



Bacillus subtilis Spore Resistance to Simulated Mars Surface Conditions

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OPEN ACCESS

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Specialty section:

This article was submitted to
Extreme Microbiology,
a section of the journal
Frontiers in Microbiology

Received: 24 October 2018

Accepted: 08 February 2019

Published: 26 February 2019

Citation:

Cortesão M, Fuchs FM,
Commichau FM, Eichenberger P,
Schuerger AC, Nicholson WL,
Setlow P and Moeller R (2019)
Bacillus subtilis Spore Resistance
to Simulated Mars Surface
Conditions. *Front. Microbiol.* 10:333.
doi: 10.3389/fmicb.2019.00333

In a Mars exploration scenario, knowing if and how highly resistant *Bacillus subtilis* spores would survive on the Martian surface is crucial to design planetary protection measures and avoid false positives in life-detection experiments. Therefore, in this study a systematic screening was performed to determine whether *B. subtilis* spores could survive an average day on Mars. For that, spores from two comprehensive sets of isogenic *B. subtilis* mutant strains, defective in DNA protection or repair genes, were exposed to 24 h of simulated Martian atmospheric environment with or without 8 h of Martian UV radiation [M(+)-UV and M(-)-UV, respectively]. When exposed to M(+)-UV, spore survival was dependent on: (1) core dehydration maintenance, (2) protection of DNA by α/β -type small acid soluble proteins (SASP), and (3) removal and repair of the major UV photoproduct (SP) in spore DNA. In turn, when exposed to M(-)-UV, spore survival was mainly dependent on protection by the multilayered spore coat, and DNA double-strand breaks represent the main lesion accumulated. *Bacillus subtilis* spores were able to survive for at least a limited time in a simulated Martian environment, both with or without solar UV radiation. Moreover, M(-)-UV-treated spores exhibited survival rates significantly higher than the M(+)-UV-treated spores. This suggests that on a real Martian surface, radiation shielding of spores (e.g., by dust, rocks, or spacecraft surface irregularities) might significantly extend survival rates. Mutagenesis were strongly dependent on the functionality of all structural components with small acid-soluble spore proteins, coat layers and dipicolinic acid as key protectants and efficiency DNA damage removal by AP endonucleases (ExoA and Nfo), non-homologous end joining (NHEJ), mismatch repair (MMR) and error-prone translesion synthesis (TLS). Thus, future efforts should focus on: (1) determining the DNA damage in wild-type spores exposed to M(+/-)-UV and (2) assessing spore survival and viability with shielding of spores via Mars regolith and other relevant materials.

Keywords: *Bacillus subtilis*, spore resistance, DNA repair, SASP, Mars, contamination, radiation, planetary protection

INTRODUCTION

Mars is a cold and dry planet, with intense UV (190–400 nm) and ionizing radiation in the form of galactic cosmic radiation (GCR) and solar particle events (SPE) (Guo et al., 2018). The Martian atmosphere is also highly oxidizing due to the OH radicals and oxygen atoms produced by photolysis which result in surface oxidation and the formation of O₂, O₃ and H₂O₂ (Gargaud et al., 2011). In addition, the Mars surface exhibits: temperature shifts from –125°C to +20°C; extremely low water vapor pressure (Davila et al., 2010; Fox-Powell et al., 2016); and very low atmospheric pressure. These extreme conditions are stressful to all known life forms, causing physiological, biochemical and structural damage, which can be lethal for most terrestrial organisms (Jakosky et al., 2003). At the molecular level, this damage can affect membrane lipids, proteins, RNA and, most importantly, DNA. Specific DNA damage includes single strand breaks (SSB), double strand breaks (DSB), and photolesions such as cyclobutane-type pyrimidine dimers (CPDs), 6-4 photoproducts (6-4 PPs) and the thymine dimer 5-thymine-5,6-dihydrothymine, commonly known as the spore photoproduct (SP) (Setlow, 2014).

Nonetheless, despite complex stress-induced damage, spores of the Gram-positive bacterium *Bacillus subtilis* have repeatedly demonstrated their resistance to many space-related extremes, becoming one of the model organisms in the field of Space Microbiology. Studies have shown *Bacillus* spores survive in extreme dryness, high levels of UV and ionizing radiation, and outer space conditions in Low Earth Orbit (LEO), where they were exposed to solar UV, high vacuum, GCR, and temperature fluctuations (Dose et al., 1995; Horneck et al., 2001, 2010; Nicholson and Schuerger, 2005; Fajardo-Cavazos et al., 2010; Moeller et al., 2012b).

Because of their extreme resistance, spores of *B. subtilis*, and other spore-forming bacteria, present a challenge for bio-sterilization in spacecraft facilities, calling for the development of new and more efficient sterilization regimens (Stapelmann et al., 2013; Khodadad et al., 2017). *Bacillus subtilis* spores were also shown to survive in Mars analog soils, confirming a potential forward contamination risk to Mars sites with liquid brines (Schuerger et al., 2017).

Resistance of spores to extreme conditions does not rely on one single mechanism, but rather on a combination of several strategies (Setlow, 2014). The first line of action is “damage prevention.” The overall spore structure is composed of the core, inner membrane, cortex, coat, and crust layers (Figure 1), and has a wide number of properties and components that protect spores from many stress factors. Specifically, the spore core has low water content (25–55% of wet weight), due in some fashion to the spore’s peptidoglycan cortex, that provides resistance to wet heat. Within the core, high levels (~25% of core dry weight) of pyridine-2,6-dicarboxylic acid – dipicolinic acid (DPA), in a 1:1 chelate with Ca²⁺ (Ca-DPA) help to protect spores from desiccation and DNA-damaging agents and maintain spore dormancy (Magge et al., 2008). The core’s high levels of α/β-type small, acid-soluble spore proteins (SASP) (Magge et al., 2008) that saturate spore DNA are one of the main factors

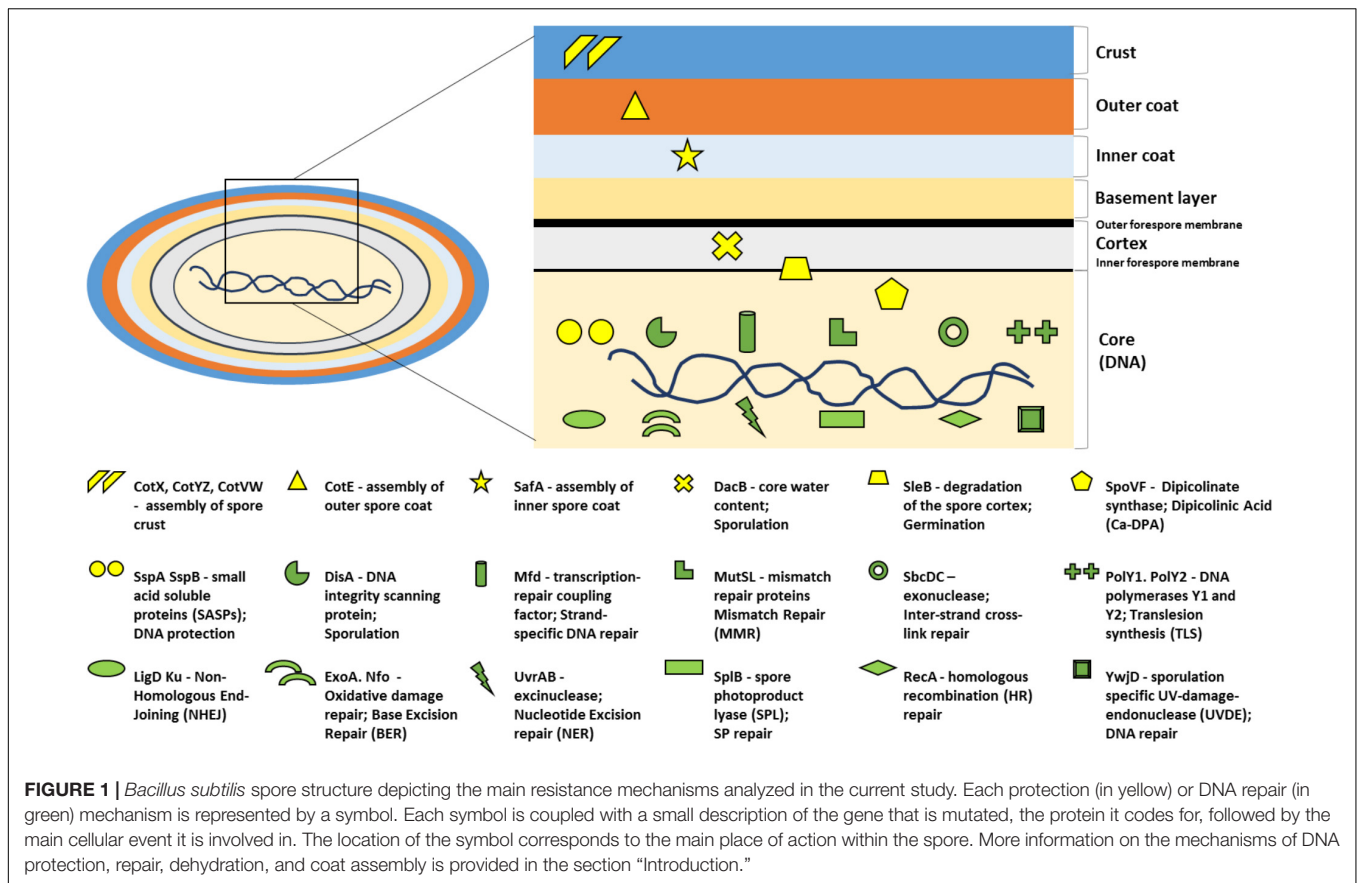
protecting spores from genotoxic chemicals, desiccation, dry and wet heat, as well as UV and γ-radiation (Mason and Setlow, 1986; Moeller et al., 2008). Moreover, the thick proteinaceous coat and crust layers, as well as the inner membrane, function as barriers to many toxic chemicals minimizing their ability to access the spore core where DNA and most spore enzymes are located. The spore coats also contain melanin-like pigments that absorb UV radiation, and there is evidence that such pigments can play a significant role in spore resistance to UV-B and UV-A radiation (Hullo et al., 2001; Moeller et al., 2008, 2014; Setlow, 2014).

