

Proteolysis in hyperthermophilic microorganisms

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Summary Proteases are found in every cell, where they recognize and break down unneeded or abnormal polypeptides or peptide-based nutrients within or outside the cell. Genome sequence data can be used to compare proteolytic enzyme inventories of different organisms as they relate to physiological needs for protein modification and hydrolysis. In this review, we exploit genome sequence data to compare hyperthermophilic microorganisms from the euryarchaeotal genus *Pyrococcus*, the crenarchaeote *Sulfolobus solfataricus*, and the bacterium *Thermotoga maritima*. An overview of the proteases in these organisms is given based on those proteases that have been characterized and on putative proteases that have been identified from genomic sequences, but have yet to be characterized. The analysis revealed both similarities and differences in the mechanisms utilized for proteolysis by each of these hyperthermophiles and indicated how these mechanisms relate to proteolysis in less thermophilic cells and organisms.

Keywords: Archaea, Bacteria, protease, *Pyrococcus*, *Sulfolobus solfataricus*, *Thermotoga maritima*.

Introduction

Proteases are critical to the maintenance of cellular function. They hydrolyze both external and internal nutrient sources and recognize and break down unneeded or abnormal polypeptides, the latter produced as a result of environmental stress, mutation or errors in biosynthetic processes (Tomoyasu et al. 2001). Cells have an array of proteases for processing proteins and polypeptides (e.g., Allison and Macfarlane 1990, Guedon et al. 2001) and for maintaining metabolic function under abnormal conditions (Arsene et al. 2000). Proteases range from simple monomeric hydrolases to complex, multi-subunit structures with molecular masses in the order of 1 MDa. Some proteases have a high functional and structural complexity, particularly those that are ATP-dependent, e.g., Lon, ClpXP, ClpYQ, FtsH and the proteasome (Gottesmann 1996, Maupin-Furlow et al. 2000), but whether simple or complex, all proteases must be precisely regulated to avoid destruction of the cell's metabolic machinery.

Here, we exploit genomic sequence data, in conjunction with physiological, biochemical and biophysical information, to investigate relationships among proteolytic inventories of

hyperthermophilic microorganisms (capable of growth at 80 °C) of the euryarchaeotal genus *Pyrococcus*, the crenarchaeote *Sulfolobus solfataricus* and the bacterium *Thermotoga maritima*. *Thermotoga maritima*, initially isolated from Vulcano, Italy, has an optimum growth temperature of 80 °C and is a fermentative anaerobe that reduces sulfur facultatively and prefers simple and complex sugars as growth substrates (Huber et al. 1986). *Sulfolobus solfataricus*, initially isolated from a solfataras field near Naples, Italy (Zillig et al. 1980), is an aerobe that grows at acidic pHs as low as 2.0, with an optimal growth temperature of 80 °C (Brock et al. 1972). This archaeon grows chemolithotrophically by oxidizing metal cations (Fe²⁺) or sulfur as well as heterotrophically on simple sugars. *Pyrococcus* is a marine hyperthermophilic genus that includes species with optimal growth temperatures between 96 and 100 °C. *Pyrococcus* spp. have been isolated from deep-sea hydrothermal vent systems, such as those found along the North Fiji basin (*P. abyssi*, Erauso et al. 1993) and Okinawa Trough (*P. horikoshii*, Gonzalez et al. 1998), as well as from shallow marine environments, such as those found around Vulcano Island, Italy (*P. furiosus*, Fiala and Stetter 1986). *Pyrococcus* spp. are strict anaerobes that reduce sulfur facultatively and grow heterotrophically by fermentation of proteinaceous compounds and sometimes simple sugars and α -keto acids such as pyruvate.

Inferring protease inventory from genomic sequences

Initial efforts to assess the extent and variety of proteases in hyperthermophiles by biochemical methods significantly underestimated this biocatalytic feature. For example, Connaris et al. (1991) and Blumentals et al. (1990) reported that gelatin-based zymograms of cell-free extracts from *P. furiosus* revealed the presence of up to 13 clearing zones, some of which were later attributed to multiple versions of a single protease (Halio et al. 1996, Chang et al. 2001). Similar experiments with *T. maritima* revealed an even more limited set of proteases than observed in *P. furiosus* (Hicks et al. 1998). Genome sequence data, however, indicate that the proteolytic genotypes of these organisms are more expansive than can be inferred from zymogram analyses. Tables 1 and 2 show the confirmed and putative protease-related genes in the genomes of *P. furiosus* (<http://comb5-156.umbi.umd.edu/genemate/>), *P. abyssi*,

Table 1. Protease inventory in *Pyrococcus* species, *Sulfolobus solfataricus* and *Thermotoga maritima*.

