UV-Induction of Thymine-Containing Dimers in *Saccharomyces cerevisiae*

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(Z. Naturforsch. **30 c**, 811–817 [1975]; received August 5, 1975)

Far UV, Kinetics of Dimer Formation, Dimer Yield Ratio

In haploid and diploid *S. cerevisiae* the dimer yield ratio $\hat{TT}/\hat{CT}$ is found to be 1.2/1 and 1.3/1, resp., at the UV (254 nm) unit dose 1 erg/mm², the share of $\hat{TT}$ and $\hat{CT}$ in a UV (254 nm) lethal hit being 0.7 $\hat{TT}$ and 0.6 $\hat{CT}$. A general formulation of the UV lethal hit is given and discussed. The $\hat{TT}+\hat{CT}$ yields obtained for *S. cerevisiae* are compared to those reported for other organisms. It is found that there obviously exists a directly proportional linear correlation between genome size and $\hat{TT}+\hat{CT}$ yield for the UV dose range well below the stationary levels of the $\hat{TT}$ and $\hat{CT}$ formation kinetics.

Introduction

In a recent paper we presented an assay of thymine-containing dimers UV-induced in the yeast *S. cerevisiae* employing (5′-dTMP) DNA-specific labelling [1]. The method was reported to allow quantitative analysis down to UV doses of at least 500 erg/mm² and thus is as sensitive as the methods of radio-dimer assay in bacteria and mammalian cells which are based on (Thy or Thd) DNA-specific labelling. Here we wish to present some further data about UV-induction of Thy-containing dimers in *S. cerevisiae*.

Materials and Methods

Strains

Strain 211-1aMT6-425 of *S. cerevisiae* [= T6-425 in the text; haploid and respiratory deficient (*rho*⁻)]; strain 211-1aMT6-425 *tmp1-51* of *S. cerevisiae* (= T6-425 *tmp1-51* in the text; haploid and *rho*⁻); strain MB1052 *tmp1-3* of *S. cerevisiae* (diploid and *rho*⁻): as cited in Fäth and Brendel [1].

Labelling of cells, UV-irradiation, and dimer assay

This was essentially performed as previously described [1], the UV-wavelength used being 254 nm.

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Mathematical

A. $\hat{TT}$ and $\hat{CT}$ dimer yield per yeast genome were determined with following assumptions: 1. Performing (5′-dTMP) DNA-specific labelling in *S. cerevisiae* as described in [1] is expected to yield stationary cells where the DNA-Thy has approx. the same specific activity as the 5′-dTMP offered in the labelling medium [2]. Thus the Thy-radioactivity found in the formic acid hydrolysates is expected to be directly proportional to the Thy-contents of the analysed DNA-hydrolysate. 2. Yeast nuclear DNA is assumed to contain 30.5% Thy and 19.5% Cyt [3], and the size of a haploid (diploid) yeast genome is assumed to be 1.35×10^7 (2.7×10^7) base pairs or 8.9×10^9 (1.8×10^{10}) dalton with an average weight of 660 dalton per base pair [4]. Then the number of Thy molecules per haploid (diploid) yeast genome is 8.4×10^6 (1.7×10^7). 3. The Thy in $\hat{TT}$ and $\hat{CT}$ has the same specific activity as the total DNA-Thy and the $\hat{CT}$ is labelled in the Thy-moiety only whereas the $\hat{TT}$ is labelled in either Thy-moiety.

Then the number of $\hat{TT}$ and $\hat{CT}$ dimers, resp., UV-induced in a haploid (diploid) yeast genome by an incident UV-dose D_i is

$$= D_i \times 8.9 \times 10^9 \times \frac{0.305}{322} \times f_{\hat{TT}} \times 0.5$$

for $\hat{TT}$ per haploid genome,

Abbreviations: 5′-dTMP, deoxythymidine-5′-monophosphate; Pyr, pyrimidine; Thy, thymine; Cyt, cytosine; Thd, thymidine; $\hat{TT}$, thymine-thymine dimer; $\hat{CT}$, cytosine-thymine dimer; $\hat{UT}$, uracil-thymine dimer; $\hat{CC}$, cytosine-cytosine dimer; PyrPyr, pyrimidine dimer.

