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Submitted on 28 May 2014

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Genetic and Physical Interactions between Tel2 and the Med15 Mediator Subunit in *Saccharomyces cerevisiae*

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Abstract

**Background:** In budding yeast, the highly conserved Tel2 protein is part of several complexes and its main function is now believed to be in the biogenesis of phosphatidyl inositol 3-kinase related kinases.

**Principal Findings:** To uncover potentially novel functions of Tel2, we set out to isolate temperature-sensitive (ts) mutant alleles of Tel2 in order to perform genetic screenings. MEDI15/GAL11, a subunit of Mediator, a general regulator of transcription, was isolated as a suppressor of these mutants. The isolated tel2 mutants exhibited a short telomere phenotype that was partially rescued by MED15/GAL11 overexpression. The tel2-15 mutant was markedly deficient in the transcription of EST2, coding for the catalytic subunit of telomerase, potentially explaining the short telomere phenotype of this mutant. In parallel, a two-hybrid screen identified an association between Tel2 and Rvb2, a highly conserved member of the AAA+ family of ATPases further found by in vivo co-immunoprecipitation to be tight and constitutive. Transiently overproduced Tel2 and Med15/Gal11 associated together, suggesting a potential role for Tel2 in transcription. Other Mediator subunits, as well as SUA7/TFIIB, also rescued the tel2-ts mutants.

**Significance:** Altogether, the present data suggest the existence of a novel role for Tel2, namely in transcription, possibly in cooperation with Rvb2 and involving the existence of physical interactions with the Med15/Gal11 Mediator subunit.

Introduction

**TEL2** is a highly conserved gene that has been found in all eukaryotic organisms examined so far. Before describing the very important and fundamental roles of Tel2 known to date, it is worth briefly describing the chronology of Tel2’s history. Tel2 was originally isolated as a potential regulator of telomere length in the budding yeast *Saccharomyces cerevisiae*, but became eventually, over twenty years later, highly suspected, in humans at least but also in the fission yeast *Schizosaccharomyces pombe*, of having nothing to do with telomeres [1]. In the meantime, several, sometimes contradictory, telomere studies on Tel2 from various organisms had accumulated. The Tel2 story begins in 1986, when Lustig and Petes isolated, on the basis of telomere tracts length, two *S. cerevisiae* mutant strains that had abnormally short telomeres and named them *tel1* and *tel2* [2]. Telomeres, specialized nucleoprotein complexes, represent the natural ends of linear chromosomes and their integrity is essential for genome stability. Telomeres protect against unwanted chromosome end-to-end fusions, against degradation by DNA modifying enzymes and prevent chromosome ends from being mistaken for DNA double-strand breaks [3]. The genes corresponding to the short telomere mutants isolated by Lustig and Petes [2], *TEL1* and *TEL2*, were cloned around ten years later [4,5]. Tel1, as well as its human ortholog, ATM (Ataxia Telangiectasia Mutated), have been since extensively documented as they both play pivotal roles in genome stability as well as in the response of the cell to DNA damage, while Tel2 remained poorly documented for many years following its identification. In fact, Tel1 has a true role in telomere biology in budding yeast as it was recently found to localize at the ends of the shortest telomeres in the cell, an event which then favors telomerase recruitment and telomere re-elongation [6-8].

On the other hand, early experiments on *S. cerevisiae* Tel2 revealed that it could bind telomeric DNA, at least in *vivo* [9,10]. Not long later, probably led by the potential implication of *S. cerevisiae* Tel2 in telomeric functions, several studies on Tel2 from other organisms aiming at looking for telomeric functions were undertaken. Thus, human *TEL2*, also known as *HCL2*, and *Caenorhabditis elegans* *TEL2*, also known as RAD-5 or *CLK-2*, were implicated in the control of telomere length [11-13]. Meanwhile, other studies investigated in other directions and, as a consequence, Tel2 was also implicated in the response to DNA damage, in *C. elegans* [12,14], *S. pombe* [15] and humans [16,17]. This was also the case in *S. cerevisiae*, as Tel2 was found to physically bind Tel1, an event that was needed to recruit Tel1 at DNA double-strand breaks, as well as Mec1, an ATR ortholog [18,19]. Given the localization of Tel1 at short telomeres [6,7], it would be extremely important to know whether Tel2 is needed to recruit Tel1 at short telomeres, as it does at DNA double-strand breaks [18,19]. In mammals, Tel2 physically associated with - and was required for the stability - of all six mammalian phosphoinositol 3-kinase related kinases (PIKKs), ATM, ATR, DNA-PKcs, mTOR,
SMG1 and TRRAP [17]. These PIKKs complexes are important for basic transactions associated with DNA damage signaling/repair and associated cell cycle control, nutrient sensing and cell growth control, degradation of mRNA and control of gene expression, principally [1,20]. Strikingly, however, the study on mammalian TEL2 failed to reveal any evidence for telomeric phenotypes associated with TEL2 genetic inactivation [17], in spite of the fact that ATM is pivotal in the response of telomeres to mammalian TEL2 failed to reveal any evidence for telomeric expression, principally [1,20]. Strikingly, however, the study on repair and associated cell cycle control, nutrient sensing and cell maintenance. These PIKKs complexes are important for the rescue of telomeric instability in the maturation of PIKK complexes [29]. It has been recently reported that TEL2 might act as a scaffold to coordinate the recruitment of RNA polymerase II to activated promoters (see, for instance, [33]). We therefore considered the possibility that increased expression of MED15 might activate the transcription of TEL2, thus resulting in increased TEL2 protein levels being responsible for the observed suppression of tel2-ts growth defects by the Ycp50#8 and YEp24#2 plasmids. By Western analysis, the levels of either HAp-Tel2 or Myc-Tel2, both expressed under the control of native promoter from the tagged construct integrated at TEL2 locus, did not vary whether MED15 was expressed from either the centromeric or multi-copy plasmid, in addition to endogenous Med15, or expressed from endogenous locus only, in cells transformed with plasmid alone (Figure 1D). These data therefore suggest that suppression of the thermosensitivity of tel-15 or tel2-26 by Ycp50-MED15 or YEp24-MED15, respectively, is not due to increased amounts of TEL2 protein. In addition, we also verified that the suppression was not due to increased transcription of TEL2 (Figure 1C).

