UV-inducible cellular aggregation of the hyperthermophilic archaeon *Sulfolobus solfataricus* is mediated by pili formation

Sabrina Fröls,1,2 Malgorzata Ajon,3 Michaela Wagner,3 Daniela Teichmann,1 Behnam Zolghadr,2 Mihaela Folea,4 Egbert J. Boekema,4 Arnold J. M. Driessen,3 Christa Schleper1,2* and Sonja-Verena Albers3

1Department of Genetics in Ecology, Vienna Ecology Center, University of Vienna, Althanstrasse 14, 1090 Vienna, Austria.
2Center for Geobiology, Department of Biology, University of Bergen, Realfagbygget, Allegaten 41, N-5007 Bergen.
3Department of Microbiology, Groningen Biomolecular Sciences and Biotechnology Institute and the Zernike Institute for Advanced Materials, University of Groningen, Kerklaan 30, 9751 NN Haren, the Netherlands.
4Department of Biophysical Chemistry, Groningen Biomolecular Sciences and Biotechnology Institute, University of Groningen, Nijenborgh 4, 9747 AG Groningen, the Netherlands.

Summary

The hyperthermophilic archaeon *Sulfolobus solfataricus* has been shown to exhibit a complex transcriptional response to UV irradiation involving 55 genes. Among the strongest UV-induced genes was a putative pili biogenesis operon encoding a potential secretion ATPase, two pre-pilins, a putative transmembrane protein and a protein of unknown function. Electron microscopy and image reconstruction of UV-treated cells showed straight pili with 10 nm in diameter, variable in length, not bundled or polarized and composed of three evenly spaced helices, thereby clearly being distinguishable from archaeal flagella. A deletion mutant of SSO0120, the central type II/IV secretion ATPase, did not produce pili. It could be complemented by reintroducing the gene on a plasmid vector. We have named the operon *ups* operon for UV-inducible pil operon of *Sulfolobus*. Overexpression of the pre-pilins, Ups-A/B (SSO0117/0118) in *Sulfolobus* resulted in production of extremely long filaments. Pronounced cellular aggregation was observed and quantified upon UV treatment. This aggregation was a UV-dose-dependent, dynamic process, not inducible by other physical stressors (such as pH or temperature shift) but stimulated by chemically induced double-strand breaks in DNA. We hypothesize that pili formation and subsequent cellular aggregation enhance DNA transfer among *Sulfolobus* cells to provide increased repair of damaged DNA via homologous recombination.

Introduction

The ability of *Bacteria* and *Archaea* to form multicellular structures is observed in a variety of biological systems. This fascinating phenomenon of a collective behaviour can be manifested in the formation of biofilms from mixed microbial mats, cellular aggregates or microcolonies. Multicellular structures represent an essential strategy for adaptation to changing environmental conditions or even survival (Shapiro, 1998; Davey and O’Toole, 2000; Battin et al., 2007). Cells organized in biofilm-like structures show a higher resistance to toxic compounds, as for example antimicrobials (Patel, 2005) or to physical stress, like shifts in temperature or pH, or exposure to UV light (Ojanen-Reuhs et al., 1997; Roine et al., 1998; Elasri and Miller, 1999; Martinez and Casadevall, 2007). In addition, microorganisms benefit from the attachment on substrates like, e.g. suspended particles, which provides a higher nutrient availability (Davey and O’Toole, 2000). Also genetic transfer, i.e. DNA exchange via conjugation, plays an important role in biofilms to disseminate specific genes of metabolic pathways (Gasson and Davies, 1980; Molin and Tolker-Nielsen, 2003). The rate of conjugal DNA exchange in biofilm structures is enhanced and conjugative pili stabilize the biofilm structure (Gasson and Davies, 1980; Ghigo, 2001; Molin and Tolker-Nielsen, 2003; Reisner et al., 2006).

Cellular aggregation is mainly reported for organisms of the domain *Bacteria*, while comparably few but quite...
diverse examples have been found in the domain of the *Archaea*. In anoxic sediments of the ocean anaerobic methane-oxidizing archaea form synergistic communities with sulphate-reducing bacteria in the form of structured consortia (Boetius *et al.*, 2000). An unusual microbial community organized in string-of-pearls was found in cold sulphurous water. It is formed by the euryarchaeon SM1 that grows in close association with the bacterium *Thiotrix* sp. and forms complex and unusual cellular appendages (Moissl *et al.*, 2003; 2005). Single-strain cultures of the hyperthermophilic euryarchaeote *Archaeoglobus fulgidus* form a protein- metal- and polysaccharide-containing heterogeneous biofilm, which is inducible by various environmental stressors (LaPaglia and Hartzell, 1997). *Pyrococcus furiosus* can form surface attached microcolony structures mediated by multifunctional flagella, which can also form cable-like structures to mediate cell–cell contacts (Näther *et al.*, 2006; Schopf *et al.*, 2008).

Beside adherent multicellular structures that are found attached to diverse surfaces, non-adherent floating multicellular structures are also described for archaea. *Methanosarcina mazei*, for example, forms aggregates during exponential growth (Mayerhofer *et al.*, 1992) and halophilic archaea do so in the presence of divalent cations (Kawakami *et al.*, 2005; 2007). For the halophilic euryarchaeote *Halobacterium volcanii* and the hyperthermophilic crenarchaeote *Sulfolobus* sp. cellular aggregation was observed in context with conjugal DNA transfer (Rosenshine *et al.*, 1989; Schleper *et al.*, 1995).

Characteristic for all types of cellular aggregation is the attachment between single cells, mostly mediated or stabilized by exopolysaccharides (EPS) and/or proteins as was shown for many bacterial systems (Davey and O’Toole, 2000; Klemm *et al.*, 2004; Kawakami *et al.*, 2007). Some microorganisms like *Xanthomonas* and *Pseudomonas* use type IV pili to initiate or mediate the cellular aggregation (Ojanen-Reuhs *et al.*, 1997; Bhattacharjee *et al.*, 2001). A *Pseudomonas aeruginosa* mutant defective in the type IV pilus biogenesis was unable to attach on surfaces and form microcolonies (O’Toole and Kolter, 1998; O’Toole *et al.*, 2000).

