

# Influence Of Deubiquitinating Enzymes On Mutagenesis In *Saccharomyces Cerevisiae*

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## Citation

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## Abstract

In recent years, it became clear that the mutagenic effect of base alterations in a DNA template is dependent on bypass synthesis, carried out by one or more translesion polymerases. A critical role for proliferating cell nuclear antigen (PCNA) and its ubiquitination following DNA damage has been established. Among *Saccharomyces cerevisiae* deletion mutants in which UV mutagenesis is compromised, we identified and characterized a mutant of the ubiquitin recycling protein Doa4. Similar cases may be represented by Doa1, previously described by others, as well as Bro1 and Ubi4. We discuss overall altered ubiquitin levels or failure to deubiquitinate specific target proteins as likely explanations. This study is of relevance for understanding and possibly modifying the mutagenic effect of DNA-damaging agents in environmental toxicology, cancer treatment and cancer prevention.

## INTRODUCTION

The cellular responses to various kinds of DNA damage have by now been elucidated to a significant degree in pro- and eukaryotes (Friedberg et al., 2006). However, concepts explaining one of the most severe consequences of DNA damaging treatments – the enhancement of mutagenesis – have emerged only during the last few years. With the discovery of translesion polymerases, however, the frequently postulated replicative bypass of altered bases of reduced coding capacity gained a mechanistic foundation. Data from the eukaryotic model budding yeast (*Saccharomyces cerevisiae*) were essential for this progress and the basic mechanisms appear to be evolutionarily conserved.

Pathways leading to mutation are best understood for DNA damage by UV-C radiation, resulting in pyrimidine dimers. The prototype of an error-prone polymerase is polymerase  $\eta$ , the complex of proteins Rev3 and Rev7 (Nelson et al., 1996b). This polymerase is responsible for most induced and spontaneous mutagenic events. Of equal importance is Rev1, a deoxycytidyl transferase with an independent structural role in mutagenesis, possibly as a platform for several bypass polymerases (Acharya et al., 2005; Acharya et al., 2007; Acharya et al., 2006; Guo et al., 2006a; Nelson et al., 1996a).

In contrast to this error-prone bypass, a mostly error-free

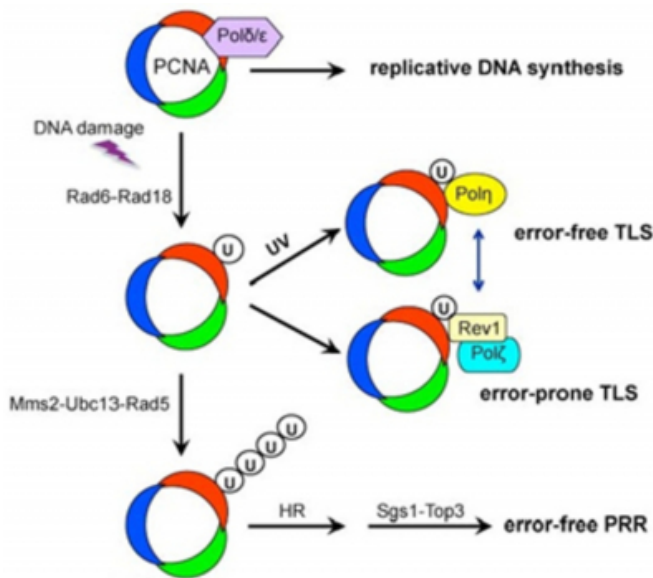
bypass of the most frequent UV photoproducts, dipyrimidine cyclobutane-type dimers is catalyzed by polymerase  $\epsilon$  (Johnson et al., 1999; Yu et al., 2001). Consequently, the enzyme's action lowers overall mutability since it competes with error-prone bypass mechanisms. A second major error-free tolerance pathway of different mechanism is the Rad5 pathway that appears to involve template switching (Li et al., 2002; Zhang and Lawrence, 2005).

