Multiplexed mRNA in-situ Hybridization Chain Reaction (HCR) in Sycon ciliatum

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- PROTOCOL -

Day 1 - Sample preparation (version with xylene clearing)

From Kojima & Funayama, 2022.

This protocol refers to samples that have been already fixed and stored in pure methanol at $-20\,^{\circ}\text{C}$.

- 1. Wash samples for 15 min with 500 µL (or 1 mL) of 100% ethanol at RT.
- 2. Clear samples for $30 \min$ with 500 μ L (or 1 mL) of 50% xylene in ethanol at RT.

Always use xylene in glass containers (as it dissolves plastic) and under a chemical safety hood.

- 3. Wash samples for 15 min with 500 µL (or 1 mL) of ice-cold 100% ethanol at 4 °C.
- 4. Wash samples for $\underline{15\,\text{min}}$ each with a graded series of 500 μ L (or 1 mL) ice-cold ethanol (75, 50 and 25%) in 0.25× HS at 4 °C.
- 5. Wash samples for $\underline{10 \text{ min}}$ with 500 μ L (or 1 mL) of **ice-cold 0.25**× **HS** at 4 °C.
- 6. Wash samples for $\underline{10 \text{ min}}$ with 500 μ L (or 1 mL) of **ice-cold 1**× **PBS** at 4 °C.
- 7. Post-fix samples for 30 min with 500 µL (or 1 mL) of ice-cold fixative solution at 4 °C.

Pre-heat probe-hybridization buffer to 37 °C (you will need 700 μ L per tube [500 μ L for the pre-hybridization, and 200 μ L for the probe solution]).

8. Wash samples for 4×10 min with 500 μ L (or 1 mL) of **PBST** at 4 °C.

Day 1 – Sample preparation (version with proteinase-K permeabilisation and acetic anhydride acetylation)

From Fortunato et al., 2012; Voigt et al., 2017.

This protocol refers to samples that have been already fixed and stored in pure methanol at -20 °C.

- 1. Wash samples for 15 min with 500 µL (or 1 mL) of ice-cold 100% ethanol at 4 °C.
- 2. Wash samples for $\underline{15\,\text{min}}$ each with a graded series of 500 μ L (or 1 mL) ice-cold ethanol (75, 50 and 25%) in PBST at 4 °C.
- 3. Wash samples for 2 \times 10 min with 500 μ L (or 1 mL) of **PBST** at RT.
- 4. Rock samples for 15 min with 500 µL (or 1 mL) of 7.5 µg/mL proteinase K in PBST at 37 °C.
- 5. Wash samples for two times without incubation with 500 µL (or 1 mL) of **PBST** at RT.
- 6. Quench samples for 10 min with 500 μL (or 1 mL) of 2 mg/mL glycine in PBST at RT.

- 7. Wash samples for $3 \times 10 \, \text{min}$ with 500 μL (or 1 mL) of **PBST** at RT.
- 8. Acetylate samples for $\underline{15\,\text{min}}$ each with a graded series of 500 μL (or 1 mL) **0.1 M triethanolamine** containing **0, 1.5 and 3 \mu\text{L/mL} acetic anhydride** ar RT.
- 9. Wash samples for $2 \times 10 \text{ min}$ with $500 \,\mu\text{L}$ (or $1 \,\text{mL}$) of **PBST** at RT.
- 10. Post-fix samples for $30 \, \text{min}$ with $500 \, \mu\text{L}$ (or $1 \, \text{mL}$) of **fixative solution** at RT.

Pre-heat probe-hybridization buffer to 37 °C (you will need 700 μ L per tube [500 μ L for the pre-hybridization, and 200 μ L for the probe solution]).

11. Wash samples for $2 \times 10 \text{ min}$ with $500 \,\mu\text{L}$ (or $1 \,\text{mL}$) of **PBST** at RT.

Day 1 - Sample preparation (version with proteinase-K permeabilisation and sodium borohydride clearing)

This protocol refers to samples that have been already fixed and stored in pure methanol at -20 °C.

- 1. Wash samples for 15 min with 500 µL (or 1 mL) of ice-cold 100% ethanol at 4 °C.
- 2. Wash samples for $\underline{15\,\text{min}}$ each with a graded series of 500 μ L (or 1 mL) ice-cold ethanol (75, 50 and 25%) in PBST at 4 °C.
- 3. Wash samples for $2 \times 10 \, \text{min}$ with 500 μL (or 1 mL) of **PBST** at RT.
- 4. Rock samples for 15 min with 500 µL (or 1 mL) of 7.5 µg/mL proteinase K in PBST at 37 °C.
- 5. Wash samples for two times without incubation with 500 µL (or 1 mL) of **PBST** at RT.
- 6. Wash samples for 10 min with 500 μL (or 1 mL) of **PBST** at RT.
- 7. Post-fix samples for 30 min with 500 µL (or 1 mL) of **fixative solution** at RT.