<i>Pyrococcus furiosus</i>		<i>Pyrococcus abyssi</i>		<i>Pyrococcus horikoshii</i>	
Locus	Function	Locus	Function	Locus	Function
ATP-dependent proteases					
pf_481472	ATP-dependent LA (Lom) ¹	PAB1313	ATP-dependent LA (Lon) ¹	PH0452	ATP-dependent LA (Lon) ¹
pf_119316	ATP-dependent regulatory subunit	PAB2233	ATP-dependent regulatory subunit	PH0201	ATP-dependent regulatory subunit
pf_169930	Proteasome beta subunit (PsmB-2)	PAB2199	Proteasome beta subunit (PsmB-2)	PH0245	Proteasome beta subunit (PsmB-2)
pf_1318448	Proteasome beta subunit (PsmB-1)	PAB1867	Proteasome beta subunit (PsmB-1)	PH1402	Proteasome beta subunit (PsmB-1)
pf_1467425	Proteasome alpha subunit	PAB0417	Proteasome alpha subunit	PH1553	Proteasome alpha subunit
ATP-independent proteases					
pf_301754	Pyrolysin	PAB1252	Pyrolysin-like	PH0310	Pyrolysin-like
pf_251719	Periplasmic serine protease, putative	PAB2437	Periplasmic serine protease, putative	PH0282	Periplasmic serine protease, putative
pf_176949	Metalloprotease	PAB2195	Protease, putative	PH0256	Protease, putative
pf_401364	Metalloprotease	PAB1063	Metalloprotease	PH0351	Metalloprotease
pf_472643	Metalloprotease	PAB1319	Metalloprotease	PH1569	Hypothetical protease IV
pf_699579	Subsillin-like protease	PAB1960	Hypothetical protease IV	PH1704	Intracellular protease I (PfpI)
pf_1479679	Protease IV	PAB0311	Intracellular protease I (PfpI)	PH0979	Hydrogenase maturation protease (hyc I)
pf_1553191	Alkaline serine protease	PAB0576	Hydrogenase maturation protease (hyc I)	PH0630	Hypothetical neutral protease
pf_1757236	Putative protease	PAB0555	CAAX Prenyl protease	PH0585	Hypothetical neutral protease
pf_1599202	Intracellular protease I (PfpI)				
pf_637303	Hydrogenase maturation protease (hyc I)				
pf_754933	Hypothetical protein				
pf_1136394	Conserved hypothetical protein (bacteriocin homolog)				
Peptidases					
pf_471039	Carboxypeptidase I	PAB1320	Carboxypeptidase I174	PH0465	Carboxypeptidase I
pf_334012	Protein similar to acylaminoacyl peptidase	PAB1418	Protein similar to acylaminoacyl peptidase	PH0594	Protein similar to acylaminoacyl peptidase
pf_181525	O-sialoglycoprotein endopeptidase (gcp-1)	PAB1159	O-sialoglycoprotein endopeptidase (gcp-1)	PH1987	O-sialoglycoprotein endopeptidase (gcp-1)
pf_488067	O-sialoglycoprotein endopeptidase (gcp-2)	PAB1047	O-sialoglycoprotein endopeptidase (gcp-2)	PH0445	O-sialoglycoprotein endopeptidase (gcp-2)
pf_561253	Methionine aminopeptidase (MAP)	PAB1434	Methionine aminopeptidase (MAP)	PH0628	Methionine aminopeptidase (MAP)
pf_707740	Proline-dipeptidase related protein	PAB2178	Proline-dipeptidase related protein	PH1902	Proline-dipeptidase related protein
pf_743892	Putative proline-dipeptidase	PAB2178	X-Pro dipeptidase	PH1902	Putative proline-dipeptidase
pf_803543	Prolyl endopeptidase	PAB0762	Prolyl endopeptidase	PH1262	Prolyl endopeptidase
pf_848157	Membrane dipeptidase	PAB2388	Membrane dipeptidase	PH1026	Membrane dipeptidase
pf_1775248	D-aminopeptidase	PAB0045	D-aminopeptidase	PH0078	D-aminopeptidase
pf_1898123	Putative aminopeptidase	PAB1637	XAA-Pro dipeptidase (proline dipeptidase)	PH1149	XAA-Pro dipeptidase (proline dipeptidase)
pf_1902688	Putative aminopeptidase	PAB1419	Pyroglutamyl-peptidase I	PH0596	Pyroglutamyl-peptidase I
pf_1906416	Putative aminopeptidase	PAB2375	Aminopeptidase from M42 family	PH0519	Aminopeptidase from M42 family
pf_1262501	XAA-Pro dipeptidase (proline dipeptidase)	PAB0437	Aminopeptidase from M42 family	PH1527	Aminopeptidase from M42 family
pf_1224347	Pyroglutamyl-peptidase I	PAB2096	Aminopeptidase from M42 family	PH1821	Aminopeptidase from M42 family
pf_383398	Endoglucanase/peptidase	PAB0723	Acetylornithine deacetylase (ArgE)/peptidase	PH1153	Acetylornithine deacetylase (ArgE)/peptidase
pf_1444497	Endoglucanase (ceIM)/peptidase	PAB0581	Succinyl-diaminopimelate desuccinylase/peptidase	PH1288	Succinyl-diaminopimelate desuccinylase/peptidase
pf_1717470	Endo-1,4-beta-glucanase/peptidase	PAB0966	Signal sequence peptidase I (SEC11)	PH0590	Signal sequence peptidase I (SEC11)
pf_1131554	Acetylornithine deacetylase (ArgE)/peptidase	PAB0869	Peptidase, putative	PH0737	Peptidase, putative
pf_1890964	Succinyl-diaminopimelate desuccinylase/peptidase	PAB1781	X-Pro aminopeptidase pepQ-3	PH0974	Hypothetical dipeptidase
pf_329163	Signal sequence peptidase I (SEC11)				
pf_679507	Hypothetical protein				

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Table 1 Cont'd. Protease inventory in *Pyrococcus* species, *Sulfolobus solfataricus* and *Thermotoga maritima*.

<i>Sulfolobus solfataricus</i>		<i>Thermotoga maritima</i>	
Locus	Function	Locus	Function
ATP-dependent proteases			
SSO0278	Proteasome beta subunit	TM1633	ATP-dependent protease LA (Lon)
SSO0738	Proteasome alpha subunit	TM1869	ATP-dependent protease LA, putative
SSO0766	Proteasome beta subunit	TM0198	ATP-dependent Clp protease, ATPase (clpC-1)
SSO0271	26S proteasome regulatory subunit	TM1391	ATP-dependent Clp protease, ATPase (clpC-3)
ATP-independent proteases			
SSO1886	Thermopsin precursor, probable	TM0146	ATP-dependent Clp protease, ATPase (clpX)
SSO2037	Thermopsin precursor, probable	TM0873	ATP-dependent Clp protease, ATPase (clpC-2) frameshift
SSO2194	Thermopsin precursor-related protein	TM0695	ATP-dependent Clp protease, proteolytic subunit (clpP)
SSO2551	Serine protease, subtilase family, putative	TM0521	Heat-shock protein HslV (clpQ) proteolytic subunit
SSO1141	Protease related protein	TM0522	Heat-shock protein HslU (clpY) ATPase
SSO2045	Protease	TM0580	Cell division protein FisH
SSO2098	Tricorn protease	ATP-independent proteases	
SSO1067	Intracellular protease (PipI)	TM0747	Carboxy-terminal protease
SSO1759	Protease, putative	TM0516	Clostripain-related protein
SSO2015	Protease, putative	TM0643	Clostripain-related protein
SSO2612	HtrA-like Serine protease (periplasmic)	TM1589	Clostripain-related protein
SSO0464	Hypothetical protein, put. protease	TM1823	FisH protease activity modulator HflC (hflC)
SSO0087	Hypothetical protein, put. metalloprotease	TM1822	FisH protease activity modulator HflK (hflK)
Peptidases			
SSO3115	Tricorn Protease interacting F factor F1	TM1346	Processing protease, putative
SSO2154	Tricorn Protease interacting F factor F2	TM0785	Protease, bacteriocin
SSO2675	Tricorn Protease interacting F factor F3	TM0145	Secreted metalloendopeptidase Gep, putative
SSO0010	X-pro aminopeptidase	TM0409	Conserved hypothetical, probable secreted proteinase
SSO0363	Prolidase	TM0890	Conserved hypothetical, probable membrane metalloprotease
SSO0433	O-sialoglycoprotein endopeptidase	TM1704	Hypothetical protein (homology to protease maturation)
SSO0434	O-sialoglycoprotein endopeptidase	TM0916	Periplasmic serine protease, putative
SSO1355	Thermostable carboxypeptidase (cpsA-1)	Peptidases	
SSO1952	Thermostable carboxypeptidase (cpsA-2)	TM0963	Oligoendopeptidase, putative
SSO3105	Thermostable carboxypeptidase 1	TM0847	Conserved hypothetical protein
SSO1465	Pyrrolidone carboxylate peptidase (pcp)	TM0445	Conserved hypothetical protein
SSO1607	Pyrrolidone carboxylate peptidase, put. (pcp-like)	TM1572	Signal peptidase I, putative
SSO1864	Microsomal dipeptidase	TM1696	Type IV prepilin peptidase
SSO0098	Methionine aminopeptidase 2	TM0129	Carboxypeptidase G2, putative
SSO2088	Peptidase, putative	TM0874	Conserved hypothetical protein
SSO2181	Peptidase related protein	TM0463	Lipoprotein signal peptidase
		TM0772	Conserved hypothetical
		TM1048	Endoglucanase (peptidase)
		TM1049	Endoglucanase (peptidase)
		TM1050	Endoglucanase (peptidase)
		TM0042	Aminopeptidase P, putative
		TM0365	Aminopeptidase, putative
		TM1713	Proline dipeptidase, putative
		TM1478	Methionine aminopeptidase (map)

