The X World Sponge Conference, Galway 24.06 – 01.07. 2017

Regeneration in sponges

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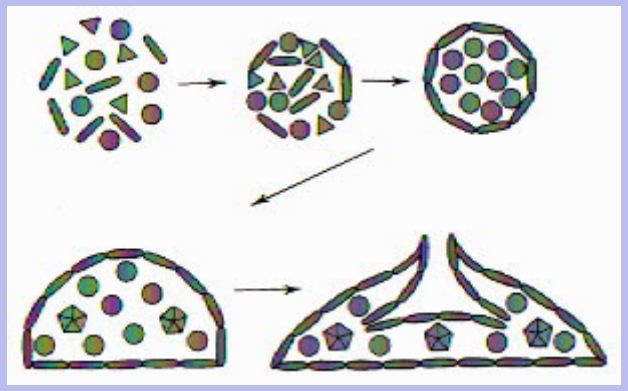
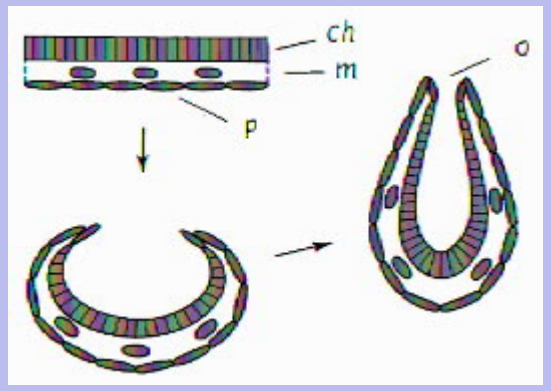
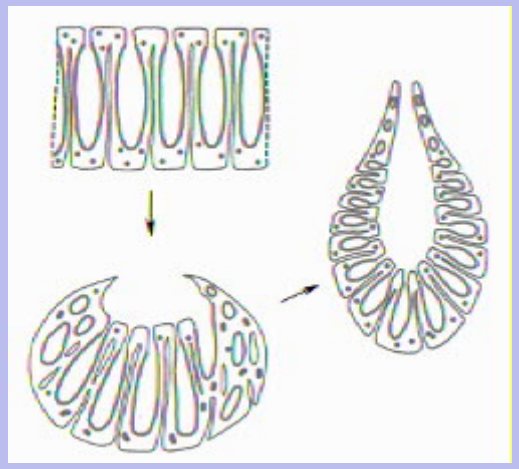
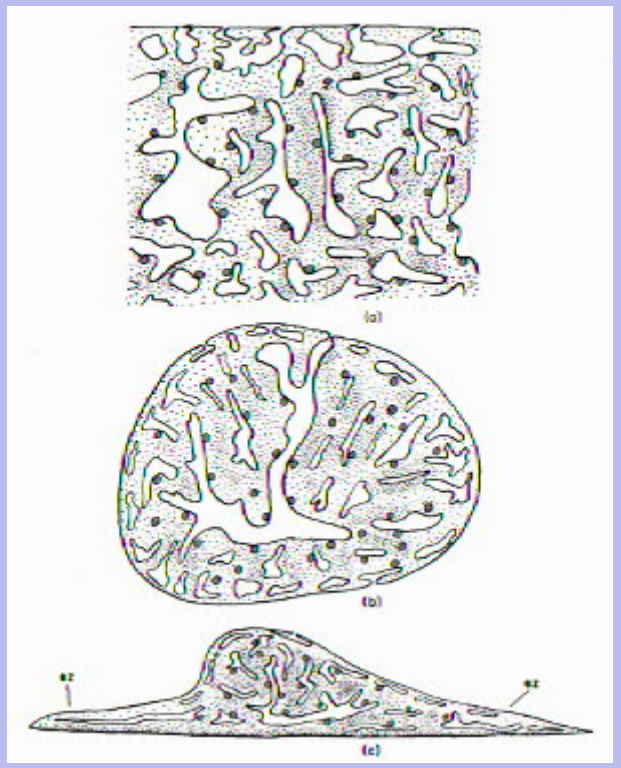






