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COMMUNICATION

DEAD-box RNA helicases Dbp2, Ded1 and Mss116 bind to G-quadruplex nucleic acids and destabilize G-quadruplex RNA†

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We identified 29 G-quadruplex binding proteins by affinity purification and quantitative LC-MS/MS. We demonstrated that the DEAD-box RNA helicases Dbp2, Ded1 and Mss116 preferentially bind to G-quadruplex nucleic acids in vitro and destabilize RNA quadruplexes, suggesting new potential roles for these helicases in disruption of quadruplex structures in RNA.

G-quadruplexes (G4) are non-canonical, four-stranded nucleic acid structures, consisting of stacked planar guanine tetrads, in which guanines are held together by Hoogsteen hydrogen bonds.1 G4 structures are of important biological significance in processes such as regulation of gene transcription and translation.2,3 They are also associated with genetic instability and human diseases.4,5 Several proteins have been reported to bind to G4. These proteins include but are not limited to the RNA helicases DHX36/RHAU,6 DHX9,7 and DDX21,8 and the DNA helicases XBP,9 XPD,9 BLM,10 and Pif111,12 and the nucleolar protein nucleolin,13 transcription factor SP1,14 yeast tRNA binding protein Arc1/G4p1,15 yeast transcription coactivator Sub1 and its human homolog PC4.16 Herein, we report that DEAD-box RNA helicases Dbp2, Ded1, and Mss116 preferentially bind to both G4DNA and G4RNA and destabilize G4RNA.

Using affinity purification from Saccharomyces cerevisiae whole cell lysates with a G4DNA bait followed by quantitative LC-MS/MS analysis16 (Fig. 1), we systemically identified 29 proteins as G4 binding proteins (Table 1). The complete list of proteins identified by mass spectrometry is in Table S2 (ESI†). Arc1/G4p1 is a known G4DNA binding protein,15 and we recently characterized the G4DNA interaction of Sub1, a global transcriptional coactivator, and confirmed that it preferentially binds to G4DNAs.16 The sequences of G-quadruplex DNA interacting proteins identified in our proteomics screen were analysed with the MEME package,17 an online motif finder tool. A discriminatory search was performed using non-G4 binding sequences.18 The RGG motif was the top scoring motif found in seven of the G4DNA binding proteins [Fig. S1, ESI†], which is consistent with previous reports that RGG motifs in proteins such as nucleolin and FMRP can interact with G-quadruplexes.19–21 The next two most highly enriched motifs are conserved motifs from the DEAD-box RNA helicase Dbp2. In addition to Dbp2, three other DEAD-box RNA helicases (Ded1, Dbp1, and Mss116) were incubated with G4DNA or in a separate experiment, ssDNA. Isolated proteins were identified by quantitative mass spectrometry to determine those proteins enriched upon binding to G4DNA.

Fig. 1 Scheme of experimental strategy. Lysates of YPH499 yeast cells were incubated with G4DNA or in a separate experiment, ssDNA. Isolated proteins were identified by quantitative mass spectrometry to determine those proteins enriched upon binding to G4DNA.

† Electronic supplementary information (ESI) available: Detailed experimental methods, supplementary tables and figures. See DOI: 10.1039/c8cc10091h
Results from proteomics screen for G4DNA binding proteins 