P. horikoshii (Kawarabayasi et al. 1998), *S. solfataricus* (She et al. 2001) and *T. maritima* (Nelson et al. 1999). This information was also used to examine other hyperthermophilic and mesophilic organisms (for more information see <http://www.che.ncsu.edu/extremophiles/>). Protease-related genes were identified through BLAST analyses of completely sequenced prokaryotic genomes, the online database at the Kyoto Encyclopedia of Genes and Genomes (<http://www.genome.ad.jp/kegg/>), and the AlignAce output files (http://arep.med.harvard.edu/microbial_motifs/). Putative protease/peptidases were analyzed for known motifs with ScanProsite (<http://ca.expasy.org/tools/scnpsit1.html>), the presence of signal peptides using SignalP (<http://www.cbs.Dtu.dk/services/SignalP/>) and genomic organization using the STRING analy-

sis method (Snel et al. 2000), for possible protease-gene relationships. Homology was confirmed when amino acid sequence identities were at least 25% over 50% or more of the protein. Genomic analysis showed that *Pyrococcus* spp., *S. solfataricus* and *T. maritima* have numerous protease homologs to putative and confirmed proteases in other archaea and bacteria, although there are many differences among these organisms in protease inventory. This is true even when comparing the protease inventory of the three species within the genus *Pyrococcus*.

The ATP-dependent proteases in hyperthermophiles

All prokaryotic genomes sequenced to date, including hyper-

[†] The Lon protease in *Pyrococcus* lacks the ATP-binding domain, but was placed in the ATP-dependent protease section because there is no experimental evidence aside from the sequence to suggest otherwise.

Table 2. Protease-related genes in selected microorganisms.

Species	ATP-dependent proteases	ATP-independent proteases	Peptidases	Total
<i>Thermotoga maritima</i>	9	14	16	39
<i>Pyrococcus furiosus</i>	5	13	22	40
<i>Pyrococcus abyssi</i>	5	9	20	34
<i>Pyrococcus horikoshii</i>	5	9	20	34
<i>Archaeoglobus fulgidus</i>	4	7	11	22
<i>Sulfolobus solfataricus</i>	4	13	16	33
<i>Escherichia coli</i>	13	16	31	60

thermophiles, indicate the presence of several ATP-dependent proteases, although there is some variation in the roster of these enzymes among organisms. These proteases are typically implicated in protein and peptide turnover, and stress response (for reviews see Gottesman 1996, 1999, Porankiewicz et al. 1999, Schmidt et al. 1999). Although it is unclear how particular functional or abnormal proteins are selected for proteolytic processing by ATP-dependent proteases, it is a key issue in understanding cellular function.

The Lon protease

Lon protease is unique among ATP-dependent proteases in that it is not based on the assemblage of small subunits (i.e., 15–25 kDa) into stacked rings that interact with separate ATPases. Rather, Lon protease is a homotetramer, composed of 87-kDa subunits, each containing an active site serine and a single ATP-binding site (Maurizi 1992). Lon is ubiquitous across all three domains of life and seemed at one point to be the only such ATP-dependent protease. Analysis of the *T. maritima* genome revealed a homolog to the *Escherichia coli* Lon, TM1633, referred to here as LonA. However, a second open reading frame, TM1869, was also annotated as a possible Lon homolog, designated LonB, which was previously not identified. LonA has both the active site and ATP-binding site motifs typically noted in other versions of Lon. LonB contains the active site region (with the conserved serine residue), but not the ATP-binding site (Figure 1). Homologs to both LonA and LonB were noted in several bacterial genomes. However, euryarchaeal genomes appear to encode only a single LonB homolog. In *Pyrococcus* spp., the *lon* gene contains an intein (http://www.neb.com/neb/frame_tech.html), a self-splicing element functional at the protein level. Whether this impacts its regulation or the expression of the encoded protein is unknown. No Lon homolog could be identified in the *S. solfataricus* genome. The archaeal Lons also have one or two putative transmembrane regions, which are absent in the Eubacteria, suggesting that they may be membrane-associated. LonA and LonB are distinct enzymes, as is readily apparent when a phylogenetic tree is constructed based on their amino acid sequences (Figure 2). Although it is clear that LonA and LonB are distinct enzymes, their metabolic roles and biochemical specifics are unknown.

The FtsH (or HflB) proteinase

FtsH (or HflB) is an ATP-dependent proteinase with a zinc metalloprotease motif that is present in Bacteria, mitochondria, and chloroplasts, but not in Archaea (Schumann 1999, Langer 2000). Unlike the proteasome, Lon protease and Clp protease, which are cytoplasmic, the FtsH protein is anchored to the cytoplasmic membrane through two transmembrane regions. Among hyperthermophiles, FtsH has been located only in the bacteria *Aquifex aeolicus* and *T. maritima* (see Table 1). Although Archaea lack FtsH, we speculate that the archaeal Lon, which has one to two putative transmembrane regions, may replace FtsH from a metabolic standpoint.

