

The ciliate cryptosystem

Marion Scheepers

BoiseCrypt Fall 2009

Outline

- 1 What are ciliates?
- 2 Ciliates and Cryptography
- 3 What is the encryption cipher?
- 4 Programmability
- 5 Computational Power

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Single cell organisms - I.

Prokaryotic

Genome

Organized in a circular DNA molecule. No nuclear membrane.

Proliferation

By binary cell division.

Eukaryotic

Genome

Organized in linear DNA molecules. Enclosed in a nuclear membrane.

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Single cell organisms - II.

Prokaryotic

Genetic Diversity

Maintained by plasmid donation.

Eukaryotic

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Maintained by genetic exchange.

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Ciliates - Nuclear Duality.

Macro Nucleus (MAC)

Ploidy

Polyploid.

Transcription

Transcriptionally active.

Micro Nucleus (MIC)

Ploidy

Diploid.

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Transcriptionally silent.

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The Ciliate MIC.

Fact

Only the MIC undergoes meiosis and mitosis.

Fact

Ciliates exchange only MIC data during conjugation.

Fact

The MIC is an encrypted version of the MAC.

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- 1 What are ciliates?
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The ciliate MIC exchange protocol.

The MIC-exchange protocol is essentially a Diffie-Hellman key exchange protocol:

- 1 Conjugants form a cytoplasmic bridge

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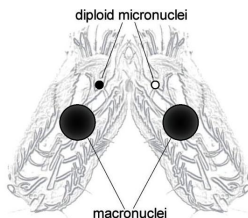
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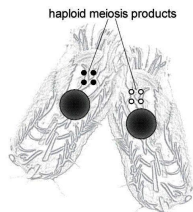
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- 2 Each conjugant meiotically divides a MIC into four haploid copies
- 3 Each conjugant produces a cache of MIC derived RNA, micRNA

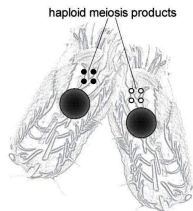
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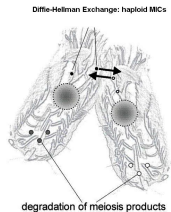
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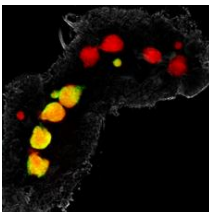
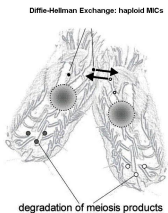
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DH-MIC decryption.

Conjugants now are in possession of:

- 1 their original nuclei O-MIC and O-MAC, as well
- 2 the just obtained DH-MIC.

Each conjugant subsequently:

- 1 replicates the DH-MIC;
- 2 selects one DH-MIC for decryption;
- 3 decrypts the DH-MIC data to obtain the DH-MAC data;
- 4 destroys all copies of O-MIC and O-MAC.

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Grille ciphers

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Pattern: 1-4-6-8-7-5-3-2

Final Message: **The man was absorbed in his own destiny, deaf to the ideas of others.**

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Examples

Gene	Organism	Pattern
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	<i>Stylonychia Lemnae</i>	3-4-5-6-7-8-10-2-1-9
	<i>O. Trifallax</i>	3-4-6-5-7-9-10-2-1-8
	<i>Uroleptus Pisces</i>	1-2-4-8-6-15plus 3-5-7-10-13-12-9-14-16-11
α TBP	<i>Oxytricha Nova</i>	1-3-5-7-9-11-2-4-6-8-10-12-13-14
	<i>O. Trifallax</i>	1-3-5-7-10-12-2-4-6-8-9-11-13-14-15-16-17
	<i>S. Mytilus</i>	like O. Nova
USG1	<i>Uroleptus sp</i>	1-2-3-4-7-8-9-10-11-12-13-14-15-5-6
Upr	<i>Uroleptus sp</i>	1-2-4-5-6-8-11-13-15-16 and 7-9-3-10-12-14

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	<i>O. Trifallax</i>	1-3-5-7-10-12-2-4-6-8-9-11-13-14-15-16-17
	<i>S. Mytilus</i>	like O. Nova
USG1	<i>Uroleptus sp</i>	1-2-3-4-7-8-9-10-11-12-13-14-15-5-6
Upr	<i>Uroleptus sp</i>	1-2-4-5-6-8-11-13-15-16 and 7-9-3-10-12-14

Examples

Gene	Organism	Pattern
Actin I	<i>Oxytricha Nova</i>	8-7-1-2-4-3-5-9-6
	<i>Stylonychia Lemnae</i>	3-4-5-6-7-8-10-2-1-9
	<i>O. Trifallax</i>	3-4-6-5-7-9-10-2-1-8
	<i>Uroleptus Pisces</i>	1-2-4-8-6-15plus 3-5-7-10-13-12-9-14-16-11
α TBP	<i>Oxytricha Nova</i>	1-3-5-7-9-11-2-4-6-8-10-12-13-14
	<i>O. Trifallax</i>	1-3-5-7-10-12-2-4-6-8-9-11-13-14-15-16-17
	<i>S. Mytilus</i>	like O. Nova
USG1	<i>Uroleptus sp</i>	1-2-3-4-7-8-9-10-11-12-13-14-15-5-6
Upr	<i>Uroleptus sp</i>	1-2-4-5-6-8-11-13-15-16 and 7-9-3-10-12-14