Pre-heat probe-hybridization buffer to 37 °C (you will need 700 μ L per tube [500 μ L for the pre-hybridization, and 200 μ L for the probe solution]).

- 8. Wash samples for $2 \times 10 \text{ min with } 500 \,\mu\text{L}$ (or 1 mL) of **PBST** at RT.
- 9. Treat samples for 20 min with 500 µL (or 1 mL) of fresh 0.1% SBI at RT.

SBI solutions should be prepared fresh, and used always under a fume hood, as it release molecular hydrogen, which is a highly flammable gas.

10. Wash samples for $2 \times 10 \text{ min with } 500 \,\mu\text{L}$ (or 1 mL) of **PBST** at RT.

Day 1 - HCR detection stage

1. Pre-hybridize samples for $30 \, \text{min}$ with $500 \, \mu\text{L}$ of **pre-warmed probe hybridization buffer** at $37 \, ^{\circ}\text{C}$.

If reusing probes, pre-warm probe solution to 37 °C, then skip to Step 3.

At this step, samples can be stored in probe hybridization buffer at -20 °C for several months.

2. Prepare probe solution by adding 0.8 μ L (0.8 pmol) of each **probe set 1 \muM stock solution** to 200 μ L of **probe hybridization buffer** (final concentration of 4 nM) at 37 °C.

Note: if using 500 μ L of probe solution, add 2 μ L (2 pmol) of each probe set.

3. Incubate samples for >12 h (overnight) with 200 µL of pre-warmed probe solution at 37 °C.

Pre-heat probe wash buffer at 37 °C (you will need 500 μLper tube per 4 washes).

Day 2 - HCR amplification stage

Pre-equilibrate amplification buffer to room temperature (you will need 700 μ L per tube [500 μ L for pre-amplification, and 200 μ L for the hairpin solution]).

1. Wash samples for 4×20 min with 500 µL of **probe wash buffer** at 37 °C.

Probe solution can be saved and reused for 2–3 times; store at -20 °C.

- 2. Wash samples for $3 \times 5 \min$ with 500 μ L (or 1 mL) of $5 \times$ **SSCT** at RT.
- 3. Pre-amplify samples for 30 min with 500 µL of amplification buffer at RT.
- 4. Snap cool in separate tubes $4\,\mu\text{L}$ of **hairpin H1** (30 pmol) and $4\,\mu\text{L}$ of **hairpin H2** (30 pmol) $3\,\mu\text{M}$ stock solutions: heat at 95 °C for 90 s and cool to RT in the dark for 30 min.

If reusing hairpin solutions, heat at 95 °C and cool at RT, then skip at Step 6.

5. Prepare hairpin solution by adding **snap-cooled H1 hairpins** and **snap-cooled H2 hairpins** to 200 µL of **amplification buffer** (final concentration of each hairpin of 60 nM) at RT.

Note: if using 100 μ L of amplification buffer, add 2 μ L (15 pmol) of each hairpin. Note: if using 500 μ L of amplification buffer, add 10 μ L (75 pmol) of each hairpin.

6. Incubate samples for >12 h (overnight) with 200 µL of hairpin solution at RT.

Day 3 - HCR conclusion

1. Wash samples for 2×5 min, 2×30 min, and 1×5 min with $500 \,\mu$ L (or 1 mL) of $5 \times$ **SSCT** at RT.

Hairpin solution can be saved and reused for 2-3 times; store at -20 °C.

At this step, samples can be stored in the dark in $5 \times$ SSCT for several days at room temperature.

Day 3 - Sample mounting

1. Wash samples for 3×5 min with 500 μ L (or 1 mL) of $1 \times PBS$ at RT.

If using VECTASHIELD® PLUS Antifade Mounting Medium with DAPI (H-2000), skip directly to Step 4.

- 2. Incubate samples for $20 \min$ with 500 μ L (or 1 mL) of **DAPI staining solution** at RT.
- 3. Wash samples for 3×5 min with 500 μ L (or 1 mL) of $1 \times PBS$ at RT.
- 4. Incubate samples for 30-60 min with 1 mL of 50% glycerol in 1× PBS at RT.
- 5. Incubate samples for 30-60 min with 1 mL of 75% glycerol in $1 \times PBS$ at RT.

Maintaining samples at pH 7.40 is critical for the stability of fluorophores and long-term storage of mRNA in-situ HCR samples.

At this step, samples can be stored in the dark in 75% glycerol for several month at 4°C.

- 6. Collect precipitated samples from the 75 % glycerol solution and place them on a cleaned (bridged, if necessary) slide.
- 7. Add \sim 15–20 µL of mounting medium (or VECTASHIELD® PLUS Antifade Mounting Medium with DAPI [H-2000]) directly on samples.
- 8. Seal the slide with nail polish and store in the dark at 4 °C.

