Across the tree of life, radiation resistance is governed by antioxidant Mn$^{2+}$, gauged by paramagnetic resonance

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Despite concerted functional genomic efforts to understand the complex phenotype of ionizing radiation (IR) resistance, a genome sequence cannot predict whether a cell is IR-resistant or not. Instead, we report that absorption-display electron paramagnetic resonance (EPR) spectroscopy of nonirradiated cells is highly diagnostic of IR survival and repair efficiency of DNA double-strand breaks (DSBs) caused by exposure to gamma radiation across archaea, bacteria, and eukaryotes, including fungi and human cells. IR-resistant cells, which are efficient at DSB repair, contain a high cellular content of manganous ions (Mn$^{2+}$) in high-symmetry (H) antioxidant complexes with small metabolites (e.g., orthophosphate, peptides), which exhibit narrow EPR signals (small zero-field splitting). In contrast, Mn$^{2+}$ ions in IR-sensitive cells, which are inefficient at DSB repair, exist largely as low-symmetry (L) complexes with substantially broadened spectra seen with enzymes and strongly chelating ligands. The fraction of cellular Mn$^{2+}$ present as H-complexes (H-Mn$^{2+}$), as measured by EPR of live, nonirradiated Mn-replete cells, is now the strongest known gauge of biological IR resistance between and within organisms representing all three domains of life: Antioxidant H-Mn$^{2+}$ complexes, not antioxidant enzymes (e.g., Mn superoxide dismutase), govern IR survival. As the pool of intracellular metabolites needed to form H-Mn$^{2+}$ complexes depends on the nutritional status of the cell, we conclude that IR resistance is predominantly a metabolic phenomenon. In a cross-kingdom analysis, the vast differences in genomic efforts, the level of cellular IR resistance cannot be predicted by a genome sequence (1, 2). Without the identification of a distinct set of genes responsible for IR resistance, sequence-based approaches to gauging the wide range of radiosensitivities encountered in prokaryotes, simple eukaryotes, and even human-derived cancer cell lines have been futile (2–4). Indeed, genetic heterogeneity appears to be a central characteristic of IR resistance phenotypes in general (5, 6). Instead, it was long ago suggested that manganous ions (Mn$^{2+}$) accumulated in cells are responsible for extreme radiation resistance (7).

Reactive oxygen species (ROS) generated through the radiolysis of H$_2$O in cells subjected to IR are the primary molecular agents of cellular damage. In particular, irradiated cells rapidly form superoxide (O$_2^-$) ions by radiolytic reduction of both atmospheric O$_2$ and O$_2$ released through the intracellular decomposition of IR-generated H$_2$O$_2$ as catalyzed by both enzymatic and nonenzymatic metal ions. Importantly, because O$_2^-$ is charged, it cannot easily cross membranes and builds up in irradiated cells, selectively damaging proteins, not DNA (8). Nonenzymatic cellular mechanisms exist to resist superoxide damage. Notably, the IR-resistant bacterium Lactobacillus plantarum, which naturally lacks antioxidant enzymes, can efficiently convert high concentrations of IR-induced O$_2^-$ generated under anaerobic conditions back to membrane-permeable H$_2$O$_2$ (O$_2^-$ + 2H$^+$ → H$_2$O$_2$), which escapes irradiated cells. This intracellular reaction is catalyzed in L. plantarum by antioxidant low-molecular-weight (LMW) Mn$^{2+}$ complexes (9–12). By comparison, the O$_2^-$-scavenging, manganese-dependent enzyme superoxide dismutase (MnSod) becomes increasingly less effective as a catalyst as concentrations of O$_2^-$ rise (13). This could explain why MnSod has repeatedly been shown to be dispensable for IR resistance in bacteria.

Significance

Decades of functional genomic efforts have failed to predict the ability of cells to survive ionizing radiation (IR). Evidence is mounting that small high-symmetry antioxidant complexes of manganous ions with metabolites (H-Mn$^{2+}$) are responsible for cellular IR resistance, and that H-Mn$^{2+}$ protects the proteome, not the genome, from IR-induced reactive oxygen species. We show that the amount of H-Mn$^{2+}$ in nonirradiated living cells is readily gauged by electron paramagnetic resonance (EPR) spectroscopy and highly diagnostic of their DNA repair efficiency and survival after gamma-radiation exposure. This spectroscopic measure of cellular H-Mn$^{2+}$ content is the strongest known biological indicator of cellular IR resistance between and within organisms across the three domains of the tree of life, with potential applications including optimization of radiotherapy.

