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DIVERSITY OF CRISPR SYSTEM In the euryarchaeal pyrococcales [1]

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CRISPR-Cas systems: RNA-interference-based immune systems in procaryotes

CRISPR-cas systems are found in approximately 48% of sequenced bacteria and 90% of sequenced archaea. They function as **prokaryotic immune systems**, in that they confer resistance to exogenous genetic elements.

CRISPRs (Clustered Regularly Interspaced Short Palindromic Repeats) are arrays of direct variable short repeats separated by sequences called spacers or guides that generally derived from invader genetic elements such as plasmids and prophages. CRISPR-associated (*cas*) genes are often located adjacent to the CRISPR locus. They



- Acquisition: new spacers are incorporated into the genome between CRISPR after repeats, each foreign exposure to new element.
- Expression: small non-coding CRISPR RNAs (crRNAs) are generated. A long precursor is first produced then processed between repeats and matured into crRNAs.
- Interference: crRNAs-Cas protein complexes bind to invading nucleic acid target and cleave it

Bioinformatic tools for studying the diversity of CRISPR and cas genes in six pyrococcal



GTTCCAATAAGACTAAAAAATTGAAAAG

Group1	BRE/TATA	\checkmark	DR1	Group2		
P.furiosus	crl … GGGTAAGTTGGATGCCCCGTAAAGGTTATAAATTCGAGTGA	TATAGTTACTCCGTAGGAGTATTGGGGCCGAAAJ	AAGCCCCCTGTTCCAATAAGACTAAAATAGAATTGAAAG			
	Cr6 ··· GGGTAAGTTGGATGCCCCGTAAGGGTTATAAATTCAAGTGAT	TATAATTACTCCATAGGAGTATTGGGGCCGAAAJ	AAGCCCCCTGTTACAATAAGACTAAAATAGAATTGAAAG			
	Cr7 ··· GGGTAAGTTGGATGCCCCGTAAGGGTTATAAATTCAAGTGA	TATAATTACTCCATAGGAGTATTGGGGCCGAAA/	AAGCCCCCTGTTCCAATAAGACTACAAAAGAATTGAAAG	P.horikoshi		
	Cr2 ··· GGGTAAGGTTGATGTCCCGTAAGGCTTATAAA-~TTCGAGTGA	TATAGTTACTCTGTAGGAGTATTGGGGGCAAAA	AAGCCCCCTGTTCCAATAAGACTACAAAAGAATTGAAAG	G		
	CT8 ··· GGGGAAGGTGGATGTCCCGTAAGGCTTATAAATTCGAGTGAY	TATAATTACCCCAATGGGGAATTAGGGCAAAA	AAGCCCACTGTTCCAATAAGACTACAAAAGAATTGAA~G			
	Cr5 CectaasttegatsccccgtaaggttataaaTtcaagtga	TATAATTACTCCATAGGAGTATTGGGGCGAAAZ	AAGCCCCCTGTTACAATAAGACCAAAATAGAATTGAAAG	P. STO4		
	CL4 ···· TGATAAGICTAACACCCCGTAAGCCTTATAAATTCGAGTGA	IGTAGTCACTCCGTAGGAGAATTAGGACGAAAA	AAGCTCCCTGTTCCAATAAGACTACAAAAGAATTGAAAG			
P.yayanosii	CF2 COTTAAGACCCCCCTCGCCAAAAGATTTATAAAA TCCAAGACT	CCCAAGAAAAGCATAGAAGAAAACAAGCAAAAA	AACCCACCTGTTCCAATAAGACTCAAAGAGAATTGAAAG			