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Actin I	<i>Oxytricha Nova</i>	8-7-1-2-4-3-5-9-6
	<i>Stylonychia Lemnae</i>	3-4-5-6-7-8-10-2-1-9
	<i>O. Trifallax</i>	3-4-6-5-7-9-10-2-1-8
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α TBP	<i>Oxytricha Nova</i>	1-3-5-7-9-11-2-4-6-8-10-12-13-14
	<i>O. Trifallax</i>	1-3-5-7-10-12-2-4-6-8-9-11-13-14-15-16-17
	<i>S. Mytilus</i>	like O. Nova
USG1	<i>Uroleptus sp</i>	1-2-3-4-7-8-9-10-11-12-13-14-15-5-6
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	<i>O. Trifallax</i>	3-4-6-5-7-9-10-2-1-8
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α TBP	<i>Oxytricha Nova</i>	1-3-5-7-9-11-2-4-6-8-10-12-13-14
	<i>O. Trifallax</i>	1-3-5-7-10-12-2-4-6-8-9-11-13-14-15-16-17
	<i>S. Mytilus</i>	like O. Nova
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	<i>Stylonychia Lemnae</i>	3-4-5-6-7-8-10-2-1-9
	<i>O. Trifallax</i>	3-4-6-5-7-9-10-2-1-8
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	<i>O. Trifallax</i>	1-3-5-7-10-12-2-4-6-8-9-11-13-14-15-16-17
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USG1	<i>Uroleptus sp</i>	1-2-3-4-7-8-9-10-11-12-13-14-15-5-6
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Actin I	<i>Oxytricha Nova</i>	8-7-1-2-4-3-5-9-6
	<i>Stylonychia Lemnae</i>	3-4-5-6-7-8-10- $\bar{2}$ - $\bar{1}$ -9
	<i>O. Trifallax</i>	3-4-6-5-7-9-10- $\bar{2}$ - $\bar{1}$ -8
	<i>Uroleptus Pisces</i>	1-2-4- $\bar{8}$ - $\bar{6}$ -15plus 3-5-7-10-13- $\bar{12}$ - $\bar{9}$ -14-16- $\bar{11}$
α TBP	<i>Oxytricha Nova</i>	1-3-5-7-9-11-2-4-6-8-10-12-13-14
	<i>O. Trifallax</i>	1-3-5-7-10-12-2-4-6-8-9-11-13-14-15-16-17
	<i>S. Mytilus</i>	like O. Nova
USG1	<i>Uroleptus sp</i>	1-2-3-4-7-8-9-10-11-12-13-14-15-5-6
Upr	<i>Uroleptus sp</i>	1-2-4-5-6-8-11-13-15-16 and 7-9-3-10-12-14

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	<i>O. Trifallax</i>	1-3-5-7-10-12-2-4-6-8-9-11-13-14-15-16-17
	<i>S. Mytilus</i>	like O. Nova
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	<i>Uroleptus Pisces</i>	1-2-4- $\bar{8}$ - $\bar{6}$ -15 plus 3-5-7-10-13- $\bar{12}$ - $\bar{9}$ -14-16- $\bar{11}$
α TBP	<i>Oxytricha Nova</i>	1-3-5-7-9-11-2-4-6-8-10-12-13-14
	<i>O. Trifallax</i>	1-3-5-7-10-12-2-4-6-8-9-11-13-14-15-16-17
	<i>S. Mytilus</i>	like <i>O. Nova</i>
USG1	<i>Uroleptus sp</i>	1-2-3-4-7-8-9-10-11-12-13-14-15-5-6
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	<i>Uroleptus Pisces</i>	1-2-4- $\bar{8}$ - $\bar{6}$ -15plus 3-5-7-10-13- $\bar{12}$ - $\bar{9}$ -14-16- $\bar{11}$
α TBP	<i>Oxytricha Nova</i>	1-3-5-7-9-11-2-4-6-8-10-12-13-14
	<i>O. Trifallax</i>	1-3-5-7-10-12-2-4-6-8-9-11-13-14-15-16-17
	<i>S. Mytilus</i>	like O. Nova
USG1	<i>Uroleptus sp</i>	1-2-3-4-7-8-9-10-11-12-13-14-15-5-6
Upr	<i>Uroleptus sp</i>	1-2-4-5-6-8-11-13-15-16 and 7-9-3-10-12-14

Examples

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Outline

- 1 What are ciliates?
- 2 Ciliates and Cryptography
- 3 What is the encryption cipher?
- 4 Programmability**
- 5 Computational Power

Reprogramming DH-MIC Decryption

For a sequence σ present in the DH-MIC the decryption program can be caused to:

- 1 retain σ as a member of DH-MAC, even if it is normally deleted.
- 2 delete σ as member of DH-MAC even if it is normally retained.
- 3 permute subsequence of σ even when σ is normally retained in DH-MAC.

This intervention does not require transforming the micronucleus.

As long as σ is not essential/detrimental to ciliate survival the clonal offspring of the ciliate maintain the reprogrammed state of σ until subsequent reprogramming.

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Speed, energy efficiency and space

In certain ciliate species we have the following benchmarks per DH-MIC decryption:

Speed: more than a million rearrangement processes per second.

Energy Efficiency of rearrangement processes, “optimized” over evolutionary time, is vastly superior to corresponding *in silico* technology.

Space: Over 90% of the DH-MIC genome is discarded. This constitutes a vast supply of randomly accessible σ that can be recruited for supplemental computational tasks not interfering with ciliate survival.

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Credits

The diagrams of ciliate conjugations and the photo were graciously provided by H.J. Lipps' Laboratory at the University of Witten-Herdecke in Germany.