Most, if not all, of the characteristics required for survival of life exposed to radiation are embodied by Deinococcus radiodurans, a nonsporulating bacterium capable of surviving doses of ionizing radiation (IR), X-rays and gamma rays (12–16 kGy), 10-fold greater than the yeast Saccharomyces cerevisiae, 20-fold greater than the bacterium Escherichia coli, and 3,000-fold greater than human cells (1). Despite concerted functional genomic efforts, the level of cellular IR resistance cannot be predicted by a genome sequence (1, 2). Without the identification of a distinct set of genes responsible for IR resistance, sequence-based approaches to gauging the wide range of radiosensitivities encountered in prokaryotes, simple eukaryotes, and even human-derived cancer cell lines have been futile (2–4). Indeed, genetic heterogeneity appears to be a central characteristic of IR resistance phenotypes in general (5, 6). Instead, it was long ago suggested that manganous ions (Mn$^{2+}$) accumulated in cells are responsible for extreme radiation resistance (7).
(7–10, 14, 15) and archaea (16), even though oxidative stress plays a major role in causing IR toxicity (8, 17).

The least frequent and most dangerous form of DNA damage caused by IR is the double-strand break (DSB). Impaired DSB repair currently provides the best available correlation with IR-induced cell death. Generally, any process that inhibits DSB repair, whether by mutation of repair genes or by ROS-mediated oxidative damage to repair enzymes, will severely limit a cell’s ability to recover from IR. This is established, first, by the greatly increased radiosensitivity of specific DNA repair-deficient mutants (8). Second, evidence has mounted that oxidative protein damage is causative in IR toxicity, and antioxidant LMW complexes of Mn$^{2+}$ with metabolites are the source of ROS production (15). We have previously found that MnSod-deficient mutants (Sod1 and Sod2) of strain BY4741, and four diploid environmental S. cerevisiae strains that were found to display significantly different IR resistances (Fig. 1, Upper and Table 1). We added the basidiomycete Rhodotorula tairwanensis, which is a moderately IR-resistant yeast with a larger genome (~20 Mbp). Under standard conditions for cell irradiation and pulsed-field gel electrophoresis (PFGE), we determined that the production of IR-induced DSBs for yeasts (BY4741, FY1679, EXF-6219, and EXF-6761) ranges between 0.0006 and 0.0009 DSB per mega-base pair per gray (DSB/Mbp/Gy) (SI Appendix, Fig. S1 C and D). We also examined nine bacterial strains, D. radiodurans, a D. radiodurans MnSod-deficient mutant (sodA−), Deinococcus fuscus, and Deinococcus geothermalis, Rubrobacter xylanophilus, E. coli, Pseudomonas putida, Enterococcus faecium, and Acinetobacter radioreistantes with representatives previously characterized for IR-induced DSB yields by PFGE (7) and, similarly, for two archaea, Halobacterium salinarum and Haloferax volcanii (16). As a representative of mammalian cells, which are far more susceptible to IR-induced DSBs than prokaryotes and yeasts due to their massive genome size (~3 Gbp) (5, 27), we chose cultured Jurkat T cells. Jurkat cells are considered to be IR-resistant for human cells (D$_{10}$, 4 Gy) (28), but extremely IR-sensitive compared with prokaryotes and fungi, based on D$_{10}$ (Table 1). For each of the cell types, we present the IR survival index, D$_{10}$, as well as the DNA repair efficiency index, DSBD$_{10}$, defined as DSBD$_{10}$ = [D$_{10}$ (Gy)] × [DSB Yield (DSB/ Mbp/Gy)]/[Genome size (Mbp)]. This DSBD$_{10}$ index equals the number of DSBs inflicted per haploid genome at the IR dose that kills 90% of the population (Fig. 1, Upper). It corresponds to an irradiated cell’s maximum survivable number of IR-induced DSBs, and reflects its efficiency in repairing the most lethal form of DNA damage: the DSB (5) (Table 1 and SI Appendix, Fig. S1 C and D).

The tabulated values of DSBD$_{10}$ for this cell panel (Table 1) indeed span the gamut of IR resistance. Thus, as we have described (5), the D. radiodurans strains are most efficient at DSB repair (DSBD$_{10}$ = 118), whereas E. coli (DSBD$_{10}$ = 6) and P. putida (DSBD$_{10}$ = 5) are the least efficient, with the others arranged between these extremes. It is useful to emphasize that, as reported, the extremely high IR survival (D$_{10}$) of wild-type D. radiodurans is undiminished in the D. radiodurans MnSod-deficient mutant (sodA−) growing under high-level chronic gamma radiation (50 Gy/h) or exposed to massive acute doses (12 kGy) (7, 15, 29) (Table 1); thus, this enzyme cannot be responsible for the high IR resistance of these cells.