**TEL2 genetically interacts with other Mediator subunits, as well as with SUA7/TFIIB**

In parallel with the genetic screenings described above, we performed a two-hybrid screen using Tel2 as the bait. Only one clone scored positive, identifying *S. cerevisiae Rvb2* cDNA (see Appendix S1 in the Supporting information and Figures S1, S2).

Rvb1/2, two highly conserved members of the AAA+ family of ATPases, are parts of several distinct complexes, namely, the SWR1 and INO80 complexes of chromatin modification, the R2TP complex, which, together with the Hsp90 chaperone, regulates the accumulation and stability of snoRNPs, and the ASTRA complex, the function of which is presently unknown [23-24,33-35]. In all of these multi-protein complexes, the presence of Rvb1 and that of Rvb2 were reported to be essential for their proper function. In addition, Rvb1/pontin and Rvb2/reptin have been implicated in general transcription, not only in *S. cerevisiae* in which roughly 5% of all genes were found to be deregulated in *rpb2* mutants [36,37] but also in Vertebrates [38].

In view of the solid and constitutive physical association between Rvb2 and Tel2 and of the genetic interaction between TEL2 and the MEDI15 Mediator subunit, described above, we hypothesized that Tel2 might also function as a general regulator of transcription. Suα7, budding yeast TFIIB, an essential component of RNA polymerase II [39] has previously been reported to bind Tel2 by two-hybrid [40]. This putative physical interaction, obtained from high-throughput data, has not been retested and cannot therefore be used to draw any valid conclusion. However, this arose our curiosity and we set out to test the potential existence of genetic interactions between TEL2 and SUA7. Interestingly, continuous overexpression (on agar-based semi-solid medium) of *SUa7* under the control of the GAL1-10 promoter resulted in the suppression of tel2-19 and tel2-23 growth defects at 35 and 32°C, respectively.

**Results**

**Temperature-sensitive tel2 mutants**

We first set out to isolate temperature-sensitive (ts) mutants of *S. cerevisiae* TEL2 (see Materials and Methods). We could isolate six such tel2 alleles. We could distinguish two classes of tel2 mutants, based on the severity of the temperature-associated growth defects and the capacity to form colonies at 34–37°C (Figure 1A) and the nature of the mutations harbored (Table 1). Death in these tel2 mutants was accompanied by cell lysis, which appeared to occur at any of the cell cycle stages. FACS analysis, performed on alpha factor-synchronized populations of tel2-15 and tel2-19 mutant cells, as well as examination in the light microscope, failed to reveal any obvious cell-cycle defect at restrictive temperatures for growth (Figure 1B and data not shown).

The **MEDI15 Mediator subunit is a suppressor of tel2-ts mutations**

All six tel2 alleles identified in the present study were used to perform genetic screens in order to try and isolate extragenic suppressors. Only one such gene, namely GAL11, was isolated in these genetic screens, besides TEL2 itself. GAL11 behaved both as a low-copy and a high-copy suppressor. Thus, GAL11 was contained in the YCp50#8 centromeric (GEN4, URA3) plasmid (from the YCp50 genomic library; [30]) isolated as a weak rescuer of tel2-15 at 31°C (see below), as well as in the YEp24#2 multi-copy (episomal, 2 μ, URA3) plasmid (from the YEp24 genomic library; [31]), strong rescuer of tel2-26 at 34°C. Restriction analysis identified the GAL11 gene and surrounding sequences as responsible for the rescue in YCp50#8 and YEp24#2, both around 4.2 kb in length (GAL17 ORF is 3243 base pairs in length).

In addition, TEL2 itself expressed from a YEp24 library plasmid was isolated twice as a strong rescuer of tel2-19 and tel2-25 at 35 and 33°C, respectively (see below). Gal11, which according to a unified nomenclature should now be referred to as Med15 [32], is a subunit of the yeast Mediator, a large complex required for the recruitment of RNA polymerase II to activated promoters (see, for instance, [33]). We therefore considered the possibility that increased expression of MED15 might activate the transcription of TEL2, thus resulting in increased TEL2 protein levels being responsible for the observed suppression of tel2-ts growth defects by the Ycp50#8 and YEp24#2 plasmids. By Western analysis, the levels of either HAp-Tel2 or Myc-Tel2, both expressed under the control of native promoter from the tagged construct integrated at TEL2 locus, did not vary whether MED15 was expressed from either the centromeric or multi-copy plasmid, in addition to endogenous Med15, or expressed from endogenous locus only, in cells transformed with plasmid alone (Figure 1D). These data therefore suggest that suppression of the thermosensitivity of tel-15 or tel2-26 by Ycp50-MED15 or YEp24-MED15, respectively, is not due to increased amounts of TEL2 protein. In addition, we also verified that the suppression was not due to increased transcription of TEL2 (Figure 1C).

