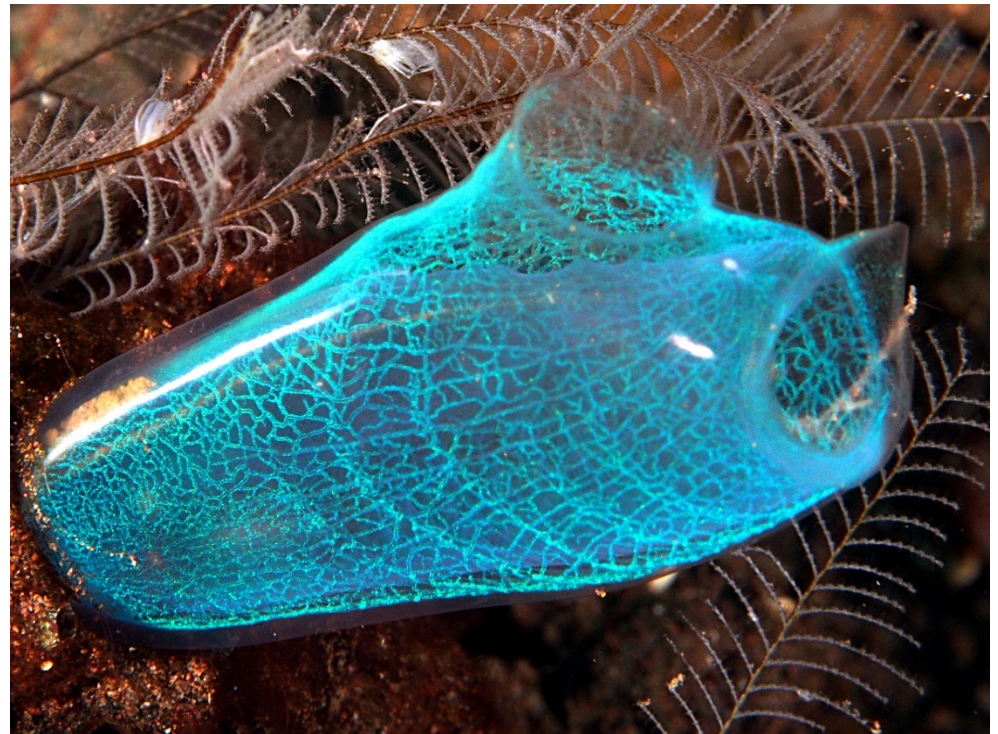


Shedding sun light on the ascidians genome

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Intro. To Genomics 485

Fall 2020



Outline

- General information



Outline

- General information
- Genome paper



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- General genome information
- Sequencing strategy



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- Sequencing Methods



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- Sequencing Methods
- Genome assembly



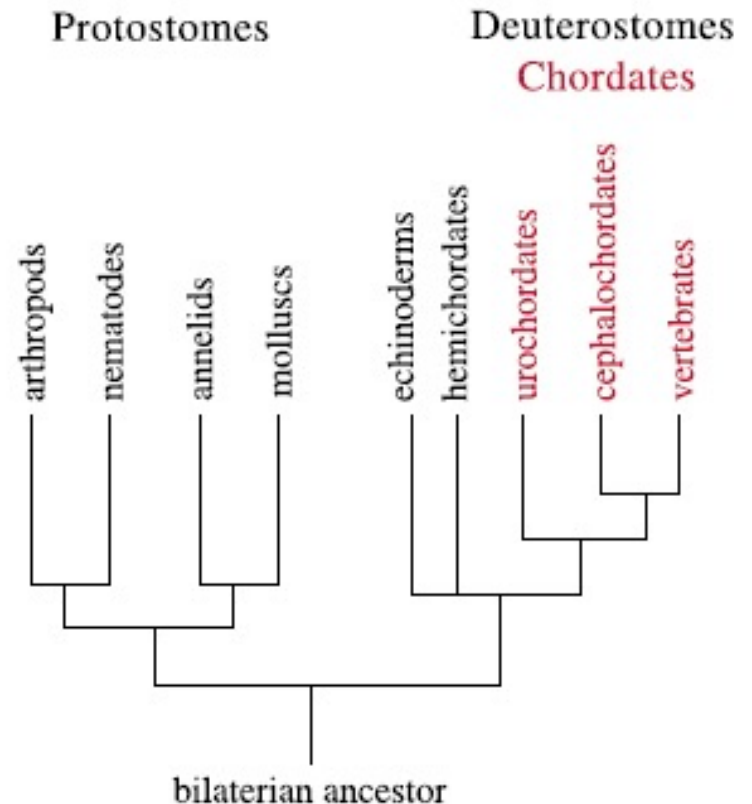
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- General information
- Genome paper
- General genome information
- Sequencing strategy
- Sequencing Methods
- Genome assembly
- Genome outcome