**Results**

**IR Resistance.** We determined survival (D$_{10}$) following gamma irradiation for a panel of cells from across the three domains of life: archaea; bacteria; and eukaryotes, including fungi and human cells. This panel incorporates eight S. cerevisiae strains with similarly sized genomes (10–14 Mbp) (Table 1 and SI Appendix, Fig. S1 A and B) from a collection of yeasts (SI Appendix, Table S1): two model laboratory strains (a haploid BY4741 and its diploid FY1679 counterpart), two MnSod-deficient mutants (Sod1 and Sod2) of strain BY4741, and four diploid environmental S. cerevisiae strains that were found to display significantly different IR resistances (Fig. 1, Upper and Table 1). We added the basidiomycete Rhodotorula tairwanensis, which is a moderately IR-resistant yeast with a larger genome (~20 Mbp). Under standard conditions for cell irradiation and pulsed-field gel electrophoresis (PFGE), we determined that the production of IR-induced DSBs for yeasts (BY4741, FY1679, EXF-6219, and EXF-6761) ranges between 0.0006 and 0.0009 DSB per mega-base pair per gray (DSB/Mbp/Gy) (SI Appendix, Fig. S1 C and D). We also examined nine bacterial strains, D. radiodurans, a D. radiodurans MnSod-deficient mutant (sodA−), Deinococcus fuscus, and Deinococcus geothermalis, Rubrobacter xylanophilus, E. coli, Pseudomonas putida, Enterococcus faecium, and Acinetobacter radioreistantes with representatives previously characterized for IR-induced DSB yields by PFGE (7) and, similarly, for two archaea, Halobacterium salinarum and Haloferax volcanii (16). As a representative of mammalian cells, which are far more susceptible to IR-induced DSBs than prokaryotes and yeasts due to their massive genome size (~3 Gbp) (5, 27), we chose cultured Jurkat T cells. Jurkat cells are considered to be IR-resistant for human cells (D$_{10}$, 4 Gy) (28), but extremely IR-sensitive compared with prokaryotes and fungi, based on D$_{10}$ (Table 1). For each of the cell types, we present the IR survival index, D$_{10}$, as well as the DNA repair efficiency index, DSBD$_{10}$, defined as DSBD$_{10}$ = [D$_{10}$ (Gy)] × [DSB Yield (DSB/ Mbp/Gy)]/[Genome size (Mbp)]. This DSBD$_{10}$ index equals the number of DSBs inflicted per haploid genome at the IR dose that kills 90% of the population (Fig. 1, Upper). It corresponds to an irradiated cell’s maximum survivable number of IR-induced DSBs, and reflects its efficiency in repairing the most lethal form of DNA damage: the DSB (5) (Table 1 and SI Appendix, Fig. S1 C and D).

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**Thirty-Five–Gigahertz EPR Measurements.** To carry out EPR measurements of Mn$^{2+}$ speciation and test for correlations with the measured IR survival (D$_{10}$) and repair efficiency (DSBD$_{10}$), cells for each member of the experimental panel (Table 1) were harvested at the middle- to late-exponential growth phase, and the 35-GHz (Q-band) absorption-display EPR spectra were collected from the intact, viable cells. We had previously found (15, 26) that the Q-band (35 GHz) continuous wave (CW) absorption-display EPR spectra, but not derivative spectra at X- or Q-bands (or, in fact, at any frequency), reveal that cellular Mn$^{2+}$ exists as two distinct pools of Mn$^{2+}$ complexes. First, as illustrated in Fig. 1, Lower, the g-2 region of the spectrum (~12 kG) is dominated by a narrow signal (<1 kG in width) associated with antioxidant H-Mn$^{2+}$ complexes with simple...
metabolites (e.g., orthophosphate), which displays a sextet pattern arising from hyperfine interactions with the $^{55}$Mn (nuclear spin, $I = 5/2$) nucleus [hyperfine coupling, $A \sim 90$ G (30, 31)]. Then, this central H-feature “rides on” and is flanked by broad “wings” extending from fields of $\sim 2$ kG to fields well above the magnet limit, which are associated with a heterogeneous population of low-symmetry (L) Mn$^{2+}$ complexes. The previous, limited observations further suggested to us the hypothesis that the relative amounts of the two pools might track with IR survival, $D_{10}$. In this regard, Mn$^{2+}$ in $D.\text{radiodurans}$ cells, which are extremely IR-resistant, exists almost exclusively as antioxidant H-complexes, whereas Mn$^{2+}$ in $E.\text{coli}$ cells, which are IR-sensitive, exists primarily as L-complexes (15). In vivo, H-Mn$^{2+}$ complexes in bacteria protect proteins, but not DNA, from IR-induced ROS (7, 11, 18, 19); similarly, synthetic H-Mn$^{2+}$ complexes provide strong in vitro protection of proteins, but not DNA, from ROS (11, 19–24). Moreover, H-Mn$^{2+}$-accumulating yeasts consistently display elevated ROS-scavenging capacities (Fig. 2, Upper) that protect proteins from gamma radiation (Fig. 2, Lower), but have no effect on IR-induced DSB yields (SI Appendix, Fig. S1 C and D).

Qualitative inspection of the absorption-display 35-GHz EPR spectra for bacteria and yeasts (Fig. 1, Lower) supports this hypothesis. In these normalized spectra, the intensity of the wings, which reflect the amount of L-Mn$^{2+}$ relative to H-Mn$^{2+}$, monotonically decreases with increasing cellular IR survival as measured by $D_{10}$ (Table 1). However, human Jurkat T cells, which are IR-sensitive, display a spectrum essentially identical to that of the paradigmatic IR-resistant bacterium, $D.\text{radiodurans}$, whereas its $D_{10}$ value indicates extreme IR sensitivity (Fig. 1, Lower and Table 1). Below, we return to and resolve this apparent contradiction.