The current concept of bypass pathway choice is based upon PCNA and its modifications by ubiquitin (Ub) and SUMO (Fig. 1). Monoubiquitination of PCNA (at K164 in yeast) is found after methylmethane sulfonate (MMS) or UV treatment (Hoegge et al., 2002; Kannouche et al., 2004) and a requirement of ubiquitinated PCNA for UV mutagenesis has indeed been demonstrated (Stelter and Ulrich, 2003; Zhang et al., 2006). The Rad6-Rad18 complex can bind to single-stranded DNA (Bailly et al., 1994; Bailly et al., 1997) which emerges as a consequence of blocked replication. The Ub conjugating activity of Rad6 catalyzes monoubiquitination of PCNA at K164 which increases its affinity for bypass polymerases (Guo et al., 2006b; Kannouche et al., 2004). Monoubiquitination of PCNA attracts error-prone polymerases mediating a mutagenic bypass, presumably through the ubiquitin-binding domain of Rev1. On the other hand, the signal for the error-free bypass by template-switching is subsequent K63-linked polyubiquitination, resulting from the action of the Ubc13-Mms2-Rad5

complex, with the Ubc13-Mms2 heterodimer functioning as the ubiquitin-conjugating (E2) enzyme in conjunction with the Rad5 (E3) ubiquitin ligase (Hoegge et al., 2002; Ulrich and Jentsch, 2000).

**Figure 1**

Fig. 1: Ubiquitination of PCNA and translesion synthesis. From (Zhang et al., 2011), reproduced with permission. See text for details



Given the importance of Ub for translesion synthesis, it is perhaps surprising that the impact of cellular Ub concentration on mutagenesis has not been studied in detail. For example, whereas a deletion of the polyubiquitin gene UBI4 (encoding a protein of five consecutive Ub as the major Ub source in yeast) is not lethal, altered stress resistance is detectable (Finley et al., 1987). However, an analysis of spontaneous or induced mutability has never been reported for this mutant.

Posttranslational protein modification by Ub and specifically by K48-linked polyUb has been traditionally linked with promoting degradation through the 26S proteasome. Ub is a long lived-protein and, consequently, deubiquitination enzymes (DUBs) that recycle Ub from proteins marked for degradation play an important role in Ub homeostasis. DUBs are also needed to reverse ubiquitination from target proteins whose activity or localization was altered by Ub and from those that were accidentally ubiquitinated. This is a topic of considerable complexity, given the identification of more than 100 DUBs in humans (Amerik and Hochstrasser, 2004; Reyes-Turcu et al., 2009).

Our interest in exploring the relationship between DUBs and

induced mutagenesis stems from the isolation of a mutant of Doa4, a DUB important for Ub homeostasis, in a screen for mutants defective in UV mutagenesis (Gong and Siede, 2009). Doa1 may represent a similar case, studied by other investigators (Lis and Romesberg, 2006). Here, we present a characterization and discussion of the role of Doa4 in DNA-damage-induced mutagenesis.

**MATERIAL AND METHODS**

**STRAINS**

The initially used strains were all derivatives of BY4741 (MATa his3Δ1 leu2Δ0 met15Δ0 ura3Δ0) and part of the systematic yeast gene deletion collection, purchased from Open Biosystems. Using PCR-mediated transplacement (Rothstein, 1989) and Li-acetate transformation (Gietz and Schiestl, 1995), selected deletions were transferred into strain Y300 (MATa ade2-1 ura3-1 trp1-1 his3-11,15 leu2-3,112 can1-100), originally obtained from Dr. Stephen Elledge.

**MUTAGEN TESTING**

Cells were grown to logarithmic phase for 16 h or to saturation for 48 h in YPD (1% yeast extract, 2% peptone, 2% dextrose) at 30°C. For UV radiation assays, cells were washed and resuspended in sterile water, appropriate dilutions were plated on synthetic media plates with or without canavanine or tryptophane (Amberg et al., 2005) and irradiated (germicidal UV-C). For MMS assays, cells were incubated in YPD at a titer of 2x10<sup>7</sup> cells/ml for 1 h at 30°C, washed and plated. Colonies were counted after 3-5 days of incubation. Fractions of surviving cells and mutants per surviving cells were calculated.