The type IV pilus biogenesis pathways of bacteria are not only closely related to the type II protein secretion systems (Sauvonnet *et al.*, 2000; Köhler *et al.*, 2004), but also to the archaeal flagella systems. This was shown by bioinformatic and biochemical analyses (Faguy *et al.*, 1994; Bardy and Jarrell, 2002; Peabody *et al.*, 2003). In addition, it has been shown that the flagella of *Halobacterium salinarum* and *Sulfolobus shibatae* are in symmetry and structure more closely related to the bacterial type IV pili than to bacterial flagella (Cohen-Krausz and Trahtenberg, 2002; 2008). The core components of the bacterial and archaean systems are: (i) a type II/IV secretion system ATPase, (ii) a multistacking transmembrane protein, and (iii) the pre-pilin-like proteins with a characteristic N-terminal signal sequence (termed class III signal peptides) that form the structure of the pilus (Peabody *et al.*, 2003). In the genome of the crenarchaeote *Sulfolobus solfataricus* three putative type IV pili loci were identified (Albers and Driessen, 2005). The operon SSO2316 (named after the central ATPase) codes for the flagellum of *S. solfataricus* (Szabó *et al.*, 2007a). The operon SSO2680 encodes a recently described bindosome assembly system (Bas) needed for the functional surface localization of sugar-binding proteins (Zolghadr *et al.*, 2007). The biological function of the third operon SSO0120, spanning ORFs sso0117 through sso0121, was unclear. Using whole-genome microarray studies to analyse the UV response of *S. solfataricus* we observed that the genes sso0117 to sso0121 were among the most highly induced genes using a UV dose of 75 J m⁻² at 254 nm (Fröls *et al.*, 2007). A strong upregulation of the operon was also observed by an independent study of White and co-workers using a higher UV dose of 200 J m⁻², with *S. solfataricus* and *S. acidocaldarius* (Dorazi *et al.*, 2007; Götz *et al.*, 2007). In parallel to the strong transcriptional UV response we observed a massive aggregation of the cells, which disappeared after regeneration (Fröls *et al.*, 2007).

In this study we demonstrate that extracellular pili-like structures, thinner than flagella, are formed upon UV light treatment. They are encoded by the UV-inducible (type IV-like) pil operon, as shown by targeted gene knockouts. Furthermore, we show that these pili structures are essential for the UV-dependent auto-aggregation of *S. solfataricus* cells and that this phenomenon is driven by double-strand breaks (DSB) in the DNA, but not by other stressors, such as pH or temperature shifts.

**Results**

**UV-inducible expression of the sso0117–sso0121 gene cluster**

The induction of the genes *sso0118* and *sso0117* occurred as one of the strongest and fastest transcriptional reactions detected in an earlier genome-wide microarray study on the impact of UV light exposure of *S. solfataricus* cells (Fröls *et al.*, 2007). These genes belonged to a cluster, and possibly an operon of five genes (*sso0117* through *sso0121*) all of which were strongly induced with a maximal induction of 14-fold for *sso0118* (Fröls *et al.*, 2007). The transcriptional increases were observed at 1.5–5 h after UV treatment. Over the time-course of 8.5 h, a similar transcriptional reaction pattern for these genes was observed, but not for the upstream or downstream flanking genes (*sso0116* and...
The putative pili operon was well conserved in the order *Sulfolobales*, with the same gene arrangement in the strains *Sulfolobus tokodaii* and *S. acidocaldarius* (Table S2 and Szabó et al., 2007b). Further similarities were only found to genes of the hyperthermophilic crenarchaeon *Metallosphera sedula*, belonging to a closely related order. In *M. sedula*, homologues of *sso0120, sso0119* and *sso0117* form an operon structure whereas *sso0118* is located in a different genomic region.

**Maturation of pre-pilins**

Both *sso0117* and *sso0118* encode predicted proteins of 15 and 16 kDa, respectively. They contain a signal sequence with the predicted cleavage site for the type IV pre-pilin peptidase PibD (Albers et al., 2003; Szabó et al., 2007b). In *sso0117* and *sso0118* only 6 and 16 amino acids would be cleaved by PibD respectively (Fig. 1B). The ORFs of *sso0117* and *sso0118* were cloned into an *Escherichia coli* expression vector already containing PibD (Szabó et al., 2007b). Using the *in vivo* assay the expression of the pre-pilin proteins was induced for 2 h before the expression of the peptidase was induced. Western blot analysis of crude membrane extracts of the recombinant *E. coli* cells showed that *sso0118* was processed by PibD resulting in a faster running protein species when compared with the full-length protein (Fig. 1C, lanes 2 and 3). Cleavage of *sso0118* was already observed before induction of the expression of PibD, most likely because the promoter used for the expression is leaky and the enzyme cleaves the substrate very efficiently. Cleavage of the signal peptide of *sso0117* could not be observed, most probably because the difference between the precursor and the processed form do not differ enough to be separated on SDS-PAGE. Experiments to separate these two forms in isoelectric focusing gel electrophoresis failed.

**UV-induced pili formation**

To identify pili, cells were analysed by electron microscopy after UV treatment. To exclude that any extracellular structures were not artefacts of flagella we used the *S. solfataricus* knockout strain *ΔflaJ* that does not produce flagella (Szabó et al., 2007a). Only on the surface of the UV-treated cells, pili-like structures were observed (Fig. 2A). These pili structures were spread over the whole surface and were not polarized at one cell side. Most of the cells of a UV-treated culture contained many pili, some had less or very few (only two to three pili), and few cells did not express pili on their surfaces at all. A time-course experiment showed that the first pili-like structures were observed at 1 h after UV treatment.
In comparison with the flexible flagella, the pili showed a more straight and rigid structure. Pili of up to 16 μm in length or even longer were observed. However, such long filaments where only found detached from the cells, which indicated that they are more fragile than flagella. Because the pili appeared straight for most of their length, it was possible to process them by single-particle analysis selecting straight segments of almost up to 100 nm. About 700 segments were extracted from long pili, aligned and averaged. The final average projection map is shown in Fig. 2B. The structure appeared to consist of three evenly spaced helices. The pitch (repeating unit) of the pili was 15.5 nm and the maximal diameter was about 10 nm. In the negatively stained samples the single helices appeared almost uniformly stained without any clear density differences that could give clues about the handedness (left- or right-handed) of the helices.

**Cellular aggregation after UV treatment**

The appearance of pili upon UV treatment that could mediate cell-to-cell contacts inspired us to analyse microscopically the formation of cell aggregates (Fröls et al., 2007). We have shown earlier that aggregation occurs with high frequency independent of the *S. solfataricus* genotypes, because experiments with four different strains [P1, PH1, PH1-M16, PH1(SSV1)] showed the same phenotypic reaction. With increasing time after UV treatment, an increasing number of cells were found in aggregates with the highest amount of aggregation found at 6–8 h after UV treatment (Fröls et al., 2007 and Fig. 6).

The aggregates increased also in size. While three to five cells were found in the early aggregates, bigger complexes formed at later time points. The shape of the early aggregates seemed to be random, as variations of pyramids, circle shapes, straight and branching chains were observed (not shown). In the later stages (6 h) the cells accumulated to big clusters of >100 cells. As it was impossible to count the number of cells in such aggregates, our quantitative data (% cells in aggregates of total cell count) generally represent an underestimate.