The second line of defense is “damage repair,” which takes place soon after spores germinate and begin outgrowth. *Bacillus subtilis* spores are armed with enzymes of multiple DNA repair pathways, thus marshaling multiple mechanisms that ensure spore survival. The main known mechanisms for repair of DNA damage in spores are: (1) homologous recombination (HR), (2) non-homologous end joining (NHEJ), (3) nucleotide excision repair (NER), (4) DNA integrity scanning, (4) inter-strand cross-link repair, (5) base excision repair (BER), (6) SP repair by spore photoproduct lyase (Spl), (7) mismatch repair (MMR), (8) endonuclease-dependent excision repair (UVER), and (9) error-prone translesion synthesis (TLS) (Xue and Nicholson, 1996; Rebeil et al., 1998; Duigou et al., 2005; Moeller et al., 2007b, 2012a; Lenhart et al., 2012).

The continuous and ongoing efforts to characterize the geochemistry, mineralogy and consequent habitability of the Martian surface (Skelley et al., 2005; Davila et al., 2010; Fox-Powell et al., 2016) have led to recent findings of the presence of water on Mars. This finding suggested that ancient Martian environments could have supported microbial life, and therefore Mars has become the focus of space exploration and life-detection studies (Grotzinger et al., 2014, 2015; Fox-Powell et al., 2016).

To help ensure the legitimacy of life-detection studies and to prevent forward contamination, there are international planetary protection policies restricting the number of microorganisms on spacecraft surfaces, and Special Regions of Mars have been identified where proliferation of known microbes could take place (Schuerger et al., 2013; Rummel et al., 2014; Rettberg et al., 2016). Hence, it is of concern that extremely resistant microorganisms, including *B. subtilis*, have been detected in spacecraft-associated facilities (Venkateswaran et al., 2014; Checinska et al., 2015; Moissl-Eichinger et al., 2016), and that these organisms (and most importantly, their spores), might pose a threat to the forward contamination of surface terrains, or the search for past or present life on Mars (Fajardo-Cavazos et al., 2008; Horneck et al., 2010; Goetz et al., 2016). In spite of its importance, there is a paucity of experimental data on the molecular mechanisms of spore survival of Earth microorganisms in the Martian environment. Consequently, if we are to design adequate planetary protection measures and prevent forward contamination, it is of utmost importance to expand our knowledge on how microorganisms are able to resist Mars’ environmental conditions, and thus, potentially survive on this planet.

In the current study, a systematic screening was performed to determine if and how *B. subtilis* spores could survive an average day on Mars. A number of spores of *B. subtilis* strains



lacking protective elements and/or DNA repair proteins were exposed to 24 h of simulated Martian surface conditions with or without 8 h of UV radiation, and spore survival and mutagenesis were measured. The results of this study reveal the molecular mechanisms behind *B. subtilis* spore resistance in a Martian environment and assess the possibility of microbial contamination due to spores on the Martian surface.

MATERIALS AND METHODS

Bacterial Strains, Growth, Sporulation, and Spore Purification

The two sets of *B. subtilis* strains used in this work are listed in **Tables 1, 2**, and all are isogenic with their respective wild-type strains, either PS832, PY79 or 168. One set of spores was chosen to determine the role of various spore protection mechanisms, including SASP, Ca-DPA, the spore core hydration level and the spore coat and crust, in spore survival (**Table 1**); the other set was used to study the importance of different DNA repair mechanisms (**Table 2**).

The *ligD ku* genes were deleted in strain 168. The deletion cassette was constructed using the oligonucleotide pairs KK294/295 (5'-CCGAGCGCCTACGAGGAATTTGTATCGCAACCCGCAAGACGAAACCGCTTAG/5'-CGATGATGGCAGCAAAGACCGCACT), KG297/KG298 (5'-C

CTATCACCTCAAATGGTTCGCTGCTTTAGTGTGAAGAGAAGGAGTACGATTCATG/5'-GCGATATCTCCAAAAGACGGGACGGA) and *kan-fwd/kan-rev* (5'-CAGCGAACCATTTGAGGTGATAGG/5'-CGATACAAATTCCTCGTAGGCGCTCGG) which were used to amplify the flanking regions and the *aphA3* kanamycin resistance gene. The deletion cassette was used to transform *B. subtilis* using a previously described protocol (Kunst and Rapoport, 1995). Transformants were selected on LB agar plates supplemented with 10 $\mu\text{g mL}^{-1}$ kanamycin. The resulting strain was designated as BP141.

Spores were obtained by cultivation under vigorous aeration at 37°C for 7 days in double-strength liquid Schaeffer's sporulation medium (SSM) (Schaeffer et al., 1965) and in a few cases with DPA added to 100 $\mu\text{g mL}^{-1}$. Spores were purified and stored as described previously (Moeller et al., 2006). Antibiotics [i.e., chloramphenicol (5 $\mu\text{g mL}^{-1}$), neomycin (10 $\mu\text{g mL}^{-1}$), spectinomycin (100 $\mu\text{g mL}^{-1}$), erythromycin (1 $\mu\text{g mL}^{-1}$), or tetracycline (10 $\mu\text{g mL}^{-1}$)] were used when needed (Paidhungat et al., 2000) (**Tables 1, 2**). Final spore suspensions consisted of single spores with no detectable clumps, and were free (>99%) of vegetative cells, germinated spores, or cellular debris, as seen in phase-contrast microscopy (data not shown).

Sample Preparation

Spore suspensions were prepared in sterile distilled water such that a 50 μL aliquot contained 5×10^8 spores. Each sample for

TABLE 1 | *B. subtilis* strains deficient in spore components used in this study.

Strain	Genotype	Absent component(s)/ protection mechanism(s)	Reference
PS832	Wild-type parental strain of PS and FB strains (prototroph; Trp ⁺ revertant of strain 168)	None/wild-type/full protection capabilities	Popham et al., 1995
PY79	Wild-type parental strain of all PE strains (prototroph)	Wild-type/full protection capabilities	McKenney and Eichenberger, 2012
PS283	$\Delta sspA$	α -Type small, acid-soluble protein (SASP)/DNA protection	Mason and Setlow, 1986
PS338	$\Delta sspB$	β -Type SASP/DNA protection	Mason and Setlow, 1986
PS483	$\Delta sspE$	γ -Type SASP/no protection function	Hackett and Setlow, 1988
PS356	$\Delta sspA \Delta sspB$	α - and β -Type SASP/DNA protection	Loshon et al., 1999
PS482	$\Delta sspA \Delta sspB \Delta sspE$	α -, β -, and γ -Type SASP/DNA protection	Tovar-Rojo and Setlow, 1991
PS1899	<i>dacB::cat</i>	Carboxypeptidase DacB/core dehydration	Popham et al., 1995
PS2211	<i>dacB::cat</i> $\Delta sspA \Delta sspB$	<i>dacB</i> , α/β -type SASP/core dehydration and DNA protection	Popham et al., 1995
PS3394	$\Delta cotE$; Tet ^R	CotE protein/outer coat assembly	Young and Setlow, 2003
PE566	$\Delta cotVW$; Erm ^R	CotVW proteins/spore crust assembly	Eichenberger et al., 2004
PE620	$\Delta cotX \Delta cotYZ$; Neo ^R	CotX and CotYZ proteins/spore crust assembly	McKenney and Eichenberger, 2012
PE618	$\Delta cotE$; Cat ^R	CotE protein/outer coat assembly	McKenney and Eichenberger, 2012
PE277	$\Delta safA$; Tet ^R	SafA protein/inner coat assembly	McKenney and Eichenberger, 2012
PE1720	$\Delta cotE \Delta safA$; Cat ^R Tet ^R	CotE and SafA proteins/inner and outer coat assembly	Raguse et al., 2016
PS3395	$\Delta cotE \Delta sspA \Delta sspB$; Tet ^R	CotE and α/β -type SASP/outer coat assembly and DNA protection	Young and Setlow, 2003
FB122	$\Delta sleB \Delta spoVF$; Spc ^R Tet ^R	Enzymes SleB and dipicolinate synthase (SpoVF)/degradation of the spore cortex in germination and DPA synthesis in the mother cell	Magge et al., 2008
PS3664	$\Delta sleB \Delta spoVF \Delta sspA \Delta sspB$; Spc ^R Tet ^R	SleB and SpoVF, α/β -type SASP/DPA formation and DNA protection	Setlow et al., 2006
PS3747	$\Delta cotE::cam \Delta sleB$; Spc ^R $\Delta spoVF \Delta sspA \Delta sspB$; Tet ^R	<i>cotE</i> , DPA, α/β -type SASP/outer coat assembly, DPA synthesis and DNA protection	Setlow et al., 2006