| Name   | Description                                      | T15 | G4  | p-value |
|--------|--------------------------------------------------|-----|-----|---------|
| DBP2   | ATP-dependent RNA helicase DBP2                  | 6   | 178 | 9.4 × 10⁻¹² |
| KSP1   | Serine/threonine-protein kinase KSP1              | 3.1 | 98  | 2.5 × 10⁻⁷  |
| RPL2A  | 60S ribosomal protein L2                          | 15  | 177 | 2.7 × 10⁻⁷  |
| MSC3   | Meiotic sister-chrom. recomb. protein             | 0.2 | 53  | 2.8 × 10⁻⁵  |
| RPS6A  | 40S ribosomal protein S6                          | 18  | 143 | 3.1 × 10⁻⁵  |
| DED1   | ATP-dependent RNA helicase DED1                   | 14  | 128 | 3.2 × 10⁻⁵  |
| SUB1   | RNA pol II transcriptional coactivator            | 1.1 | 51  | 2.6 × 10⁻⁵  |
| SBP1   | Single-stranded nucleic acid-binding              | 0.2 | 35  | 5.7 × 10⁻⁴  |
| GUS1   | Glutamyl-RNA synthetase                          | 1.1 | 46  | 0.0018    |
| VIF5   | Uncharacterized protein                           | 0.2 | 26  | 0.0033    |
| RPS8A  | 40S ribosomal protein S8                          | 6   | 64  | 0.0034    |
| SSV1   | Cyclin (Bur2p)-depend. protein kinase             | 0.2 | 27  | 0.0043    |
| PRP42  | U1 small nuclear ribonucleoprotein                | 9.1 | 18  | 0.0060    |
| RPL4A  | 60S ribosomal protein L4-A                        | 21  | 119 | 0.0061    |
| RPL21A | 60S ribosomal protein L21-A                      | 25  | 122 | 0.0067    |
| RPS17  | Putative RNA-binding protein                      | 67  | 238 | 0.016     |
| NPL3   | Nuclear protein 3                                 | 17  | 92  | 0.016     |
| DBP1   | ATP-dependent RNA helicase DBP1                  | 8   | 57  | 0.020     |
| SSIB   | Heat shock protein SSIB                          | 0.2 | 17  | 0.020     |
| BRE1   | E3 ubiquitin-protein ligase BRE1                 | 0.2 | 21  | 0.028     |
| RPL34A | 60S ribosomal protein L3-A                       | 1.1 | 21  | 0.029     |
| ARC1   | Aminoacyl-tRNA synthetase cofactor               | 0.2 | 28  | 0.029     |
| AIR2   | Protein AIR2                                     | 0.2 | 19  | 0.031     |
| RPL3   | 60S ribosomal protein L3                          | 14  | 70  | 0.034     |
| MSS116 | ATP-dependent RNA helicase MSS116                | 0.2 | 16  | 0.034     |
| NOP1   | rRNA 2'-O-methyltransferase fibrillarin           | 0.2 | 14  | 0.037     |
| YRA1   | RNA annealing protein YRA1                       | 0.2 | 14  | 0.041     |
| RPL5   | 60S ribosomal protein L5                         | 0.2 | 21  | 0.042     |
| RPL11B | 60S ribosomal protein L13-B                      | 7   | 81  | 0.046     |

Table 1 contains proteins which were significantly (p-value less than 0.05) enriched on G4DNA (G4) relative to ssDNA (T15) by spectra counting. Numbers indicated in T15 and G4 columns represent the total number of spectra obtained for that protein when enriching with the corresponding oligonucleotide. A value of 0 was replaced with 0.1 in each replicate to allow the log of the value to be calculated in subsequent calculations. Proteins characterized in this study are italicized.

Constant ($K_d$) of 0.55 ± 0.1 nM (Fig. 2b). Binding to tailed G4DNA is about three-fold tighter than binding to the tailless cMYC G4DNA ($K_d = 1.9 ± 0.3$ nM), 10 fold tighter than binding to the ssDNA ($K_d = 5.4 ± 0.9$ nM), and 62 fold tighter than its binding affinity for the duplex DNA ($K_d = 34 ± 11$ nM). Dbp2 also tightly binds to tailless ScTEL G4DNA ($K_d = 0.72 ± 0.28$ nM), and tailless hTEL G4DNA ($K_d = 3.0 ± 0.4$ nM). Thus, Dbp2 binds preferentially to G4DNAs, including parallel and hybrid G4DNAs.

Ded1 also binds to tailed cMYC G4DNA ($K_d = 1.3 ± 0.2$ nM), 2.5 fold tighter than its binding affinity to the tailless cMYC G4DNA ($K_d = 3.4 ± 0.7$ nM), 4.5 fold tighter than binding to the ScTEL G4DNA ($K_d = 5.8 ± 2.5$ nM), and 21 fold tighter than binding to the ssDNA ($K_d = 27 ± 3$ nM) (Fig. 2c). Ded1 does not show affinity to duplex DNA nor to hTEL G4DNA. These results demonstrate that Ded1 preferentially binds to G4DNAs, including parallel and some hybrid G4DNAs.