**SUA7/TFIIB**

In parallel with the genetic screenings described above, we performed a two-hybrid screen using Tel2 as the bait. Only one clone scored positive, identifying *S. cerevisiae Rvb2* cDNA (see Appendix S1 in the Supporting information and Figures S1, S2).
On the other hand, under the same conditions, overexpression of RVB2, also under GAL1-10 promoter control, did not rescue the growth defects in the thermo-sensitive tel2-19 and tel2-25 mutants and, in fact, aggravated these defects (data not shown).

Next, to see whether tel2-ts rescue by MED15 might reflect a general property of Mediator, we constructed plasmids to express one of several additional Mediator subunits under the control of the strong, inducible GAL1-10 promoter in a multi-copy (2 µ) plasmid. Among the MED1, MED2, MED5, MED12, MED16,
The Med15 Mediator subunit has physical affinities with Tel2

The genetic interaction between Med15 and Tel2, described above, prompted us to look for possible physical interactions between the two proteins, interactions that are frequently suspected of taking place under similar circumstances. Therefore, we assessed possible Tel2-Med15 physical interactions under conditions of increased expression by using a GAL1-10 promoter-controlled inducible system. Such a system in which the duration of induction of the promoter in galactose-based liquid culture medium is controlled is currently used in genome-wide analyses because it presents the advantage compared to other systems of assessing in vivo interactions between proteins in their native configuration. Upon induction of the GAL1-10 promoter for 2 hr at 29°C, we could readily detect in vivo physical interactions between Tel2-Myc and Med15-HA (Figure 2). Thus, full length Tel2-Myc was found to specifically bind the first half of Med15 (Med15<sup>1–343</sup>-HA), but not the second half of Med15 (Med15<sup>344–540</sup>-HA) (Figure 2B, C). Additional restriction of the expressed proteins showed that the first quarter of Med15 (Med15<sup>1–108</sup>-HA) efficiently bound the first half of Tel2 (Tel2<sup>1–342</sup>-HA) (Figure 2D). Therefore, given the genetic suppression of tel2-ts mutants by MED15, as well as the physical affinity between Med15 and Tel2, it is tempting to speculate that the Rvb2-Tel2 module might play an important role during transcription. The previously established physical interaction between Tel2 and Sua7/TFIIH [40] supports this view.

Finally, under transient overexpression conditions, Med15<sup>1–340</sup>-HA still physically associated with the temperature-sensitive Tel2-15-Myc protein at either 29°C or 34°C (Figure 2E). Tel2-15 was chosen for these experiments because it confers a tighter ts phenotype than Tel2-19. Note that all five mutations in Tel2-15 (Table 1) lie in the part of Tel2 (amino acids 1–343) that is relevant for interaction with Med15 (Figure 2D). One can therefore reasonably conclude that these mutations do not affect association with Med15.

Short telomeres of tel2 mutants rescued by MED15 overexpression

Prior to isolation of the temperature-sensitive tel2 mutants described above, we had been searching for tel2 mutants with altered telomere length (see Materials and Methods), and found one of them (out of 200 hundreds screened mutants), tel2-12, that exhibited shortened telomeres. The mutations in tel2-12 were later found to be identical to those in the tel2-19 mutant ([Table 1](#) and later found to confer temperature sensitivity. Upon further analysis of these mutants, we found that both the tel2-15 and tel2-19 mutants exhibited telomere shortening, just like the tel2-12 mutant, when grown at either permissive, 24°C, (Figure 3A) or semi-permissive for growth of 29°C (Figure 3B). To further document the telomere length deregulation occurring in the tel2-ts mutants, we additionally constructed tel2-ts-based double mutants. Importantly, we observed the absence of an additional effect on telomere length when the tel1 null and tel2-19 mutations were combined (tel1 null also confers telomere shortening; [2]; Figure 3B), as expected from the previous observation that Tel1 and Tel2 function in the same pathway of telomere length regulation [2]. We also observed that telomeres in the tel1Δ yku70Δ double mutants were shorter than in the two corresponding single mutants (Figure 3C). This indicated that tel1Δ cells have telomeres that can get even shorter when they are in combination with an additional mutation, thus serving as a positive control for the present situation in which the tel2 mutation fails to further shorten telomeres in the tel1 mutant background (Figure 3B). This point had been previously established by a study reporting that the tel1 hdf1/yku70 null double mutant had telomeres shorter than either of the two single tel1 and hdf1 single mutants and that the double mutant lost telomeres at an accelerated rate compared with the single mutants [41]. In contrast, combining the tel2-19 (or tel2-15) and yku70 null mutations [yku70 null] also confers telomere shortening; [42] provoked an additive effect on telomere shortening (Figure 3C). This finding was expected since previous data showed that Tel1 and Yku70 are in separate genetic pathways for telomere length regulation [41] while Tel1 and Tel2 are in the same pathway [2].