Antibiotic resistance: Cat^R, resistance to chloramphenicol (5 $\mu\text{g mL}^{-1}$); Erm^R, resistance to erythromycin (2 $\mu\text{g mL}^{-1}$); Neo^R resistance to neomycin (10 $\mu\text{g mL}^{-1}$); Spc^R, resistant to spectinomycin (100 $\mu\text{g mL}^{-1}$); Tet^R, resistance to tetracycline (10 $\mu\text{g mL}^{-1}$).

exposure was prepared by applying 50 μl of spores onto a 10 mm \times 20 mm aluminum coupon (Model M4985, Seton, Inc., Branford, CT, United States) to ensure that the spores spread homogeneously on the coupons by complete covering of the surface, yielding spore multilayer samples with a thickness of \sim 25 spore layers (Tauscher et al., 2006). In our study, coupons were chosen to simulate surface materials of a spore-contaminated spacecraft. Each set of spore samples was tested in three replicates of each genotype with the same spore concentration. Spore samples were air-dried under ambient laboratory conditions (20°C, 33 \pm 5% relative humidity) for 1 day prior to exposure to simulated Mars surface conditions.

Spore Exposure in the Mars Simulation Chamber

Spore-inoculated coupons were exposed for 24 h to simulated Martian conditions in a cylindrical Mars Simulation Chamber (MSC) (50 cm in diameter by 70 cm long) with a regimen of 8 h simulated Martian solar irradiation exposure and 16 h exposure in the dark. The UVC (200–280 nm) flux on spores in the MSC was measured as 4.04 W m⁻², which converts to 14.4 kJ m⁻² h⁻¹ (or 115 kJ m⁻² d⁻¹) (Table 3). During the 8 h of simulated Martian solar irradiation, one sample set was exposed

to full Martian UV conditions [designated as M(+)]UV and the other sample set was covered with aluminum foil, which shielded all applied photonic energy [designated M(-)]UV. The overall simulated Martian conditions of temperature, pressure, and gas composition inside the chamber are listed in Table 3. Regarding irradiation conditions, the 8 h of radiation exposure represents a worst-case scenario for high UV flux (note that no ionizing radiation was simulated), and thus likely to give the maximum UV effects on *B. subtilis* spores under Martian conditions. In parallel, two additional sample sets were prepared; one was stored for the same time under ambient laboratory conditions (Earth atmosphere, pressure, room temperature, and protected from light) and the remaining sample set was stored at 4°C in a refrigerator. The MSC was developed as part of an ongoing series of Mars astrobiology and planetary protection projects, and has been described previously (Schuerger et al., 2008, 2011).

Spore Recovery and Survival Assay

To recover *B. subtilis* spores from aluminum coupons, spore layers were covered by a 10% aqueous polyvinyl alcohol solution (PVA) and after drying the spore-PVA layers were removed as described (Horneck et al., 2001), and suspended in 1 ml of sterile distilled water, resulting in >95% recovery

TABLE 2 | DNA repair-deficient *B. subtilis* strains used in this study.

Strain	Genotype	Absent component/repair mechanism(s)	Reference
168	<i>trpC2</i>	Wild-type/full DNA repair capabilities	Laboratory collection (Gunka et al., 2012)
GP987	<i>trpC2 ΔdisA</i> ; Tet ^R	DNA integrity scanning protein DisA/sporulation initiation	Mehne et al., 2013
GP1503	<i>trpC2 ΔexoA::aphA3 Δnfo</i> Cat ^R	Apurinic and apyrimidinic (AP) endonucleases ExoA and Nfo/base excision repair pathway (BER)	Gunka et al., 2012
BP141	<i>trpC2 ΔligD ku::aphA3</i>	Ku homodimer and DNA Ligase D/non-homologous end joining (NHEJ)	This study
GP1167	<i>trpC2 Δmfd</i> ; Erm ^R	Transcription-repair coupling factor Mfd/strand-specific DNA repair	Gunka et al., 2012
GP1190	<i>trpC2 ΔmutSL::aphA3</i>	MutS and MutL proteins/mismatch repair (MMR)	Gunka et al., 2012
PERM715	<i>trpC2 pMUTIN4::yqjH (polY1) ΔyqjW (polY2)</i> ; Em ^R Kan ^R	DNA polymerases Y1 and Y2/translesion synthesis (TLS)	Rivas-Castillo et al., 2010
BP469	<i>trpC2 ΔrecA</i> , Erm ^R	RecA protein/homologous recombination (HR)	This study
GP894	<i>trpC2 ΔsbcDC::aphA3</i>	Exonuclease SbcDC/inter-strand cross-link repair (ISCLR)	Gunka et al., 2012
BP130	<i>trpC2 ΔsplB</i> ; Spc ^f	Spore photoproduct lyase (SP lyase)/SP repair	Djouia et al., 2018
RM1010	<i>trpC2 Δdis ΔsplB</i> ; Tet ^R Spc ^f	SP lyase and DisA/SP repair and sporulation initiation	This study GP987 → BP130
RM1011	<i>trpC2 ΔexoA::aphA3 Δnfo ΔsplB</i> ; Cat ^R Spc ^R	SP lyase, ExoA and Nfo/AP endonucleases and BER	This study GP1503 → BP130
RM1012	<i>trpC2 ΔligD Δku ΔsplB</i> ; Spc ^R Kan ^R	SP lyase, Ku and LigD/SP repair, NHEJ	This study BP141 → BP130
RM1013	<i>trpC2 Δmfd ΔsplB</i> ; Erm ^R Spc ^R	SP lyase and Mfd/SP repair and strand-specific DNA repair	This study GP1167 → BP130
RM1014	<i>trpC2 ΔmutSL::aphA3 ΔsplB</i> ; Spc ^R	SP lyase, MutS and MutL/SP repair and MMR	This study GP1190 → BP130
RM1015	<i>trpC2 pMUTIN4::yqjH (polY1) ΔyqjW (polY2) ΔsplB</i> ; Em ^R Kan ^R Spc ^R	SP lyase, PolY1 and PolY2/SP repair and TLS	This study WN1127 → BP130
RM1016	<i>trpC2 ΔsbcDC::aphA3</i> ; Kan ^R ΔsplB; Spc ^R	SP lyase and exonuclease SbcDC/SP repair and ISCLR	This study GP894 → BP130
RM1017	<i>trpC2 ΔrecA ΔsplB</i> ; Erm ^R Spc ^R	SP lyase and RecA/SP repair and HR	This study BP469 → BP130
GP1175	<i>trpC2 ΔuvrAB</i> ; Erm ^R	Excinuclease/nucleotide excision repair (NER)	Gunka et al., 2012
RM1019	<i>trpC2 ΔuvrAB</i> ; Erm ^R ΔsplB; Spc ^R	SP lyase and UvrAB/SP repair and NER	This study GP1175 → BP130
PERM639	<i>ΔywjD::lacZ</i> ; Erm ^R	UV-damage-endonuclease (UVDE)/UV damage repair	Ramirez-Guadiana et al., 2012
RM1021	<i>trpC2 ΔywjD::lacZ</i> ; Erm ^R	UVDE/UV damage repair	This study PERM639 → 168
RM1022	<i>trpC2 ΔywjD::lacZ</i> ; Erm ^R ΔsplB; Spc ^R	SP lyase and UVDE/SP repair and UV damage repair	This study PERM639 → BP130

Arrows indicate constructions made by transformation. Antibiotic resistance: Cat^R, resistance to chloramphenicol (5 μg mL⁻¹); Erm^R, resistance to erythromycin (2 μg mL⁻¹); aphA3: resistance to kanamycin (10 μg mL⁻¹); Spc^R, resistant to spectinomycin (100 μg mL⁻¹); Tet^R, resistance to tetracycline (10 μg mL⁻¹).

of the spores (data not shown). The PVA procedure has no geno- or cytotoxic effect on the spore viability (Horneck et al., 2001). Spore survival was determined from serial dilutions in distilled water as colony-forming units after incubation overnight at 37°C on nutrient broth (NB) agar plates (Difco, Detroit, MI, United States) (Moeller et al., 2007b, 2010). Spore survival was determined by observing standard colony formation of macroscopic visible colonies on NB agar containing the appropriate selective antibiotic, as described above (Horneck et al., 2001). The relative sensitivity of spores of each mutant strain was determined with respect to that of the corresponding wild-type spores, and in some cases with *splB* spores, results were compared statistically using the Student's *t*-test and differences with *P*-values of ≤0.05 were considered statistically significant.