**High-Frequency/High-Field EPR.** As noted above, MnSod is not responsible for the high IR survival of wild-type $D.\text{radiodurans}$ studied here, as the IR resistance is undiminished in the isogenic $D.\text{radiodurans}$ MnSod-deficient mutant (sod$^{4-}$), as reported earlier (7, 10, 15, 17) and confirmed here (Table 1). Nonetheless, in consideration of reports based on high-frequency/high-field (HFHF) EPR spectroscopy that Mn$^{2+}$Sod is abundant, and indeed critical in the IR survival of $D.\text{radiodurans}$, rather than the H-Mn$^{2+}$ complexes (32), we used HFHF derivative-display EPR spectroscopy (33) (SI Appendix, Materials and Methods) to determine the amount of Mn$^{2+}$Sod present in the $D.\text{radiodurans}$ strains. HFHF EPR is more sensitive to the presence of Mn$^{2+}$Sod (32) than 35-GHz spectroscopy, which gave no evidence of Mn$^{2+}$Sod (15). The spectrum of Mn$^{2+}$Sod collected at 321 GHz (SI Appendix, Fig. S4) shows sharp, but low-intensity, peaks across the g-2 region. In particular, it shows signature features to low and high fields of the typical $^{55}$Mn sextet at g-2 that comprises the spectrum for the H-Mn$^{2+}$ of $D.\text{radiodurans}$ (SI Appendix, Fig. S4). Through use of simulations of the $D.\text{radiodurans}$ Mn$^{2+}$ and Mn$^{2+}$Sod spectra (SI Appendix, Fig. S5) to calibrate spectrum amplitudes, we find that Mn$^{2+}$Sod is present in negligible amounts, comprising, at most, $\sim 5\%$ of the total Mn$^{2+}$ pool (SI Appendix, Materials and Methods). As XANES (X-ray absorption near-edge structure) measurements show an absence of cellular Mn$^{2+}$ (11), the EPR measurements complement the survival measurements on the MnSod knockout strains by indicating that not only is Mn$^{2+}$Sod not responsible for the observed high cellular IR survival in these wild-type cells harvested in log phase (Table 1) but that, in fact, they contain little holo-MnSod of any kind. This is consistent with earlier HFHF measurements of MnSod populations in log phase (32). However, it was incorrectly concluded from the high MnSod population found in the late-stationary phase that MnSod is responsible for high cellular survival throughout the growth cycle (32). Earlier data for the $D.\text{radiodurans}$ MnSod-deficient mutant (Dr$^{sodA}$) showed that this enzyme does not contribute to acute IR survival of log-phase cells. Although late-stationary-phase cells were not tested (15, 29),
DrsodA is dominant. Guided by our recent experience with the f0.9 for DSBD and rising rapidly with increasing IR exposure, we model the broad features contributed by the heterogeneous cellular L-Mn2+ pool to the EPR spectrum of a cell type was modeled as an optimized function of the IR DNA repair efficiency index, DSBD, for each cell type studied. As an illustration of the range of values, we furthermore note that DrsodA displays luxuriant growth on solid medium under high-level chronic IR (50 Gy/h, 137Cs) irrespective of the growth stage of inoculated cells (7). Moreover, E. coli sodA (14) and yeast sod2 mutants (Table 1) are IR-resistant, if not more resistant, than the wild types. Finally, the earlier HHHF work reported only the central portion of the MnSod spectrum, as in SI Appendix, Fig. S4 (32); for completeness, collection and analysis of the full Mn2+ sod spectrum here (SI Appendix, Fig. S6) now confirm the reported magnitudes of the parameters that define the EPR spectrum of MnSod [the so-called zero-field splitting (ZFS) parameters], and further yield the sign of the dominant parameter (23, 24) (SI Appendix, Materials and Methods).