Attempts to destroy the cell–cell connections by shear force experiments resulted in cell lysis at all stages but not in disaggregation, indicating a high stability of the aggregates. The induction of cellular aggregation was UV-dose-dependent (see Fig. 3). We treated the cells with seven different UV doses ranging from 5 to 1000 J m$^{-2}$. Growth retardation of the respective cultures was directly proportional to the applied UV dose (data not shown). The highest cellular aggregation was observed 6 h after UV treatment, i.e. at the expected maximum. The highest amount of cellular aggregation was found with 75 J m$^{-2}$ (up to 50% and sometimes even 70% of cells in aggregates, Fig. 3A and Fröls et al., 2007) and with 50 J m$^{-2}$ (at least 40% of the cells were in aggregates of ≥3 cells, Fig. 3A). Even the lowest dose of UV light of 5 J m$^{-2}$ induced the cellular aggregation, whereas the high UV doses of 200 and 1000 J m$^{-2}$ showed a very low and no significant aggregation reaction respectively. We also observed a strong correlation between the size and amount of cellular aggregates (Fig. 3B). Low doses of 5 and 10 J m$^{-2}$ resulted in cellular aggregates of <7 cells.
Only upon a UV dose of 50–75 J m^{-2}, large aggregates of 10–20 cells or many more were generated frequently. Because cells in these biggest aggregates could not be counted, our numbers in Fig. 3A represent an underestimate for 50 and 75 J m^{-2}. In the case of the high UV doses of 200 and 1000 J m^{-2} no aggregates > 4 cells were observed.

By using different vital staining techniques (see Experimental procedures), we investigated whether dead cells accumulate in aggregates (see Table 1). In the case of the lowest UV dose of 5 J m^{-2} only 8% of the total cells in aggregates (≥3 cells) were dead. The amount of dead cells increased proportionally with the UV dose but was far lower than the number of living cells. The majority of the cells (64%) present in the infrequent aggregates at 200 J m^{-2} were not alive. At lower UV dose, like 75 J m^{-2}, even large aggregates of >20 cells were almost uniformly composed of living cells (Fig. 3C).

Fig. 3. Aggregation of S. solfataricus cells after treatment with different UV doses.
A. Quantitative analysis of cellular aggregation at 6 h after UV treatment. Exponential cultures were treated with 0, 5, 10, 25, 50, 75, 200 and 1000 J m^{-2}. The percentage amount of cells in aggregates (≥3 cells) is given in relation to the total cells. For each UV dose the amount of cells in and outside aggregates were counted until 500 single cells were found. The bars display the mean of three independent experiments, except for 5 and 10 J m^{-2} (see asterisk), where only one experiment was performed.
B. Light micrograph of S. solfataricus cell aggregates at 6 h after UV treatment with different UV doses. The size of the aggregates increased with the UV dose; the biggest aggregates were found after treatment with 50 and 75 J m^{-2}.
C. Fluorescence micrograph of a S. solfataricus cell aggregate at 6 h after UV treatment at 75 J m^{-2}. Cells were stained with the LIVE DEAD Baclight (Invitrogen) assay. Living cells are labelled in green and dead cells in red. Big aggregates of >20 cells were mostly found at 3 h after treatment. For quantitative analysis of the cell vitality at different UV doses see Table 1.
Gene knockout in the UV-inducible pili operon abolishes pili formation and cellular aggregation

To prove that pili were indeed assembled from components expressed from the putative pili operon, a deletion mutant was constructed in which the ATPase (sso0120) was replaced by insertion of a lacS cassette containing the lacS gene with its natural promoter and terminator region via a double cross-over. The successful deletion of the sso0120 gene was confirmed by Southern analysis and RT-PCR (see Fig. 4A and B). The RT-PCR showed that under inducing conditions the sso0120 mRNA was absent, while the downstream genes of the operon were still expressed, probably because of readthrough of the lacS terminator by the RNA polymerase. After UV treatment of the mutant Δsso0120 we could not observe any pili-like structures on the cellular surfaces by electron microscopy (Fig. 4C, Ia and Ib). As control, we used the parent strain PBL2025 (Scheelert et al., 2004) which clearly showed pili-like structures beside the flagella upon exposure to UV light (Fig. 4C, IIa and IIb). When the mutant strain Δsso0120 was complemented with pSVA99 containing sso0120 under the control of the araS promoter, pili were again observed after UV treatment, but only when the cells were additionally incubated with arabinose (Fig. 5A). Overexpression of both pilin genes, sso0117 and sso0118, in the ΔflaJ strain using the virus-based vector construct pSVA96 resulted in the assembly of fewer, but extremely long and irregular pili (Fig. 5B). The overexpression of the whole operon, sso0121-0117, using pSVA125 led to the formation of pili around the whole cell surface (Fig. 5C), whereas the expression of a cytoplasmic control protein from pSVA31 did not result in the assembly of surface structures (data not shown). Together these data demonstrate that formation of the pili is dependent on expression of sso0120 and that the two pre-pilins (or one of them) most likely form the subunits of the UV-inducible pili.

Table 1. Cell vitality of *S. solfataricus* cells in aggregates formed after treatment with UV light.

<table>
<thead>
<tr>
<th>UV dose (J m⁻²)</th>
<th>Vital cells % a</th>
</tr>
</thead>
<tbody>
<tr>
<td>5</td>
<td>92</td>
</tr>
<tr>
<td>10</td>
<td>88</td>
</tr>
<tr>
<td>25</td>
<td>83</td>
</tr>
<tr>
<td>50</td>
<td>66</td>
</tr>
<tr>
<td>75</td>
<td>56</td>
</tr>
<tr>
<td>200</td>
<td>36</td>
</tr>
</tbody>
</table>

a. At 6 h after UV treatment a live and dead stain was performed (see Experimental procedures and also Fig. 3C). A minimum of 50 aggregates ≥ 3 cells were counted per each UV dose and the fraction of vital cells is given in relation to the total cells found in aggregates.

Fig. 4. Analysis of the sso0120 knockout strain.
A. Southern blot analysis of wild-type PBL2025 (B) and the Δsso0120 (A) strain. Genomic DNA was each digested with HindIII or EcoRI respectively.
B. RT-PCR analysis of PBL2025 (B) and Δsso0120 (A) strain after UV stress. The position of the primers used for the PCR reactions are indicated by the same number above the gel and the map of the operon.
C. Electron micrographs 3 h after UV treatment. Only long flagellar but no pili can be observed in the Δsso0120 strain (Ia and b) while the surface of PBL2025 (IIa and b) is covered with pili.