Mss116 protein shows little to no binding to the ssDNA, duplex DNA, tailless ScTEL or tailless hTEL (Fig. 2d). However, Mss116 binds to both the tailed cMYC G4DNA ($K_d = 10 ± 1$ nM) and the tailless cMYC G4DNA ($K_d = 19 ± 5$ nM). The affinity of Mss116 for cMYC G4DNAs is also tighter than that for dsRNA ($K_d ≈ 120$ nM). Thus, Mss116 preferentially binds to parallel G4DNA.

All three DEAD-box helicases (Dbp2, Ded1, and Mss116) bind to tailed cMYC G4DNA with higher affinity than that of tailless G4DNA (Fig. 2), suggesting the tail or the junction between the tail and G4DNA may also contribute to the binding. However, each of these helicases also bind the tailless cMYC G4DNA with high affinity indicating that the G4 structure itself recognized by the helicases. Although these three DEAD-box helicases bind to G4DNAs preferentially, none of them is capable of unfolding a G4DNA substrate containing either a 5’- or 3’-ssDNA extension (Fig. S3, ESIF†).

Next, we conducted a bioinformatic search of yeast transcriptome, and found that the most frequently occurring G4RNA sequences in the yeast transcriptome are two-tetrad ribonucleotide sequences (Table S3, ESIF†). We selected the top four G4RNA sequences from yeast transcriptome, and confirmed that they form stable G4RNA structures by circular dichroism spectra analysis (Fig. S2b, ESIF†). The YNL098C G4RNA is the most common G4RNA sequence present in the yeast transcriptome, and it forms a parallel G4 structure in vitro (Fig. S2b and c, ESIF†).

We measured the binding affinities of these three DEAD-box RNA helicases to G4RNA vs. ssRNA (Fig. 3). Dbp2 binds to YNL098C G4RNA very tightly ($K_d = 0.84 ± 0.12$ nM), more than 200 fold tighter than that of ssRNA ($K_d = 210 ± 20$ nM) (Fig. 3b). Ded1 also binds to YNL098C G4RNA very tightly ($K_d = 1.18 ± 0.5$ nM), 14 fold tighter than that of ssRNA ($K_d = 16.6 ± 3.3$ nM) (Fig. 3c). For Mss116, binding to YNL098C G4RNA ($K_d = 43 ± 10$ nM, Fig. 3d) is approximately 4 fold tighter than binding to the ssRNA ($K_d = 180 ± 10$ nM, Fig. S4, ESIF†). Thus, Dbp2, Ded1, and Mss116 bind preferentially to G4RNA.

We then examined whether binding of these DEAD-box RNA helicases to G4RNA destabilizes the G4RNA structures.
In conclusion, we have identified 29 G4 binding proteins by affinity purification using G4DNA bait and LC-MS/MS analysis. The diversity of proteins enriched on G4DNA implies that G4 structures play critical roles in multiple biological functions. We demonstrated three DEAD-box RNA helicases (Dbp2, Ded1, and Mss116) bind preferentially to G4DNA and G4RNA in vitro. Binding of Dbp2, Ded1 or Mss116 to G4DNA does not affect G4DNA structure. However, their binding destabilizes G4RNA in an ATP-independent manner. Our observation that binding of these proteins to G4RNA is sufficient to unfold the structure, and provides one possible explanation for the recent observation that G4RNAs are globally unfolded in eukaryotic cells. A recent X-ray crystal structure and single-molecule analysis captured a G4DNA which was partially unfolded in a transient ATP-independent manner due to binding of the RNA helicase, DDX36. Either of these mechanisms could be involved in the ATP-independent G4RNA destabilization by DEAD-box RNA helicases.

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Conflicts of interest
There are no conflicts to declare.

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