- RECIPES -

Fixative solution

Compound	Quantity	Molar mass (g/mol)	Final concentration (for 100 mL)
36–38% formaldehyde	$3.7\mathrm{mL}$	30.03	3.7%
25 % gluteraldehyde	$0.2\mathrm{mL}$	100.12	0.05%
10× PBS	$10.0\mathrm{mL}$	_	$1 \times$
Ultrapure water	_	_	_

- 1. Add 3.7 mL of 36-38% formaldehyde to a graduated cylinder.
- 2. Add 0.2 mL of 25 % gluteraldehyde to a graduated cylinder.
- 3. Fill up to 100 mL with ultrapure water.
- 4. Store the fixative solution at 4 °C.

1× Holtfreter's solution (HS)

Compound	Quantity	Molar mass (g/mol)	Final concentration (for 1 L)
NaCl	3.46 g	58.44	0.05900 M
KCl	$0.05\mathrm{g}$	74.55	0.00067 M
$CaCl_2$	0.10 g	110.98	0.00076 M
$or \operatorname{CaCl}_2 \cdot 2\operatorname{H}_2\operatorname{O}$	0.13 g	120.04	0.00090 M
$NaHCO_3$	0.20 g	84.00	0.00240 M
Ultrapure water	_	_	_

- 1. Dissolve solutes in 800 mL of ultrapure water, by continuous stirring.
- 2. Fill up to 1 L with ultrapure water.
- 3. Store the $0.25 \times$ HSindefinitely at RT.

1× PBS with 0.1% Tween 20 (PBST or PTw)

Compound	Quantity	Molar mass (g/mol)	Final concentration (for 50 mL)
Tween 20	50 . 0 μL	1,227.54	0.01%
$20 \times PBS$	5.0 mL	_	$ exttt{1} imes$
Ultrapure water	_	_	_

- 1. Add $5\,\text{mL}$ of $20\times$ PBS to a graduated cylinder.
- 2. Add 50 µL of Tween 20.
- 3. Fill up to 50 mL with ultrapure water.

$5 \times$ SSC 0.1% Tween 20 (SSCT)

Compound	Quantity	Molar mass (g/mol)	Final concentration (for 50 mL)
Tween 20	50 . 0 μL	1,227.54	0.01%
$20 imes \mathrm{SSC}$	12.5 mL	_	$5 \times$
Ultrapure water	_	_	_

- 1. Add 12.5 mL of $20 \times$ SSC to a graduated cylinder.
- 2. Add $50 \,\mu\text{L}$ of Tween 20.
- 3. Fill up to $50\,\mathrm{mL}$ with ultrapure water.

Proteinase K working solution

Compound	Quantity	Molar mass (g/mol)	Final concentration (for 10 mL)
20 mg/mL proteinase K stock solution	3.75 μL	_	7.5 µg/mL
PBST	_	_	_

- 1. Add 3.75 μL of 20 mg/mL proteinase K stock solution to 8 mL of PBST.
- 2. Fill up to 10 mL with PBST.

1:500 DAPI staining solution

Compound	Quantity	Molar mass (g/mol)	Final concentration (for 500 μL)
DAPI	1.0 μL	_	1:500
$1 \times PBS$	499.0 µL	_	_

- RESOURCES -

1. mRNA fluorescent in-situ HCR in Sycon spp.

- *Fortunato, S., Adamski, M., Bergum, B., Guder, C., Jordal, S., Leininger, S., ... & Adamska, M. (2012). Genome-wide analysis of the sox family in the calcareous sponge *Sycon ciliatum*: multiple genes with unique expression patterns. *EvoDevo*, 3, 1-11. 10.1186/2041-9139-3-14
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- Voigt, O., Adamska, M., Adamski, M., Kittelmann, A., Wencker, L., & Wörheide, G. (2017). Spicule formation in calcareous sponges: coordinated expression of biomineralization genes and spicule-type specific genes. *Scientific Reports*, 7(1), 45658. 10.1038/srep45658

2. mRNA in-situ HCR in other sponges.

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- Larroux, C., Fahey, B., Adamska, M., Richards, G. S., Gauthier, M., Green, K., & Degnan, B. M. (2008). Whole-mount *in situ* hybridization in *Amphimedon. CSH protocols*, pdb-prot5096. 10.1101/pdb.prot5096
- Musser, J. M., Schippers, K. J., Nickel, M., Mizzon, G., Kohn, A. B., Pape, C., & Arendt, D. (2021). Profiling cellular diversity in sponges informs animal cell type and nervous system evolution. *Science*, 374(6568), 717-723. 10.1126/science.abj2949
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