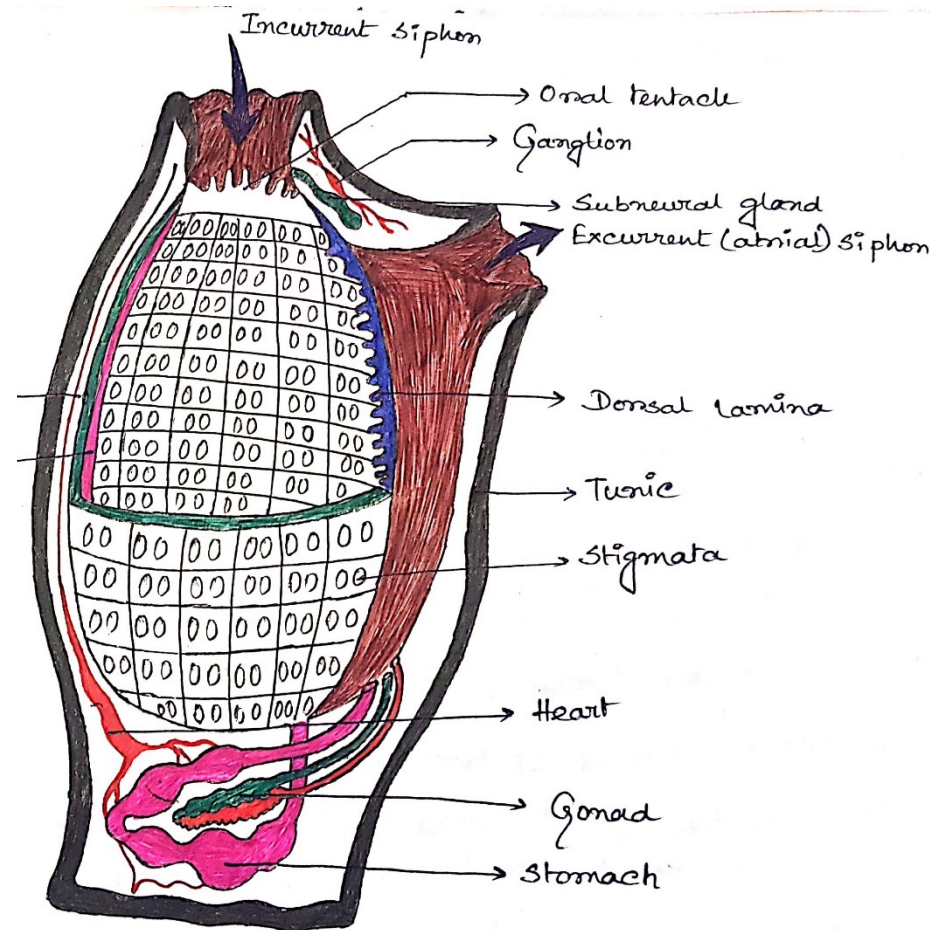
General information - phylogeny

- Subphyla: urochordates also known as tunicates (ascidians).