**RESULTS**

The key data that initiated this project originated from a screen of the haploid *S. cerevisiae* deletion mutant collection for mutants that reduce the probability of UV-induced mutations (Gong and Siede, 2009). We used the well-studied system of forward mutation to canavanine resistance which selects for defects in arginine permease, thus preventing the uptake of the toxic arginine analog canavanine. Not surprisingly, deletion mutants of many genes known to be required for induced mutagenesis such as REV3 were reisolated. We also isolated mutants of genes not previously known to influence UV mutagenesis including DOA4 which encodes a DUB (Gong and Siede, 2009). The defect in UV-induced forward mutation to canavanine resistance conferred by a deletion of DOA4 was quantified with the original deletion strain (Table 1, BY4741 as genetic background).

After testing a cross-section of yeast DUB deletions in quantitative single-dose assays, it was suggested that this phenotype is shared with mutants of Bro1 (a Doa4 interacting protein), Doa1 and Ubi4 (polyubiquitin) but not with other DUB deletions tested (Table 1); others rather seem to increase mutability. Interestingly, decreased mutability appears to be accompanied by decreased UV resistance of colony formation – primarily in case of *doa1Δ* and less so for *doa4Δ*, *bro1Δ*, or *ubi4Δ*.

**Figure 2**

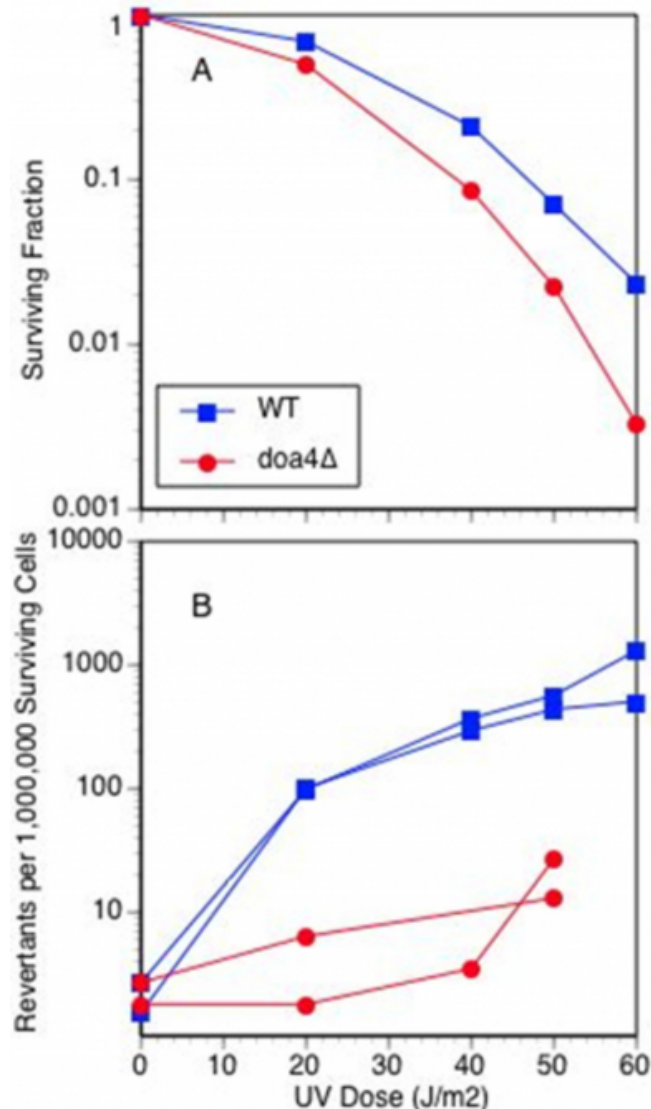
Table 1

Strain (Genotype)	% Survival (30 J/m <sup>2</sup> UV)	UV-Induced Can <sup>r</sup> mutants per 10 <sup>6</sup> surviving cells
WT	24	74
<i>doa1Δ</i>	7	6
<i>doa4Δ</i>	19	<3
<i>ubp1Δ</i>	26	170
<i>ubp2Δ</i>	51	48
<i>ubp5Δ</i>	51	130
<i>ubp6Δ</i>	40	222
<i>ubp8Δ</i>	40	130
<i>ubp12Δ</i>	43	145
<i>bro1Δ</i>	35	<2
<i>ubi4</i>	37	2

To prove the general validity of our observation, we transferred the DOA4 deletion to an unrelated strain (Y300) and tested a mutational system that is very different from canavanine forward mutation (*trp1-1* reversion). A partial defect in UV mutagenesis was indeed confirmed over a range of doses. The influence was similar in saturated cultures (Fig. 2) and in logarithmic-phase cultures (Fig. 3).