© 2008 The Authors
Journal compilation © 2008 Blackwell Publishing Ltd, *Molecular Microbiology*, 70, 938–952
The Δsso0120 strain was further tested for its ability to form cellular aggregates upon UV exposure. After a treatment with a UV dose of 50 J m\(^{-2}\) no significant cellular aggregation of more than four cells was observed (Fig. 6). The amount of cells in aggregates accounted for less than 10% in the UV-treated culture and the control (mock-treated) culture, similar to the amount of cells in aggregates observed for the mock-treated cultures of the other four tested S. solfataricus strains. The S. solfataricus strain P1 and PH1-M16 (P1 ΔlacS) showed a maximum aggregation at 6–8 h after treatment, with an average of 45–50% cells in aggregates. In the same experiment, the PBL2025 and the ΔflaJ strains exhibited a shifted maximum at 8–10 h and a lower amount of aggregation with an average of 20%. The weaker reaction is most probably due to the different genotypes of these strains, which stem from PBL2025, an isolate from Yellowstone National Park S. solfataricus 98/2s (Scheffert et al., 2004). Comparable results were observed when using a lower UV dose of 25 J m\(^{-2}\) (see Fig. S1). Again, no significant cellular aggregation was observed for strain Δsso0120. The P1 and PH1-M16 strains showed a lower amount of aggregation with 30–40%, as expected in relation to the lower UV dose. The amount of cells in aggregates in the case of the PBL2025 strain stayed the same, whereas with the ΔflaJ strain the amount of cells in aggregates increased to >30% and the maximum shifted to 6 h. Based on these results we conclude that the UV induction of the putative pili operon, the inducible pili production and the cellular aggregation are functionally linked to each other. We therefore named the newly identified operon UPS for UV-inducible (type IV-like) pili operon of Sulfolobus, represented by the genes upsX, upsE (ATPase), upsF (TM protein), upsA and upsB (pre-pilins).

Fig. 5. Electron micrographs of S. solfataricus cells assembling pili. (A) shows a UV-treated Δsso0120 cell expressing sso0120 under the control of the araS promoter. (B) depicts a ΔflaJ cell overexpressing the pilins SSO117/118 and overexpressing the whole operon comprising SSO0121-117 (C). In (B) two pictures were assembled to show the length of the pilus; in (A) and (C) pili are indicated by the arrows.

Fig. 6. Quantitative analysis of the UV-induced cellular aggregation of different S. solfataricus strains at 0–10 h after UV treatment (UV) and mock treatment (C). The graph is based on four independent UV experiments for each strain. Cellular aggregation was observed at 3, 6, 8 and 10 h after UV treatment with 50 J m\(^{-2}\) (254 nm). The bars display the percentage amount of cells in aggregates (≥3 cells) in relation to the total amount of evaluated cells (500–1000 single cells were counted).

No UV-induced cellular aggregation was observed in the knockout strain Δsso0120. Similar results were observed by using a UV dose of 25 J m\(^{-2}\) (254 nm) displayed in Fig. S1.
Aggregate formation of different S. solfataricus strains after treatment with bleomycin (B) (3 μg ml⁻¹) and mock treatment (C). No significant cell aggregation was observed with the knockout strain Δsso0120. The bars display the percentage amount of cells in aggregates (≥ 3 cells) in relation to the total amount of evaluated cells (500 single cells were counted).

**Cellular aggregation is not inducible by other environmental stressors or in late growth phases**

To analyse if cellular aggregation can be induced by conditions other than UV exposure, four strains that harbour the wild type of the ups operon were used: S. solfataricus strains P1, PH1-M16, PBL2025 and ΔflaJ. We monitored and quantified the extent of cellular aggregation after a temperature shift from 78°C to 88°C (heat shock) and down to 65°C (Kagawa et al., 2003), which corresponded to non-lethal heat- and cold-shock conditions that might be often encountered in hot springs. Shifts from pH 3 to 4 and down to pH 2.5 were similarly investigated. No significant cellular aggregation was observed under the tested conditions in any of the four tested strains. The amount of cells in aggregates (≥ 3 cells) was always below 10% (see Fig. S2). We also monitored the extent of cellular aggregation in the late growth phases of the cultures, from stationary to dead phase. Only at the beginning of the late stationary phase, i.e. at the start of growth retardation, a slightly increased cellular aggregation was noted. For strain P1 up to 24% of the cells were found in aggregates of four to seven cells at most, while the amount of cells in aggregates (≥ 3 cells) were lower than 10% in all other growth phases (see Fig. S2).

**Cellular aggregation is induced by treatment with DNA double-strand breaking-inducing agents**

As a response of S. solfataricus to UV light we observed earlier the formation of DSB in the genomic DNA (Fröls et al., 2007). Whereas cis-syn-cyclobutane pyrimidine dimers (CPDs) represent direct DNA damages caused by the UV light effect, DSB are probably formed as a result of collapsing replication forks at unrepaird sites in the genomic DNA. It has been speculated earlier that DSB might represent an intracellular signal for further cellular reactions. Therefore we determined whether the formation of DSB is connected to the formation of cellular aggregates. The induction of cellular aggregation of the different S. solfataricus strains P1, PH1-M16, PBL2025 and Δsso0120 in response to the DSB-inducing agents bleomycin (3 μg ml⁻¹) (Fig. 7) and mitomycin C (5, 10 and 15 μg ml⁻¹) was investigated (Cannio et al., 1998; Reilly and Grogan, 2002; Kosa et al., 2004) (Table 2). The concentrations we applied were non-lethal to the cells as investigated by plating efficiencies and growth behaviour in liquid cultures (data not shown). Cellular aggregation was monitored at 3, 6 and 8 h after the treatment and with bleomycin additionally at 1 and 10 h. All tested strains, except for the Δsso0120 strain, showed a significant cellular aggregation in response to the agents. Eight hours after the treatment with bleomycin, strains P1, PH1-M16 and PBL2025 exhibited 25–35% of cells in aggregates (Fig. 7), while aggregation in the mock-treated cultures and the bleomycin-treated strain Δsso0120 remained below 10%. Similarly, although less strongly, mitomycin C induced aggregate formation in the ups operon containing wild-type strains (P1, PBL2025), but not in the knockout strain (Table 2). These observations indicate that DNA damage and in particular DSB might be a direct or indirect signal for inducing aggregate formation.

**Discussion**

The special living conditions of Archaea in extreme environments make them interesting objects to study adaptations and stress responses. In particular hyperther-

**Table 2.** Cellular aggregation in percentage after treatment with mitomycin C.a

<table>
<thead>
<tr>
<th>Strain</th>
<th>Mitomycin C dose</th>
<th>3 h</th>
<th>6 h</th>
<th>8 h</th>
</tr>
</thead>
<tbody>
<tr>
<td>P1 (wild-type)</td>
<td>5 μg ml⁻¹</td>
<td>5</td>
<td>10</td>
<td>10</td>
</tr>
<tr>
<td></td>
<td>10 μg ml⁻¹</td>
<td>8</td>
<td>10</td>
<td>16</td>
</tr>
<tr>
<td></td>
<td>Control</td>
<td>1</td>
<td>2</td>
<td>2</td>
</tr>
<tr>
<td>PBL2025</td>
<td>5 μg ml⁻¹</td>
<td>1</td>
<td>10</td>
<td>9</td>
</tr>
<tr>
<td></td>
<td>15 μg ml⁻¹</td>
<td>6</td>
<td>12</td>
<td>10</td>
</tr>
<tr>
<td></td>
<td>Control</td>
<td>1</td>
<td>1</td>
<td>3</td>
</tr>
<tr>
<td>PBL2025:Δsso0120</td>
<td>5 μg ml⁻¹</td>
<td>1</td>
<td>1</td>
<td>2</td>
</tr>
<tr>
<td></td>
<td>15 μg ml⁻¹</td>
<td>0</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td></td>
<td>Control</td>
<td>0</td>
<td>1</td>
<td>0</td>
</tr>
</tbody>
</table>