**Correlation of IR Sensitivity and EPR.** To quantify the correlation between increasing IR survival and an increasing population of H-Mn2+ complexes revealed in Fig. 1, Upper and Lower, a simple “quantitation by simulation” procedure (34, 35) using the EasySpin program (36) was developed to decompose the cellular Mn2+ 35-GHz absorption–display EPR spectra into fractional contributions from spectra that represent the L- and H-pools (SI Appendix, Materials and Methods). The contribution of the H-Mn2+ pool to the EPR spectrum of a cell type was modeled as an optimized sum of a simulated exemplar spectrum that corresponds to that of the Pi complex of Mn2+ (SI Appendix, Fig. S2; denoted H′) and of a simulated exemplar spectrum corresponding to that of Mn2+ with bound imidazole (SI Appendix, Fig. S2; denoted H); the presence of an H′ contribution is generally required when H-Mn2+ is dominant. Guided by our recent experience with the EPR of Mn2+ complexes (37), we model the broad features contributed by the heterogeneous cellular L-Mn2+ pool with a single exemplar spectrum (SI Appendix, Fig. S2) in which the parameters that govern the breadth of an Mn2+ spectrum (ZFS parameters) (30, 31) are larger and more widely distributed than those for H-Mn2+ (SI Appendix, Materials and Methods). For each cell type, these exemplars are then summed in proportions that yield a match to the experimental spectrum. The total fraction of the H-Mn2+ contribution is given by the sum of the fractional contributions of the H-exemplars, fH = fH′ + fH″; the cellular L-Mn2+ pool then has a fraction, fL = 1 − fH. An example of a two-component decomposition (H = H′, L) is shown for yeast strain EXF-6218, for which fL = 0.20 (Fig. 1, Lower Inset). SI Appendix, Fig. S3 shows the decomposition of the Jurkat T cell spectrum, for which fH = 0.95 and which required a contribution from H′. Table 1 lists the fL for each cell type studied. As an illustration of the range of speciation observed for the cell panel under normal growth conditions (Table 1), the Mn2+ of D. radiodurans and Jurkat cells is associated almost exclusively with H-Mn2+ complexes, fH ≈ 0.95, whereas E. coli represents an opposite extreme, with a dominant population of L-Mn2+ complexes: fL = 0.17, fH = 0.83.

**Tabulated quantities:** D10, dose at 10% survival (kGy); DSBD10 = [D10 (Gy)] × [DSB Yield (DSB/Mbp/Gy)] × [Genome Size (Mbp)], DSBs per haploid genome; DSB yield (DSB/Mbp/Gy). Gamma-radiation–induced cellular DSB damage is linear with dose, with DSB yields falling within narrow ranges: for circular genomes of prokaryotes (0.002 ± 0.002 DSB/Mbp/Gy), for linear genomes of animal cells (0.006 ± 0.002 DSB/Mbp/Gy), and for linear genomes of yeasts (0.0006 ± 0.0003 DSB/Mbp/Gy) (2, 5, 27) (SI Appendix, Fig. S1). Estimated uncertainties for fL are <5% (SI Appendix, Materials and Methods). The source column lists citations for IR-induced DSB yields and genome sizes. fL, fraction of H-Mn2+; GS, genome size (Mbp); USU, Uniformed Services University.

**Table 1. Values for prokaryotes and eukaryotes of the cell panel of the IR resistance indexes DSBD10 (DSB repair efficiency) and D10 (survival), DSB yield, genome size, and the Mn2+ speciation index fL, as assessed by EPR**

| Name                  | Short name | DSBD10 | D10, kGy | DSB yield | GS, Mbp | fL       | Source          |
|-----------------------|------------|--------|----------|-----------|---------|----------|-----------------|
| Bacteria              |            |        |          |           |         |          |                 |
| D. radiodurans ATCC BAA-816 | Dr          | 118    | 12.0     | 0.003     | 3.3     | 0.94     | (5, 7)          |
| D. radiodurans sodA- | Dr sodA-    | 118    | 12.0     | 0.003     | 3.3     | 0.94     | (5, 15)         |
| D. geothermalis DSM 11300 | Dg          | 118    | 12.0     | 0.003     | 3.3     | 0.94     | (7)             |
| D. fuscus KS 0460 | Df          | 84     | 7.0      | 0.003     | 4.0     | 0.97     | (2, 7)          |
| R. xylanophilus DSM 9941 | Rx          | 59     | 6.0      | 0.003     | 3.3     | 0.97     | (46)            |
| A. radioresistens MD929, USU | Ar          | 48     | 5.0      | 0.003     | 3.2     | 0.7      | (This study)     |
| E. faecium ATCC 19434 | Ef          | 18     | 2.0      | 0.003     | 3.0     | 0.81     | (7)             |
| E. coli K-12, MG1655 | Ec          | 6      | 0.7      | 0.002     | 4.6     | 0.17     | (5, 7)          |
| P. putida ATCC 47054 | Pp          | 5      | 0.3      | 0.003     | 6.1     | 0.13     | (5, 7)          |
| Human cells           |            |        |          |           |         |          |                 |
| Jurkat T4 human cells ATCC TIB-152 | JT         | 72     | 0.004    | 0.006     | 3,000   | 0.95     | (27, 28)        |
| Archaean               |            |        |          |           |         |          |                 |
| H. salinarum ATCC 700922 | Hs         | 39     | 5.0      | 0.003     | 2.6     | 0.95     | (43, 45)        |
| H. volcanii DS-70 | Hv          | 18     | 1.5      | 0.003     | 4.0     | 0.84     | (43, 45)        |
| Yeast                 |            |        |          |           |         |          |                 |
| S. cerevisiae EXF-6761 |             | 6761   | 32       | 3.5       | 0.0009  | 10       | 0.51 (Fig. 1, Upper and SI Appendix, Fig. S1) |
| S. cerevisiae EXF-5735 |             | 5735   | 20       | 2.6       | 0.00075 | 10       | 0.3 (Fig. 1, Upper and SI Appendix, Fig. S1) |
| S. cerevisiae FY1679 |             | 1679   | 20       | 2.4       | 0.0007  | 12       | 0.26 (Fig. 1, Upper and SI Appendix, Fig. S1) |
| R. taiwanensis MD1149, USU | Rt          | 16     | 0.8      | 0.001     | 20      | 0.35     | (This study)     |
| S. cerevisiae BY4741 |             | 4741   | 10       | 1.0       | 0.0008  | 12       | 0.21 (Fig. 1, Upper and SI Appendix, Fig. S1) |
| S. cerevisiae BY4741, sod1- |             | 4741   | 10       | 1.4       | 0.0008  | 12       | 0.21 (This study) |
| S. cerevisiae BY4741, sod2- |             | 4741   | 10       | 1.1       | 0.0008  | 12       | 0.21 (This study) |
| S. cerevisiae EXF-6219 |             | 6219   | 7        | 0.8       | 0.0006  | 14       | 0.23 (Fig. 1, Upper and SI Appendix, Fig. S1) |
| S. cerevisiae EXF-6218 |             | 6218   | 8        | 0.8       | 0.00075 | 14       | 0.2 (Fig. 1, Upper and SI Appendix, Fig. S1) |
Materials and Methods