$$= D_i \times 1.8 \times 10^{10} \times \frac{0.305}{322} \times f_{\hat{TT}} \times 0.5$$

for $\hat{TT}$ per diploid genome,

$$= D_i \times 8.9 \times 10^{9} \times \frac{0.305}{322} \times f_{\hat{UT}}$$

for $\hat{CT}$ per haploid genome,

$$= D_i \times 1.8 \times 10^{10} \times \frac{0.305}{322} \times f_{\hat{UT}}$$

for $\hat{CT}$ per diploid genome,

with $f_{\hat{TT}}$ and $f_{\hat{UT}}$ = fraction of nuclear DNA-Thy present or found in $\hat{TT}$ and $\hat{UT}$ dimer, resp., at the unit dose 1 erg/mm² of incident UV (254 nm), and with the nominator term "322" = MWT of dTMP in dalton.

B. For the composing of our Fig. 1 the originally obtained data were transformed as follows:

$N_{\hat{TT},\,Pyr} \leftarrow N_{\hat{TT},\,Thy} \times 0.61$;
$N_{\hat{CT},\,Pyr} \leftarrow N_{\hat{CT},\,Thy} \times 0.61$,

with

$N_{\hat{TT},\,Thy}$ = $\hat{TT}$-region radioactivity at a given incident dose UV (254 nm) minus $\hat{TT}$-region radioactivity at zero dose UV (dpm) $\times 1/2$ / total Thy-radioactivity per chromatographical run (dpm),

$N_{\hat{CT},\,Thy}$ = $\hat{UT}$-region radioactivity at a given incident dose UV (254 nm) minus $\hat{UT}$-region radioactivity at zero dose UV (dpm) / total Thy-radioactivity per chromatographical run (dpm),

and

$$0.61 = \frac{\text{yeast nuclear DNA Thy contents}}{\text{yeast nuclear DNA Thy + Cyt contents}}.$$

C. Estimation of the value of term

$$L_{\hat{TT}} \times F_{\hat{TT}} \times 1\,\hat{TT} + L_{\hat{CT}} \times F_{\hat{CT}} \times 1\,\hat{CT} + L_{\hat{CC}} \times F_{\hat{CC}} \times 1\,\hat{CC}$$

for haploid *S. cerevisiae:* 1. Meistrich [5] reports 3.3 "thymine dimers" per lethal hit for phage T4 *vx* after UV (>310 nm) + acetophenon D (AcΦD). As UV (>310 nm) + AcΦD is a pure $\hat{TT}$ inducer [6] this means that

$$L_i \times F_i \times 1\,I = L_{\hat{TT}} \times F_{\hat{TT}} \times 1\,\hat{TT} = L_{\hat{TT}} \times 3.3 = 1 \text{ for phage T4 } vx.$$

Then $L_{\hat{TT}} = 1/3.3 = 0.30$ results for phage T4 *vx*. 2. It be assumed that this value for $L_{\hat{TT}}$ is valid for *S. cerevisiae*, too, and that in this organism $L_{\hat{TT}} = L_{\hat{CT}} = L_{\hat{CC}}$ is valid. 3. We found 0.7 $\hat{TT}$ + 0.6 $\hat{CT}$ dimers per lethal hit of UV (254 nm) in *S. cerevisiae* by retrapolation of our measured data to an LD_{37} (254 nm) = 0.06 erg/mm² which is reported for haploid *S. cerevisiae rad1 rad18 rad51* [68]. If it is assumed that the dimer yield ratio $\hat{CT}/\hat{CC} = 1/1$ [9] is approx. correct, then one could estimate 1.9 $\hat{Pyr}\hat{Pyr}$ per lethal UV hit in a haploid *S. cerevisiae rad1 rad18 rad51*. Then for *S. cerevisiae* one would obtain $\Sigma L_i \times Fi \times 1\,I \rightarrow L_{\hat{TT}} \times 1.9\ \hat{Pyr}\hat{Pyr} = 0.30 \times 1.9 = 0.57$. i = $\hat{TT}$; $\hat{CT}$; $\hat{CC}$.