a. The percentage amount of cells in aggregates (≥ 3 cells) in relation to the total number of evaluated cells is given (a minimum of 500 single cells were counted).
mophilic and acidophilic *Archaea* like *S. solfataricus* have to deal with a constant stress and DNA damage in their harsh environments. Here we present the identification and characterization of an archaeal pili system that mediates cellular aggregation of *S. solfataricus* in response to UV damage. The genes encoding the now called *ups* operon for UV-inducible (type IV-like) pili operon of *Sulfolobus* had earlier been identified to be UV-dependently induced in a genome-wide DNA microarray analysis (Fröls et al., 2007).

To our knowledge this is the first reported study on a UV-inducible pili-mediated auto-aggregation system. As discussed below, its induction seems to be coupled to the DNA DSB caused by UV irradiation. We suspect that cellular aggregation mediates DNA repair via a conjugation-like process, as an enhanced exchange of chromosomal markers has been observed upon UV irradiation as well as increase in the transcripts levels of genes involved in homologous recombination.

**UV-inducible pili mediate cellular aggregation**

By electron microscopic analysis we found a strong correlation between the formation of extracellular pili on the cellular surface after UV treatment and the expression of the *ups* operon, both of which appeared first at 1 h after UV treatment and reached a maximum within 5–6 h. To test our hypothesis that the gene products of the *ups* operon are responsible for the production of the pili we used the recently developed genetic system (Albers and Driessen, 2007) to produce a specific knockout of the putative secretion ATPase *UpsE* (SSO0120). No pili structures were observed on the cellular surface of the Δ*sso0120* strain. By testing this strain in a quantitative cellular aggregation analysis, we proved that the pili are necessary for the cellular aggregation of *S. solfataricus* after UV treatment. Cellular aggregates were as infrequent (i.e. lower than 10% of all cells) as in mock-treated controls of four different *S. solfataricus* strains. Image analysis of isolated pili structures showed that the pili are much thinner in diameter and clearly distinguishable from the flagella of *S. solfataricus* (Szabó et al., 2007a). A detailed structural analysis of another archaeal pilus has recently been published from a methanogenic euryarchaeote *Methanococcus maripaludis* (Wang et al., 2008).

The pili-like structures of *S. solfataricus* are spread over the whole cellular surface. They are not bundled or polarized like the cable-like flagellar bundles of *P. furiosus*, which mediate cell attachment (Náther et al., 2006) or the type IV pili of the Tad system from *Actinobacillus* species that mediate non-specific adherence (Kachlany et al., 2000; 2001). Experiments to disconnect cellular aggregates by shearing forces failed, indicating that the cell–cell contacts were highly stable once formed and showing that the cellular aggregates were not a result of an unspecific accumulation. The latter was also ruled out by a live and dead stain analysis (Fig. 3C and Table 1). The detailed mechanisms of auto-aggregation is, however, still unknown. It has been reported that the bacterial type IV pili are bound with their tip on surface structures or other cells (Mattick, 2002). So far, we did not observe any attachment to surfaces. However, our experiments were performed under moderate shaking in glass flasks, such that one cannot rule out the possibility of surface attachment under different conditions.

**UV-inducible cellular aggregation is highly dynamic**

A quantitative assay was developed in this study to analyse the dynamics of cellular aggregation in more detail. We showed that the aggregation is a fast process induced by the UV-dependent reaction of *S. solfataricus* and seems to occur in two phases. First, small aggregates of three to five cells accumulate, which later aggregate to larger forms. The maximum of aggregation was reached at 6–8 h after UV treatment, followed by a clear disappearance, interpreted as an active disaggregation. One has to note that the absolute amount of cellular aggregation is by far underestimated because cell aggregates of more than 20 cells were uncountable and the biggest aggregates with even up to 100 and more cells were found frequently at 6 h after UV treatment. Furthermore, cell aggregates of two were not incorporated in the calculations in order to exclude dividing cells.

In correlation to the cell cycle length of *S. solfataricus*, which is around 7 h, the dynamics of this process are relatively fast. For example, the cellular packets of *M. mazei* need 2–6 days to form the lamina structures, and then remain stable over 6–11 days until the culture reaches stationary growth phase and the lamina disaggregates (Mayerhofer et al., 1992). The stress induced biofilm formation of *A. fulgidus* occurs in 2–12 h, but in this case no disaggregation was reported (LaPaglia and Hartzell, 1997).

**UV light is the only identified stressor to induce auto-aggregation**

It is reported that cells organized in multicellular structures show a higher resistance to different environmental stressors, like temperature, pH and also UV light (Ojanen-Reuhs et al., 1997; Roine et al., 1998; Martinez and Casadevall, 2007). Treatment of the hyperthermophilic archaeon *A. fulgidus*, with a high dose of UV light and other physical or toxic stressors, results in a biofilm production (LaPaglia and Hartzell, 1997). Mutants of plant pathogen bacteria *Pseudomonas syringae* and *Xan-*
thomonas campestris defect in the auto-aggregation showed a higher sensibility to UV irradiation than the wild type capable of forming multicellular structures (Ojanen-Reuhs et al., 1997; Roine et al., 1998). A decreased sensitivity to UV light and other environmental stressors was also reported for biofilms of the yeast-like fungi Cryptococcus neoflormans (Martinez and Casadevall, 2007). None of the stressors that we used for S. solfataricus induced cellular aggregation, nor did late growth phase stages. This stands in contrast to all given examples of multicellular structures, which are typically interpreted as an advantageous life form under harsh or specialized environmental conditions. Thus S. solfataricus shows a unique multicellular formation which is not a general effect of a stress response.

Interestingly, the extent of cellular aggregation (aggregate sizes and the number of cells involved) was dependent on the UV dose. Relatively high doses of UV light, like 200 or 1000 J m\(^{-2}\), resulted in an insignificant amount of small aggregates (≤ 4 cells) and killed most of the cells. In contrast a relatively low dose of UV light, like 5 J m\(^{-2}\), induced cellular aggregation. In nature sunlight composed of up to about 96% UV-A reaches the ground with c. 4% UV-B that is the most DNA-damaging factor. The daily dose of DNA-damaging UV-B light on a sunny day in the northern and southern world hemispheres is measured.