Proteins, irradiated to the indicated doses, were mixed with purified E. coli as captured by the EPR-derived index of the Jurkat cells does not account for the large Jurkat genome size limitations of $D_{10}$ as a molecular measure of IR resistance. Overall, Fig. 3 shows that for all domains of life, over a range of thousands of grams, the Mn$^{2+}$ speciation within non-irradiated viable cells as determined by absorption-display EPR, $f_{H}$, has high predictive value for DSB repair efficiency, as measured by the DSBD$_{10}$ and thus for resistance to IR exposure.

Molecular Interpretation. Consistent with our earlier results (7), SI Appendix, Fig. S8, Left shows that is, at best, a loose correlation between DSBD$_{10}$ and total cellular Mn concentration, [Mn]; namely, the figure shows a broad cluster of points for cells with high [Mn] and high DSBD$_{10}$ and, similarly, for cells with low values for both. SI Appendix, Fig. S8, Right shows a more significant correlation between the total H-Mn concentration, [H-Mn] = $f_{H}$ [Mn], but the correlation is poorer than that between $f_{H}$ itself and DSBD$_{10}$, as revealed in Fig. 3 and SI Appendix, Fig. S7. This difference may well reflect, in some part, imprecise values for [Mn], which are determined from the number of Mn ions per cell, as measured by inductively coupled plasma MS, and an average cell volume, an imprecision that translates to [H-Mn] (SI Appendix, Table S2). Regardless, at this stage, in considering IR resistance it is most revealing to focus on $f_{H}$; future improvements in the concentration measurements may allow a refinement of this approach. A molecular interpretation of the isotherm/Hill plot correlation between the EPR and DSBD$_{10}$ measures emerges from a simple