Results and Discussion

Kinetics of $\hat{TT}$ and $\hat{CT}$ formation

Fig. 1 depicts the kinetics of $\hat{TT} + \hat{CT}$, $\hat{TT}$, and $\hat{CT}$ formation in a haploid and a diploid strain of *S. cerevisiae* for the range of incident UV doses $10^3 - 2 \times 10^4$ erg/mm². The originally obtained data – Thy-radioactivity found as dimer/total Thy

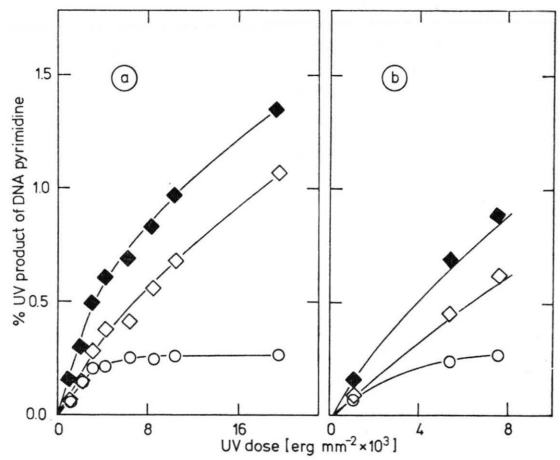

Fig. 1. UV (254 nm)-induced $\hat{Pyr}\hat{Pyr}$ formation in haploid *rho*⁻ (a) and diploid *rho*⁻ (b) *S. cerevisiae*. ◆–◆, $\hat{TT}$+ $\hat{CT}$; ◇–◇, $\hat{TT}$; ○–○, $\hat{CT}$.

radioactivity – were transformed to dimers/DNA-Pyr (Materials and Methods) to allow direct comparison with the data reported in [7–12]. It must be pointed out, however, that the yeast strains used in our experiments are respiratory deficient (*rho*⁻) whereas those used by the authors mentioned obviously were respiratory proficient (*rho*⁺). We find that – for the dose range analysed – the dimer formation curves are essentially identical for haploid and diploid yeast. Furthermore our results are in

good agreement with those in [7–12], for incident UV (254 nm) doses well above 1000 erg/mm², but not for UV doses near 1000 erg/mm² (see below).

Dimer yield per UV unit dose of 1 erg/mm²

Extrapolation from dimer yield data obtained for UV doses far above the unit dose is a delicate matter as it assumes the characteristics of the dimer formation kinetics at the unit dose to be the same as those found at the "high" dose. We are fully aware of this and wish our extrapolation data to be viewed with these limitations.

In Table I column 4 these extrapolation values are separately given for $\hat{TT}$ and $\hat{CT}$ based on the data obtained for the incident UV dose 1080 erg/mm². It may be discussed whether the "high" dose dimer yields are reasonable estimates for the unit dose dimer yields or not: 1. A first necessary condition for reasonable extrapolation is that at the "high" dose chosen for retrapolation the dimer formation kinetics are well below their stationary level. 2. The second necessary condition is that between the "high" dose and the zero dose the course of the dimer formation kinetics must not attain a concave shape. It should be linear or just slightly convex.

Literature is abundant of cyclobutane dimer yield data and cyclobutane dimer formation kinetics for pyrimidine dinucleotides [13–18], synthetic polynucleotides [15, 19–26], viral, procaryotic and eucaryotic DNA *in vitro* and *in vivo* [7–12, 27–59]. With respect to this cited literature we conclude the course of the $\hat{TT}$ and $\hat{CT}$ formation kinetics to be generally linear in the range between the zero dose UV and at least 1000 erg/mm² UV and also to be well below their stationary levels. Thus we think – in analogy to those sources – that our extrapolation from the UV dose 1080 erg/mm² to the UV unit dose 1 erg/mm² is reasonable.