Cellular aggregation is induced by DNA DSB and might mediate a recombinational repair among chromosomes of mating cells

Between 2 and 8 h after UV treatment we observed the formation of DNA DSB, probably resulting from replication fork collapse at damaged DNA sites (Fröls et al., 2007). These observations inspired us to investigate in this study if the cellular aggregation is causally linked to the presence of DSB in the genome. Indeed, the DSB-inducing agents bleomycin and mitomycin C caused the same phenotype of cellular aggregation as UV light. Similarly, the proliferation of the S. shibatae virus 1 (SSV1) can be induced by mitomycin C as well as UV light (Martin et al., 1984) indicating that the same internal signal cascades are involved.

However, it is still unclear how DSB DNA might be sensed in the cells and how the signal is further transferred to induce the cellular aggregation and DNA-repair reactions. A phototaxis mechanism is reported for H. salinarum that regulates the motor switch of the flagella. The UV light is sensed by the sensory rhodopsin (Htr) and activates a Che-like two-component system (Nutsch et al., 2003). However, neither of these components is known in Sulfolobales. In Synecochystis PCC6803 Che-like histidine kinases control the cell orientation to the light and type IV pilus biosynthesis (Bhaya et al., 2001).

We observed that strain Δss0120 was more sensitive than wild type to DSB-inducing agents, suggesting that cell aggregation is required for efficient DNA repair. Although aggregation could simply reduce the exposure of cells to UV light by shading, we believe that aggregation might play a role in mediating the formation of mating pairs that allow DNA repair via homologous recombination among the partners.

Significantly enhanced exchanges of chromosomal markers upon treatment with UV light have been described for Sulfolobus (Wood et al., 1997; S. Fröls and C. Schleper, unpublished).

Furthermore, we found a slight, but significant upregulation of the mre11 operon upon UV treatment in S. solfataricus using whole-genome microarrays (Fröls et al., 2007). This operon encodes homologues of the eukaryotic system involved in the DSB repair via homologous recombination (Hopfner et al., 2002; Constantinesco et al., 2004).

By integrating our observations and those cited above we think that recombinational repair via homologous recombination and DNA exchange via cell–cell contacts might be an important strategy to overcome DNA damage in Sulfolobus caused by UV light. Future studies will aim at investigating if this is indeed the case. It will also be interesting to elucidate the transcriptional regulation of the UV-induced genes, with the perspective to clarify the signal transduction pathways that sense UV irradiation or DNA damage in crenarchaeota.

Experimental procedures

Strains and growth

Sulfolobus solfataricus P1 (DSM1616), PH1 (Schleper et al., 1994), PH1-M16 (Martusewitsch et al., 2000) and PBL2025 (Schelert et al., 2004) and derived deletion mutants were grown aerobically at 80°C in the medium described by Brock et al. (1972), adjusted to pH 3 with sulphuric acid and supplemented with 0.1% (w/v) of tryptone and 0.2% (w/v) of arabinose under moderate agitation (150 r.p.m. in a New Brunswick shaker). Growth of cells was monitored by measuring the optical density at 600 nm. Solid media were prepared by adding gelrite to a final concentration of 0.6% and MgCl\(_2\) and CaCl\(_2\) to 0.3 and 0.1 M respectively. Plates were incubated for 5 days at 78°C. For the propagation of plasmids, E. coli strain DH5α was used. For the virus containing
plasmids ElectroMAX™ E. coli Stbl4™ cells (Invitrogen, Germany) were used.

**UV light exposure**

UV treatment of cells was performed under red dimmed light. Aliquots of 10 ml of *S. solfataricus* culture (OD₆₀₀ 0.3–0.5) were transferred to a 110 mm plastic Petri dish and treated with a defined UV dose (λ, 254 nm, UV-Stratalinker 1800, Stratagene). Treated cell suspensions were combined to a final volume of 20 ml. The mock-treated cultures were set for 5 s under red dimmed light. Treated cells were stored in the dark at room temperature for 15 min and were re-incubated at 78°C and 150 r.p.m. Samples taken at different time points were used for microscopy, cell vitality and electron microscopy.

**Electron microscopy and single-particle analysis**

For image processing, cells with attached pili were negatively stained with 2% uranyl acetate on glow-discharged carbon-coated copper grids. Electron microscopy was performed on a Philips CM120 electron microscope operating at 120 kV with a LaB6 filament. Images were recorded with a 4000 SP 4K slow-scan CCD camera at 60 000× magnification at a pixel size of 5.0 Å at the specimen level with ‘GRACE’ software (Oostergetel et al., 1998). Single-particle analysis was performed with the Groningen Image Processing (‘GRIP’) software package on a PC cluster. Non-overlapping pili segments were extracted from the micrographs and aligned with correlation methods. The aligned projections were treated with multivariate statistical analysis in combination with hierarchical classification before final averaging (van Heel et al., 1992; Penczek et al., 1992).

**Plasmid construction for expression in *S. solfataricus* and E. coli**

The genes sso0117 and sso0118 were cloned using primers 118-forward-NcoI and 117-reverse-BamHI in the same arrangement as found in the genomic context into the virus-based expression vector pMJ05 (Jonuscheit et al., 2003) via the entry vector pMZ1 (Zolghadr et al., 2007) yielding pSVA96. To express the whole ups operon genes sso0121-117 were cloned using primers 121-forward-NcoI and 117-reverse-BamHI via pMZ1 into pMJ05 resulting in pSVA125. To construct the expression plasmid for the signal peptide cleavage assay, sso0118 was amplified using 118-forward-NcoI and 118-reverse-BamHI and cloned into pZa7, which added a HA-tag to the C-terminus of the protein and resulted in pSVA133. By NcoI–HindIII restriction the sso0118-HA part was then transferred into pBAD/Myc-HisA yielding pSVA134. To achieve coexpression with the peptidase a fragment containing pibD under the control of the T7 promoter was cloned from pUC18-pibD into pSVA134 by Spel restriction resulting in pSVA135. All plasmid vectors used in this study are listed in Table 3.

For the expression of SSO117/118 and the ups operon in the ΔflaJ strain, cells were grown to an OD₆₀₀ of 0.2, and transformed with pSVA96, pSVA125 and pSVA31 as a control as described by Jonuscheit et al. (2003). After 2 days, cultures were transferred to medium containing 0.4% arabinose to induce the expression of the desired genes. After one transfer, cells were analysed at an OD₆₀₀ of 0.7 cells by electron microscopy.

**Construction of plasmids for the directed deletion of genes**

The up- and downstream flanking regions of sso0120 were amplified using primer pairs KO-UP forward/KO-UP reverse and KO-DOWN forward/KO-DOWN reverse respectively (Table S1). The resulting fragments were cloned using KpnI/NcoI for the upstream flanking region (1099 bp) or BamH/NotI for the downstream flanking region (924 bp) in PET2268, a vector containing the lacS cassette for selection, yielding pSVA37. Electroporation of the knockout plasmids and selection for correct deletion mutants were performed as described (Albers and Driessen, 2007).