The Clp family of proteases

The Clp family occurs in both the eubacteria and eukaryotes, including hyperthermophilic bacteria, but appears to be absent in hyperthermophilic archaea. Two types of Clp proteases are known, with either ClpP or ClpQ (HslV) as the proteolytic subunit. For full proteolytic activity, ClpP and ClpQ must associate with their respective ATPase subunits. In the case of ClpP this can be either ClpX or ClpA ATPases, whereas ClpQ associates with ClpY (HslU) ATPase (Porankiewicz et al. 1999). Both the ClpP and ClpQ proteases, as well as their respective ATPase subunits ClpC (three homologs), ClpX and ClpY were identified in the genomes of *T. maritima* and *A. aeolicus* (Deckert et al. 1998). In both *T. maritima* and *A. aeolicus*, the *clpP* gene is preceded by a putative trigger factor. The trigger factor may be involved in the export of proteins, acting as a chaperone to keep them in an open conformation. Moreover, ClpP in the *A. aeolicus* genome is followed by ClpX. In *T. maritima*, the Clp ATPases are scattered throughout the genome and are not linked to other proteases. However, ClpC-1 in *T. maritima* (TM0198) is linked to *radA*, which is involved in DNA repair. We postulate that these genes are involved in stress response and are coordinately regulated. The genes encoding ClpQ and ClpY are linked on the *T. maritima* genome and are likely co-transcribed, whereas they occur separately in the *A. aeolicus* genome. As more is learned about gene regulation in these two hyperthermophiles, the significance of these alternative arrangements for ClpQ and ClpY should become clearer.

In *E. coli*, expression of *lon*, *clpP* and the ATPase subunits *clpX* and *clpB*, are all σ^{32} -dependent (Bukau 1993), whereas in gram-positive *Bacillus subtilis* and *Lactococcus lactis*, the

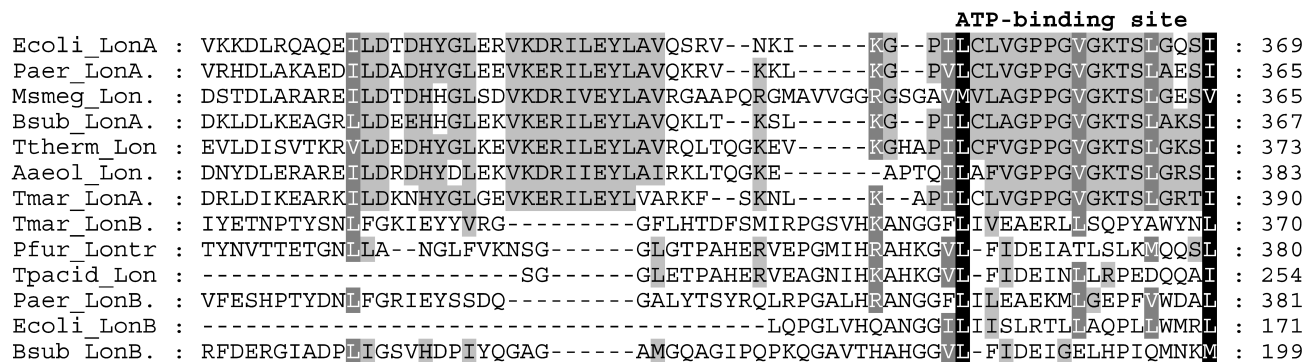


Figure 1. Multiple sequence alignment using CLUSTALX of the ATP-binding domain and active site region of the LonA and LonB homologs. Abbreviations: Ecoli = *Escherichia coli*; Paer = *Pseudomonas aeruginosa*; Msmeg = *Mycobacterium smegmatis*; Bsub = *Bacillus subtilis*; Ttherm = *Thermus thermophilus*; Aaeol = *Aquifex aeolicus*; Tmar = *Thermotoga maritima*; Pfur = *Pyrococcus furiosus*; and Tpacid = *Thermoplasma acidophilum*.

heat-shock response involves at least three classes of heat-inducible genes (Hecker et al. 1996). It has recently been found that, in gram-positive bacteria, *clpP* is under the control of a novel regulator, CtsR, belonging to Class III, which is σ^B -independent and lacks the *cis*-acting CIRCE operator sequence (Hecker et al. 1996). Analysis of the *T. maritima* genome reveals 70 putative transcriptional regulators that have moderate degrees of identity to regulators from both gram-positive and gram-negative sources (Nelson et al. 1999). Among these are homologs to the *E. coli* sigma E (*rpoE*) and the heat-shock operon repressor (HcrA) from *B. subtilis* (Nelson et al. 1999).

However, homologs to *E. coli* σ^{32} and the gram-positive regulator CtsR could not be identified. It is possible that *T. maritima* uses a novel mechanism, or a regulatory pathway that is a hybrid of that in gram-positive and gram-negative organisms.

The proteasome

The 20S proteasome, or multicatalytic proteinase (MCP), is a cylindrically shaped protease found in the Archaea, Eukarya and the gram-positive actinomycetes (Bochtler et al. 1999, Barber and Ferry 2001). The lack of the proteasome in other bacteria suggests that actinomycetes acquired the protease

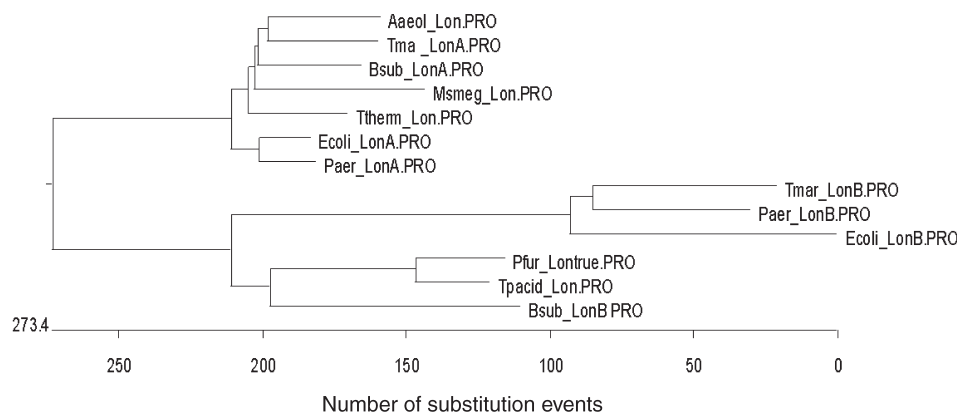


Figure 2. Phylogenetic tree of Lon proteins.