**Figure 3**

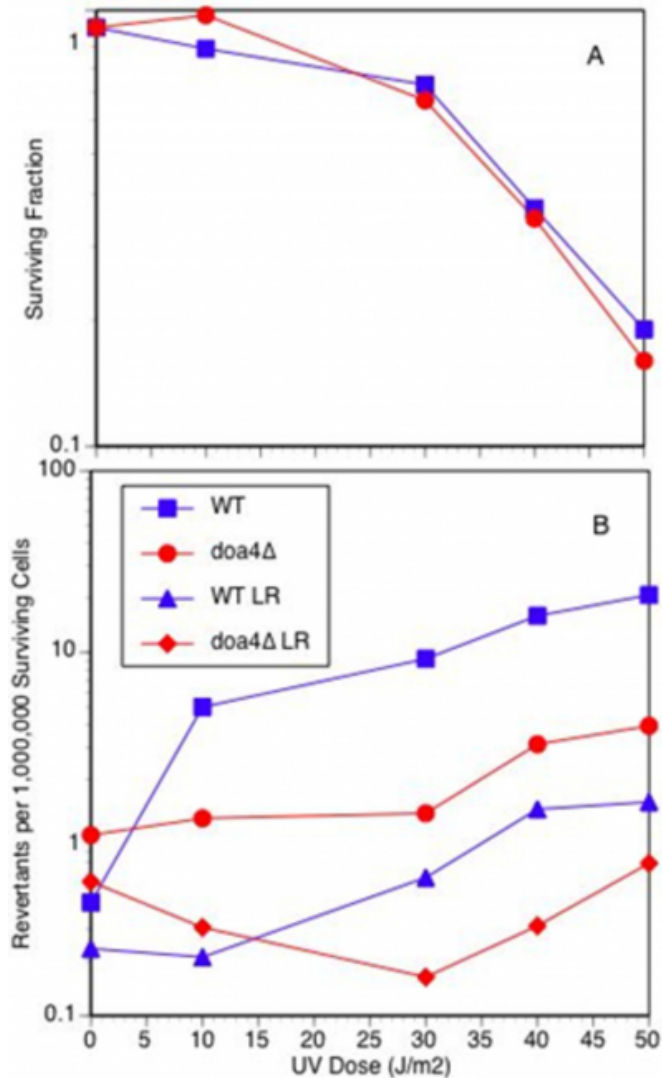
Fig. 2: UV survival (A) and mutation frequencies (reversion, two independent experiments, B) for WT and isogenic  $\Delta$ . Cultures were grown to saturation (cultured for 48 h in YPD).



We noted a small fraction of distinct fast growing mutants of the *trp1-1* nonsense allele. We assume that these are certain locus-specific revertants among various kinds of suppressor mutants. If the frequencies of these revertants were plotted separately, a defect in mutagenesis in the *doa4* deletion was still evident. Whereas the WT showed some mutant induction as a function of UV dose, the *doa4* mutant shows frequencies that remain indistinguishable from the spontaneous background mutant frequency (Fig. 3).