**Southern blotting**

Genomic DNA (8 ng) was digested with the appropriate enzymes and separated on 0.8% agarose gel. The gel was

---

**Table 3. Plasmids used in this study.**

<table>
<thead>
<tr>
<th>Plasmid name</th>
<th>Reference</th>
</tr>
</thead>
<tbody>
<tr>
<td>pET2268 Vector</td>
<td>ElectroMax™ by Stratagene.</td>
</tr>
<tr>
<td>pZa7</td>
<td>Transfer vector to add HA-tag to proteins.</td>
</tr>
<tr>
<td>pUC18-pibD pUC18 containing pIB under the control of a T7 promoter.</td>
<td></td>
</tr>
<tr>
<td>pMz1</td>
<td>Entry vector for virus vector.</td>
</tr>
<tr>
<td>pMJ05v Virus-based shuttle vector for <em>S. solfataricus</em></td>
<td></td>
</tr>
<tr>
<td>pSVA31 pMJ05 containing ABCF1 under control of araS promoter.</td>
<td></td>
</tr>
<tr>
<td>pSVA57 PET2268 containing up- and downstream flanking regions of sso0120</td>
<td></td>
</tr>
<tr>
<td>pSVA96 pMJ05 containing sso117/118 under control of araS promoter.</td>
<td></td>
</tr>
<tr>
<td>pSVA99 pMJ05 containing sso0120 under control of araS promoter.</td>
<td></td>
</tr>
<tr>
<td>pSVA125 pMJ05 containing sso121-117 under control of araS promoter.</td>
<td></td>
</tr>
<tr>
<td>pSVA133 pZa7 containing sso0118</td>
<td></td>
</tr>
<tr>
<td>pSVA134 pBAD/Myc-HisA containing sso0118-HA</td>
<td></td>
</tr>
<tr>
<td>pSVA135 pSVA134 containing pibD</td>
<td></td>
</tr>
</tbody>
</table>

a. Plasmids labelled bold are shuttle vectors for *S. solfataricus/E. coli.*
equilibrated in 20× SSC and the DNA was transferred overnight to a positively charged nylon membrane (BIO-RAD, the Netherlands). DNA hybridization was performed in standard hybridization buffer. PCR products of both lacS and the sso0120 gene were digoxigenin-labelled with the HighPrime Kit (Roche, the Netherlands). Detection was performed with a Lumilimager (Roche, the Netherlands).

**Gene expression analysis**

Total RNA isolation and cDNA synthesis were performed as described previously (Zolghadr et al., 2007). Gene-specific primer sets (1–7, Table S1) were used to detect the presence of the genes in the ups operon. PCR products were analysed on 0.8% agarose gels.

**Isolation of E. coli crude membranes**

BL21(DE3) (pLysS) E. coli cells were transformed with plasmids pSW017, pSW018, pSW019 and pSW020. The signal sequence cleavage assay was performed as described before (Szabó et al., 2007b). At an OD$_{600}$ of 0.6, the expression of the precursor genes, sso0117/118, was induced by addition of 0.2% l-arabinose for 2 h. Subsequently, the expression of pibD was induced with 0.1 mM isopropyl-beta-D-thiogalactopyranoside (IPTG) for 2 h. The cultures were harvested, and cell pellets were re-suspended in 2 ml of buffer (50 mM TrisCl, pH 7.5, 1 mM EDTA). Crude membranes were isolated as described previously (Szabó et al., 2007b) and re-suspended in 50 mM TrisCl, pH 7.5. Cleavage of substrates was determined by SDS-PAGE and Western blot analysis of 5 µg of crude membranes using monoclonal antihemagglutinin (HA Tag) antibodies (Sigma).

**Microscopy and quantitative analysis of cell aggregate formation**

Cell aggregate microscopy was performed as described (Fröls et al., 2007). To quantify the formation of aggregates, the number of cells in aggregates and the number of aggregates were counted until 1000 or 500 single cells were observed. At least seven fields of views were analysed for each time point. To exclude that the cellular aggregates were not artefacts of the microscopic slide preparation only fields of views were analysed where the cells showed an even spreading. For statistic analysis the percentage of cells in aggregates ≥ 3 cells (to exclude the dividing pairs of cells) against the total amount of cells was calculated. Additionally the percentage of each aggregates size (from 3 to 15 cells) against the total amount of cells was determined to observe the time- and dose-dependent formation of cellular aggregates in a higher resolution.

**Analysis of the cell viability**

To analyse the cell viability the LIVE DEAD Baclight (Invitrogen) assay was used according to the manufacturer’s instructions. Alternatively, a combined 4′,6-diamidino-2-phenylindole (DAPI) propidium iodide stain was used. At 6 h after UV treatment, samples of 20 µl of liquid cultures were mixed with 2 µl of propidium iodide (1:30 dilution in 10 mM TrisCl pH 7.5) and incubated for 15 min in the dark at room temperature. Microscopic slides were coated with 1% agar (10 mM TrisCl, pH 7.5) containing 0.2 µg ml$^{-1}$ DAPI. Propidium iodide-stained culture (5 µl) was spread on the coated slide and immediately examined. To analyse the number of dead cells in aggregates in relation to the living cells, a minimum of 50 cellular aggregates of ≥ 3 cells were counted for each UV dose.

**Testing of various stress factors**

For the temperature shift, exponentially grown S. solfataricus cultures (OD$_{600}$ of 0.3–0.5) were transferred from 78°C to 88°C or to 65°C. Additionally control cultures were transferred to 78°C with gentle shaking at 150 r.p.m., and at time points up to 10 h after transfer, samples were analysed for aggregation.

For the pH shift experiments, exponential-grown S. solfataricus cells were harvested and re-suspended in an identical volume of Brock’s basal salt medium supplemented with β-arabinose (0.2%) and tryptone (0.1%) at pH values of 2.5, 3 and 4 respectively. Growth was continued at 78°C. Samples for the quantitative analysis of the cellular aggregation were taken up to 8 h after the pH shift. For the treatment with the DSB-inducing antibiotics, an exponential S. solfataricus culture was treated with 3 µg ml$^{-1}$ bleomycin (Bleocin, Calbiochem) or 5, 10 and 15 µg ml$^{-1}$ mitomycin C (Sigma). Growth was continued at 78°C and cell samples taken up to 10 h after antibiotics additions were plated on Brock’s solid media. Survival rates confirmed the use of a non-lethal drug concentration for both antibiotics as described (Cannio et al., 1998; Reilly and Grogan, 2002; Kosa et al., 2004).

**Acknowledgements**

The work has been funded by Deutsche Forschungsgemeinschaft within SPP1112 and by the University of Bergen. D.T. is funded by the Marie Curie research training network MRTN-CT-2006-033499. S.-V.A. and B.Z. were supported by a VIDI grant from the Dutch Science Organization (NWO). M.A. was funded by an Ubbo-Emmius scholarship of the University of Groningen.