through lateral gene transfer (Lupas et al. 1997). Although most bacteria lack a version of the proteasome, they contain the related complex ClpQY (or HslVU), which shares a similar fold and catalytic mechanism with the proteasome (Bochtler et al. 1997). The proteasome from the thermophilic archaeon *Thermoplasma acidophilum* yielded the first structure of the proteasome and it has since become a prototype for the three-dimensional structure and topology of the molecule (Lowe et al. 1995). Native versions of the archaeal proteasome have been isolated and characterized from *Methanosarcina thermophila*, *Methanococcus jannaschii* and *P. furiosus* and appear to share many structural and biochemical properties with the *T. acidophilum* proteasome (Maupin-Furlow and Ferry 1995, Bauer et al. 1996, Wilson et al. 2000). The 20S structure comprises four heptametrical rings stacked on top of one another (Rechsteiner et al. 1993). Each ring comprises either α - or β -type subunits, arranged in the order $\alpha_7\beta_7\beta_7\alpha_7$, with a centralized hollow channel running the entire length of the complex (DeMartino and Slaughter 1999). To safeguard against unwanted protein degradation, the proteasome confines proteolytic activity to the interior region of this self-compartmentalized structure (DeMartino and Slaughter 1999, Goldberg 2000). Although the archaeal 20S proteasome functions as a discrete protease in vitro, it is not known if the 26S proteasome is the only functional form in vivo (Maupin-Furlow et al. 2000). Archaeal proteasomes contain various peptidase activities; most have only chymotrypsin-like activity, although some also have high trypsin-like or caspase-like activity. The archaeal proteasome acts in a processive manner, chopping protein substrates at multiple places to yield peptide fragments of three to 30 amino acids in length (Kisselev et al. 1998). Although the physiological role of the archaeal proteasome is unclear, inhibitor-based studies show that *T. acidophilum* cells can proliferate without a functional proteasome under normal growth conditions, but cannot grow without proteasome activity under heat shock conditions (Ruepp et al. 1998).

All archaeal genomes sequenced to date contain homologs of the 20S proteasome core structure, including members of both Crenarchaeota and Euryarchaeota (see Tables 1 and 2). The genomes of *Aeropyrum pernix*, *Pyrococcus* spp. and *S. solfataricus* each contain two different β subunit homologs (see Tables 1 and 2), and two different α subunits have been identified in the halophilic archaeon *Haloferax volcanii* (Wilson et al. 1999). In Archaea, the genes encoding the α and β proteasome subunits appear to be transcribed as a part of independent operons that have conserved gene organization, whereas the genes surrounding *pan* (proteasome activating nucleotidase) do not appear to be conserved (Maupin-Furlow et al. 2000). In addition, the archaeal proteasome appears to be a part of a superoperon containing subunits of the exosome, indicating a possible functional link between RNA processing and proteolysis in this domain (Koonin et al. 2001).

It is clear that hyperthermophiles, like their mesophilic counterparts, have a full complement of ATP-dependent proteases at their disposal. However, the proteases differ between the two domains, the proteasome and Lon proteases being

present in Archaea and the Lon, Clp and FtsH being present in Eubacteria. Although much is known about ATP-dependent proteases and their metabolic roles in mesophilic eubacteria, one cannot assume that they have identical roles or regulation patterns in hyperthermophilic bacteria. Moreover, little is known about the metabolic roles and regulation of the proteasome and Lon in Archaea.

ATP-independent proteases in hyperthermophiles

Most heterotrophic hyperthermophiles can grow on proteinaceous substrates as primary carbon and energy sources. Such substrates must initially be acted on by extracellular proteases, which may or may not be cell-associated. The products of extracellular hydrolysis are transported into the cell, presumably by an ABC-type transporter, where they are further broken down to individual amino acids by the concerted action of intracellular proteases and peptidases. It is thought that peptides can be oxidized to CO_2 in *Thermoproteus tenax*, *Archaeoglobus fulgidus* and *S. solfataricus*, with sulfur, thio-sulfate, sulfate, oxygen, nitrite and nitrate serving as terminal electron acceptors (Schönheit and Schäfer 1995). In species from the genera *Thermococcus*, *Pyrococcus*, *Thermotoga*, *Desulfurococcus* and *Pyrodictum*, peptides are likely fermented to free acids, such as acetate, isovalerate, butyrate and phenylpyruvate, generating ATP by substrate-level phosphorylation (Schäfer et al. 1993, Schönheit and Schäfer 1995). Parts of these pathways can be constructed by analysis of the genomes of these organisms, although the details of metabolic schemes involved in peptide fermentation in these organisms are unknown.

Proteases and peptidases presumably involved in the initial steps in protein and peptide utilization have been isolated from hyperthermophilic archaea, including *Pyrococcus* spp. (Halio et al. 1996, Voorhorst et al. 1996, Chang et al. 2001), *Thermococcus stetteri* (Klingeberg et al. 1995), *A. pernix* (Sako et al. 1997) and *P. abyssi* (Dib et al. 1998) (see Table 3). The only protease isolated from *T. maritima* thus far is a homomultimeric protease that has moderate amino acid sequence identity to bacteriocins from mesophilic bacteria (Hicks et al. 1998). Within the classical classification scheme for proteases, namely, serine, aspartic, metallo and cysteine, the majority of the enzymes characterized to date from hyperthermophiles has been extracellular, and belongs to the serine class. Although these enzymes have been well characterized biochemically, little is known about their metabolic significance and even less about their regulation.

Proteolysis in hyperthermophilic bacteria is poorly understood, despite the availability of complete genomic sequences for *T. maritima* (Nelson et al. 1999) and *A. aeolicus* (Deckert et al. 1998). To date, only two proteases (Hicks et al. 1998, Choi et al. 1999) and a leucine aminopeptidase (Khan et al. 2000) have been characterized biochemically from hyperthermophilic bacteria. A 43-kDa serine protease was identified in *Aquifex pyrophilus* using a sequence tag specific for serine proteases (Choi et al. 1999). The gene encoding the protease was sequenced and found to contain a putative signal se-

Table 3. Proteases and peptidases isolated from hyperthermophilic microorganisms. Abbreviations: (NP) = recombinant form, not purified from host; M = metalloprotease; Ser = serine; Cys = cysteine; E = extracellular; I = intracellular; and MA = membrane associated.