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D_{10} = \text{efficient live cells, the fraction of antioxidant } H-Mn \text{ as measured by inductively coupled plasma MS, and an average cell volume, an imprecision that translates to [H-Mn] (SI Appendix, Table S2). Regardless, at this stage, in considering IR resistance it is most revealing to focus on } f_{H}; \text{ future improvements in the concentration measurements may allow a refinement of this approach. A molecular interpretation of the isotherm/Hill plot correlation between the EPR and DSBD}_{10} \text{ measures emerges from a simple }
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**Fig. 2.** Antioxidant capacity of LMW extracts (U, ultrafiltrates) of bacteria (e.g., PpU) and yeasts (e.g., 6767U). (Upper) ROS-scavenging capacity of U assessed by oxygen radical absorbance capacity assay (47, 48). Net AUC, net area under the fluorescence decay curve. The U’s were diluted to 0.01x, 0.02x, 0.03x, 0.04x, 0.05x, 0.1x, or 0.2x for the assay. (Lower) Capacity of U of the indicated strains to protect proteins during gamma irradiation. Indicated U’s were mixed with purified E. coli proteins, irradiated to the indicated doses (kGy), and assayed for protein damage (e.g., strand breaks, cross-links), manifest as smears. DrU, D. radiodurans ultrafiltrates; EcU, E. coli ultrafiltrates; PpU, P. putida ultrafiltrates.
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DSBD_{10} \text{ such a plot (Fig. 3) indeed exhibits the strong linear correlation expected for an IR resistance/binding isotherm (SI Appendix, Materials and Methods); Pearson correlation coefficient } r = 0.883, P = 5.50 \times 10^{-7}; \text{ Spearman rank correlation coefficient } r_s = 0.849, P = 4.25 \times 10^{-6}. \text{ Conversely, this correlation over a range, } 5 \leq DSBD_{10} \leq 118 \text{ implies that the speciation in live cells, the fraction of antioxidant } H-Mn^{2+} \text{ as captured by the EPR-derived index } f_{H}, \text{ is a powerful predictor of the index of DSB repair efficiency, DSBD}_{10}, \text{ which is based on survival as controlled for the genome size of the organism.}
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Below, we consider possible implications of this and other alternative correlations between properties of intracellular Mn$^{2+}$ and IR resistance. We first note that Fig. 3 shows that $D_{10}$ is a suitable IR survival metric at the organism level (e.g., yeasts), which naturally scales with genome size. The figure further provides evidence that DSBD$_{10}$, instead, is the proper metric of IR resistance at the molecular level. In other words, the survival index, $D_{10}$, is a suitable measure of IR resistance only for cells of similar genome size, and for such cells, the speciation from EPR is roughly correlated with $D_{10}$ (Fig. 3, Inset), as expected, although not as well correlated as with DSBD$_{10}$ (Fig. 3). However, comparing the use of these two IR tolerance measures for the human Jurkat cells clearly distinguishes between them. The Mn$^{2+}$ EPR phenotype for Jurkat cells is “high H-Mn$^{2+}$”, namely, high $f_{H}$ (Fig. 1, Lower), implying high DSB repair efficiency, which is in excellent correspondence with their DSBD$_{10}$ (Fig. 3). However, in the Hill plot of $f_{H}$ versus the IR survival index (D$_{10}$), the Jurkat cells are hugely off the correlation shown by the other cells (Fig. 3, Inset) because the extremely low D$_{10}$ index of the Jurkat cells does not account for the large Jurkat genome, and therefore the total number of DSBs, which scales with genome size. Thus, the two plots in Fig. 3 demonstrate the genome size-based limitations of D$_{10}$ as a molecular measure of IR resistance.
heuristic analysis of ligand binding by intracellular Mn$^{2+}$ (SI Appendix, Materials and Methods). Guided by the decomposition of the cellular EPR spectra into contributions from two pools (Fig. 1, Lower, Inset), we first divide Mn$^{2+}$ complexes and their ligands into two types, H and L, with H representing an “average” H’/H’-ligand. We further assume that n H-ligands compete with n L-ligands for binding to the cellular Mn$^{2+}$. In all cell types, the concentration of Mn$^{2+}$ is much less than the concentration of either ligand type, which ensures that there is a negligible amount of free Mn$^{2+}$. For example, under standard growth conditions, D. radiodurans accumulates $\sim$10$^5$ Mn atoms per cell (7, 11, 15, 19), but millimolar in IR resistance of such cells further exceeds that of the L-ligands. The H-ligands overwhelmingly outcompete any L-ligands present, including the apoperoxidase dismutase polypeptide if present, driving the Mn$^{2+}$ speciation to near-quantitative existence as LMW, IR-protective H-Mn$^{2+}$ complexes (f$_H$ ≈ 1). The observations reported here thus imply that in Mn$^{2+}$- and nutrient-replete cells, the antioxidant H-Mn$^{2+}$ complexes, as quantified by absorption-display EPR spectroscopy, govern IR survival in yeasts, archaea, bacteria, and human cells, but not influenced by antioxidant enzymes, namely, MnSod. This indicator of Mn$^{2+}$ speciation will be further strengthened with a widened panel of cell-type calibrants, studies of how f$_H$ changes during cell growth and aging, and further refinement of the EPR spectroscopic approach, as well as its complementation by electron-nuclear double-resonance studies (15, 26). In particular, human cells and their cancer counterparts can display large differences in their IR sensitivities (6), and the H-Mn$^{2+}$ content may provide a suitable metric to determine dosing regimens for different cancer types during radiation therapy (Fig. 3).

Discussion
We have revealed that in Mn- and nutrient-replete cells, the fraction of antioxidant metabolite complexes of Mn$^{2+}$, the H-Mn$^{2+}$, as captured by the EPR-derived index f$_H$, strongly correlates with the DSB repair efficiency index, DSBD$_{10}$ (Fig. 3, Eqs. 2 and 3, and SI Appendix, Materials and Methods). This strong association is remarkable, considering the vast differences in taxonomic status, genome size, and radioresistance between studied cell types. In contrast, the antioxidant enzyme MnSod plays a negligible part in IR survival in such cells (7, 9, 10, 14–16), as confirmed here. The cellular content of H-Mn$^{2+}$ complexes is now the strongest biological indicator of cellular IR resistance between and within organisms representing the three domains of life.