Detection of Sporulation Deficiency

To verify mutation induction caused by exposure to Martian conditions, 250 *B. subtilis* colonies arising from survivors of each Martian exposure tested were picked and streak-purified on SSM-agar plates solidified with 1.5% agar, containing the appropriate antibiotic(s), and incubated at 37°C for 7 days. Sporulation deficiencies were determined visually by changes

in colony morphology and pigmentation. Sporulated *B. subtilis* colonies show brownish pigmentation after extended incubation on sporulation plates, whereas a decrease in pigmentation and a translucent appearance are characteristic of asporogenous or Spo⁻ *B. subtilis* mutants (Piggot and Coote, 1976; Hullo et al., 2001; Fajardo-Cavazos et al., 2005). The frequency of Spo⁻ mutants was expressed as the ratio of the Spo⁻ colonies to the total 250 colonies picked after 7 days of incubation on SMM plates. To verify the Spo⁻ mutation rates, plate from spores that had been exposed in colonies were individually transferred into 5 mL of SSM media and incubated for 24 h at 37°C. Sporulation was then induced by diluting the overnight culture 1:100 into 5 mL of SSM medium. To determine the number of spores formed, after 24 h of cultivation, appropriate dilutions of cultures were plated on NB agar before and after a heat-shock (80°C; 10 min) to kill growing or sporulating cells but not spores, as described (Maughan et al., 2007). Each analysis of the selected Spo⁻ mutants was repeated at least three times.

Numerical and Statistical Analysis

The surviving fraction of *B. subtilis* spores was determined from the quotient N/N_0 , with N = the number of colony-forming

TABLE 3 | Environmental conditions used during Mars environmental simulation experiments.

Parameter	Value, fluence or percentage
Pressure	0.69 ± 0.01 kPa
Temperature	-10 ± 2°C
Relative humidity	8 ± 2%
UV-VIS-NIR radiation ^a	Fluence rate per h (total applied fluence) ^b
Total UV (200–400 nm)	92.8 kJ m ⁻² h ⁻¹ (742.5 kJ/m ⁻²)
UV-C (200–280 nm)	14.4 kJ m ⁻² h ⁻¹ (115.2 kJ/m ⁻²)
UV-B (280–320 nm)	20.8 kJ m ⁻² h ⁻¹ (166.5 kJ/m ⁻²)
UV-A (320–400 nm)	57.6 kJ m ⁻² h ⁻¹ (460.8 kJ/m ⁻²)
VIS (400–700 nm)	864.0 kJ m ⁻² h ⁻¹ (6.91 MJ/m ⁻²)
NIR (700–1,100 nm)	882.0 kJ m ⁻² h ⁻¹ (7.05 MJ/m ⁻²)
Total irradiance (200–1,100 nm)	1,838.8 kJ m ⁻² h ⁻¹ (14.7 MJ/m ⁻²)
Time	24 h (with or without 8 h of radiation)
Mars Gas Mix ^c	95.54% CO ₂ ; 2.7% N ₂ , 1.6% Ar, 0.13% O ₂ , 0.03% H ₂ O

^a Fluence rates for UVC and UVB were directly measured with an International Light, model IL400A radiometer (Newburyport, MA, United States). ^b Fluence rates for UVA, total UV, VIS, and NIR were based on the models of (Schuergel et al., 2005, 2008). ^c Gas composition in the MSC system was ordered from Boggs Gases, Inc. (Titusville, FL, United States) as a commercial mixture of the top five gases in the Martian atmosphere (see Schuergel et al., 2008).

units (CFU) of the Mars-exposed sample and N_0 that of the untreated controls. The Spo⁻ mutant frequencies from the control and M(+/-)UV exposed spores were determined from three replicate samples. The frequency of Spo⁻ mutations in samples induced by exposure to the M(+/-)UV conditions was determined as $[M/N - m_S]$, with M = the total number of mutants from the exposed samples; $N = 250$; and m_S = frequency of spontaneous Spo⁻ mutations in unexposed samples. The sporulation frequency of the induced asporogenous mutants was determined by dividing the CFU after heat shock (spores) by the CFU before heat shock (growing/sporulating cells and spores). The data shown are expressed as averages ± standard deviations, and results were compared statistically using the Student's *t*-test. Values were analyzed in multigroup pairwise combinations, and differences with *P*-values of ≤0.05 were considered statistically significant (Moeller et al., 2005, 2006, 2007a,b, 2008; Horneck et al., 2008).

RESULTS

To know which spore components and molecular mechanisms are involved in *B. subtilis* spore resistance to simulated Mars surface conditions, two sets of *B. subtilis* spores were exposed to a simulated Martian atmospheric environment with or without 8 h of UV radiation (M(+/-)UV). The first set comprised spores deficient in spore protective components (Table 1), and the second set comprised spores deficient in various DNA repair mechanisms (Table 2). A summary registering which mutant genotypes, and respective missing mechanisms of protection or repair, revealed the highest and/or lowest sensitivity to M(+/-)UV tested conditions is presented in Figure 2.