As given in Table I column 5 the ratio $\hat{TT}/\hat{CT}$ is 1.2/1 and 1.3/1 for haploid *rho*⁻ and diploid *rho*⁻ *S. cerevisiae*, respectively, at the UV dose 1080 erg/mm². This finding is well reproducible. The question is whether this ratio is equally valid for UV doses near the zero dose UV or whether in fact it might be 1/1 there. Though it is known that the $\hat{TT}$ dimer is a priori more readily formed than the $\hat{CT}$ dimer [60] this possibility cannot simply be excluded, even though in yeast nuclear DNA the ratio Thy/Cyt is approx. 1.6/1 [3]. Up to now nothing is known about the true infra architecture of the yeast chromosomes, *e. g.* about the true nearest neighbour frequencies of the DNA bases. Estimations referring to this by simply employing the formula given by Josse *et al.* [61] may easily lead to a distorted picture [61]. And there is proof that the rule "$\hat{TT}$ yield > $\hat{CT}$ yield > $\hat{CC}$ yield" may be completely inverted [9]. Unfortunately, discrimination between $\hat{TT}$ and $\hat{CT}$ was not possible until Setlow and Carrier [60]. Hence the data obtained for bacteriophages before this finding [27, 28, 30, 31] could not serve as an aid to solve this problem – though for bacteriophages the course of the $\hat{TT}$ and $\hat{CT}$ formation kinetics could have been easily monitored down to UV doses close to the unit dose. And unfortunately – despite the findings of Setlow and Carrier [60] – dimer yield

Table I. Yield of Thy containing dimers UV-induced in *S. cerevisiae in vivo*.

Strain	Nuclear DNA contents [dalton]	Fraction Thy present as dimer [%] a) at D_i = 1080 erg/mm² b) at D_i = 1 erg/mm²		Dimers per Genome a) at D_i = 1080 erg/mm² b) at D_i = 1 erg/mm² c) at LD_{37} = .06 erg/mm²		Ratio $\hat{TT}/\hat{CT}$ at the incident UV dose 1080 erg/mm²
		$\hat{TT}$	$\hat{CT}$	$\hat{TT}$	$\hat{CT}$	
T6-425 *	8.9×10^9	a) 0.27 ± 0.03	0.12 ± 0.01	a) 1.1×10^4	1.0×10^4	1.1
		b) 2.5×10^{-4}	1.1×10^{-4}	b) 10.5	9.4	
				c) 0.63	0.56	
T6-425 *tmp1-51*	8.9×10^9	a) 0.30 ± 0.03	0.13 ± 0.01	a) 1.3×10^4	1.1×10^4	1.2
		b) 2.8×10^{-4}	1.2×10^{-4}	b) 11.7	10.1	
				c) 0.70	0.61	
MB1052 *tmp1-3*	1.8×10^{10}	a) 0.32 ± 0.03	0.12 ± 0.01	a) 2.7×10^4	2.0×10^4	1.3
		b) 3.0×10^{-4}	1.1×10^{-4}	b) 25.0	19.0	
				c) –	–	

The data are means [1] from at least five determinations each.

* For strain T6-425 the data are reproducibly lower than those of strain Tb-425 *tmp1-51*. This might be due to UV quenching by aminopterin and sulfanilamide [87] absorbed by the cell as strain T6-425 was labelled in medium R [1].

