



Title	Transcriptomic analysis on the physiological roles of the mixed segment in the wood-feeding termite, <i>Nasutitermes takasagoensis</i> (Abstract_論文要旨)
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Title -; Transcriptomic analysis on the physiological roles of the mixed segment in the wood-feeding termite, *Nasutitermes takasagoensis*.

(食材性シロアリ *Nasutitermes takasagoensis* における組織複合域の生理学的機能に関するトランスクリプトーム解析)

The mixed segment is a unique part of the gut present only in the most apical lineage of termites and consists of a complex of overlapping mesenteric and proctodeal epithelial tissues. It harbors numerous bacteria in the ectoperitrophic space. So far, physiological roles of the mixed segment have yet to be elucidated.

I performed sequencing of transcriptomes obtained from the mixed segment, midgut and the first proctodeal segment to understand the variety of functional enzymes and metabolic pathways acting in the mixed segment of the wood-feeding termite *Nasutitermes takasagoensis*. I found that vacuolar H⁺-ATPase (V-ATPase) subunits were predominant in the mixed segment, which was confirmed by reverse-transcriptase quantitative polymerase chain reaction (RT-qPCR) analysis. The distribution of V-ATPase enzyme activity in these three tissues was in good agreement with the expression patterns. Transcripts were annotated using the Kyoto Encyclopedia of Genes and Genomes (KEGG) database. The predominant metabolic function detected in the mixed segment was energy production via oxidative phosphorylation. KEGG orthologs involved in lysosomal and phagosomal systems were also characteristic of this segment. The transcriptome data suggest that V-ATPases appear to electrogenically drive NHE6 or NHE7 (NHE6/7) K⁺/H⁺ antiporters to stimulate K⁺ secretion, increasing gut lumen pH. The mixed segment also expressed higher levels than did the adjacent gut regions of carbonic anhydrase, another contributor to gut alkalization through HCO₃⁻ production. The dominant expressions of NHE6/7 and carbonic anhydrase in the mixed segment were further confirmed by absolute quantitative RT-qPCR. Annotations based on GO revealed the significant differences of functional variations in three tissues. Accordingly, Pfam annotation also revealed the differences in gene compositions in three tissues. Genes encoding β-glucosidases and endo-β-1,4-glucanases have been mainly identified from the midgut transcriptome and almost absent in the mixed segment transcriptome.

In conclusion, the dominantly expressed V-ATPase in the mixed segment was presumed to be electrogenetically coupled with the NHE6/7 K⁺/H⁺ antiporter to increase the luminal pH in conjunction with HCO₃⁻ transport. These mechanisms might promote the solubilization of lignocellulose during its passage to the hindgut. These novel findings will allow to enhance our knowledge of how the mixed segment contribute to the digestive physiology of higher termites on plant biomass degradation in tropical ecosystems.

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