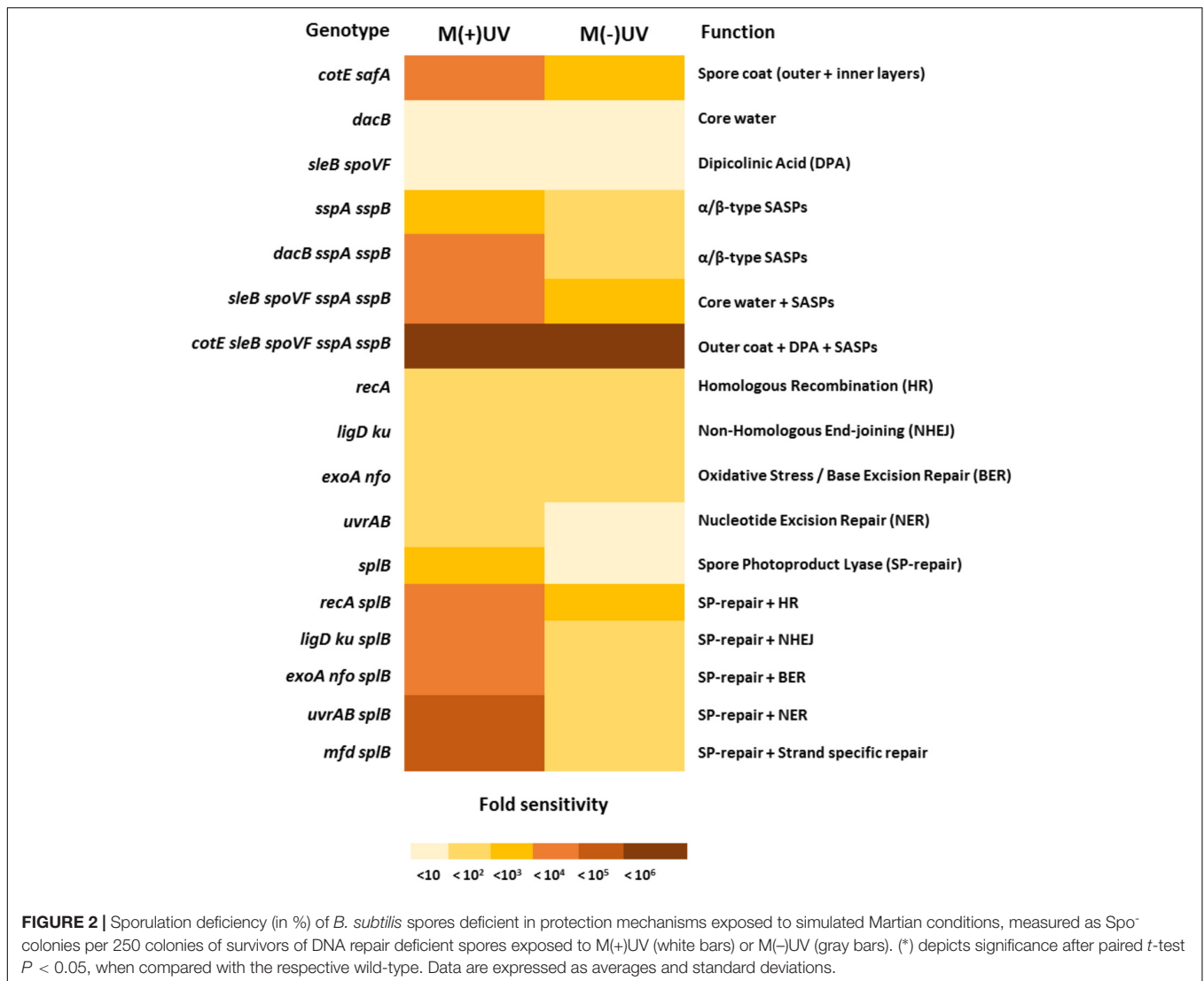
Spore Protection

When exposed to both M(+/-)UV conditions, *B. subtilis* spores lacking proteins responsible for spore coat assembly were significantly more sensitive than wild-type spores (Table 4 and Supplementary Figures S1–S3). The outer and inner spore coats provided significant protection against the Martian environment, with *cotE* PY79 spores, lacking the outer coat, being less sensitive [15-fold M(+)-UV and 18-fold M(-)UV] than *safA* spores, lacking the inner spore coat [~240-fold M(+)-UV and 63-fold M(-)UV], when compared with the wild-type spores. Spores lacking both outer and inner spore coat layers (*cotE safA* spores) exhibited astonishing increases in sensitivity of ~1000-fold in M(+)-UV, and ~200-fold in M(-)UV, compared to wild-type spores (Table 4 and Supplementary Figures S1–S3). Despite the striking effects of inner and outer coat defects on spore resistance to M(+/-)UV, the loss of the spore crust layer (*cotVW*, and *cotX cotYZ* spores) had no significant effects on spore survival under the tested conditions (Table 4 and Supplementary Figures S1–S3).

A second group of crucial protective components in spores is the α/β -type SASP that saturate spore DNA and protect it from damage. Spores lacking SASP- α and - β (*sspA sspB* spores) are thus lacking ~80% of the α/β -type SASP pool (Hathout et al., 2003). When exposed to M(+/-)UV *sspA sspB* spores had increased sensitivity when compared with the wild-type, being significantly more sensitive to M (+)UV (273-fold, with a *P*-value of 0.0015) than to M(-)UV (17-fold, with a *P*-value of 0.0021) (Table 4 and Supplementary Figures S4–S7). Interestingly, *sspE* spores, which lack the most prominent SASP, SspE, had no significant effect on spore survival in both M(+/-)UV (with a *P*-value of 0.4936, same as wild-type), but had increased sensitivity when additionally lacking SASP- α and - β (*sspE sspA sspB* spores). Results show *sspE sspA sspB* spores with 435-fold and 39-fold sensitivity in M(+)-UV (with a *P*-value of 0.0012) and M(-)UV (with a *P*-value of 0.0013), respectively, when compared with wild-type spores (Table 4 and Supplementary Figures S4–S7).

A third spore protective factor is the low water content in the spore core. Spores with higher core water content (*dacB*, and *sleB spoVF* spores) exhibited lower resistance to conditions M(+/-)UV, when compared to wild-type spores (Table 4 and Supplementary Figures S4–S7). Notably, spores lacking α/β -type SASP and either DacB (*dacB sspA sspB* spores, with a *P*-value of 0.0086) or CaDPA (*sleB spoV sspA sspB* spores, with a *P*-value of 0.0053) were more sensitive to the Martian environment than either *dacB* or *sleB spoVF* spores. Results also show that addition of DPA to the sporulation medium suppressed *sleB spoVF* spores' decreased resistance while sporulating, reaching near wild-type survivability levels (Table 4 and Supplementary Figures S4–S7).

Spores lacking an outer coat with an additional SASP deficiency (*cotE sspA sspB* spores, with a *P*-value of 0.0052), were more sensitive to Mars conditions than spores lacking either protective component alone (*cotE*, and *sspA sspB* spores) (Table 4 and Supplementary Figures S4–S7). An additional deficiency in Ca-DPA (*cotE sleB spoVF sspA sspB* spores), and consequent higher core water content, resulted in rapid



killing with a 10⁵-fold, in M(+)-UV and 10⁴-fold in M(-)-UV, greater sensitivity compared with the wild-type (with *P*-values of 0.0001 or 0.0001, respectively). However, the effects of the *sleB spoVF* mutations were again suppressed when these spores were prepared with DPA added to the sporulation medium with 10³-fold greater sensitivity compared with the wild-type in M(+)-UV and 646-fold in M(-)-UV (Table 4 and Supplementary Figures S4–S7).

Spore DNA Repair

Bacillus subtilis spores rely on a complex network of mechanisms to repair DNA damage accumulated during periods of dormancy, and ensure genomic integrity. When spores were exposed to M(+)-UV, SP lyase deficient spores (*splB* spores, with a *P*-value of 0.0004) were ~300-fold more sensitive than wild-type spores, whereas spores lacking NHEJ (*ligD ku*, with a *P*-value of 0.0049) or HR (*recA*, with a *P*-value of 0.0037) were only ~35 and ~80-fold more sensitive than wild-type spores (Table 5 and Supplementary Figures S8–S12). A number of single or

double mutations in other DNA repair genes resulted in smaller amounts of sensitization of spores to M(+)-UV, including *exoA nfo*, *uvrAB*, *mfd*, *sbcDC*, *polY1* *polY2*, and *mutSL* mutations. Mutation of the *disA* gene (lacking DNA integrity scanning protein) had only minimal (but not significant) effects on spore survival in M(+)-UV reaching near wild-type levels of survivability (with a *P*-value of 0.0943). Sensitivity of *recA* and *ligD ku* mutant spores was revealed to be in the same order of magnitude in both tested environments M(+)-UV, being of ~80- to 90-fold for *recA* spores in M(+)-UV, and ~30-fold for *ligD ku* in M(+)-UV and M(-)-UV (Table 5 and Supplementary Figures S8–S12).

Analysis of the M(+)-UV survival rates of *splB* spores additionally lacking other DNA repair genes, revealed that almost all DNA repair mutations caused significant increases in spore sensitivity, when compared to that of the *splB* single mutant spores. Spores lacking SP lyase (SP repair) and strand specific DNA repair (*mfd splB* spores, with a *P*-value of 0.0001) as well as spores lacking SP repair and NER (*uvrAB splB*

TABLE 4 | Spore surviving fraction and increased sensitivity of mutant spores lacking protection mechanisms exposed to M(+)/UV or M(-)/UV.