That MnSod confers no discernible advantage over the H-Mn$^{2+}$ complexes for IR survival (Table 1) is excerpted from earlier studies (7, 9, 10, 14–16). Metal-bound MnSod is dispensable for IR resistance (Table 1), and indeed is shown here to be absent or nearly so (SI Appendix, Fig. S4) in log-phase D. radiodurans cells with extremely high IR survival. These findings suggest that in nutrient-replete organisms, H-Mn$^{2+}$ complexes govern IR/ROS resistance. This dominant role of H-Mn$^{2+}$ in IR resistance of such cells further implies that MnSod may be more important under nutrient-limited conditions, when Mn$^{2+}$ and Pi are in lower abundance and the organic ligands (e.g., free amino acids, peptides, nucleosides) of H-Mn$^{2+}$ complexes are consumed, typically in rapidly dividing cells or following starvation in aging cells (7, 39).

This study has extended insights on the role of Mn antioxidants in the IR survival (D$_{10}$) of bacteria (see Introduction) to a group of simple eukaryotes by showing that variations in D$_{10}$ and efficiency of DNA repair (DSBD$_{10}$) among nine bacteria and nine yeasts are strongly correlated to their H-Mn$^{2+}$ (f$_H$) content (Table 1). Importantly, we also show that the IR resistance of S. cerevisiae is not affected by the presence or absence of Sod enzymes, whether the major Cu/Zn-dependent SOD1, which is localized throughout the cell, or the Mn-dependent SOD2, which is only in the mitochondrial matrix (Table 1). Also consistent with this analysis, IR-induced DSB yields in S. cerevisiae genomes (0.0006–0.0009 DSB/Mbp/Gy) (SI Appendix, Fig. S1) are similar to those reported in other organisms; IR-induced DSB yields across representative archaea, bacteria, and animal cells fall within a narrow range (0.001–0.005 DSB/Mbp/Gy) (5) (Table 1).
Based on the number and diversity of yeasts we examined (SI Appendix, Table S1), our results elucidate many environmental yeasts to the class of biology’s most radiation-resistant organisms. We believe the ability of EPR to accurately measure differences in the IR survival between numerous phylogenetically distinct yeast strains of similar genome size makes paramagnetic spectroscopy suitable for gauging the IR resistance of other eukaryotic cell types, including cancer cells. In the case of D. radiodurans, we note that the ~10^4 Mn^{2+} ions accumulated per cell are not uniformly distributed (7, 11). Rather, Mn is most concentrated in granules, often colocalized with the DNA-containing nucleol (11, 39), providing further support to the proposed Mn antioxidant role in repair of IR-induced DSBs, the most consequential form of DNA damage (5). These granules could serve as primitive antioxidant organelle-like structures, strengthening the antioxidant protection in the proximity of the genome, where functional DNA repair and replication proteins are needed most.

While the existence of high cellular content of H-Mn^{2+} complexes appears in species across archaea, bacteria, and eukaryotes, many microbes can survive vastly greater IR doses than they ever would have experienced in their natural environment over geological times. It therefore seems likely that the underlying mechanisms observed for the accumulation of antioxidant H-Mn^{2+} complexes evolved not as a response to IR but, instead, in response to other severe oxidative pressures that diminish protein functionality (17): desiccation, UV light, aging, and other stressors. Gauging the antioxidant capacity of cells by EPR may thus have applications beyond radiobiology.

Materials and Methods

Strains. Bacteria used in this study were as follows: D. radiodurans [American Type Culture Collection (ATCC) BAA-816], D. radiodurans (sodΔ^-1) (29), D. geothermophilus [Deutsche Sammlung von Mikroorganismen (DSM) 11300], D. ficus (strain MD501), D. ficus (strain MD502), and P. putida (ATCC 47054). Yeasts used in this study (eight S. cerevisiae strains and one Rhodotorula strain) examined by EPR were chosen from a collection of fungi gauged for IR resistance (D_0) (Table 1 and SI Appendix, Table S1): S. cerevisiae (6761) (EFX-6761; diploid), S. cerevisiae (5735) (EFX-5735; diploid), S. cerevisiae (1679) (FY1679; diploid) (40), S. cerevisiae (6219) (EXF-6219; diploid), S. cerevisiae (6218) (EXF-6218; diploid), S. cerevisiae (4741) (BY4741; haploid) (41), S. cerevisiae (Scsod1^-1) (BY4741-ΔSOD1; haploid) (42), S. cerevisiae (Scsod2^-1) (BY4741-ΔSOD2; haploid) (42), and R. taiwanensis (MD1149; USHIS; accession number: PRJNA352283). Archaea used in these studies were H. salinarum (ATCC 700922; strain) (43) and H. volcanii (DS-70). Human cells used in this study were Jurkat T cells (ATCC TIB-152).

More information about growth, acute ^60Co irradiations, ultrafiltrates, intracellular antioxidant capacity of ultrafiltrates, PFGE, and Monte Carlo simulation is provided in SI Appendix, Materials and Methods.

EPR. As reported (37), cryogenic (2 K) Q-band (35 GHz) CW, 100-kHz field-modulated, dispersion-mode, rapid-passage absorption-display EPR spectra were collected on a spectrometer previously described (44). HHF EPR spectra were recorded on a laboratory-built spectrometer at the EPR Laboratory of the National High Magnetic Field Laboratory (33) (SI Appendix).
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