

<https://doi.org/10.17221/104/2021-PPS>

Biological and molecular characterisation of two Polish *Wheat streak mosaic virus* isolates and their transmission by wheat curl mites

KATARZYNA TRZMIEL^{1*}, WIKTORIA SZYDŁO^{2,3}, BEATA HASIÓW-JAROSZEWSKA¹

¹Department of Virology and Bacteriology, Institute of Plant Protection-National Research Institute, Poznań, Poland

²Center for Advanced Technology, Adam Mickiewicz University, Poznań, Poland

³Population Ecology Lab, Faculty of Biology, Adam Mickiewicz University, Poznań, Poland

*Corresponding author: k.trzmiel@iorpib.poznan.pl

ELECTRONIC SUPPLEMENTARY MATERIAL (ESM)

The authors are fully responsible for both the content and the formal aspects of the electronic supplementary material. No editorial adjustments were made.

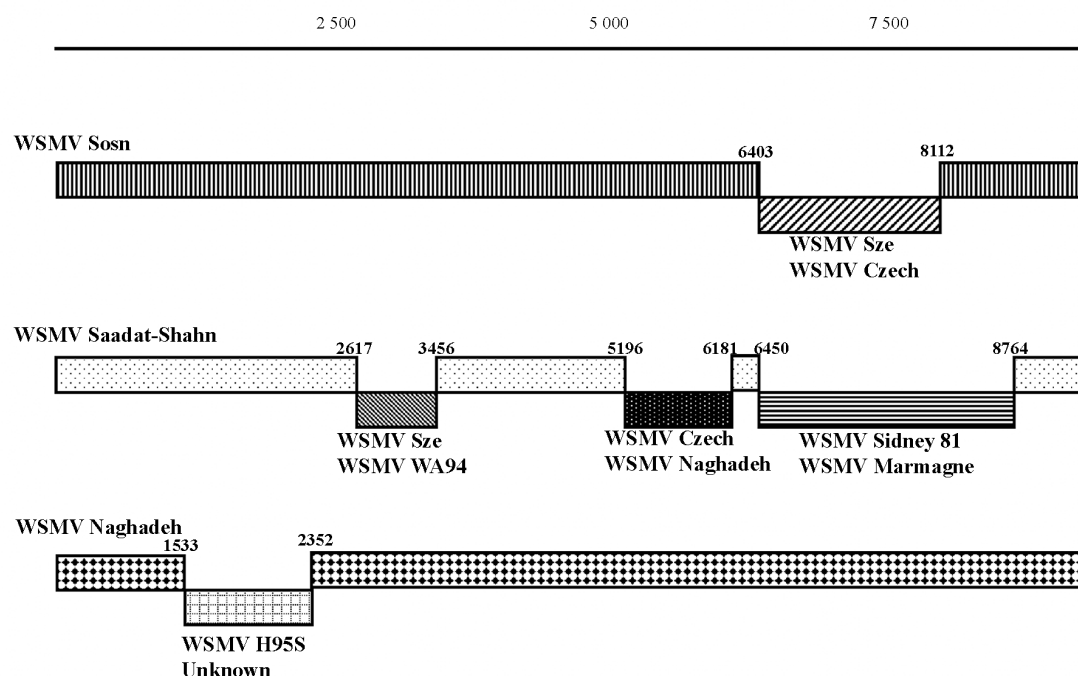


Figure S1. Recombination analysis of the complete *Wheat streak mosaic virus* genomes

The analyses were performed using seven algorithms implemented in RDP4; only recombination events with a *P*-value below 0.05 detected by at least four different methods are shown; in all the cases, the potential major and minor parent is indicated; the scale bar/the upper line shows the nucleotide count.