Organism	Protease	Type	T _{opt} (°C)	pH _{opt}	MW (kDa)	Location	Reference
Crenarchaeota							
<i>Sulfolobus acidocaldarius</i>	Thermopsin	Acid	90	2	Calc. 32.6, App 46–51	E	Fusek et al. 1990, Lin et al. 1991
<i>Sulfolobus solfataricus</i>	Aminopeptidase	M (Co ²⁺ /Mn ²⁺)	75	6.75	4 × 80 (320)	I	Hammer et al. 1990
<i>S. solfataricus</i>	Carboxypeptidase	M (Zn ²⁺)	85	5.5–7/9	4 × 42 (170)	I	Colombo et al. 1992, 1995
<i>S. solfataricus</i>	Proteinase I	Ser	> 90	6.5–8	2 × 54 (118)	I	Burlini et al. 1992
<i>Aeropyrum pernix K1</i>	Aeropyrolysin	M	100 (- CaCl ₂) 110 (+ CaCl ₂)	6.0–8.0	52	E	Sako et al. 1997
<i>A. pernix K1</i>	Pemilase	Ser	90	9	50	I	Chavez Crocker et al. 1999
<i>Desulfurococcus mucosus</i>	Archaeolysin	Ser	90–95	7.2	43–54	E	Cowan et al. 1987
<i>Pyrobaculum aerophilum</i>	Aerolysin (NP)	Ser				E?	Volkl et al. 1994
Euryarchaeota							
<i>Pyrococcus abyssi</i> st 549	Protease from <i>Pub</i> (PPA)	Ser	95	9	60, 105, 150	E	Dib et al. 1998
<i>Pyrococcus furiosus</i>	Carboxypeptidase (PfuCP)	M (Co ²⁺)	90–100	6.2–6.5	2 × 58–9 (128)	I	Cheng et al. 1999
<i>P. furiosus</i>	Deblocking aminopeptidase (DAP)				10–12 subunits (size not reported)	I	Tsunasawa 1998
<i>P. furiosus</i>	Methionine aminopeptidase (PMAP) (NP)	M (Co ²⁺)	~90	7.0–8.0	32.74	I	Tsunasawa et al. 1997, Tahirov et al. 1998
<i>P. furiosus</i>	Proline dipeptidase/prolidase	M (Co ²⁺)	100	7	2 × 39.4–42 (79)	I	Ghosh et al. 1998
<i>P. furiosus</i>	Prolyl endopeptidase/oligopeptidase (POP)	Ser	85–90	7.0–8.0	Calc. 70–1, App 59	I	Robinson et al. 1995, Harwood et al. 1997, Harris et al. 2001
<i>P. furiosus</i>	Protease I (PfpI)	Cys	105	7	18.8 subunit, 60 and 120 native	I	Blumentals et al. 1990, Hailo et al. 1996, 1997, Du et al. 2000, Chang et al. 2001
<i>P. furiosus</i>	Pyrolysin	Ser	115	6.5–10.5	150	MA	Voorhorst et al. 1996
<i>P. furiosus</i>	Pyroglutamate carboxyl peptidase (PpPCP) (NP)	Cys	~90	6.0–9.0	4 × 22.8 (96.3)	I	Tsunasawa et al. 1998
<i>Pyrococcus horikoshii</i>	Aminopeptidase (NP)	Ser	95	7.5	X × 36.9 (440)	I	Ando et al. 1999
<i>Thermococcus kodakaraensis</i>	Subtilisin-like protease (NP)	Ser	80	9.5	43.8	E?	Kamman et al. 2001
<i>T. kodakaraensis</i>	Thiol protease (TT)	Cys	110	7	44	E	Morikawa et al. 1994
<i>Thermococcus litoralis</i>	Pyroglutamate carboxyl peptidase (NP)	Cys	70 or 75		4 × 24 (96)	I	Singleton et al. 1999, 2000
<i>T. stetteri</i>	Stetterlysin	Ser				MA	Voorhorst et al. 1997
<i>T. stetteri</i>	SDS-resistant protease	Ser	85	8.5–9	68	E	Klingeberg et al. 1995
<i>Staphylothermus marinus</i>	STABLE protease	Ser	90	9	150	MA	Peters et al. 1995, Mayr et al. 1996
<i>Thermoplasma acidophilum</i>	Tricorn protease (TRI)	Ser	65	8.5–8.8	120 (monomer); 720 (hexamer); 14,600 (icosahedral capsid/20 hexamers)	I	Tamura et al. 1996
Bacteria							
<i>Aquifex pyrophilus</i>	Serine-type protease (NP)	Ser	85	7.0–9.0	43	MA	Choi et al. 1999
<i>Fervidobacterium pennivorans</i>	Fervidolysin	Ser	80	10	73 (precursor); 58 (mature protease); 130 (Friedrich – native purif.)	MA	Friedrich and Antranikian 1996, Kluskens et al. 2001
<i>Thermotoga maritima</i>	Maritimacin		90–93	6.0–9.0	X × 31 (> 669)	I	Hicks et al. 1998, 2001

quence. The protease was identified in the cell wall fraction of *A. pyrophilus*, demonstrating that the protease is expressed in the native organism and that it is exported from the cell. However, the role of the protease is unclear because *Aquifex* spp. appear unable to use peptides as a carbon or nitrogen source (Deckert et al. 1998). Choi et al. (1999) suggested that the protease is associated with the cellular S-layer, but whether it is involved in protein degradation or is involved in S-layer formation is unclear. Similarly, in *T. maritima*, analysis of the genome identified about 35 proteases and peptidases, 12 of which may be exported (see Tables 1 and 2). However, growth of *T. maritima* on peptides as sole carbon and energy sources has not been reported.