	CI3 ··· CGTTAAGACCCCCCTCGCCAAAAGATTTATAAAA-TCCAAGACT	CCCAAGAAAAGCATAGAAGAAAACAAGCAAAAA	AACCCACCTGTTCCAATAAGACTCAAAGAGAATTGAAAG	P. abvssi		
	CI4 ···· CGTTAACACCCCCTTCLCCCAAAAGATTTATAAAA-TCCCAGGACTC	CCCARGAAAAGCATAGAAGAAAACAAGCAAAAA	AACCCACLTGTTCCAATAAGACTCAAAGAGAATTGAAAG			
		SCIANGANGNGI AGGAAGAAAACAAGCAAAAA	AGCCCGCLTGTTCCAATAAGACTCAAAGAGAATTGAAAG			
P. norikosnii	GF6 ····· ARAAGTAGCAGGATACCCAAAAGTCTTATAAAA-TTTGAGTGAG	IATAGTAACTUCAGTAGAGAAATAAAGCAAAA	ITGGCTCCTGTTCCAATAAGA4TAAAATAGAATTGAAAC			
		TATAGTAACTCTAGTAGAGAAATAAAGCAAAAT	TTGGCTCCTGTTCCAATAAGACTAAAATAGAATTGAAAG	G P.yayanosii		
	CED TGATAAGTCTAACACCCGTAAGCCTTATAAATTCGAGTGA	IGIAGICACICCGIAGGAGAATTAGGACGAAAA	AAGCTCCCTGTTCCAATAAGACTATAAGAGAATTGAAAG			
P.sp5104	642 ···· TAAAAAAGeeeeerea-caaaaacettataaaaateaaggeaa	JGAAAATACTACAAAAACAAAAAACACCCAAAAA	AAGCCCCCTGTTCCCAATAAGACTATAAGAGAATTGAAAG			
	GE6 ···· TAAAAAGCCCCCCTCCAGCAAAAACCCTTATAAAAAATCAAG-~AG	JAATAAT~GT-~AAAAACAAAAAACACCCAAAAA	AAGCCCCCTGTTCCCAATAAGACTAAAAAAGAATTGAAAG	P.horikoshii		
	CES ···· AAAAACAACCCCCTTGCCAAAAACCTTATAAAAAACAAGA-CAA	AAGAACAACGTAAAAACAAAAAACACCCAAAAA	AAGCCCCCAGTTCCAATAAGACTAAAAAAGAATTGAAAG	2.2.0		
P.spNA2	CEA CLAAATAATCCCTCCACCAAAAATCTTATAAAAATT-ARCCCA	JARGARCAGTATGARAACAAAAAACACCCAAAAA	ARGCCTCCTGTTCCAATAAGAC CATAAGAGAATTGAAAT			
	CFZ ···· CAGAGGGCTCCAATACCAGAAAAGCTTATAAAA-TTAGAGTAA	IGTAATTUUTUTATAGGAGAAATAGAGCAAAAA	ATCGCGCCTGTTCCAATAAGACTAAAAGAGAATTGAAAG	P 5704		
	CES GGGAAACCATCGATATCCAAAAAGCTTATAAAA-TTGGAGTAA	···· GOGAAACCATCGATATCCAAAAAGCTTATAAAA-TTGGAGTAATCCACTATAGAGGAAAATAGAGCAAAAATCGCGCCCTGTCCCAATAAGACTAAAATAGAATTGAAAG				
P.aDyssi	CTI ···· CAATGAACTCCAATACCAGAAAAGCTTATAAAA-TTGAAGCGAG	CGTAACTCCTTTATAGGGAAAATAAAGCAAAA	ACGGCCCCTGTTCCCAATAAGACTAAAATAGAATTGAAAG			
	CE4 TATCAAGGCACGTTACCAGAAACCCCTTATAAGA-TCGGAGGAT		atcgaccetsffccaataagastaaaatagaattgaaag	P.abyssi		

#GTTTCCGTAGAAC_TAATAGTGTGGAAAG

Conclusions

Three different *cas* genes types were identified within the six pyrococcal genomes (subtypes I-A, III-A and III-B). Subtype I-A is ubiquitously represented. Sequence alignments show strong homologies between CRISPRs and Cas proteins belonging to similar systems.

The diversity of CRISPR system situations in the Pyrococcales illustrates the modularity and instability of





Model of pyrococcal CRISPR mode of action

CRISPR systems.

There are lot of things that we still do not understand but knowledge in the CRISPR field is added as quickly as guide sequences in an active CRISPR array.

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