<https://doi.org/10.17221/104/2021-PPS>Table S1. Percentage of nucleotide and (amino acid) sequence identity of the different genome regions between WSMV-Sze and other known type B isolates of *Wheat streak mosaic virus*

Genome region	WSMV-Sze					
	-Sosn	-Austria	-Czech	-Hoym	-Marmagne	-Saadat-Shahr
Complete genome	98.2 (99.1)	97.6 (98.5)	98.1 (99.1)	98.0 (98.7)	98.4 (98.7)	91.6 (97.9)
5'-UTR	97.6	97.6	99.2	98.4	96.9	95.3
P1	97.4 (97.4)	97.8 (97.7)	97.5 (97.7)	97.8 (96.8)	97.7 (97.4)	91.8 (95.4)
HC-Pro	97.2 (99.4)	96.6 (98.9)	97.8 (99.4)	97.6 (99.4)	98.5 (98.9)	87.8 (95.8)
P3	98.4 (98.9)	98.8 (99.2)	98.8 (100)	98.9 (99.6)	99.6 (100)	95.2 (99.2)
6K1	99.3 (100)	99.3 (98.0)	98.6 (100)	98.6 (100)	99.3 (100)	98.6 (100)
CI	97.9 (99.2)	97.6 (98.6)	97.9 (99.3)	98.0 (99.2)	98.1 (98.2)	87.1 (98.7)
6K2	98.6 (96.0)	96.7 (96.0)	98.6 (96.0)	97.3 (94.1)	98.6 (96.0)	97.3 (96.0)
NIa-Vpg	97.9 (98.9)	97.4 (97.9)	98.3 (98.4)	98.1 (98.4)	98.6 (97.9)	97.4 (98.9)
NIa-Pro	99.4 (100)	97.2 (99.1)	98.8 (100)	98.6 (99.1)	98.6 (99.5)	91.7 (99.1)
NIb	99.7 (100)	97.6 (98.7)	98.1 (98.7)	98.2 (98.9)	98.3 (99.1)	93.5 (98.5)
CP	97.8 (100)	97.6 (99.1)	97.7 (99.7)	97.4 (99.1)	98.5 (99.4)	91.8 (99.1)
3'-UTR	98.6	99.3	99.3	98.6	100.0	98.6

<https://doi.org/10.17221/104/2021-PPS>

Table S2. Percentage of nucleotide and (amino acid) sequence identity of the different genome regions between WSMV-Sosn and other known type B isolates of *Wheat streak mosaic virus*

Genome region	WSMV-Sosn					
	-Sze	-Austria	-Czech	-Hoym	-Marmagne	-Saadat-Shahr
Complete genome	98.2 (99.1)	97.9 (98.8)	98.6 (99.3)	98.5 (99.1)	97.9 (98.8)	91.8 (98.3)
5'-UTR	97.6	98.4	98.4	99.2	97.6	96.1
P1	97.4 (97.4)	98.3 (99.1)	98.5 (99.7)	98.5 (98.8)	97.7 (98.8)	92.6 (97.4)
HC-Pro	97.2 (99.4)	97.4 (99.4)	98.7 (100)	98.5 (100)	97.3 (98.4)	88.6 (96.3)
P3	98.4 (98.9)	98.6 (98.2)	98.9 (98.9)	99.0 (98.5)	98.5 (98.9)	95.0 (98.2)
6K1	99.3 (100)	98.6 (98.0)	98.0 (100)	98.0 (100)	98.6 (100)	98.0 (100)
CI	97.9 (99.2)	97.9 (98.7)	100 (100)	98.6 (98.0)	100 (100)	98.6 (100)
6K2	98.6 (96.0)	98.0 (98.0)	98.6 (96.0)	97.3 (94.1)	98.6 (96.0)	97.3 (96.0)
NIa-Vpg	97.9 (98.9)	97.8 (98.9)	98.9 (99.4)	98.8 (99.4)	97.9 (98.9)	97.8 (100)
NIa-Pro	99.4 (100)	97.2 (99.1)	98.8 (100)	98.6 (99.1)	98.3 (99.5)	91.4 (99.1)
NIb	99.7 (100)	97.4 (98.7)	98.0 (98.7)	98.1 (98.9)	98.1 (99.1)	93.3 (98.5)
CP	97.8 (100)	98.1 (99.1)	99.2 (99.7)	98.9 (99.1)	98.5 (99.4)	92.3 (99.1)
3'-UTR	98.6	97.9	97.9	97.3	98.6	97.3