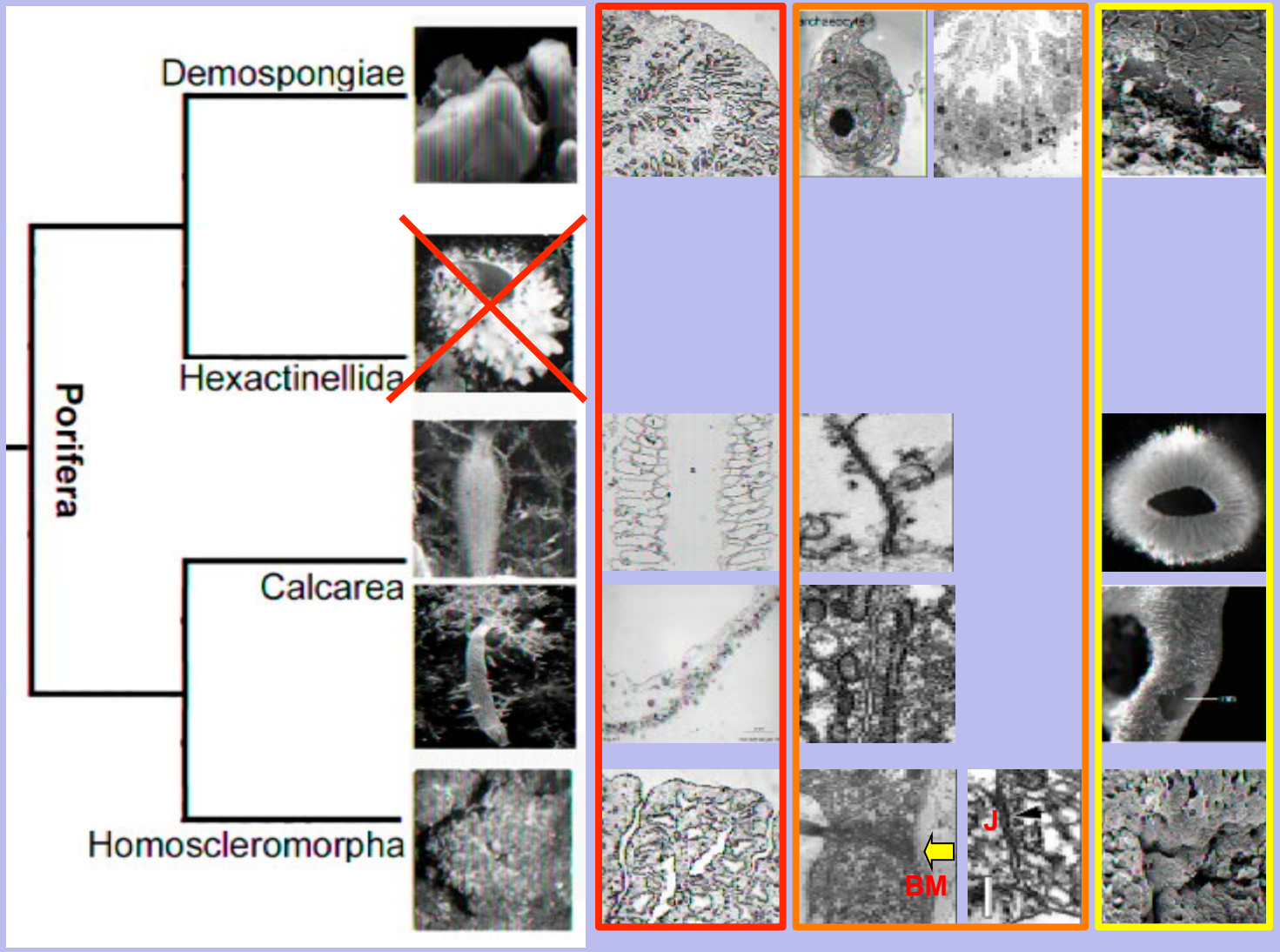


- **The aims of this study are:**

- 1) To show the variety of morphogeneses during reparative regeneration in different sponges;
- 2) To discover the cells, involved in the regeneration ;
- 3) To highlight the correlation between tissue organization and morphogenetic mechanisms involved in sponge's regeneration.

