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Rigorózní práce

**A new *Sodalis* lineage from bloodsucking fly *Craterina melbae*
(Diptera, Hippoboscoidea) originated independently of the tsetse
flies symbiont *Sodalis glossinidius***

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Anotace:

This study provides description of a new lineage of the symbiotic bacterial genus *Sodalis* from a blood-sucking fly *Craterina melbae*. Using molecular data, it explores its phylogenetic position and evolutionary features.

Potvrzuji, že Eva Nováková, první autorka, přispěla zásadním způsobem ke vzniku předložené práce.

Václav Hypša

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A new *Sodalis* lineage from bloodsucking fly *Craterina melbae* (Diptera, Hippoboscoidea) originated independently of the tsetse flies symbiont *Sodalis glossinidius*

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Sodalis; symbiont; molecular phylogeny; 16S rRNA gene; type three secretion system; *Craterina*.

Introduction

The symbiotic bacterium *Sodalis glossinidius* (Dale & Maudlin, 1999) was originally reported as one of three phylogenetically distant bacteria inhabiting tissues of tsetse flies (Aksoy *et al.*, 1997). The other two bacteria are the mutualistic *Wigglesworthia glossinidia* (Aksoy, 1995) and the broadly distributed parasite of the genus *Wolbachia* (O'Neill *et al.*, 1993). Since its discovery, *Sodalis glossinidius* has become an important subject of a symbiosis-centered research due to several favorable circumstances. Primarily, it attracted attention as a companion of an important blood-sucking insect and was recognized as a possible factor influencing the vector competence/capacity (Maudlin & Ellis, 1985). While this view was later opposed by several authors (Moloo & Shaw, 1989; Geiger *et al.*, 2005b), the research of *Sodalis glossinidius* further accelerated after Dale *et al.* (2001) demonstrated that it utilizes the machinery of the type three secretion system (TTSS) to enter the host cell. Owing to this finding and the fact that *Sodalis* could be maintained in *in vitro* laboratory cultures (Welburn *et al.*, 1987), *Sodalis glossinidius* became a model organism, particularly in studying host cell invasion in an early stage of the symbiosis evolution. As a result of this attention, the complete genome of *Sodalis glossinidius* has recently been

Abstract

Symbiotic bacterium closely related to the secondary symbiont of tsetse flies, *Sodalis glossinidius*, has been described from the bloodsucking fly *Craterina melbae*. Phylogenetic analysis of two genes, 16S rRNA gene and component of type three secretion system, placed the bacterium closer to the *Sitophilus*-derived branch of *Sodalis* than to the tsetse symbionts. This indicates that the *Craterina*-derived lineage of *Sodalis* originated independent of the tsetse flies symbionts and documents the capability of *Sodalis* bacteria either to switch between different host groups or to establish the symbiosis by several independent events.

sequenced and analyzed (Toh *et al.*, 2006). The preliminary analysis revealed a number of genomic changes associated with the adoption of a symbiotic lifestyle and further stressed the significance of *Sodalis* as a model of evolutionary transition from free-living to symbiotic bacteria. However, genetic characterization of a symbiont and the elucidation of its molecular machineries only represent one facet of the evolutionary picture. To understand fully the biology and the evolutionary potential of such a bacterium, it is important to know its distribution among various hosts, the routes of interspecific transmission and the modes of symbiosis it can adopt in different hosts. This can be well demonstrated by the finding that *Sodalis*-related bacteria, associated with the weevils of the genus *Sitophilus*, display features typical for mutualistic primary symbionts (Heddi *et al.*, 1998; Nardon *et al.*, 2002; Lefevre *et al.*, 2004). Such a phylogenetic-distribution pattern indicates that *Sodalis* may be capable of both the horizontal transfers between different hosts, and the long-term coevolution associated with establishment of a mutualistic relation. This makes the bacterium a potentially excellent model for the study of the changes and trends accompanying the adaptation to different symbiotic modes. Unfortunately, despite the considerable number of symbiotic bacteria described annually from various insects, no other