Protective component	Surviving fraction		Increased sensitivity compared to wild-type spores (fold)	
	M(+)/UV	M(-)/UV	M(+)/UV	M(-)/UV
Wild-type (wt, PS832)	$(6.6 \pm 0.8) \times 10^{-2}$	$(7.3 \pm 0.1) \times 10^{-1}$	1.0 ± 0.1	1.0 ± 0.2
<i>sspA</i>	$(1.5 \pm 0.2) \times 10^{-2+}$ [+0.0042]	$(2.0 \pm 0.4) \times 10^{-1+}$ [+0.0247]	$4.4 \pm 0.6^+$ [+0.0053]	$3.6 \pm 0.7^+$ [+0.0041]
<i>sspB</i>	$(1.7 \pm 0.2) \times 10^{-2+}$ [+0.0058]	$(4.6 \pm 0.1) \times 10^{-1+}$ [+0.0438]	$3.8 \pm 0.4^+$ [+0.0091]	1.6 ± 0.4 [0.1062]
<i>sspE</i>	$(7.6 \pm 0.1) \times 10^{-2}$ [0.2981]	$(7.2 \pm 0.1) \times 10^{-1}$ [0.8287]	0.9 ± 0.2 [0.4936]	1.0 ± 0.1 [0.5698]
<i>sspA sspB</i>	$(2.4 \pm 0.5) \times 10^{-4+}$ [+0.0002]	$(4.2 \pm 0.9) \times 10^{-2+}$ [+0.0025]	$273 \pm 57^+$ [+0.0015]	$17 \pm 3.8^+$ [+0.0021]
<i>sspA sspB sspE</i>	$(1.5 \pm 0.3) \times 10^{-4+}$ [+0.0001]	$(1.9 \pm 0.4) \times 10^{-2+}$ [+0.0016]	$435 \pm 36^+$ [+0.0012]	$39 \pm 9.3^{+#}$ [+0.0013; #0.0402]
<i>dacB</i>	$(1.1 \pm 0.2) \times 10^{-2+}$ [+0.0032]	$(1.5 \pm 0.2) \times 10^{-1+}$ [+0.0135]	$6.1 \pm 0.9^+$ [+0.0041]	$4.8 \pm 0.6^+$ [+0.0035]
<i>dacB sspA sspB</i>	$(2.1 \pm 0.2) \times 10^{-5+}$ [+0.0001; #0.0073]	$(1.3 \pm 0.2) \times 10^{-2+}$ [+0.0011]	$3172 \pm 285^{+#}$ [+0.0001; #0.0086]	$58 \pm 9.6^{+#}$ [+0.0011; #0.0359]
<i>sleB spoVF</i>	$(5.1 \pm 0.2) \times 10^{-2}$ [0.0544]	$(1.3 \pm 0.2) \times 10^{-1+}$ [+0.0109]	1.3 ± 0.2 [0.4628]	$5.8 \pm 1.0^+$ [+0.0031]
(*) <i>sleB spoVF</i>	$(8.5 \pm 0.7) \times 10^{-2}$ [0.0653]	$(2.4 \pm 0.5) \times 10^{-1+}$ [+0.0214]	0.8 ± 0.2 [0.4897]	$3.0 \pm 0.6^+$ [+0.0068]
<i>sleB spoVF sspA sspB</i>	$(1.8 \pm 0.1) \times 10^{-5+}$ [+0.0001; #0.0081]	$(2.0 \pm 0.3) \times 10^{-3+}$ [+0.0001]	$3780 \pm 761^{+#}$ [+0.0001; #0.0063]	$356 \pm 57^{+#}$ [+0.0003; #0.0009]
(*) <i>sleB spoVF sspA sspB</i>	$(1.7 \pm 0.4) \times 10^{-4+}$ [+0.0001]	$(1.7 \pm 0.2) \times 10^{-2+}$ [+0.0009]	$394 \pm 66^+$ [+0.0012]	$44 \pm 6.2^{+#}$ [+0.0017; #0.0093]
<i>cotE</i>	$(1.6 \pm 0.3) \times 10^{-2+}$ [+0.0083]	$(8.4 \pm 0.1) \times 10^{-2+}$ [+0.0046]	$4.2 \pm 0.9^+$ [+0.0068]	$8.6 \pm 1.3^+$ [+0.0024]
<i>cotE sspA sspB</i>	$(1.7 \pm 0.3) \times 10^{-5+}$ [+0.0001; #0.0038]	$(6.9 \pm 0.1) \times 10^{-3+}$ [+0.0001]	$3793 \pm 691^{+#}$ [+0.0001; #0.0052]	$106 \pm 18^{+#}$ [+0.0009; #0.0029]
<i>cotE sleB spoVF sspA sspB</i>	$(4.8 \pm 0.3) \times 10^{-7+}$ [+0.0001; #0.0001]	$(6.8 \pm 0.1) \times 10^{-5+}$ [+0.0001]	$137245 \pm 32024^{+#}$ [+0.0001; #0.0001]	$10635 \pm 2162^{+#}$ [+0.0001; #0.0001]
(*) <i>cotE sleB spoVF sspA sspB</i>	$(7.9 \pm 0.1) \times 10^{-6+}$ [+0.0001; #0.0030]	$(1.1 \pm 0.3) \times 10^{-3+}$ [+0.0001]	$8403 \pm 2187^{+#}$ [+0.0001; #0.0024]	$646 \pm 150^{+#}$ [+0.0002; #0.0004]
<i>wt (PY79)</i>	$(1.3 \pm 0.2) \times 10^{-1}$	$(8.3 \pm 0.1) \times 10^{-1}$	1.0 ± 0.4	1.0 ± 0.2
<i>cotVW</i>	$(7.5 \pm 2.8) \times 10^{-2}$ [0.1634]	$(9.3 \pm 0.1) \times 10^{-1}$ [0.2648]	1.6 ± 0.1 [0.0653]	0.9 ± 0.1 [0.4819]
<i>cotX cotYZ</i>	$(1.0 \pm 0.8) \times 10^{-1}$ [+0.5628]	$(6.9 \pm 0.1) \times 10^{-1}$ [0.2297]	1.3 ± 0.2 [0.3984]	1.2 ± 0.2 [0.2987]
<i>cotE</i>	$(9.0 \pm 0.1) \times 10^{-3+}$ [+0.0047]	$(4.7 \pm 0.1) \times 10^{-2+}$ [+0.0089]	$15 \pm 2.4^+$ [+0.0029]	$18 \pm 3.9^+$ [+0.0072]
<i>safA</i>	$(5.5 \pm 0.7) \times 10^{-4+}$ [+0.0003]	$(1.3 \pm 0.2) \times 10^{-2+}$ [+0.0053]	$244 \pm 33^+$ [+0.0009]	$63 \pm 10^+$ [+0.0029]
<i>cotE safA</i>	$(1.3 \pm 0.3) \times 10^{-4+}$ [+0.0001]	$(2.8 \pm 0.7) \times 10^{-3+}$ [+0.0001]	$1060 \pm 237^+$ [+0.0001]	$293 \pm 74^+$ [+0.0015]

(*) DPA supplementation during sporulation. + Statistically significant different from values for wild-type spores ($P \leq 0.05$); individual P -values are given in brackets below the initial values. # Statistically significant difference between values for these mutant spores compared to values for *sspA sspB* spores ($P \leq 0.05$); individual P -values are given in brackets below the initial values. The surviving fraction was determined after a 24 h exposure to M(+/-)UV relative to that of control spores of each genotype, which were stored in air at room temperature ($20 \pm 2^\circ\text{C}$), at relative humidity of $40 \pm 5\%$ and protected from UV radiation. Increased sensitivity was determined relative to the respective wild-type spores as the ratio of the surviving fraction of wild-type over the surviving fraction of the various mutant spores. Three biological replicates were analyzed for each condition.

spores, with a P -value of 0.0001) exhibited dramatic increases in M(+)/UV sensitivity of 60- and 250-fold, respectively (Table 5 and Supplementary Figure S13).

Sporulation Deficiency

When assessing sporulation deficiency through mutagenesis in survivors of spores of various strains after M(+/-)UV exposure,

TABLE 5 | Spore surviving fraction and increased sensitivity of mutant spores lacking DNA-repair proteins exposed to M(+UV) and M(-UV).