General information (fun fact)

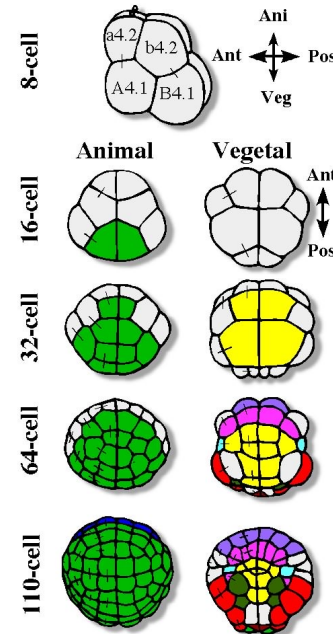
- Ascidians are characterized by a tough outer "tunic" made of a polysaccharide



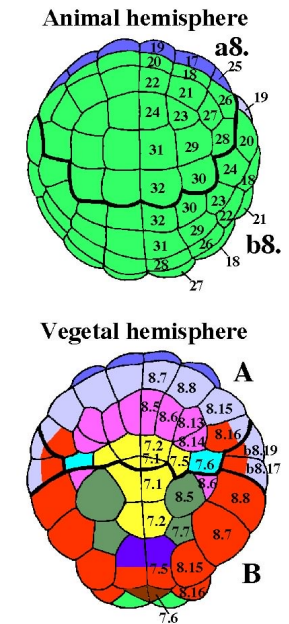
General information (fun fact)

- Ascidian embryos are used as a model system in developmental biology

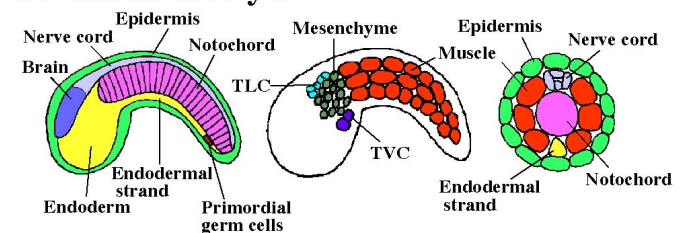
A. Fate restriction



B. Fate map



C. Tailbud embryos



General information (fun fact)

- The body itself can be divided into up to three regions
 - The pharyngeal region contains the pharynx

General information (fun fact)