Interestingly, overexpression of MED15 not only partially rescued the temperature sensitivity of the tel2-15 and tel2-19 mutants (Figure 4A), but also partially rescued their short telomere phenotype at semi-permissive temperatures for growth (Figure 4B; see also Figure 4C for the wild-type control). At the permissive temperature of 24°C, the telomere length defect of the tel2-ts mutants, which is already present (Figure 3A), was also partially rescued by overexpression of MED15 (data not shown). We noted that overexpression of MED15 caused growth defects at 24°C in the tel2-ts mutants (Figures 2A, 4A) and at all temperatures tested in the wild type (Figure 4A). While this did not prevent rescue of the tel2-ts at higher temperatures, this may be important to keep in mind. We also note that overexpression of other Mediator subunits did not result in such a toxic effect (Figure2A). Therefore, manipulating the levels of Med15 in wild-types provided a rescue strategy that might be applicable for telomere length deregulation occurring in the tel2-ts mutants.

Table 1. Sequence analysis of the amino acid changes in the tel2 mutant proteins.

<table>
<thead>
<tr>
<th>(All in tel2:Kan-MX4 YCp111-pro-tel2-tail)</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Growth defects at 34°C:</strong></td>
</tr>
<tr>
<td>Tel2-7: I204V, L303V, S384P, L675V</td>
</tr>
<tr>
<td>Tel2-19 and Tel2-26: I204V, L303V, S384P</td>
</tr>
<tr>
<td>Tel2-12 (selected as conferring short telomeres): I204V, L303V, S384P</td>
</tr>
<tr>
<td><strong>Tightly thermo-sensitive (growth arrest) at 34°C:</strong></td>
</tr>
<tr>
<td>Tel2-15: I43Y, Y90N, M141T, N178S, S206P (+silent L135)</td>
</tr>
</tbody>
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| doi:10.1371/journal.pone.0030451.t001 |
Figure 2. Increased dosage of several Mediator genes partially rescue the temperature sensitivity of the tel2-19 mutant. (A) Overexpression of the indicated genes, under the control of the GAl1-10 promoter, was continuously induced by growing on solid media containing galactose as the sole carbon source. Cells transformed with the indicated plasmid were first grown in liquid culture in selective minimal medium containing glucose as the carbon source before being re-streaked on agar-based selective minimal medium containing galactose as the carbon source. Growth was assessed after 3 days at the indicated temperature in the serially diluted cells (ten-fold dilutions from left to right in each condition). At 35°C, MED16, CDK8 and MED18 overexpression rescued tel2-19, although slightly less efficiently than MED15. (B) Tel2 and Med15 physically interact in vivo. Putative physical interactions between Tel2-Myc and Med15-HA were measured upon immunoprecipitation (IP) with anti-Med15-HA.
HA or anti-Myc monoclonal antibodies, followed by Western blotting (West.), from crude extracts from strains having transiently overexpressed the indicated constructs after incubation in galactose-based liquid selective media, for 2 hr at 29°C (same conditions for panels B–E). All experiments were conducted in parallel in strains expressing both constructs and in strains with the single constructs to take into account possible background signals. Full length Tel2-Myc3 specifically binds the first half of Med15 (Med15–540-HA) in both directions, that is to say that a positive signal was detected whether one or the other of the two proteins was immunoprecipitated. (C) In contrast, the second half of Med15 (Med15–541–1081-HA) did not associate in vivo with full length Tel2-Myc3. (D) Finally, the first quarter of Med15 (Med15–270-HA) efficiently bound the first half of Tel2 (Tel2–345-HA). (E) At the maximal permissive temperature for growth for tel2-15 of 29°C, the Tel2-15-Myc3 protein still physically interacted with Med15–540-HA, as was also the case at 34°C (data not shown). doi:10.1371/journal.pone.0030451.g002

As mentioned above, Rvb2 has been found to control the expression of around 5% of the S. cerevisiae genes [36]. If Tel2 controlled general transcription in association with Rvb2, mutations in either one should result in a similar gene expression signature. To test this possibility, we selected two genes, MGE1 and MEP2, the expression of which have been previously shown to be up-regulated and down-regulated by Rvb2, respectively [36,37] and measured their levels of expression in the tel2-15 mutant. Interestingly, the same trend in the expression of MGE1 and MEP2 was found in the tel2-15 mutant compared with that in the tel2-160 mutant, a temperature-sensitive mutant of RVB2 [37]. Indeed, MGE1 mRNA levels were severely depressed in the tel2-15 mutant, while, on the opposite, MEP2 mRNA levels were dramatically increased in that same mutant (Figure 5D), a figure similar to that found in the tel2-160/rvb2 mutant [37].

These observations next prompted us to evaluate the impact of overexpressing MED15 on EST2 transcription. Interestingly, overexpressing the MEDI15 subunit of Mediator under the control of its natural promoter resulted in a dramatic increase in EST2/telomerase transcription (Figure 5E).

We presumed that est2 null mutant cells were not temperature-sensitive during the period of time, around 75 generations, they were still alive prior to reaching telomeric senescence [43], as this has never been reported in the literature. However, to make sure that this was the case, we directly tested it and found that, indeed, the est2 null mutant cells prior to senescence were only moderately temperature-sensitive (Figure 5G) unlike the tel2-15 and tel2-19 mutants which were markedly temperature-sensitive, as seen above. Moreover, the growth defects in the est2A mutant could be explained by the damage generated by telomere erosion (see the legend to Figure 5G). These observations strongly suggested that the tel2-ts phenotype was not simply due the diminution of EST2/telomerase transcription. In addition, we note that the tel2-ts mutants arrest at various stages during the cell cycle, as seen above, while the telomerase/est2A mutants arrest at the G2/M border [43]. In fact, recent genome wide data suggest that the tel2-ts mutants are likely to harbor cumulative defects in the transcription of several genes, thereby leading, directly or indirectly, to the depressed levels of endogenous Est2 observed here. Indeed, one of the tel2-ts mutants uncovered here, tel2-7 (see mutations, Table 1) exhibited genetic interactions, under the form of synthetic growth defects, with numerous and various mutations [44]; see also the BioGRID, Toronto, at http:// thebiogrid.org; the tel2-7 mutant was provided by us to these authors). We therefore conclude that the short telomere phenotype of tel2-ts mutants is not solely due to a diminution in telomerase transcription, as proposed above and in agreement with previous observations [22].