DNA repair	Survival fraction		Increased sensitivity compared to wild-type spores		Increased sensitivity compared to <i>spB</i> spores	
	M(+UV)	M(-)UV	M(+UV)	M(-)UV	M(+UV)	M(-)UV
<i>Wild-type (wt, 168)</i>	$(3.6 \pm 0.7) \times 10^{-2}$	$(7.1 \pm 0.9) \times 10^{-1}$	1.0 ± 0.2	1.0 ± 0.1	n.a.	n.a.
<i>disA</i>	$(1.8 \pm 0.3) \times 10^{-2+}$ [+0.0164]	$(5.3 \pm 0.6) \times 10^{-1}$ [0.0943]	$2.0 \pm 0.3^+$ [+0.0439]	1.3 ± 0.2 [0.6844]	n.a.	n.a.
<i>recA</i>	$(4.1 \pm 1.0) \times 10^{-4+}$ [+0.0009]	$(9.6 \pm 2.0) \times 10^{-3+}$ [+0.0017]	$87 \pm 20^+$ [+0.0037]	$74 \pm 14^+$ [+0.0009]	n.a.	n.a.
<i>ligD ku</i>	$(1.0 \pm 0.1) \times 10^{-3+}$ [+0.0025]	$(2.4 \pm 0.5) \times 10^{-2+}$ [+0.0093]	$35 \pm 3.7^+$ [+0.0049]	$29 \pm 6.3^+$ [+0.0024]	n.a.	n.a.
<i>sbcDC</i>	$(8.4 \pm 1.0) \times 10^{-3+}$ [+0.0103]	$(1.7 \pm 0.2) \times 10^{-1+}$ [+0.0158]	$4.2 \pm 0.6^+$ [+0.0108]	$4.3 \pm 0.6^+$ [+0.0153]	n.a.	n.a.
<i>exoA nfo</i>	$(1.8 \pm 0.3) \times 10^{-3+}$ [+0.0063]	$(4.7 \pm 0.7) \times 10^{-2+}$ [+0.0065]	$20 \pm 2.8^+$ [+0.0071]	$15 \pm 2.3^+$ [+0.0085]	n.a.	n.a.
<i>mutSL</i>	$(1.5 \pm 0.3) \times 10^{-2+}$ [+0.0132]	$(1.5 \pm 0.3) \times 10^{-1+}$ [+0.0127]	$2.4 \pm 0.5^+$ [+0.0264]	$4.6 \pm 0.9^+$ [+0.0188]	n.a.	n.a.
<i>polY1 polY2</i>	$(1.7 \pm 0.3) \times 10^{-2+}$ [+0.0139]	$(2.9 \pm 0.4) \times 10^{-1+}$ [+0.0338]	$2.2 \pm 0.5^+$ [+0.0289]	$2.4 \pm 0.3^+$ [+0.0225]	n.a.	n.a.
<i>mfd</i>	$(4.3 \pm 0.7) \times 10^{-3+}$ [+0.0061]	$(1.2 \pm 0.1) \times 10^{-1+}$ [+0.0055]	$8.3 \pm 1.4^+$ [+0.0042]	$5.8 \pm 0.6^+$ [+0.0102]	n.a.	n.a.
<i>uvrAB</i>	$(1.1 \pm 0.2) \times 10^{-3+}$ [+0.0025]	$(9.3 \pm 2.0) \times 10^{-2+}$ [+0.0041]	$33 \pm 5.2^+$ [+0.0018]	$7.6 \pm 1.5^+$ [+0.0084]	n.a.	n.a.
<i>ywjD</i>	$(1.8 \pm 0.3) \times 10^{-2+}$ [+0.0325]	$(8.3 \pm 1.0) \times 10^{-1}$ [0.2978]	$2.0 \pm 0.4^+$ [+0.0323]	0.9 ± 0.1 [0.8744]	n.a.	n.a.
<i>spB</i>	$(1.2 \pm 0.2) \times 10^{-4+}$ [+0.0006]	$(4.1 \pm 0.5) \times 10^{-1}$ [0.0538]	$304 \pm 51^+$ [+0.0004]	$1.7 \pm 0.2^+$ [+0.0308]	1.0 ± 0.2	1.0 ± 0.2
<i>disA spB</i>	$(1.4 \pm 0.3) \times 10^{4+}$ [+0.0005; 0.3901]	$(1.6 \pm 0.3) \times 10^{-1+}$ [+0.0147; #0.0371]	$264 \pm 56^+$ [+0.0009]	$4.5 \pm 1.0^+$ [+0.0069]	0.9 ± 0.2 [0.8551]	$2.6 \pm 0.6^{\#}$ [#0.0319]
<i>recA spB</i>	$(1.2 \pm 0.2) \times 10^{5+}$ [+0.0001; #0.0044]	$(2.7 \pm 0.4) \times 10^{-3+}$ [+0.0009; #0.0021]	$3089 \pm 501^+$ [+0.0001]	$266 \pm 41^+$ [+0.0007]	$10 \pm 1.6^{\#}$ [#0.0157]	$154 \pm 24^{\#}$ [#0.0007]
<i>ligD ku spB</i>	$(4.9 \pm 0.7) \times 10^{6+}$ [+0.0001; #0.0006]	$(1.9 \pm 0.2) \times 10^{-2+}$ [+0.0076; #0.0268]	$7285 \pm 1110^+$ [+0.0001]	$38 \pm 4.9^+$ [+0.0024]	$24 \pm 3.6^{\#}$ [#0.0046]	$22 \pm 2.9^{\#}$ [#0.0053]
<i>sbcDC spB</i>	$(2.3 \pm 0.3) \times 10^{5+}$ [+0.0001; #0.0065]	$(1.7 \pm 0.3) \times 10^{-1+}$ [+0.0139; #0.0427]	$1568 \pm 192^+$ [+0.0001]	$4.1 \pm 0.7^+$ [+0.0127]	$5.2 \pm 0.6^{\#}$ [#0.0226]	$2.4 \pm 0.4^{\#}$ [#0.0352]
<i>exoA nfo spB</i>	$(1.9 \pm 0.4) \times 10^{5+}$ [+0.0001; #0.0038]	$(2.9 \pm 0.4) \times 10^{-2+}$ [+0.0085; #0.0326]	$1895 \pm 399^+$ [+0.0001]	$25 \pm 3.4^+$ [+0.0055]	$6.2 \pm 1.3^{\#}$ [#0.0185]	$14 \pm 1.9^{\#}$ [#0.0078]
<i>mutSL spB</i>	$(1.1 \pm 0.2) \times 10^{4+}$ [+0.0001; 0.5734]	$(3.9 \pm 0.6) \times 10^{-2+}$ [+0.0092; #0.0378]	$316 \pm 60^+$ [+0.0005]	$18 \pm 2.9^+$ [+0.0087]	1.0 ± 0.2 [0.9258]	$10 \pm 1.7^{\#}$ [#0.0105]
<i>polY1 polY2 spB</i>	$(6.3 \pm 1.0) \times 10^{5+}$ [+0.0001; #0.0125]	$(2.6 \pm 0.5) \times 10^{-1+}$ [+0.0341; 0.0537]	$568 \pm 86.5^+$ [+0.0003]	$2.7 \pm 0.5^+$ [+0.0265]	$1.9 \pm 0.3^{\#}$ [#0.0435]	1.6 ± 0.3 [0.2495]
<i>mfd spB</i>	$(1.8 \pm 0.4) \times 10^{6+}$ [+0.0001; #0.0005]	$(6.2 \pm 1.0) \times 10^{-2+}$ [+0.0032; #0.0043]	$20092 \pm 4969^+$ [+0.0001]	$11 \pm 2.3^+$ [+0.0105]	$66 \pm 16^{\#}$ [#0.0012]	$6.6 \pm 1.3^{\#}$ [#0.0194]
<i>uvrAB spB</i>	$(4.6 \pm 0.7) \times 10^{7+}$ [+0.0001; #0.0001]	$(5.0 \pm 0.7) \times 10^{-2+}$ [+0.0065; #0.0025]	$77260 \pm 12195^+$ [+0.0001]	$14 \pm 1.9^+$ [+0.0096]	$254 \pm 40^{\#}$ [#0.0007]	$8.3 \pm 1.1^{\#}$ [#0.0183]
<i>ywjD spB</i>	$(1.8 \pm 0.3) \times 10^{5+}$ [+0.0001; #0.0036]	$(7.3 \pm 0.1) \times 10^{-1}$ [0.7152; #0.1986]	$1958 \pm 357^+$ [+0.0001]	1.0 ± 0.2 [0.8749]	$6.4 \pm 1.2^{\#}$ [#0.0175]	0.7 ± 0.2 [0.7541]

n.a., not applicable. + Statistically significant difference from values for wild-type spores ($P \leq 0.05$); individual P -values are given in brackets below the initial values. # Statistically significant difference between values for these mutant spores compared to values for *spB* spores ($P \leq 0.05$); individual P -values are given in brackets below the initial values. The surviving fraction was determined after 24 h exposure to M(+/-)UV relative to that of control spores of each genotype, which were stored in air at room temperature ($20 \pm 2^\circ\text{C}$), at relative humidity of $40 \pm 5\%$ and protected from UV radiation. Increased sensitivity was determined relative to the respective wild-type or *spB* spores as the ratio of the surviving fraction of wild-type or *spB* spores over the surviving fraction of the various mutant spore. Three biological replicates were analyzed for each condition.

~3% of survivors of wild-type spores exposed to M(-)UV had accumulated Sp^- mutants. Under Mars(+UV) conditions, spore components exhibited importance in mutagenesis, in order from highest to lowest frequency: major SASPs > intact spore coats > DPA > reduced spore core water. Sp^- ratio (calculated as in sections “Detection of Sporulation Deficiency”

and “Numerical and Statistical Analysis”) was similar to that for *disA*, *ywjD*, and *spB* spores exposed to M(-)UV. Survivors of all other DNA repair mutant strains exposed to M(-)UV exhibited increased mutagenesis, from ~20% in *ligD ku* spores to ~30% in *exoA nfo* and *mutSL* spores. As expected, levels of Sp^- mutants were increased with M(+UV) exposure of spores

crust mutants were recently suggested to yield different phenotypes with respect to the double crust mutant spores (tested in this study) (McKenney and Eichenberger, 2012; Krajcikova et al., 2017).

Spore Decreased Core Water Content Is Key for Survival

During spore formation, spore core dehydration and mineralization is established, in part, as DPA is taken up into the forespore and chelates Ca^{2+} ions (Ca-DPA), displacing core water (reviewed in Setlow, 2014). The compression of the forespore that takes place later in sporulation also displaces significant amounts of core water, further reducing core water content (Magge et al., 2008). How the latter takes place is not known, but likely involves the spore cortex peptidoglycan in some fashion (Zhang et al., 2012). In the current study, two different core water deficiencies were tested: (1) *dacB* spores, which have an altered cortex and thus present elevated core water levels and (2) *sleB spoVF* spores, which lack Ca-DPA due to the *spoVF* mutation, are stabilized against spontaneous spore germination by the *sleB* mutation, and have elevated core water because Ca-DPA has been replaced by water (Paidhungat et al., 2001). Results demonstrated *dacB* spores to be significantly more sensitive in both M(+/-)UV, when compared with the wild-type spores. This increased sensitivity was perhaps due to greater molecular damage (at least some to DNA) induced by oxidative stress when in the high vacuum/desiccation of the Martian environment. Calcium-DPA-deficient *sleB spoVF* spores were shown to be more sensitive to M(+/-)UV than Ca-DPA-replete spores, in particular to exposed to M(+)UV, as shown previously (Setlow et al., 2006; Magge et al., 2008). This happens because *sleB spoVF* sporulating cells are unable to synthesize DPA, but exogenously added DPA can enter the spore, reaching near wild-type levels. Although, whether the latter effects are due only to the spore elevated core water content, or to some direct protective effect of Ca-DPA is not clear.