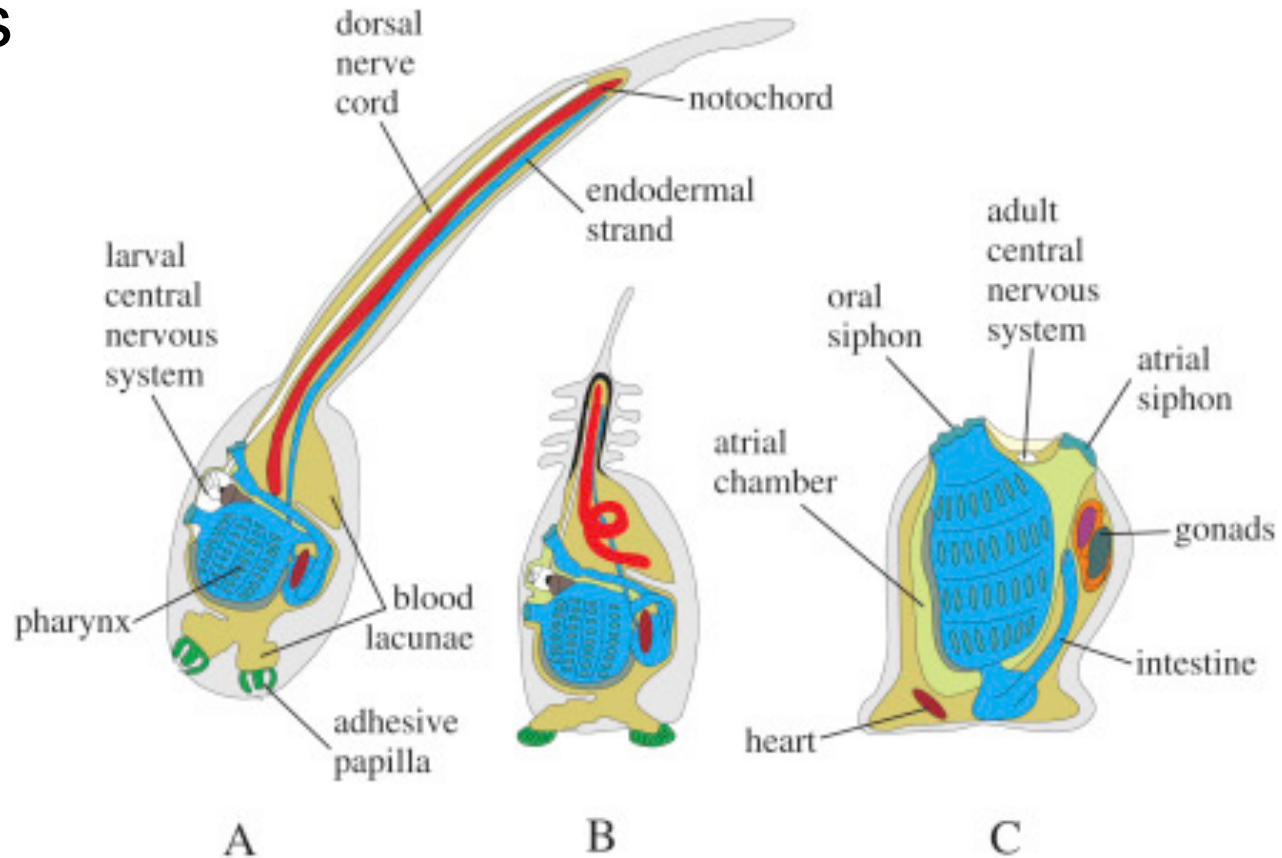
- The body itself can be divided into up to three regions
 - The pharyngeal region contains the pharynx
 - Abdomen contains most of the other bodily organs

General information (fun fact)

- The body itself can be divided into up to three regions
 - The pharyngeal region contains the pharynx
 - Abdomen contains most of the other bodily organs
 - The post-abdomen contains the heart and gonads

General information (fun fact)

- The body itself can be divided into up to three regions



Genome paper

RESEARCH ARTICLES

The Draft Genome of *Ciona intestinalis*: Insights into Chordate and Vertebrate Origins