Discussion

The present study does not bring much more information concerning the possible telomeric functions of S. cerevisiae Tel2, with the exception of a possible general role in EST2/telomerase transcription (but also in the transcription of other genes).
However, unexpectedly, we find that the MED15 subunit of Mediator (a general regulator of transcription) is a genetic suppressor of the tel2-ts mutations isolated in the present study. This genetic interaction was further documented by the finding of an in vivo interaction between Tel2 and Med15. Overexpression of other Mediator subunits, as well as of SUA7/TFIIB, also rescued the tel2-ts growth defects. We also report here the existence of a physical association between Tel2 and Rvb2. Potentially, based on the already known role of Rvb2 in controlling transcription, the Tel2-Rvb2 interaction might represent a necessary basis for the functional interactions between Tel2 and Med15.

In addition to the recently discovered role of human RUVBL1/2 in mRNA stability (at least those of the PIKKs) via the SGM1-mediated nonsense-mediated mRNA decay (NMD) pathway [28], there is overwhelming evidence that they regulate transcription when functioning in the SRCAP, TIP60 and INO80 chromatin-modifying complexes [34,38]. Most likely, S. cerevisiae Rvb1/2 perform similar tasks in regulating transcription when part of the respective homologous complexes, SWR1, NuA4 and INO80 [34]. In view of the present results, it is interesting to speculate that the S. cerevisiae Rvb2-Tel2 module might play a major role in the expression of multiple genes, as already demonstrated for Rvb2 [34–37], including of EST2/telomerase, as shown here. This is further supported by the observation that Med15-HA2 physically interacted with Rvb2-Myc3 when both were transiently overproduced (NG, MC, unpublished data). Interestingly, genetic inactivation of pontin/ hRUVBL1 or of reptin/hRUVBL2 was recently found to result in decreases in mRNA levels of kTERT, the catalytic subunit of human telomerase, effect partly exerted through binding of reptin to kTERT proximal promoter [45]. Moreover, overexpression of reptin was observed in primary gastric cancer specimens [45]. In a separate study, on colon cancer cells, RUVBL1 was also found to regulate kTERT transcription [46]. Regarding EST2/telomerase expression in S. cerevisiae, it is worth mentioning that its levels of mRNA, as well as those of other genes coding for telomeric proteins, namely Est1, Est3, Snt1 and Ten1, were found to be regulated by the NMD pathway [47], thus establishing a potential link between the Rvb2-Tel2 module and the NMD pathway, as shown for human RUVBL1/2 [28].

The putative role of Tel2 in transcription might be parallel and distinct from its role in the biogenesis of the PIKKs complexes. Because MED15 overexpression rescued the growth defects of the tel2-ts mutants, and Med15 can physically associate with Tel2, we further speculate that the function of Tel2 in transcription uncovered here probably depends on physical interactions with the Mediator via its Med15 subunit. A possible clue stems from the observation of genetic interactions between Tel2 and Sua7, uncovered here, as well as between Sua7 and Med15/Gal11 [48]. SUA7 encodes yeast TFIIB, a general transcription factor required for the initiation of transcription by RNA polymerase II [39]. Mediator’s general function is to recruit RNA polymerase II at sites of active transcription [32,33]. Med15/Gal11 was found to partially suppress deletions of GAL4 and GCN4, encoding two general transcriptional activators [48]. These authors proposed that transcriptional activators work by raising the local concentration of the limiting factor Med15/Gal11, and that Med15/Gal11 works by recruiting Mediator and Taf14-containing transcription factors like TFIIH and SWI/SNF and by competing general repressors like Ssn6-Tup1 off the target promoters [48]. Potentially, transcriptional activators might recruit the Mediator, via Med15, to the chosen site of transcription, while simultaneously recruiting Sua7 via Tel2. The role of Tel2 in these interactions might merely be to assist in chromatin remodeling in cooperation with Rvb1/2 in order to facilitate physical interactions between Sua7 and the Mediator.

Another possible clue to explain the events observed here is related to telomere position effect (TPE), a phenomenon that reversibly silences genes situated close to telomeres [49]. Interestingly, in S. cerevisiae, both Tel2 and Med15 have been reported to affect telomere position effect. Thus, the tel2-1 mutation reduced TPE but had no detectable effect on silencing of HMLα and HMRα, the silent mating type cassettes [5]. However, to our knowledge, the reasons for the implications of Tel2 in TPE have not been uncovered since, except for the proposal that Tel2 may be required for chromatin assembly at telomeres and elsewhere in the genome [5]. On the other hand, a mutation in GAL11/MED15 or, on the contrary, its overexpression, both affected TPE and telomere structure [50]. Moreover, a mutation in GAL11/SDS4/MED15 was found to strongly suppress a raf1-induced silencing defect at the telomeres and the HMR locus [51]. In fact, very recently, it was established that the Mediator directly associated with heterochromatin at telomeres, thereby influencing the exact boundary between active and inactive chromatin [52]. Mutations in Mediator subunits also resulted in increased levels of H4K16 acetylation near telomeres and in desilencing of subtelomeric genes, an effect that appeared to be distinct from the role of Mediator as a co-transcriptional activator [52]. Therefore, the interactions between Tel2 and Med15 described in the present work might theoretically have something to do with their effect on telomere structure. Further work will be required to test these hypotheses, which might be complex and difficult to experimentally approach. For the moment, we have ruled out a role for Tel2 in telomere end protection, as our tel2-ts mutants did not activate the DNA damage checkpoint, unlike mutants defective in telomere protection such as cdc13-1, for instance (NG, MC, unpublished data). However, more subtle defects of telomere structure resulting from Tel2 inactivation, such as those discovered in early studies [5], might be responsible for the functional interactions with MED15 uncovered here.

