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Data Article

Data on structural transitions in domains of hordeivirus TGB1 protein forming ribonucleoprotein complex

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ABSTRACT

This data article is related to the research article entitled "*in vitro* properties of hordeivirus TGB1 protein forming ribonucleoprotein complexes" (Makarov et al., 2015 [1]), demonstrating that upon incubation with viral RNA the poa semilatent hordeivirus (PSLV) TGB1 protein (the movement 63 K protein encoded by the first gene of the triple gene block) *in vitro* forms RNP structures resembling filamentous virus-like particles and its internal domain (ID) performs a major structural role in this process. This article reports the additional results on the structural lability of ID and the structural transitions in the C-terminal NTPase/helicase domain (HELD) induced by interaction with tRNA and phosphorylation.

Specifications Table

Subject area	*Biology*
More specific subject area	*Structural virology*

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Type of data	*Figures*
How data was acquired	*CD and absorption spectra, electrophoresis image*
Data format	*Analyzed*
Experimental factors	*Isolation of recombinant proteins, measurement of CD and absorption spectra on Chirascan CD and Hithachi UV-2900 instruments*
Experimental features	*Structural transitions in deletion mutants of hordeivirus TGBp1*
Data source location	*Belozersky Institute of Physico-Chemical Biology and Department of Virology, Lomonosov Moscow State University, Leninsky Gory, Moscow, 119992, Russia*
Data accessibility	*Data are provided with this article*

Value of the data

- The data show that structural conversion (increasing of β-structure content) in the TGBp1 internal domain (ID) is initially induced by interaction with RNA and leads to protein multimerization/aggregation. These data further demonstrate the importance of β-structure for RNA-protein and protein-protein interactions.
- The data demonstrate that the ID phosphorylation [2] is accompanied by the domain secondary structure transition to a predominantly disordered state and may explain common mechanisms of RNP complex destabilization.
- The increasing in the content of the β-component upon incubation RNA with HELD is mainly due to the structural transitions in the NTPase sub-domain displaying RNA-binding activity [3]. These data may be of interest for studying rearrangement of SF1 helicase structure induced by interaction with RNA.

1. Data

An essential step for realization of hordeivirus TGBp1 structural functions such as formation or remodeling/destabilization of transport RNP particles is based on the protein secondary structure conversion [1].

In this article, we display additional data on structural transitions in the internal domain (ID) and the NTPase sub-domain of HELD as a result of their interactions with RNA or phosphorylation.

2. Experimental design, materials and methods

2.1. Isolation of recombinant proteins

Expression of recombinant protein genes in *Escherichia coli* cells, their isolation and purification of $(His)_6$ recombinant proteins were performed as described previously [3,4]. Mutants of the PSLV TBGp1 (63K protein) are indicated according to their previous designations [3,4] (Figs. 1 and 2).

2.2. Measurement of the CD and absorption spectra

Protein samples at the concentration of 100 μg/ml in 1 mM HEPES buffer pH 7.0 were loaded into 1–2-mm cells, and CD spectra were recorded from 185 to 260 nm at 25 °C in a Chirascan CD spectrometer (Applied Photophysics, England). The CD spectra were recorded at rate 0.5–1.0 nm/s with base-line subtraction. The measured spectra were smoothed using the instrument software. The [θ] value calculations were based on mean amino acid residue molecular weight of 110. Absorption spectra were measured in 1 cm cells on Hithachi UV-2900 (Hitachi, Japan).

