analysis of *Glossina palpalis gambiense* experimentally infected or not with *Trypanosoma brucei gambiense* aimed to detect Differentially Expressed Genes (DEGs) associated with infection. Specifically, we selected candidate genes governing tsetse fly vector competence that could be used in the context of an anti-vector strategy, to control human and/or animal trypanosomiasis. The present study aimed to verify whether gene expression in field tsetse flies (*G. p. palpalis*) is modified in response to natural infection by trypanosomes (*T. congolense*), as reported when insectary-raised flies (*G. p. gambiense*) are experimentally infected with *T. b. gambiense*. This was achieved using the RNA-seq approach, which identified 524 DEGs in infected vs. non-infected tsetse flies, including 285 downregulated genes and 239 upregulated genes (identified using DESeq2). Several of these genes were highly differentially expressed, with log₂ fold change values in the vicinity of either +40 or -40. Down regulated genes were primarily involved in transcription/translation processes, whereas encoded upregulated genes governed amino acid and nucleotide biosynthesis pathways. The Bio Cys metabolic pathways associated with infection also revealed that downregulated genes were mainly involved in fly immunity processes. Importantly, our study demonstrates that data on the molecular cross-talk between the host and the parasite (as well as the always present fly microbiome) recorded from an experimental biological model has a counterpart in field flies, which in turn validates the use of experimental host/parasite couples.

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