As stressed above, Tel2 has long been an enigmatic protein, implicated in a myriad of apparently unrelated biological processes in various organisms. However, recent studies have uncovered what appears to be the main function of Tel2, namely in PIKK biogenesis, and other more recent studies have begun to unravel these mechanisms at the molecular level. However, a recent analysis showed that C. elegans CLK-2/TEL2 depletion did not phenocopy PIKK kinase depletion and, in addition,
implicated CLK-2/TEL2 in multiple developmental and cell cycle related processes [53]. The genetic approach developed here has provided new clues to further understand Tel2 functions and, unexpectedly, orientate the research on Tel2 towards directions that had not been suspected before. The present data will hopefully serve as a starting point for further exploring the role of this pivotal protein, Tel2, in potentially novel mechanisms of regulation of transcription.

**Materials and Methods**

**Yeast strains, plasmids and inducible overexpression by galactose**

Yeast strains used in this study were derivatives of BF264-15Daub (ade1 his2 leu2-3,112 trp1-1a ura3Δ), as described previously [54]. Yeast cultures were grown at the indicated temperatures in YEP (1% yeast extract, 2% bacto-peptone,
Figure 5. Tel2 controls transcription of EST2/telomerase (but not that of the telomerase RNA subunit TLC1) and is regulated by the Med15 Mediator subunit. (A) Northern blot analysis of endogenous TLC1 RNA levels indicates an absence of deregulation in the indicated tel2 mutants. rvb2 mutants that exhibit slight and stable telomere shortening (NG, MC, submitted for publication) were also used in that experiment. A
null strain was used to ascertain that the highlighted band indeed corresponds to TLC1 RNA. ACT1 and SCR1 RNA levels were measured to serve as loading controls. (B) Immunoprecipitation-Western experiments aiming at assessing Myc-tagged levels (construct integrated at EST2 genomic locus, under the control of native promoter) indicate that EST2 telomerase levels are depressed in the tel2-15 ts mutant strain grown at the semi-permissive temperature for growth of 29 °C for 2 hr or overnight (ON). The rvh2-2 and rvh2-24 mutants (NG, MC, submitted for publication) were used as controls. (C) Levels of EST2 mRNA, coding for the protein subunit of budding yeast telomerase, were measured relative to those of ACT1, in wild-type cells (wt, normalized to 1.0) and in the temperature-sensitive tel2-15 (left panel) and tel2-19 (right panel) mutants. The mean values ± standard error correspond to 4 experiments performed with the tel2-15 mutant and 5 experiments with the tel2-19 mutant, each sample being performed in triplicate. (D) MAE1 and MEF2 mRNA levels in the tel2-15 ts mutant, at the indicated temperatures. Results are from two experiments, each sample being performed in triplicate. (E) Continuous overexpression of the MED15 Mediator subunit, achieved by transforming the strains of the indicated relevant genotype with an episomal (2 μ) vector harboring MED15 ORF flanked by upstream and downstream natural genomic sequences, resulted in a dramatic increase in EST2 mRNA levels. Data are from two experiments using the wild type and the two mutants, each sample being performed in triplicate.

doi:10.1371/journal.pone.0030451.g005

0.005% adenine, 0.005% uracil) supplemented with 2% glucose (YPD), sucrose or galactose, or in selective minimal medium. All strains were made isogenic by back crossing at least twice against our genetic background. Strain origins, prior to back crossing, were as follows. The rvh2::KanMX4/RVB2, tel2::KanMX4/TEL2, est2::KanMX4/EST2, tel1::KanMX4 and yka70::KanMX4 strains were purchased at Euroscarf (Frankfurt, Germany). The tel1::TRP1 strain was from the Gottschling laboratory.

Two-hybrid experiments using the pACT2 and pAS2 vectors and pACT1 cDNA library were performed as described previously [55].

All constructs were made by using Polymerase Chain Reaction (PCR) to adapt the relevant restriction sites to the sequence of the genes and details of the constructs will be made available upon request. To confirm the two-hybrid interaction between Tel2 and Rvb2 and delineate the domains of interaction, we opted for a transient overexpression system, currently used in genome-wide analyses, which presents the advantage of measuring in vivo interactions of proteins in their native configuration. To have accurate control of the extent of expression, we used the galactose-inducible GAL1-10 promoter and activated it only in a transient manner to avoid possible deleterious effects of heavy overexpression. RVB2 was tagged with a 2 HA-6 His (hereafter referred to as HA2 because an anti-HA monoclonal antibody was used throughout) and TEL2 with a 3 Myc (Myc3) epitope tag, both at their 3’ end. Induction of genes placed under the control of the GAL1-10 promoter was done by transferring cells growing in liquid culture in glucose-containing medium into galactose-containing medium after several washes by centrifugation. In experiments involving expression of protein parts under GAL1-10 promoter control, a supplementary methionine residue was added in front of the truncated sequence (if starting from places other than the natural initiating ATG) to initiate efficient translation.