**References**


Albers, S.V., Jonuscheit, M., Dinkelaker, S., Urich, T., Kletzin,


**Supporting information**

Additional supporting information may be found in the online version of this article.
UV-inducible cellular aggregation of the hyperthermophilic archaeon *Sulfolobus solfataricus* is mediated by pili formation

Sabrina Fröls¹², Magorzata Ajon³, Michaela Wagner³, Daniela Teichmann¹, Behnam Zolghadr³, Mihaela Folea⁴, Egbert J. Boekema⁴, Arnold J.M. Driessen³, Christa Schleper¹²# and Sonja-Verena Albers³

¹ Department of Genetics in Ecology, Vienna Ecology Center, University of Vienna, Althanstrasse 14, 1090 Vienna, Austria
² Center for Geobiology, Department of Biology, University of Bergen, Realfagbygget, Allegaten 41, N-5007 Bergen
³ Department of Microbiology, Groningen Biomolecular Sciences and Biotechnology Institute and the Zernike Institute for Advanced Materials, University of Groningen, Kerklaan 30, 9751 NN Haren, The Netherlands
⁴ Department of Biophysical Chemistry, Groningen Biomolecular Sciences and Biotechnology Institute, University of Groningen, Nijenborgh 4, 9747 AG Groningen, The Netherlands

#Correspondence to C. Schleper, e-mail: christa.schleper@univie.ac.at,
tel: +43 14277 57800, fax: +43 14277 9578
Fig. S1: Quantitative analysis of the UV-induced cellular aggregation of different S. solfataricus strains. Cellular aggregation was observed at 3, 6, 8, and 10 hours after UV-treatment with 25 J/m² (254 nm). The graph is based on three independent UV-experiments; in the case of the strains PBL2025, ΔflaJ and Δsso0120 and 2 independent UV-experiments for the strains P1 and PH1-M16 (only one experiment at 8 h, respectively). The bars display the % amount of cells in aggregates (≥ 3 cells) in relation to the total amount of evaluated cells (at minimum 500 single cells were counted, but mostly up to 1000).
**Fig. S2:** Quantitative analysis of the cellular aggregation under different environmental stressors and cell growth: non-lethal pH shift, from pH 3 to pH 4 and down to pH 2.5 and a non-lethal temperature shift from 78°C up to 88°C and down to 65°C, early stationary growth phase until dead phase. The bars represent the mean of the results obtained for the four *sso0120* wild type strains; P1, PH1-M16, PBL2025 and Δ*flaJ*. The % amount of cells in aggregates (≥ 3 cells) in relation to the total amount of evaluated cells (500 single cells, or a minimum of 250 single cells were counted).
Table S1: Primers used in this study

<table>
<thead>
<tr>
<th>Primer name</th>
<th>Sequenz (5'-3')</th>
</tr>
</thead>
<tbody>
<tr>
<td>1 RT forward</td>
<td>ATAGGTCAAGTGATGGGTTA</td>
</tr>
<tr>
<td>1 RT reverse</td>
<td>CATCTGCTGCAAGTATCTTT</td>
</tr>
<tr>
<td>2 RT forward</td>
<td>GCCTATACGCATGGTTTCAC</td>
</tr>
<tr>
<td>2 RT reverse</td>
<td>AAGGGTCAGCTAAGGGTACA</td>
</tr>
<tr>
<td>3 RT forward</td>
<td>AGCAAGAAGATCACGTACTA</td>
</tr>
<tr>
<td>3 RT reverse</td>
<td>CTGGAGTATCCTCTATGGTAAT</td>
</tr>
<tr>
<td>4 RT forward</td>
<td>GATCTAGAAGAGTTCAAGTGGTT</td>
</tr>
<tr>
<td>4 RT reverse</td>
<td>AGACCTTGGCTCTGCTTTCC</td>
</tr>
<tr>
<td>5 RT forward</td>
<td>ACACAAGTGGTAGTCAATA</td>
</tr>
<tr>
<td>5 RT reverse</td>
<td>TTTGCAGCGAGTTCTCCTAA</td>
</tr>
<tr>
<td>6 RT forward</td>
<td>AGGGCGATTCGCAACTTTAG</td>
</tr>
<tr>
<td>6 RT reverse</td>
<td>ATATCTGTGTGCTGCGCGGTA</td>
</tr>
<tr>
<td>7 RT forward</td>
<td>GCTGGGTTGTCTACTTTATG</td>
</tr>
<tr>
<td>7 RT reverse</td>
<td>AGTACTGCCAGCAGTTA</td>
</tr>
<tr>
<td>118 forward-Ncol</td>
<td>CCCCCCCATGGTACAACTAATGAAAGGAGG**</td>
</tr>
<tr>
<td>118 reverse-BamHI</td>
<td>CCCCCGGATCCCGCTATTGGAAGCGCA</td>
</tr>
<tr>
<td>117 reverse-BamHI</td>
<td>CCCCCGGATCCCATCCGGTGCCAGGTTGA</td>
</tr>
<tr>
<td>121 forward-Ncol</td>
<td>CCCCCGATGGAATTTCCAGGACTATTCATGCAG</td>
</tr>
<tr>
<td>KO-UP forward</td>
<td>CCCGGTACCCTGCTATTACTCATGTTA</td>
</tr>
<tr>
<td>KO-UP reverse</td>
<td>CCCCCATGGCAATTCCAGATTTATCATGATCAG</td>
</tr>
<tr>
<td>KO-DOWN forward</td>
<td>CCGGATCCCAGAATTTCCATGATC</td>
</tr>
<tr>
<td>KO-DOWN reverse</td>
<td>CCCCCCCCAGCCGCCCAGGCTGCAAAGATATCCTT</td>
</tr>
</tbody>
</table>

* restriction sites are underlined
<table>
<thead>
<tr>
<th></th>
<th>Length in aa</th>
<th>S. tokodai</th>
<th>S. acidocaldarius</th>
<th>Metalosphaera sedula</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>S. solfataricus</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>SSO0121</td>
<td>695</td>
<td>ST1398</td>
<td>Saci_1493</td>
<td>Msed_2103</td>
</tr>
<tr>
<td>SSO0120</td>
<td>483</td>
<td>ST1397</td>
<td>Saci_1494</td>
<td>Msed_2104</td>
</tr>
<tr>
<td>SSO0119</td>
<td>481</td>
<td>ST1398</td>
<td>Saci_1495</td>
<td>Msed_2105</td>
</tr>
<tr>
<td>SSO0118</td>
<td>154</td>
<td>ST1399</td>
<td>Saci_1496</td>
<td>Msed_1193</td>
</tr>
<tr>
<td>SSO0117</td>
<td>137</td>
<td>ST1400</td>
<td>Saci_1496a*</td>
<td>Msed_2107</td>
</tr>
</tbody>
</table>

* not annotated, found by tblastn search on position 1275628-1275993 in the genome of S. acidocaldarius (amino acid identity 30 %, similarity 60 %)