

A de novo assembly of genomic dataset sequences of the sugar beet root maggot *Tetanops myopaeformis*, TmSBRM_v1.0

NADIM W. ALKHAROUF¹, CHENGGEN CHU², VINCINT P. KLINK³

¹Department of Computer and Information Sciences, Towson University, Towson, MD 21252, USA.

²USDA-ARS-NA- Northern Great Plains Research Laboratory, 1307 N 18TH ST Northern Crop Science Laboratory, Fargo, ND 58102, USA. ³USDA-ARS-NEA-BARC, Molecular Plant Pathology Laboratory, Building 004, Room 122, BARC-West, 10300 Baltimore Ave., Beltsville, MD 20705, USA.

CORRESPONDING AUTHOR(S): VINCENT P. KLINK (Vincent.klink@USDA.gov)

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Abstract

The sugar beet root maggot (SBRM), *Tetanops myopaeformis* (von Röder), is a devastating insect pathogen of sugar beet (SB), *Beta vulgaris*, ssp *vulgaris* (*B. vulgaris*), an important food crop, while also being one of only two plants globally from which sugar is widely produced, and accounting for 35% of global raw sugar with an annual farm value of \$3 billion in the United States alone. SBRM is the most devastating pathogen of sugar beet in North America. The limited natural resistance of *B. vulgaris* necessitates an understanding of the SBRM genome to facilitate generating knowledge of its basic biology, including the interaction between the pathogen and its host(s). Presented is the de novo assembled draft genome sequence of *T. myopaeformis* isolated from field-grown *B. vulgaris* in North Dakota, USA. The SBRM genome sequence TmSBRM_v1.0 will also be valuable for molecular genetic marker development to facilitate host resistance gene identification and knowledge, including SB polygalacturonase inhibiting protein (PGIP), and development of new control strategies for this pathogen, relationship to model genetic organisms like *Drosophila melanogaster* and aid in agronomic improvement of sugar beet for stakeholders while also providing information on the relationship between the SBRM and climate change.

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