**Figure 4**

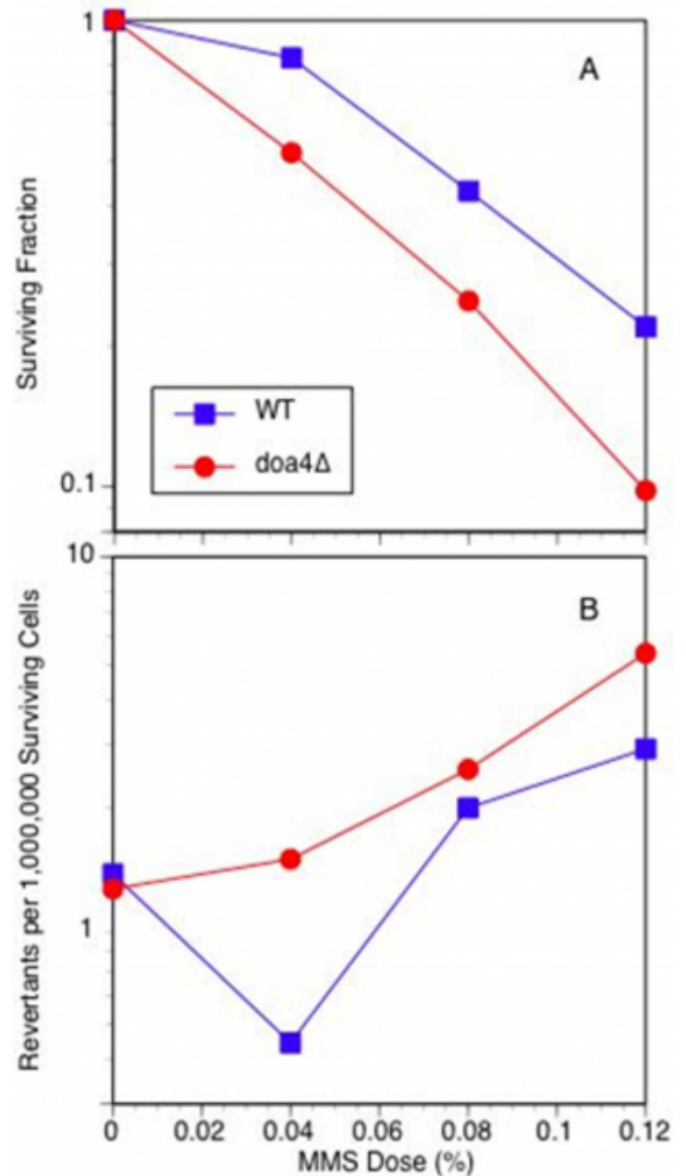
Fig. 3: UV survival (A) and mutation frequencies ( reversion, B) for WT and isogenic  $\Delta$ . Logarithmic-phase cultures were used. In B, mutation frequencies of a distinct fraction of fast-growing mutants was plotted separately (putative locus-revertants, LR, triangles/diamonds).



However, this defect in mutagenesis appeared to be damage-specific. In response to the alkylating agent MMS, *trp1-1* reversion was not compromised by the *doa4* deletion (Fig. 4).

**Figure 5**

Fig. 4: Survival (A) and mutation frequencies ( reversion, B) for WT and isogenic  $\Delta$ . Cultures grown to logarithmic phase were treated with MMS.



**DISCUSSION**

We detected a partial defect in UV mutagenesis in deletion mutants of DOA4. DOA4 (= UBP4) encodes an ubiquitin isopeptidase. Initially, genetic and physical studies indicated an interaction of Doa4 with at least a subset of 26S proteasomes and suggested a role of Doa4 in detaching Ub from proteins destined for degradation by the proteasome (Papa et al., 1999; Papa and Hochstrasser, 1993). More recent data indicate that Doa4 acts at the cytoplasmic surface of the late-stage endosome together with the ESCRT-II complex and is required to recycle Ub from membrane proteins designated for the vacuole (Amerik et al., 2000;

Swaminathan et al., 1999).

Such a role of a DUB in DNA-damage responses is not without precedence. As described by Lis and Romesberg, Doa1 appears to represent a similar case since it is required for normal resistance to MMS and hydroxyurea (Lis and Romesberg, 2006) as well as UV (our data, Table 1). The protein is required for normal Ub levels (Ghislain et al., 1996), it binds Ub and prevents the accumulation of K-48 linked Ub trimers suggesting that Doa1 (or a co-purifying protein) acts as a Ub protease (Lis and Romesberg, 2006). MMS-induced histone H2B- and PCNA monoubiquitination are not detected in *doa1* mutants (Lis and Romesberg, 2006). Especially the latter defect might result in a defect in induced mutagenesis (see Fig. 1). We have tested this hypothesis for UV radiation and found indeed a severe defect in induced mutability to canavanine resistance (Table 1 and data not shown).