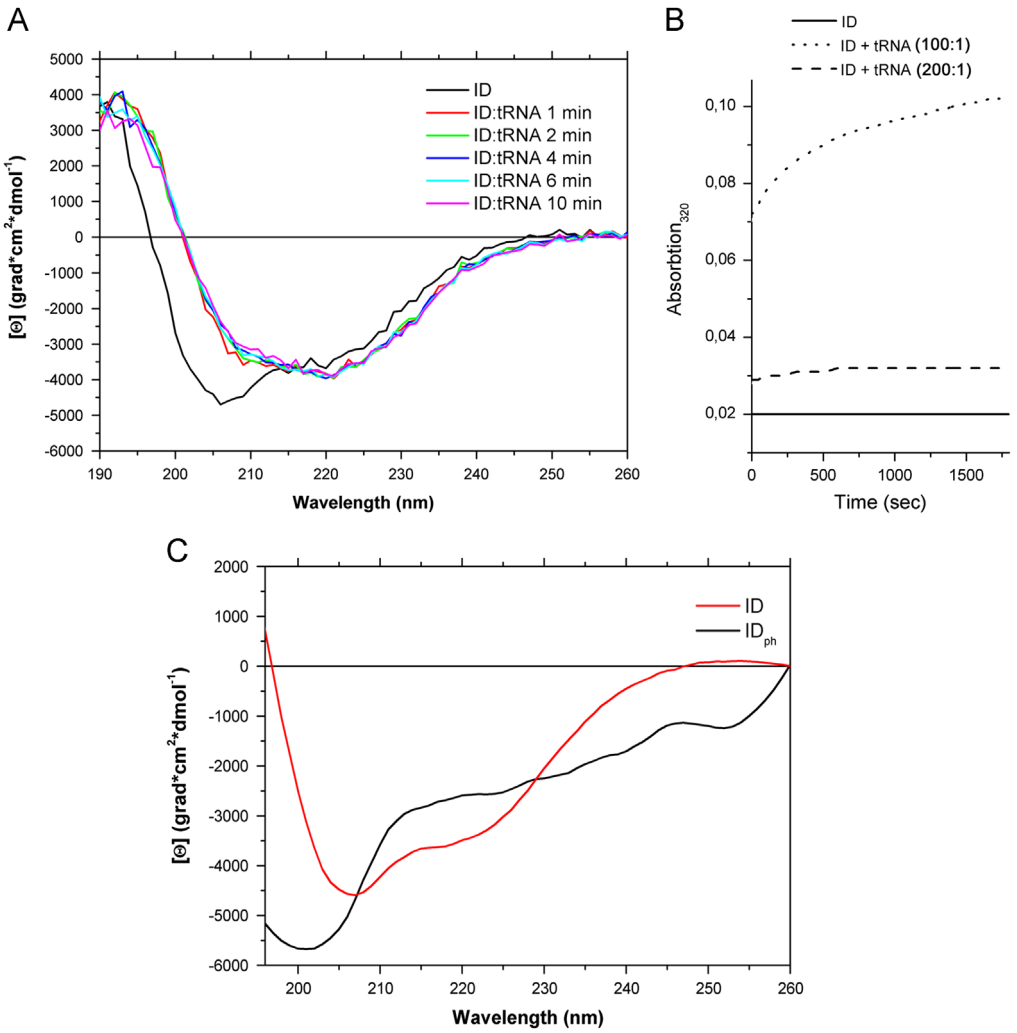

Fig. 1. Changes in circular dichroism (CD) spectra of the internal domain (ID) of PSLV TGBp1 in the presence of tRNA or after ID phosphorylation. Far-UV CD spectra of the recombinant proteins recorded at 25 °C. (A) CD spectra of ID at molar protein:RNA ratio 100:1 recorded during different time intervals; (B) kinetic of ID multimerization/aggregation (C) CD spectra of non-phospholylated ID and ID after phosphorylation by protein kinases associated with plant cell walls [2].

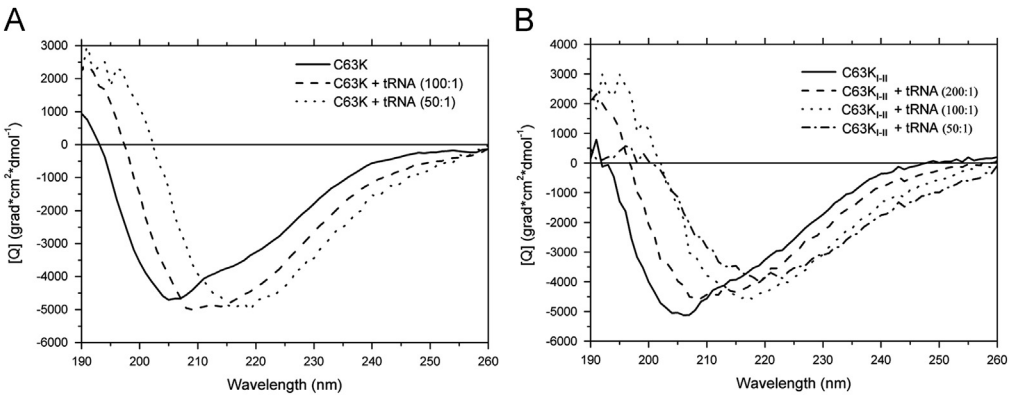

Fig. 2. Circular dichroism (CD) spectra of the C-terminal NTPase/helicase domain (HELD) of PSLV TGBp1 (C63K) and the NTPase sub-domain (C63K$_{I–II}$) without and in the presence of tRNA at different molar protein:RNA ratios. Far-UV CD spectra of the recombinant proteins recorded at 25 °C. (A) C63K; (B) C63K$_{I–II}$.

Acknowledgements

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Appendix A. Supplementary material

Supplementary data associated with this article can be found in the online version at http://dx.doi.org/10.1016/j.dib.2016.05.012.

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