Sponges are known to possess remarkable reconstitutive and regenerative abilities

Models



Halisarca dujardini: no cell junctions; no basement membrane; archaeocytes

Sycon ciliatum & *Leucosolenia complicata*: cell junctions; no basement membrane; no archaeocytes

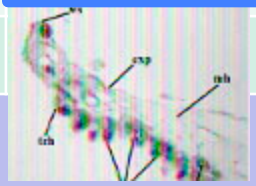
Oscarella lobularis: true epithelium; no archaeocytes

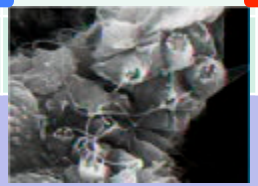
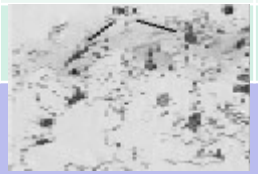
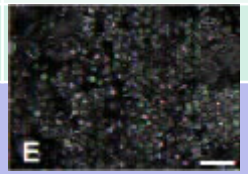
Main stages of regeneration in model sponges

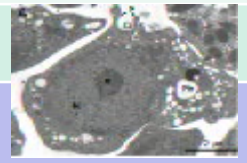
	Retraction of the wound surface	Regenerating " plug" formation	Alignment of the wound edges	Regeneration membrane (epithelization)	Formation of blastema	Restoration of ectosome & choanosome
Oscarella lobularis	+	+	+	+	-	+
Sycon ciliatum	-	+	+	+	-	+
Leucosolenia complicata	+	-	+	+	-	+
Halisarca dujardini	+	+	+	+	+	+

Basic morphogenetic and cellular processes during models regeneration

	Spreading (flattening) of epithelial sheets	Fusion of epithelial sheets	Cell transdifferentiation	Epithelial-mesenchymal transitions	Active local cell proliferation	Participation of stem-cells
Oscarella lobularis	+	+	+	-	-	-
Sycon ciliatum	+	+	+	-	-	-
Leucosolenia complicata	+	+	+	-	-	-
Halisarca dujardini	-	-	+	+	+	+



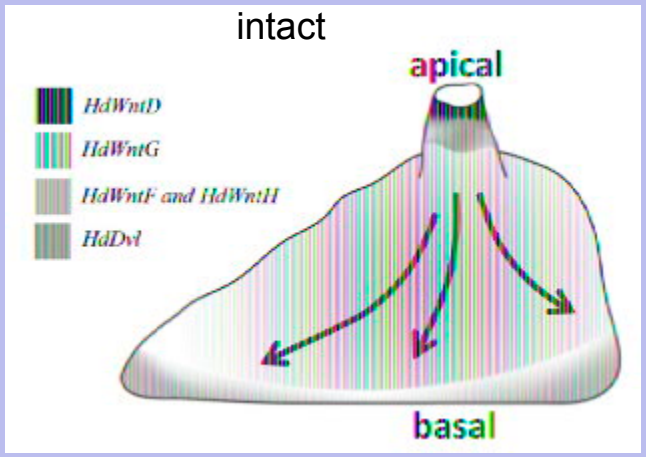


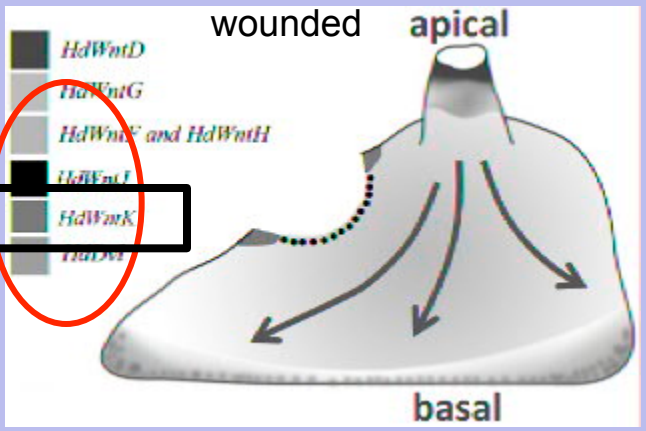
Regeneration in *Halisarca* and *Sycon*: detection of differentially expressed genes by RNA-Seq

Halisarca

At least 4 *Wnt* genes are differentially expressed along the body axis, and one *HduWntK* is expressed in cells at the edge of wound during regeneration