is often simply referred to as $\hat{T}\hat{T}$ yield or the UV product yield is expressed in terms of % UV-product radioactivity of total Thy radioactivity. We could trace but a single publication where the growth curves of $\hat{T}\hat{T}$ and $\hat{C}\hat{T}$ dimers were separately monitored in the UV dose range below 1000 erg/mm² [43]. This author has found that for *E. coli* the ratio $\hat{T}\hat{T}/\hat{C}\hat{T}$ is approx. 1.2/1 for the UV (254 nm) dose range 278 – 2222 erg/mm². For *E. coli* and *S. cerevisiae* the $\hat{T}\hat{T}$ and $\hat{C}\hat{T}$ dimer formation kinetics obviously are very similar [9]. Thus it seems reasonable to us that for *S. cerevisiae* the ratio $\hat{T}\hat{T}/\hat{C}\hat{T}$ is indeed 1.2/1 and 1.3/1 (haploid and diploid, resp.) at the UV unit dose. This is not in strict contradiction to the ratio $\hat{T}\hat{T}\,\hat{C}\hat{T} = 2/1$ reported for *S. cerevisiae* by Unrau *et al.* [9]. Although these authors obviously examined a *rho*⁺ haploid yeast strain we do not think the involvement of mitochondrial DNA in their dimer assay is the reason for the apparent difference of their results from ours. It is true that the ratio Thy/Cyt for mitochondrial DNA is 46.7/1 [62] as compared to 1.6/1 for nuclear DNA. However, usually the share of mitochondrial DNA is only approx. 15% of the total DNA in haploid *rho*⁺ yeast [2, 63] and therefore should not lead to such drastic a superelevation of $\hat{T}\hat{T}$ *versus* $\hat{C}\hat{T}$. The difference between the results of Unrau *et al.* [9] and ours should rather be a consequence of their determining $\hat{Pyr}\hat{Pyr}$ dimer ratios at the UV (254 nm) dose 3000 erg/mm² where the $\hat{C}\hat{T}$ formation kinetics is clearly close to its stationary level (Fig. 1).

UV lethal hit in terms of UV products

DNA is thought to be the principal target for the deleterious effects of UV photons on cells. And UV was found to – directly or indirectly – induce a variety of UV products in DNA. These were grouped into major UV products (cyclobutane type $\hat{Pyr}\hat{Pyr}$ dimers) and minor UV products as judged from their frequency of formation at "biological" UV doses. One was aware, of course, that the numerical preponderance of the $\hat{Pyr}\hat{Pyr}$ dimers at "biological" UV doses can by no means be a proof for their being biologically most important [64–67]. To get information about the biological importance or lethality of the various sorts of UV products made necessary 1. adequate methods for quantitative UV product determination after UV irradiation of DNA *in vivo* and 2. the construction of strains of the organism under investigation deprived of all UV lesion repair mechanisms – at least the dark repair mechanisms. Thus one could establish correlations between the UV lethal hit (l.h.) and the numbers of each UV product minimally necessary to generate UV lethality.

Presently for at least three different organisms strains are available that are thought to lack any UV lesion dark repair mechanism: bacteriophage T4 *vx* [30], *E. coli uvrA-6 rec-13* [34], and *S. cerevisiae rad1 rad18 rad51* [68], In contrast methods of direct quantitative analysis of DNA UV products are rather poorly developed: It is true that $\hat{T}\hat{T}$ and $\hat{C}\hat{T}$ dimers are well accessible to quantitative analysis. However, it has not yet been possible to develop a generally satisfactory method for quantitative assay of $\hat{C}\hat{C}$ UV-induced *in vivo* [9] – $\hat{C}\hat{C}$ being postulated to be a probable DNA UV-product *in vivo* by Setlow and Carrier [60]. Much less one did succeed in developing adequate methods for quantitative assay of the "minor" products UV-induced *in vivo* at "biological" doses – if ever one were able to get hold of all of them by direct assay [67].

Hence evaluation of the nature of UV-lethality for a given organism is commonly based on determination of the photoreactivable sector (PRS). Photolyase is reported to act differently effective on $\hat{T}\hat{T}$, $\hat{C}\hat{T}$, and $\hat{C}\hat{C}$ [64]. At least this suggests the size of the non-PRS to always be more or less overestimated for an organism thus characterized with respect to UV-sensitivity. Where the PRS is found to be near 100% – *e.g. E. coli:* 85% [82] – the question "What is the UV-product nature of UV-lethality?" is at least settled in favour of the $\hat{Pyr}\hat{Pyr}$ dimers as a whole, though it has not been decided whether all sorts of $\hat{Pyr}\hat{Pyr}$ dimers have an equal potency to be lethal or not. For *S. cerevisiae* the PRS was determined to be 0.66 [83] which suggests a significantly higher share of non-$\hat{Pyr}\hat{Pyr}$ mediated UV-lethality than in *E. coli*. This assumption must not necessarily hold true, however, as the relatively low PRS in yeast might simply be due to any yeast-inherent factor(s) that reduce photolyase efficiency. Hence, for yeast the above question cannot to be finally settled by mere knowledge of the yeast-PRS.