It is important to distinguish between a general influence on bypassing DNA damage in a mutagenic fashion and effects restricted to this specific selection system (Gong and Siede, 2009; Lemontt, 1977; Lis et al., 2008). Preferably, mutation data need to be confirmed with mutational systems of different nature. Canavanine sensitivity is quite common in mutants of the Ub/proteasome system and has indeed been described for mutants of UBI4 (Reyes-Turcu et al., 2009). Canavanine sensitivity may limit mutability. For example, a defect in detoxification may increase canavanine toxicity and counteract the emergence of canavanine-resistant mutants. Such influences can indeed be rationalized in case of mutants involved in Ub metabolism.

Consequently, we constructed a DOA4 deletion in unrelated genetic background (strain Y300) and the defect in UV mutagenesis was verified in a different mutational system (*trp1-1* reversion) (Fig. 2, 3).

Two hypotheses can be invoked to explain these observations. First, the DUB in question may be required for Ub recycling and the overall reduced Ub level may be detrimental for the mutagenic process, i.e. error-prone translesion synthesis. Certain proteins may need to be modified by mono- or K63-linked poly-ubiquitin or degraded following K48-linked polyubiquitination. Second, the DUB may be required for direct deubiquitination of a specific target protein(s) involved in mutagenesis.

The first hypothesis is preferred because of the characterized Doa4 function that has now been primarily implicated in

recycling Ub from vacuolar membrane-bound proteins (Amerik et al., 2000; Swaminathan et al., 1999). A direct interaction with DNA repair/mutagenesis proteins appears therefore somewhat unlikely.

An obvious candidate for an indirect DUB target that influences mutability is PCNA. A defect in PCNA ubiquitination following MMS treatment has already been detected for *doa1* (Lis and Romesberg, 2006) which we have shown to be defective in UV mutagenesis in this study.

However, three observations do not fit with this concept. First, UV sensitivity of the DUB mutants (Tab. 1) does not approach that of mutants of the Rad5/Mms2/Ubc13 complex, the E3/E2 enzymes required for polyubiquitination of PCNA and error-free damage tolerance (Fig. 1). If Ub homeostasis is disturbed, it is not obvious why polyubiquitination may be less reduced than monoubiquitination on which it depends. Second, a significantly lower level of free ubiquitin is found in *Doa4* mutant cells only when cells approach stationary-phase (Swaminathan et al., 1999). A defect in UV mutagenesis for *doa4*, however, was detected in both logarithmic phase and 48 h cultures (Fig. 2, 3). Third, ubiquitination of PCNA is found after UV as well as MMS treatment. A defect in induced mutagenesis, however, was not evident in MMS-treated cells (Fig. 4).

Future studies will address these discrepancies and may reveal other, relevant targets. For example, H2B represents another Ub modified protein that is important for DNA-damage transactions (Lis and Romesberg, 2006). Additional candidate targets that may need to be degraded through the proteasome pathway include the checkpoint clamp loader Rad24 (if it behaves similar to the human homolog) (Zhang et al., 2010).

In the future, it should also be explored why only certain DUBs and not others may have an influence on mutagenesis although their effect on free Ub levels might be quite comparable. The concept of Ub channeling to certain targets has been brought up in conjunction with the *doa1* phenotype (Lis and Romesberg, 2006) but the mechanism remains unknown.

Protein degradation and Ub-metabolizing proteins were found to be conserved in evolution and thus, the suggested studies may very well be relevant for higher eukaryotes. Interestingly, Usp6 as a potential human ortholog of *Doa4* is an oncogene critically important for the development of



aneurysmal bone cysts (Oliveira et al., 2006). The described chromosome translocations in this disease lead predominantly to the overexpression of Usp6.

Many additional implications can be listed. For example, manipulation of cellular Ub levels may be used to modify the outcome of cancer chemotherapy and to reduce mutagenic side effects.

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