Paramvir Dehal,^{1*} Yutaka Satou,^{2*} Robert K. Campbell,^{3,4} Jarrod Chapman,¹ Bernard Degnan,⁵ Anthony De Tomaso,⁶ Brad Davidson,⁷ Anna Di Gregorio,⁷ Maarten Gelpke,¹ David M. Goodstein,¹ Naoe Harafuji,⁷ Kenneth E. M. Hastings,⁸ Isaac Ho,¹ Kohji Hotta,⁹ Wayne Huang,¹ Takeshi Kawashima,¹⁰ Patrick Lemaire,¹¹ Diego Martinez,¹ Ian A. Meinertzhagen,¹² Simona Necula,¹ Masaru Nonaka,¹³ Nik Putnam,¹ Sam Rash,¹ Hidetoshi Saiga,¹⁴ Masanobu Satake,¹⁵ Astrid Terry,¹ Lixy Yamada,² Hong-Gang Wang,¹⁶ Satoko Awazu,² Kaoru Azumi,¹⁷ Jeffrey Boore,¹ Margherita Branno,¹⁸ Stephen Chin-bow,¹⁹ Rosaria DeSantis,¹⁸ Sharon Doyle,¹ Pilar Francino,¹ David N. Keys,^{1,7} Shinobu Haga,⁹ Hiroko Hayashi,⁹ Kyosuke Hino,² Kaoru S. Imai,² Kazuo Inaba,²⁰ Shungo Kano,^{2,18} Kenji Kobayashi,² Mari Kobayashi,² Byung-In Lee,¹ Kazuhiro W. Makabe,² Chitra Manohar,¹ Giorgio Matassi,¹⁸ Monica Medina,¹ Yasuaki Mochizuki,² Steve Mount,²¹ Tomomi Morishita,⁹ Sachiko Miura,⁹ Akie Nakayama,² Satoko Nishizaka,⁹ Hisayo Nomoto,⁹ Fumiko Ohta,⁹ Kazuko Oishi,⁹ Isidore Rigoutsos,¹⁹ Masako Sano,⁹ Akane Sasaki,² Yasunori Sasakura,² Eiichi Shoguchi,² Tadasu Shin-i,⁹ Antoinetta Spagnuolo,¹⁸ Didier Stainier,²² Miho M. Suzuki,²³ Olivier Tassy,¹¹ Naohito Takatori,² Miki Tokuoka,² Kasumi Yagi,² Fumiko Yoshizaki,¹³ Shuichi Wada,² Cindy Zhang,¹ P. Douglas Hyatt,²⁴ Frank Larimer,²⁴ Chris Detter,¹ Norman Doggett,²⁵ Tijana Glavina,¹ Trevor Hawkins,¹ Paul Richardson,¹ Susan Lucas,¹ Yuji Kohara,^{9†} Michael Levine,^{7,26†} Nori Satoh,^{2†} Daniel S. Rokhsar^{1,7,26†}

Sequencing strategy

- Source of DNA
 - Sperm was isolated
 - DNA was extracted and sheared → 3-kb fragments.
- Sequencing strategy
 - Whole-genome shotgun approach

Sequencing strategy

- The sequencing single-end
 - More than 2 million sequence fragments were obtained.
 - Bacterial artificial chromosome (BAC) and cosmid libraries were end-sequenced to 0.2× genome coverage
 - Provide longer range linking information

Genome assembly

- Genome assembly was carried out using the JAZZ suite of assembly tools
 - Developed for large whole-genome shotgun projects
- The *C. intestinalis* assembly presented here spans 116.7 Mbp of nonrepetitive sequence in 2501 scaffolds
 - Longer than 3 kbp.

Genome assembly

- Sixty Mbp is reconstructed in only 177 scaffolds
 - Longer than 190 kbp.
- 85% of the assembled sequence is found in 905 scaffolds
 - Longer than 20 kb.
- These scaffolds include 4264 contigs → 100.9 Mbp.

Genome assembly

- A total of 15,852 distinct gene models were obtained
- The average gene density
 - Higher than in *Drosophila* and far greater than the density in human
- The average gene density is 6.8 exons per gene
- The intron size distribution has a sharp peak near 60 bp

Genome outcome

- Classic studies suggest that ascidians possess organs homologous to the vertebrate thyroid, pineal, and gill slits
- *Ciona* genome contains genes encoding all the major endocrine receptors that bind peptide or protein ligands
 - In contrast to the conservation of the thyroid hormone system between ascidians and vertebrates

Genome outcome

- *Ciona* genome lacks clear orthologs for some of the P450 enzymes → vertebrate steroid hormones
 - androgens (CYP17), estrogens (CYP19), and corticosteroids and mineralocorticoids (CYP21)
- The central nervous system of the ascidian tadpole
 - a chordate nervous system in Miniature
 - with a 300-cell cerebral vesicle → containing several sensory systems

Questions

- *Why there is no mention about N50 ?*
- *Ciona* genome has P450 enzymes like vertebrate (....)
- Ascidians possess organs homologous to the vertebrate
 - 1-
 - 2-
 - 3-