Western blotting and immunoprecipitation

Techniques for block and release experiments, flow cytometry analysis (FACS), cell extract preparation, immunoprecipitation and immunoblotting (analyzed using an Odyssey Imager) have been described previously [54,55]. Mouse monoclonal anti-HA raw ascites fluid 16B12 (BabCO) and mouse monoclonal anti-HA 12CA5 antibody (Roche Diagnostics) were used for immunoprecipitation and immunoblotting, respectively. Myc-tagged proteins were visualized after immunoprecipitation and Western blotting with monoclonal anti-Myc antibody 9E10 (Roche Diagnostics). Anti-actin antibody, clone C4, was from MP Biomedicals.

Telomere length measurement

To analyze telomere length, genomic DNAs were prepared, separated in a 0.9% agarose gel (in TBE) run in TBE buffer overnight and, after denaturation, transferred and hybridized with a 270 base pair TG(3–5)P-labeled telomeric probe as described previously [55]. Following digestion of genomic DNA with XbaI, to cut within the Y′ regions of chromosomes, telomere tracts of wild-type cells appear as a broad band of ~1.1–1.3 kb which represents the average length of most chromosomes. Results were analyzed using an FLA-5100 Fuji phosphoimager and the ImageGauge software.

Northern blotting and analysis of transcription by RT-PCR

For analysis of TLC1 endogenous levels, total RNA was first isolated from yeast cell cultures according to standard procedures. Northern blot analysis was conducted according to classical techniques using a P32-labeled probe specific for TLC1 sequences. A tel1 null strain was used in all experiments to attest for the specificity of the detected signals.

The relative quantification of mRNA was performed with a quantitative RT-PCR assay. Gene-specific primers were designed using Universal Probe Library Assay Design Center (Roche Applied Science) as primer software. Two micrograms of RNA were reverse transcribed using the first strand cDNA synthesis kit from Fermentas, with gene specific primer for EST2 and random hexamers as primers for the other genes. cDNAs were then diluted from Fermentas, with gene specific primer for EST2 and random hexamers as primers for the other genes. cDNAs were then diluted to a final concentration of 10 ng/μl in sterile H2O and amplified using a BioRad Opticon instrument. Amplification was performed in 20 μl of reaction mix, containing 5 μl of diluted cDNA and 15 μl Mesa Green qPCR Master SYBR Green I (Eurogentec), together with forward and reverse primers. PCR was performed according to a two-step protocol: 3 min at 95°C, followed by 45 cycles comprising each 10 s at 95°C (denaturation) and 30 s at 60°C (annealing/extension). Quantitative data of the samples were obtained using the BioRad CFX Manager software. All cDNA samples were assayed in triplicates. We chose the ACT1 housekeeping gene as the endogenous normalizer because its expression was constant.

Mutagenesis of TEL2

Mutagenesis of TEL2 to isolate temperature-sensitive mutants was performed by mutagenic PCR coupled to the so-called gap repair method to generate in vivo the plasmids having copied the in vitro-generated mutant alleles, as described below. To mutagenize TEL2, the 2064 base pair (bp)-long TEL2 ORF plus ~215 bp upstream of the ATG and ~270 bp downstream of the stop codon was amplified by error-prone PCR under the following conditions. The concentration of dNTPs was either kept as in standard conditions (200 μM each) or one of the four dNTP concentration changed to 0.5–1.0 mM, those of the other three being kept at 200 μM, and, in both cases, the concentration of MgCl2 was changed from 1.5 to 3.0 or 4.0 mM and 0.5 mM MnCl2 added to the reaction. Standard Taq polymerase and PCR buffer (Promega) were used. Following a 30-cycle amplification, the mutated fragments were transformed into a tel2::KanMX4 strain in which
the deletion was complemented by wild-type TEL2 borne on a GEN-URA3 (YCplac33) plasmid, together with a centromeric, LEU2-based (YCplac111), plasmid carrying TEL2 ORF plus the same flanking regions and made linear by digestion with NsiI and SnaI, endogenous sites located ~50 base pairs post-initiating ATG and ~140 base pairs downstream of the stop codon, respectively. After shuffling out the wild-type TEL2 allele on 5-FOA medium (which counter-selects for URA3 in the plasmid), colonies growing at 24°C were replica plated at 33–37°C to identify thermosensitive colonies. We could isolate six such tel2 alleles. All six alleles were sub-cloned from the initial centromeric vector into a single copy vector (LEU2-based, YIp128) that was subsequently integrated at the LEU2 locus and re-transformed into the original tel2 null YCplac33-TEL2 strain, followed by 5-FOA counter-selection.

To isolate tel2 mutants potentially deregulated in telomere length control, the initial processes were similar to those exposed above. However, at the step next after shuffling out of the telomere length control, the initial processes were similar to those exposed above. Randomly from the plates, propagated for ~20 days at 24°C to attain telomere length equilibrium and selected by Southern blot analysis, as described above.

Cell viability assays
The viability of cells previously grown in liquid was determined by performing and analyzing the so-called “drop tests”. To do this, cells from exponential growth cultures were counted with a hemacytometer and the cultures were then serially diluted by 1/5th or 1/10th and spotted onto either selective plates or YEPD non-selective plates, as required, and incubated at the desired temperature for 2-3 days before being photographed.