However, we think this problem might be finally settled by making use of the following formulation of a UV-l.h.:

$$1\ \text{UV-l.h.} = \sum_i L_i \times F_i \times 1\ I = \sum_i \Pi_i = 1\,,$$

with I = any intracellularly induced UV-product; F_i = probability of its being UV-induced within the cell, and L_i = probability of its being lethal in a system without any UV dark repair mechanism.

Evaluation of this formula and consequences: In the case that indeed only the PyrPyr dimers were the potentially lethal UV-products after UV-irradiation *in vivo* the $\sum_i \Pi_i$ would shrink to the triple term

$$\sum_i \Pi_i^* = L_{\hat{TT}} \times F_{\hat{TT}} \times 1\,\hat{TT} + L_{\hat{CT}} \times {}_{\hat{CT}} \times 1\,\hat{CT} + L_{\hat{CC}} \times F_{\hat{CC}} \times 1\,\hat{CC} = 1\,.$$

Provided the partial products "$F_i \times 1$ I" are known for each PyrPyr dimer in a given organism, then the factors L_i remained to be determined. These L_i might represent what is called the chance of the replicating system not to bypass a dimer, *i. e.* to introduce a gap into the newly synthesized DNA daughter strand [69–76]. "$F_i \times 1$ I": These terms could be easily estimated for $\hat{TT}$ and $\hat{CT}$ by employing DNA-Thy DNA-specific labelling and performing direct dimer assay after UV-irradiation *in vivo*. The "$F_i \times 1$ I" would then correspond to the number of $\hat{TT}$ and $\hat{CT}$, resp., that is found per l.h. per genome for an organism without any dark repair mechanism. Determination of "$F_{\hat{CC}} \times 1\,\hat{CC}$" on the other hand would make necessary a DNA-Cyt DNA-specific labelling in general. "L_i": These factors could be calculated by employing agents that are pure PyrPyr inducers, such as *e. g.* UV (313 nm) + acetophenon (AcΦ) which obviously only induces $\hat{TT}$ in DNA [60, 77–79]. With such a pure $\hat{TT}$ inducer employed the $L_{\hat{TT}}$ should be the reciprocal of the term "$F_{\hat{TT}} \times 1\,\hat{TT}$" calculated per UV (313 nm) + AcΦ l.h. for an organism lacking any UV lesion dark repair mechanism. Referring to the data given by Meistrich [5] we have made an estimate of $\sum_i \Pi_i^*$ (i = $\hat{TT}$; $\hat{CT}$; $\hat{CC}$) for *S. cerevisiae* (Materials and Methods). According to this strongly simplified calculation we get $\sum_i \Pi_i^* = 0.57$ instead of 1. This seems to be rather a good approximation for the yeast-PRS 0.66 [83]. It must be pointed out, however, that the $\sum_i \Pi_i^* = 0.57$ calculated for yeast in the way described in Materials and Methods might equally well be a coarse underestimation of the true $\sum_i \Pi_i^*$ for yeast: Performing the same calculation for *E. coli* would give a $\sum_i \Pi_i^* \approx 0.57$, too [‡]. And the PRS for this organism is reported to be 0.85 [82]. Hence, as long as the $\sum_i \Pi_i^*$ (i = TT; $\hat{CT}$; $\hat{CC}$) is not explicitely determined no definite answer can be given about the true biological importance of PyrPyr dimers UV-induced in yeast. And if one were able to determine $L_{\hat{TT}}$, $L_{\hat{CT}}$, and $L_{\hat{CC}}$ for this organism this would finally allow an evaluation of the potential lethality of each PyrPyr dimer type.

Correlation between genome size, UV-sensitivity, and $\hat{TT} + \hat{CT}$ yield after UV-irradiation.