SspE May Provide Some Protection When SspA and SspB Are Missing

Protection of the DNA in the spore core is also dependent on the high levels of α/β -type small, acid-soluble spore proteins (SASP) (Magge et al., 2008). These act by saturating spore DNA, and are extremely important when exposed to desiccation and UV radiation (Mason and Setlow, 1986; Moeller et al., 2008). As expected, spores lacking SASP- α and - β (*sspA sspB* spores), and thus lacking ~80% of the α/β -type SASP pool (Hathout et al., 2003), had increased sensitivity to both M(+/-)UV (when compared with the wild-type), being significantly more sensitive to UV-irradiated, rather than to non-irradiated Martian environments. In contrast, *sspE* mutants lacking the most prominent SASP, SspE, which binds poorly to DNA in wild-type spores, had no significant effect on spore survival in both M(+/-)UV. However, SspE may provide some protection when SspA and SspB are missing, as suggested by the increased sensitivity in *sspE sspA sspB* spores, when compared with *sspA sspB* mutants. Removing α/β -type SASP in spore coat- or

cortex-defective spores (*cotE sspA sspB*; *dacB sspA sspB* and *sleB spoVF sspA sspB* spores) increased spore sensitivity to M(+/-)UV, confirming DNA-binding α/β -type SASP as a key factor in *B. subtilis* spore resistance to M(+/-)UV, presumably by the α/β -type SASP binding to spore DNA and converting the spore chromosome into a monogenomic toroidal shaped A-DNA structure (Setlow and Li, 2015).

Double Strand Breaks and Base Modifications in M(-)UV

The UV-exposed Martian surface conditions have direct and indirect effects on cells, either through the direct transfer of radiation energy, and consequent damage of biomolecules or through generation of reactive nitrogen species (RNS), or reactive oxygen species (ROS) that then induce biomolecular damage (Lenhart et al., 2012). Ultraviolet-induced damage is typically seen as DNA SSB or DSB, as well as photolesions such as CPDs, 6-4 PPs or SP (Setlow and Li, 2015). Spores lacking HR (*recA*), NHEJ (*lig ku*), or BER (*exoA nfo*) were significantly more sensitive to M(-)UV than wild-type spores (Table 5), indicating that DSB and base modifications comprise a substantial fraction of the DNA damage suffered, likely due to the extreme desiccation in M(-)UV (Rebeil et al., 1998; Setlow and Li, 2015; Nicholson et al., 2018).

Spore Photoproduct as Major Damage in M(+)UV

The formation of SP as a major product of UV-damage with M(+)UV exposure was expected, and has been shown previously (Xue and Nicholson, 1996). Accumulated SPs have been shown to be repaired by SP lyase (SPL), and also by the NER pathway – mechanisms that are crucial in spore UV resistance (Setlow and Li, 2015). The current study is the first to analyze the relative sensitivities of various SP repair mutant strains of *B. subtilis* spores to the Martian environment, including results with spores lacking other DNA repair mechanisms. Notably, in M(-)UV accumulated SP in spores exposed to M(+)UV were shown to be repaired by both SplB and the NER pathway, mechanisms that are crucial in spore resistance to natural UV environments (Xue and Nicholson, 1996; Setlow and Li, 2015).

YwdJ and Mfd Might Participate in SP Repair

In the current study, *ywjD* spores lacking the UV-damage endonuclease YwdJ, showed no increased sensitivity to M(+/-)UV. Yet, *ywjD splB* spores were more sensitive to M(+)UV than *splB* single mutant spores. This suggests that YwdJ might participate in SP repair, functioning as an alternative DNA repair enzyme, and is in line with previous studies (Ramirez-Guadiana et al., 2012). While *ywjD* spores showed no increased sensitivity to M(+/-)UV, spores were more sensitive to M(+)UV than *splB* spores, suggesting that YwdJ can also

participate in SP repair. Moreover, *mfd splB* spores, lacking both SP lyase and the spores also much to M(+)/UV *splB* spores indicating that transcription, had also increased sensitivity to M(+)/UV, when compared with *splB* single mutant spores. Thus, transcription-coupled repair might be involved in SP repair. This is likely due to the role Mfd plays in NER (Gomez-Marroquin et al., 2016). The lack of the DNA exonuclease SbcDC involved in inter-strand cross-link repair (ISCLR) (Mascarenhas et al., 2006; Lenhart et al., 2012) also demonstrated increased sensitivity in M(+)/UV (*sbcDC splB* spores), when compared with *splB* single mutant spores. This was not observed, however, in *polY1 polY2* spores, lacking both DNA polymerases PolY1 and PolY2, which mediate DNA repair by translesion synthesis.

Sporulation Deficiency

Strains lacking *mutSL* or *exoA nfo* shown an increased Spo⁻ rate after exposure to M(+/-)UV, suggesting their critical involvement of MMR and BER in DNA repair in order to ensure sporulation. An increased loss of viability during sporulation of strains lacking the ability to repair DNA damage by MMR had already been suggested (Modrich, 1996; Salas-Pacheco et al., 2005; Ibarra et al., 2008; Fukui, 2010), indicating *mutSL* contribution to genome stability and overall spore resistance. In turn, *exoA nfo* genes are known to encode for apurinic/apyrimidinic endonucleases involved in the repair of oxidative DNA damage through BER (Ibarra et al., 2008; Moeller et al., 2011; Campos et al., 2014). This means that spores exposed to M(+/-)UV, ensure sporulation through efficient MMR by *mutSL*, and repair oxidative damage by BER (*exoA nfo*). Especially, the absence of the proteins LigD, Ku, ExoA, Nfo, SbcDC, and MutSL showed significant increased mutation frequencies of Spo⁻, indicating their crucial role in DNA repair, genome stability and restoration. In the current study, however, the interaction between Nfo and ExoA and the DNA integrity scanning protein DisA (Campos et al., 2014) was not assessed, and would be advised for future studies on the process of oxidative DNA damage repair after exposure to simulated Martian conditions (Campos et al., 2014). This sporulation deficiency analysis is informative on the types of error-free or error-prone mechanisms leading to spore survival. For instance, **Figure 2** shows that RecA-mediated homologous recombination (HR) and wild type have similar proportions of Spo⁻ mutants, indicating that spore survival in a *recA*-mutant is error-free. Considering that other repair mechanisms such as SP, NER, NHEJ and MMR are still at least partially functional in a *recA*-deficient background, this is the best argument presented in the paper to say that UV-induced photolesions such as DNA strand breaks, dimers or AP sites are the major lesion caused by Martian exposure.

CONCLUSION

When considering a Mars exploration scenario one can expect spore killing by the Martian environment to be mostly UV-driven, as the other environmental conditions (atmospheric composition, low pressure and low temperature) were shown

to have only minimal effects on wild-type spore viability. Most importantly, the current study demonstrates that wild-type *B. subtilis* spores could survive in a Mars surface environment, if somehow shielded from UV (e.g., by dust, rocks, or spacecraft surface irregularities) It should be noted, however, that this study determined survivability by the ability to form colony forming units, and any defects in growth after exposure were not analyzed. Besides, increased spore sensitivity has been reported when in contact with Mars analog soils (Schuerger et al., 2003; Moeller et al., 2010); and vegetative cells of *B. subtilis* were found to be more sensitive the presence of perchlorates (found in Mars subglacial brines) irradiated with a Martian UV-flux (Wadsworth and Cockell, 2017). Thus, future efforts should focus on assessing spore survival and viability in real long-duration Mars mission scenarios. This can be done by: (1) directly determining DNA damage in wild-type spores exposed to M(+/-)UV, (2) address whether exposed mutants have growth defects, after germination, (3) taking into consideration the shielding of spores via Mars regolith and other relevant materials, and (4) assess the effect of Mars surface photochemistry on spore sensitivity.

AUTHOR CONTRIBUTIONS

The study was conceived by RM. Experiments were conducted by MC, FF, FC, RM, and PE. The simulation experiments in the described Mars chamber were conducted by AS. The manuscript was written by MC with input from RM, FF, FC, WN, AS, PE, and PS.

FUNDING

MC, FF, and RM were supported by the DLR grant FuE-Projekt ISS LIFE, Programm RF-FuW, Teilprogramm 475. MC was supported by the DLR/DAAD Research Fellowship – Doctoral Studies in Germany, 2017 (57370122). FC was supported by the DFG grant Co 1139/1-2. RM was supported by a DLR grant “Forschungssemester.” FF was supported by the Helmholtz Space Life Sciences Research School SpaceLife Ph.D. fellowship. AS and WN were supported by NASA Planetary Protection Office grants (AS: NNX12AJ84G and NNA05CS68G, and WN: NNA05CS68G).

ACKNOWLEDGMENTS

We acknowledge Andrea Schröder, Marina Raguse, and Katja Nagler for their assistance. We thank Mario Pedraza-Reyes and Jörg Stülke for cordially providing several *B. subtilis* strains.

SUPPLEMENTARY MATERIAL

The Supplementary Material for this article can be found online at: <https://www.frontiersin.org/articles/10.3389/fmicb.2019.00333/full#supplementary-material>

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Conflict of Interest Statement: The authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

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