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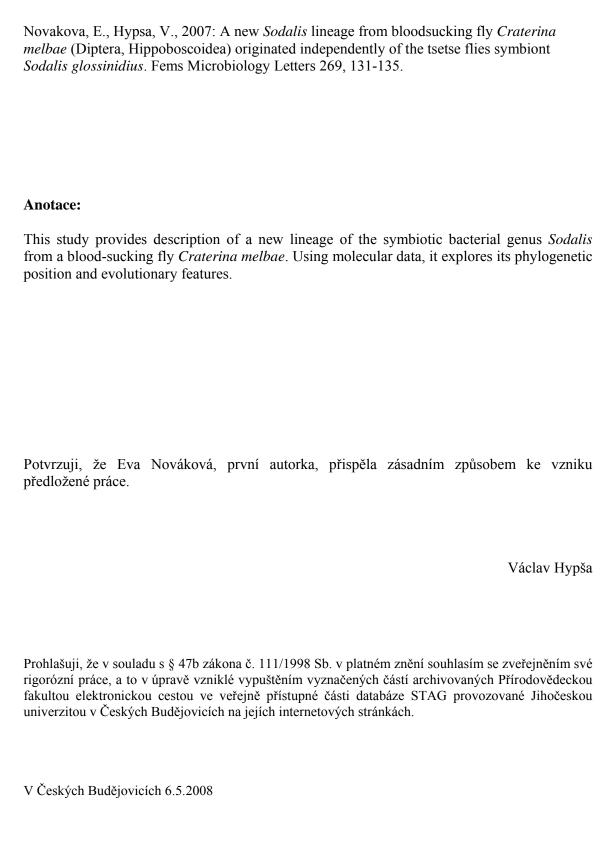


Rigorózní práce

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

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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.

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 bloodsucking 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 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 phylogeneticdistribution 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