Unfortunately, literature does not prove to be rich in $\hat{TT} + \hat{CT}$ dimer yield data adequate for a reasonable comparison to those obtained by us for *S. cerevisiae*. From the sparse yield of such ade-

Table II. Correlation between genome size, UV-sensitivity, and $\hat{TT} + \hat{CT}$ yield after UV (254 nm) irradiation.

Organism	Genome size [dalton]	ref.	LD_{37} (254 nm) [erg/mm²]	ref.	$\hat{TT} + \hat{CT}$ [erg/mm²]	ref.	$\hat{TT} + \hat{CT}$/ lethal hit
bacteriophage ΦX 174	3.6×10^6	31	62.8	31	5.9×10^{-3}	31	0.37
bacteriophage T4 *vx*	1.3×10^8	28	6.27	30	0.23	39	1.4
E. coli rec-13 uvrA-6	2.6×10^9	4	0.2	34	6.0	34	1.2
B. subtilis *	3.0×10^9	84	—		6.7	35	
S. cerevisiae rad1 rad18 rad51 (haploid, *rho*⁺)	1.0×10^{10}	86	0.06	68			
S. cerevisiae +++ (haploid, *rho*⁻)	8.9×10^9	4			21.8	[+]	1.3
S. cerevisiae +++ (diploid, *rho*⁺) +++	1.8×10^{10}	4			44.0	[+]	

† It is not clear from the data of Strauß *et al.* [35] which UV-wavelength was used in their experiments. [+], data from Table I.

‡ For *E. coli* a ratio $\hat{CT}/\hat{CC} = 1/1$ is assumed [9].

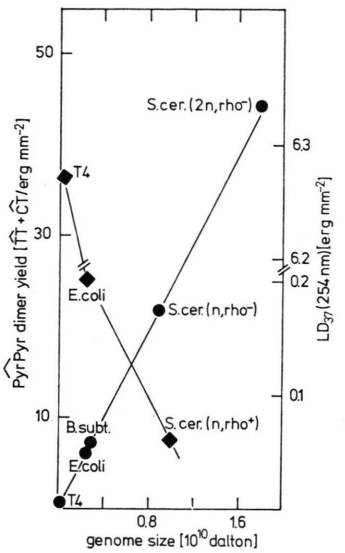

Fig. 2. Correlation between genome size and "absolute" LD_{37} (254 nm) and between genome size and UV (254 nm)-induced $\hat{TT}+\hat{CT}$. ◆—◆, "absolute" LD_{37} (254 nm) *versus* genome size; ●—●, $\hat{TT}+\hat{CT}$ yield *versus* genome size.

quate data – which are listed in Table II – we have nevertheless dared to compose Fig. 2.

Correlation between genome size and $\hat{TT}+\hat{CT}$ yield per erg mm^{-2} of incident UV (254 nm): It will seem that this correlation is a directly proportional one and that it is rather independent of the A+T contents of a genome (T4: 66%[84]; *E. coli*: 50%[61]; *B. subtilis*: 56%[61]; *S. cerevisiae:* 61%[3]). However, this finding surely requires further proof by study of more organisms.

Correlation between genome size and "absolute" UV(254 nm)-sensitivity: Here only the LD_{37} (254 nm) data for the double strand DNA organisms bacteriophage T4 *vx*, *E. coli uvrA-6 rec-13*, and haploid *rho*$^+$ *S. cerevisiae rad1 rad18 rad51* are available from the literature. It is obvious from Fig. 2 that this correlation is an indirectly proportional one. This is not surprising as DNA is generally thought to be the principal target of UV. Furthermore such a correlation was already suggested by Radman[85] who found indirect proportionality of genome size and UV-sensitivity for the bacteriophages λ and λb2. But – as can be judged from Fig. 2 – this correlation does not seem to be a linear one, at least when the data for bacteriophage T4 are included.

This research was supported by a grant of the Deutsche Forschungsgemeinschaft to the second author. The first author is deeply indepted to his wife Gerhild for her typewriting the manuscript and he greatly appreciates the excellent technical assistance of Miss Gabriele Jung.

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