Among the hyperthermophiles, proteolysis has been best studied in members of the order Thermococcales. These organisms can use peptides as sole carbon and energy sources and this is reflected in a range of proteolytic activities in their cell extracts and confirmed by genomic sequence analysis. Initial efforts to study *P. furiosus* indicated that the organism was highly proteolytic (Blumentals et al. 1990, Eggen et al. 1990, Connaris et al. 1991). Analysis of the *P. furiosus* genome has thus far revealed the presence of about 40 genes encoding proteases, protease subunits, or peptidases (Table 1). Nine of the identified proteases contain a putative signal sequence, suggesting that they are exported from the cell. A comparative genomics approach was also used to compare *P. furiosus*, *P. abyssi* and *P. horikoshii* in an effort to access the proteolytic inventory within this narrow phylogenetic range of the Thermococcales (Table 1). Similar to *P. furiosus*, both *P. abyssi* and *P. horikoshii* are highly proteolytic, with 34 genes encoding proteolytic enzymes detected in their genome sequences. It is apparent that, despite their close phylogenetic relationship, there are distinct differences between these organisms in their respective proteolytic inventories. *Pyrococcus furiosus* has four proteases (pf_699579, pf_1553191, pf_1757236 and pf_1136394) and three aminopeptidases (pf_1898123, pf_1902688 and pf_1906416) that are absent from *P. abyssi* and *P. horikoshii*. There is only one protease unique to *P. abyssi* (CAAX Prenyl protease, PAB0555), whereas no proteases yet identified are unique to *P. horikoshii*. Moreover, there is a clear distinction between the pyrolysin proteases in the Thermococcales. The pyrolysin from *P. furiosus* is only 17% identical to the pyrolysin-like proteases of *P. abyssi* and *P. horikoshii*, and 33% identical to stetterolysin from *Thermococcus stetteri*, whereas the pyrolysin-like proteases of *P. abyssi* and *P. horikoshii* are 69% identical. Differences in proteolytic content of Thermococcales can also be seen by zymogram analysis. For example, Figure 3 shows that the extracellular proteases expressed by *P. furiosus*, *P. abyssi*, *Thermococcus profundus*, *Thermococcus peptonophilus* and *Thermotoga maritima* vary when grown in the same medium at their respective temperature optima with tryptone (5 g l^{-1}) as the primary carbon and energy source.

Several extracellular (Morikawa et al. 1994, Klingenberg et al. 1995, Dib et al. 1998, Kannan et al. 2001) and membrane-associated proteases (Voorhorst et al. 1996, 1997) have been

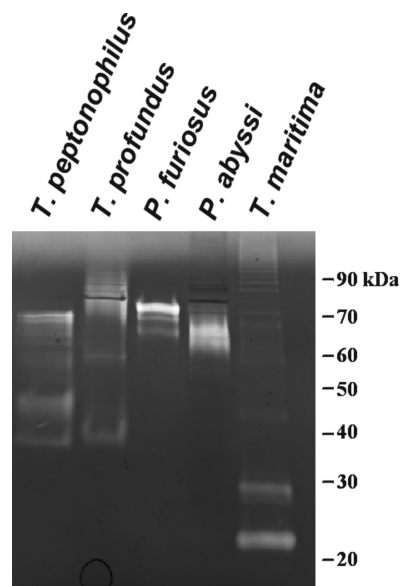


Figure 3. Extracellular proteolytic inventory from various hyperthermophiles. *Pyrococcus furiosus* and *P. abyssi* were grown at 95 °C, and *T. profundus*, *T. peptonophilus* and *Thermotoga maritima* were grown at 80 °C. The cells were removed after 14 h of growth and the extracellular enzymes were precipitated by addition of ammonium sulfate to 80%. Two μg of total extracellular protein was loaded onto a 12% SDS-polyacrylamide gel containing gelatin.

characterized biochemically from both *Thermococcus* and *Pyrococcus* spp. With the exception of the thiol protease from *T. kodakaraensis*, all the extracellular and membrane-associated proteases have been classified as serine proteases. The proteases range in size from 40 to 68 kDa and are monomeric, with the exception of the *P. abyssi* protease, which is multimeric. The serine protease from *T. kodakaraensis* has broad substrate specificity, cleaving at the carboxyl termini of Tyr, Phe, Leu, Gln, His, Thr, Ser and Ala (Kannan et al. 2001). The other serine proteases from *Thermococcus stetteri* and *P. abyssi* have fairly specific substrate specificity, preferring Arg/Phe and Aromatic/Leu at the P1 position, respectively (Klingenberg et al. 1995, Dib et al. 1998). Substrate specificity of the thiol protease was not determined.

An intracellular protease identified in *P. furiosus* (Blumentals et al. 1990) and designated *Pyrococcus furiosus* protease I (PfpI) was found to be based on a single 18.8-kDa subunit (Halio et al. 1997). The gene encoding this subunit has putative homologs in other cells and microorganisms from the three domains of life, including *M. jannaschii*, *B. subtilis*, *E. coli* and *Homo sapiens*, but not *T. maritima* or *Saccharomyces cerevisiae*. In vitro, PfpI occurs in at least three functional forms, a trimer, a hexamer and a dodecamer, and is most active as a dodecamer (Chang et al. 2001). The physiological role of PfpI is unclear, but it complements the proteasome in *P. furiosus*; in vitro, a synergistic relationship between the two proteases has been noted (Chang et al. 2001). Because *P. furiosus* lacks the tricorn protease (Table 1), we speculate that PfpI assumes this role in *P. furiosus*. It also appears to be a

predominant protease in *P. furiosus* based on zymogram analyses. The three-dimensional structure of the PfpI homolog in *P. horikoshii* (PhpI) (90% identical at the amino acid level) was recently reported (Du et al. 2000). The structure was consistent with previously reported biophysical information: PhpI is a dodecamer consisting of two identical six-member rings, each with axes of symmetry such that it consists of a dimer of trimers or a trimer of dimers. This supports the observation that, in vitro, it exists in at least three functional forms (P.M. Hicks, North Carolina State Univ., and R.M. Kelly, unpublished data). Furthermore, even though PfpI/PhpI are not ATP-dependent, the structure of PhpI suggests a similar barrel-like compartmentalization of the active site, reminiscent of the 20S proteasome and ClpP. The possible relationship of PfpI/PhpI and other ATP-independent proteases with protected active sites to ATP-dependent proteases needs to be examined, especially with respect to the evolutionary significance of the energetic requirement.

Sulfolobus solfataricus can use proteinaceous compounds as primary carbon and energy sources, and analysis of the *S. solfataricus* genome revealed the presence of 37 genes encoding proteases, protease subunits, or peptidases (Table 2). The tricorn protease as well as the interacting F factors F1, F2 and F3, which are aminopeptidases, were also identified (She et al. 2001). Although it has not been characterized in *S. solfataricus*, the tricorn protease has been well characterized in the thermophilic archaeon *Thermoplasma* (Tamura et al. 1998). Tricorn protease, in conjunction with its three interacting factors, degrades oligopeptides in a sequential manner, yielding free amino acids.