Supporting Information
Figure S1 (see Appendix S1): Physical interactions between Tel2 and Rvb2. (A) Endogenous Rvb2 and Tel2 physically associate even when telomerase access to the telomeres is restricted or even totally prevented. Immunoprecipitation-Western (IP-West.) blotting experiments on endogenous HA2-RVB2 and MYC2-TEL2 in an otherwise wild type background (2nd lane) or in strains containing either an est1 (3rd lane), a yka70 (4th lane) or est1 yka70 null mutation (5th lane) to restrict telomerase access to the telomeres either in the G1 and early S phases (yka70 null), late S, G2 and M phases (est1 null), or in all cell cycle phases (est1 null yka70 null) [2]. The 1st lane is a control with no MYC2-TEL2 expression to assess for HA2-Rvb2 background. (B) Overproduced full length Tel2-Myc3 physically interacts with full length Rvb2-HA2, in both directions. Tel2-Myc3 was specifically detected in Rvb2-HA2 immunoprecipitate (left panel, top gel) and reciprocally (right panel, bottom gel) over the background; compare, in each panel, lanes 3 (strain harboring both constructs) with lanes 1 and 2 (strains harboring the single constructs). Overexpression of the constructs, here and below in C, under the control of the inducible GAL1-10 promoter was for 2 hr at 29°C. (C) Overproduced Te12 and Rvb2 still physically associate in the absence of Tel1 (which has been previously reported to physically associate with Tel2; [3]), also creating a situation in which telomerase access to the telomeres is restricted. The association between Rvb2-HA2 and Tel2-Myc3 could be detected whether the immunoprecipitation (IP) was directed against Tel2-Myc3 (left panel) or, on the opposite, against Rvb2-HA2 (right panel), and the Western blotting (West.) realized with anti-HA and anti-Myc monoclonal antibody, respectively, as indicated below each gel. (D) Tel2 did not physically associate with amino acids 420 to 740 of Est2, comprising the entire catalytic domain when they were overproduced, for 2 hr at 29°C, under the control of the inducible GAL1-10 promoter in a high-copy vector. These experiments were performed using strains expressing either full length Tel2 (Tel2-Myc3, left panel), or Tel2-Myc3 first half (middle panel) or Tel2-Myc3 second half (right panel), as well as Est2’s catalytic domain (Est2340-740-HA2). (EPS)

Figure S2 (see Appendix S1): Delineating the Tel2 and Rvb2 fragments needed for physical interaction. (A) The first half of Tel2, Tel2(1–343)-Myc3, but not its second half, Tel2(344–688)-Myc3, had affinity with full length Rvb2-HA2. The two panels show the same thing in two distinct experiments. Note, in bottom gels, that the first 343 amino acids of Tel2 migrated at an apparent molecular weight of around 33 kD, while roughly the same number of amino acids in the second part, the last 345 ones, migrated at an apparent molecular weight of around 48 kD. (B) Full length Tel2-Myc2 physically interacted with the first half of Rvb2, Rvb2(1–235)-HA2, in both directions, as shown in left and middle panels, but barely with its second half, Rvb2(236–470)-HA2 (right panel). (C) Rvb2(1–118)-HA3, the first half of Rvb2’s first half, clearly associated with Tel2 first half, Tel2(1–343)-Myc3, while Rvb2(119–235)-HA2, the second half of Rvb2’s first half, did only faintly. (D) Rvb2(1–235)-HA2 had no clear physical interactions with the first two halves of Tel2 first half, namely Tel2(1–171)-HA2 and Tel2(172–343)-HA2, implying that sequences in both of these two Tel2 fragments are essential for association with Rvb2. (E) Schematic of Tel2-Rvb2 interactions showing in grey the regions of Tel2 and Rvb2 implicated here in physical association between the two proteins. (EPS)

Figure S3 The tel1 null yku70 null double mutant exhibited shorter telomeres than the two single mutants tel1Δ and yku70A. The mutants were grown (at 29°C) sufficiently long to harbor telomeres having attained length equilibrium. See the legend to Figure 3 for more technical detail. (EPS)

Figure S4 Immunoprecipitation-Western experiments, performed as described in the legends to Fig. 5B and S1, aiming at assessing Myc3-Est2 levels (construct integrated at EST2 genomic locus, under the control of native promoter) indicate that EST2/telomerase levels are depressed in the tel2-19 ts mutant strain grown at the semi-permissive temperatures for growth of 29°C for 2 hr or restrictive temperature of 34°C for 4 hr, but not at the permissive temperature of 24°C, as indicated. (EPS)

Figure S5 (A) est2 null mutants prior to telomeric senescence are only moderately temperature-sensitive. Therefore, the strong ts phenotype of the tel2-15 and tel2-19 mutants cannot be due to the diminution of EST2 transcript levels in these mutants. As soon as EST2 has been genetically inactivated, telomeric DNA damage accumulates, thus presumably provoking the slight growth defect seen at all temperatures tested in these cells compared with the wild type. Note that at elevated temperatures, e. g. 36°C, cells divide faster thus accelerating accumulation of damage and progression through senescence and provoking these growth defects. Finally, the absence of telomerase provokes a general destabilization of the telomeres that will eventually activate the DNA damage checkpoint and slow down cell cycle progression. Ten-fold serial dilutions (from left to right in each condition) of cultures of the indicated relevant genotype were grown for 3 days on YEPD agar...
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