Borisenko et al. 2016

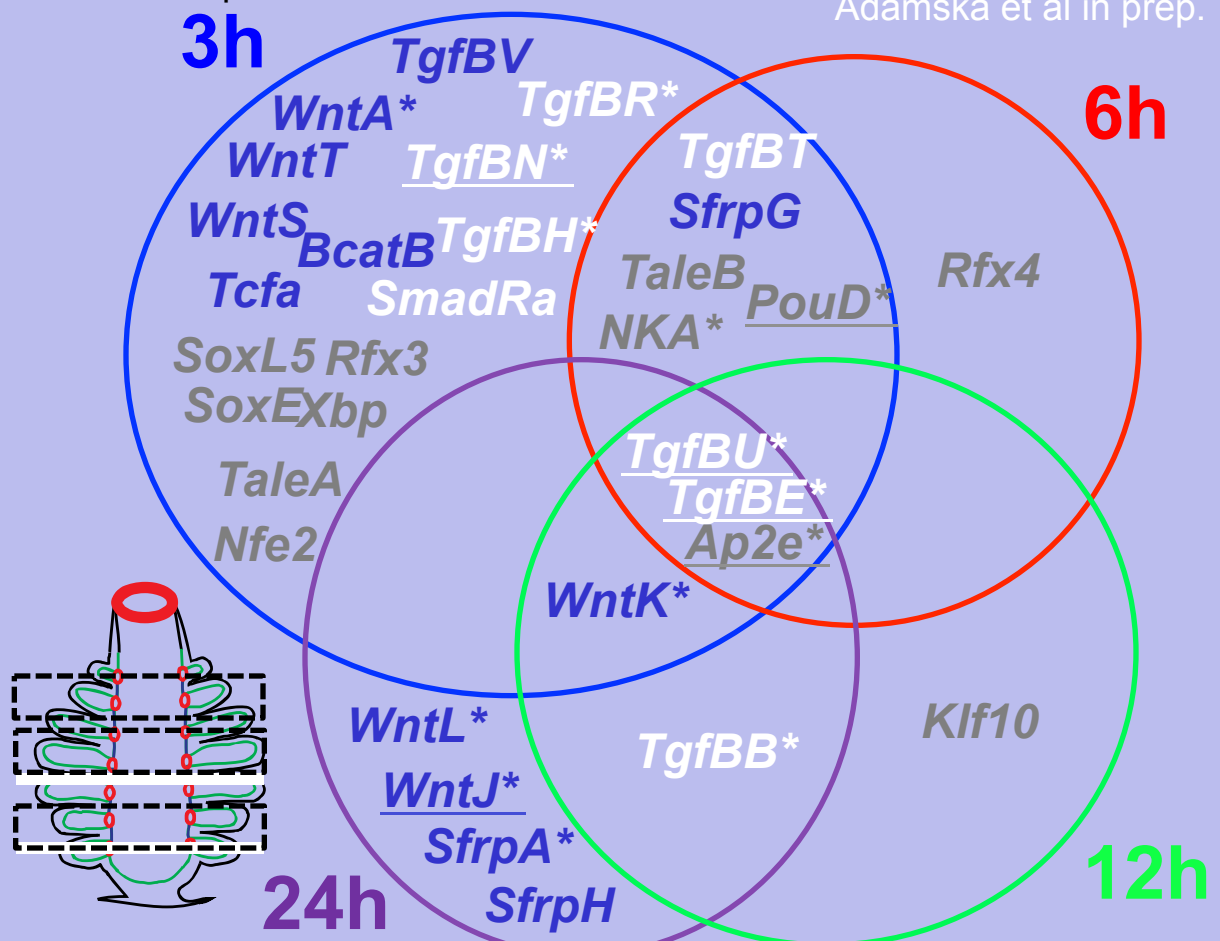




Sycon

Within hours of dissection, multiple Wnt and Tgf-beta pathway components, including their key transcrption factors are upregulated, as are also several other developmental transcription factors.

Adamska et al in prep.



Genes* with statistically significant higher expression in top than bottom.
*Genes** with statistically significant higher expression in top than middle.

General conclusions

- **Epithelial morphogenesis** discovered during **Homoscleromorpha** and **Calcaronea**, and **Mesenchymal morphogenesis** by **mesenchymal-epithelial transformations** in **Demospongiae** regeneration resemble morphogeneses in eumetazoans both morphologically and cytologically;
- Mesenchymal-epithelial transformation absent in **Calcaronea & Homoscleromorpha** regeneration;
- **Epithelial morphogenesis** absent in demosponges regeneration;
- Participation of multiple **Wnt** and **Tgf-beta pathway** components in ***Halisarca*** and ***Sycon*** regeneration are comparable to those in higher metazoan lineages.

Acknowledgements

- Grant of Russian Foundation for Basic Research (RFBR № 16-04-00084).
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- Grant the Russian Science Foundation n° 17-14-01089
- ASSEMBLE projects 2013, 2014
- Also, we thank our colleagues and friends for help
- and discussions.

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