Two proteases have been characterized in *Sulfolobus* spp.; a heat-stable intracellular serine protease from *S. solfataricus* (Burlini et al. 1992), and the acid protease thermopsin from *S. acidocaldarius* (Fusek et al. 1990, Lin et al. 1991). The protease from *S. solfataricus* has a subunit molecular mass of 54 kDa and the active form is 118 kDa, suggesting that it exists as a dimer. The enzyme has chymotrypsin-like specificity, preferring aromatic or bulky aliphatic amino acids, but differs from chymotrypsin in being unable to digest natural substrate proteins like insulin chains A and B (Burlini et al. 1992). Thermopsin has a predicted molecular mass of 32.6 kDa, but was found to be a monomer with a molecular mass of 46 kDa. The difference in molecular mass is likely because thermopsin is a glycoprotein (Lin et al. 1991). Thermopsin is capable of degrading various protein substrates, such as hemoglobin, ovalbumin, bovine serum albumin and insulin chain B (Fusek et al. 1990). The enzyme has a rather broad substrate specificity but, similar to pepsin, prefers hydrophobic residues to flank the cleavage site.

Proteases specific to hyperthermophiles

Genome sequence analysis shows that there is considerable conservation of certain proteases across all domains of life and growth temperature ranges. However, some proteases appear unique or more common to hyperthermophiles. For example, three clostripain-related proteases appear to be found only in

T. maritima. These proteases have limited homology (32% identical in a 125 amino acid region) to the heterodimeric cysteine endoprotease from *Clostridium histolyticum* (Dargatz et al. 1993). However, given the difficulties in cloning and expressing active forms of hyperthermophilic proteases in mesophilic hosts, biophysical and biochemical information for these enzymes may need to rely to a great extent on direct purification.

There are examples of proteases that, from a structural or functional perspective, may be unique to hyperthermophiles. For example, the homomultimeric protease in *T. maritima* based on an approximately 31-kDa subunit has significant homology at the amino acid sequence level to a gene encoding a mesophilic bacteriocin, linocin M18; this protease has been tentatively named maritimacin (Hicks et al. 1998). A putative homolog to this protease has also been identified in the genome sequence of *P. furiosus*, but the enzyme appears to be absent from the rest of the Archaea (Table 1). Linocin M18, a multimeric assembly of a single 31-kDa subunit isolated from *Bevibacterium linens*, was found to be antagonistic to a wide spectrum of mesophilic coryneform and other gram-positive bacteria (Valdes-Stauber and Scherer 1996). However, the physiological function of this protein in these two hyperthermophilic organisms and its relationship to bacteriocins are unknown. Initial efforts to screen the purified *T. maritima* protease for bacteriocin-like activity focused on several hyperthermophiles that are readily cultured, including hyperthermophilic archaea. However, no significant antagonistic activity was found, although the presence of the putative protease seemed to extend the lag phase for *Thermococcus litoralis* (Hicks et al. 2001).

Pyrolysin is a cell envelope-associated protease that has N-terminal sequence homology with subtilisin-like serine proteases purified from *P. furiosus* (Voorhorst et al. 1996). The enzyme exhibits endopeptidase activity and may be involved in the first step of protein utilization during proteolytic growth (Voorhorst et al. 1996). Pyrolysin exists as a mosaic of domains shared by other proteases containing 1398 amino acid residues, including a conserved pre-proenzyme region, a catalytic domain of 500 residues, and a large C-terminal extension, making it one of the largest known serine proteases (de Vos et al. 2001). Pyrolysin exhibits highest identity with the catalytic domain of the eukaryal tripeptidyl peptidases II, a subgroup of the subtilisin-like proteases (Voorhorst et al. 1996). Although the catalytic domain of pyrolysin is found in a putative subtilase from *P. furiosus*, the intact gene is absent from the genome sequences of the rest of the Archaea, including *P. horikoshii* and *P. abyssi*. However, a gene was identified in the genome sequences of *P. horikoshii* (PH0310) and *P. abyssi* (PAB1252), which includes the conserved pre-pro- and C-terminal sequences of pyrolysin, but contains a putative protease with a thiol-protease catalytic domain rather than serine protease activity (de Vos et al. 2001).

Another surface layer bound subtilisin-like protease, STABLE, has been identified in *Staphylothermus marinus* (Mayr et al. 1996) that has some relationship to pyrolysin in that specific motifs are common to both proteases. This protease pre-

sumably digests and provides peptides to this organism, which grows by sulfur-dependent, peptide fermentation.

Evolutionary aspects of proteolytic processes

Given that hyperthermophiles arguably represent an early evolutionary linkage, the question concerning the minimum set of proteases required for cellular function in these organisms arises. About half of the genes contained in hyperthermophilic genomes are still unassigned in terms of function (Nelson et al. 1999), and it seems certain that as yet undetected proteases are among those unidentified genes. About 60–70 putative and actual proteases/peptidases can be gleaned from the *E. coli* genome sequence by informatics techniques similar to those used here for the hyperthermophiles (K.R. Shockley and R.M. Kelly, unpublished data); this is about twice as many as noted in each of the five hyperthermophiles examined here (Table 2). We also note that the *E. coli* genome is about 2.5-fold larger than the pyrococcal and *T. maritima* genomes, which may relate to differences in protease inventory. However, *S. solfataricus* and *E. coli* have comparably sized genomes but differ significantly in the numbers of putative and confirmed proteases. Information about the expression and activation of specific proteases under various environmental conditions is needed to resolve the relationship between genotype and phenotype for each organism. The biochemical properties of specific proteases in these organisms will have to be reconciled with their regulation to provide some perspective on the global regulation of proteolysis.

It is intriguing to consider the origin and development of proteases based on the multimeric assembly of small (~20–30 kDa) subunits into complex ring-like structures. This is the basis for the proteasome and Clp proteases, both of which are ATP-dependent. Such structures help sequester the active sites in these proteases, presumably to avoid unwanted protein turnover. The PfpI from *P. furiosus* and its homologs are based on a similar structural organization (~19-kDa subunits arranged into two six member rings) yet have no ATP-dependence (Du et al. 2000). Furthermore, there may be an additional structural relationship between these proteases, given that antibodies raised against the eukaryotic proteasome and *E. coli* ClpP recognized PfpI in Western blots (Halio 1995). The evolutionary significance of these multi-subunit proteases and the complexity introduced through ATP-dependence merits further examination. It will be interesting to determine whether various proteolytic phenotypes recruit specific sets of proteases to certain tasks involving protein turnover under normal and stressed conditions and how the interplay between ATP-dependence and ATP-independence is regulated. If it turns out that hyperthermophiles contain fewer proteases than other cells and organisms, they may provide an interesting perspective on the complex nature of protease function and regulation.

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