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Selective protection and labelling of arginine/lysine side chains in HBSs of proteins V.3

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We use this protocol and it's working

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Abstract

Interactions between heparan sulfate proteoglycans and the partner proteins regulate many aspects of cell functions, however, their binding properties are still equivocal. Developed eight years ago was a method for selective labelling of lysine residues in the heparin binding sites of Fibroblast Growth Factors (FGFs). The labelling of arginine residues is far more challenging, due to the multiple reaction products between a dicarbonyl and a guanidino group.

Attachments



EXPERIMENTAL

PROCEDU...

22KB

Materials

STEP MATERIALS

⊗ Phenylglyoxal hydrate **Merck MilliporeSigma (Sigma-Aldrich) Catalog #142433-5G**

⊗ RapiGest SF Surfactant

⊗ (P-Hydroxyphenyl)Glyoxal **Catalog #24645-80-5**

⊗ Chymotrypsin, Sequencing Grade, 25ug **Promega Catalog #V1061**

⊗ Iodoacetamide, 15mg **Promega Catalog #VB1010**

⊗ TOYOPEARL AF-Heparin HC-650M **Catalog #0020030**

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Binding

- 1 AF-heparin beads (Tosoh Biosciences GmbH, Stuttgart, Germany; binding capacity of 4 mg antithrombin III/mL)

A mini affinity column was made by placing a plastic air filter as a frit at the end of a P10 pipette tip (Star Lab Ltd., Milton Keynes, UK) and then packed with 20 μ L AF-heparin beads.

Note

Avoid bubbles inside the mini-column

The mini-column was equilibrated with $4 \times 50 \mu\text{L}$ 200 mM NaCl, 0.2M NaHCO_3 , pH 9.5 (Na-1 buffer).

The buffer was dispensed slowly into the column using a 2 mL sterile syringe.

A minimum of 10 μg FGF protein was loaded onto the column (generally, the loading capacity of FGFs to resin was estimated at 15 mg/mL).

The loading was repeated 3 times to ensure the binding between protein and heparin beads. After binding, the column was washed with 200 μL ($4 \times 50 \mu\text{L}$) Na-1 buffer to remove any unbound protein.


 20 μL AF-heparin beads

 10 μg protein

Note

The concentration of NaCl in Na-1 Buffer could be modified, depending on the affinity of protein to heparin

[M] 0.2 Molarity (M) NaHCO_3

 TOYOPEARL AF-Heparin HC-650M Catalog #0020030

Protection of arginine side chains

- 2 PGO (Merck Ltd., UK, 97%) was used in the dark, as it is light sensitive. PGO was freshly prepared in 50% (v/v) DMSO, 50% (v/v) HPLC grade water at 1 M, which was then diluted to 0.5 M and then 0.2 M with 0.2 M NaHCO_3 , pH 9.5.

The pH was adjusted by 0.1 M NaOH to between 9.1 and 9.5 to ensure optimal reaction.

The heparin mini column was rinsed with 30 μL of the 0.2 M PGO solution to exchange buffers.

A further 30 μL PGO solution was added to the column and the bound protein was allowed to react for 60 min at room temperature in the dark.


The reaction was quenched with 5 μL 0.1% (v/v) Trifluoroacetic acid (TFA) in water so that the final concentration of TFA is 0.01% (v/v).

The mini-column was then washed with 200 μL Na-1 buffer ($4 \times 50 \mu\text{L}$). Bound proteins were eluted with $2 \times 20 \mu\text{L}$ Na-2 buffer (2 M NaCl, 0.2M NaHCO_3 , pH 9.5) containing 0.1% (w/v) RapiGest SF Surfactant (Waters, UK).

The addition of surfactant was important to ensure protein recovery in this and subsequent steps, due to the increased hydrophobicity of the protein following PGO conjugation to arginine side chains.

[M] 0.2 Molarity (M) PGO

 60:00:00 React in the dark

 Phenylglyoxal hydrate **Merck MilliporeSigma (Sigma-Aldrich) Catalog #142433-5G**

 RapiGest SF Surfactant

Labelling of Arginine side chain by HPG

- 3 The preparation of HPG was performed in the dark room as it is even more light-sensitive than PGO, following a procedure identical to that used for PGO.


The eluted protein was diluted with 400 μL 0.2M NaHCO_3 , pH 9.5 and concentrated on a 3.5 kDa MWCO centrifugal filter to a final volume of 90~100 μL .

The reaction with HPG was performed by incubating 80 μL diluted protein with 20 μL 0.5M HPG so that the final concentration of HPG in the reaction was 0.1 M.

The pH was maintained at over 9.0. The reaction was performed for 60 min at room temperature in the dark and then was quenched with 5 μL 0.1% (v/v) TFA in water.

 01:00:00 React in the dark

[M] 0.1 Molarity (M) HPG

 (P-Hydroxyphenyl)Glyoxal **Catalog #24645-80-5**

Sample preparation for Mass Spectrometry

- 4 For labeling, protein was buffer exchanged by four cycles of dilution on 3.5 kDa-MWCO centrifugal filters with 400 μL 10-fold diluted 0.2 M NaHCO_3 , pH 9.5 containing 0.1%



(w/v) RapiGest and 3 cycles of dilution with 400 μ L HPLC water containing 0.1% (w/v) RapiGest by centrifugation at 13200 rpm for 10 min.
After freezing at -80°C for 30 min, the sample was lyophilized for an hour.

Equipment

new equipment

NAME

merckmillipore

BRAND

UFC500396


SKU


3.5 kDa-MWCO centrifugal filters

SPECIFICATIONS


Incubation with Chymotrypsin/Trypsin

- 5 The freeze-dried protein was dissolved in a mixture of 80 μ L 25 mM NH_4HCO_3 and 10 μ L 1% (w/v) RapiGest ($\sim 0.1\%$ w/v in final solution) and heated at 80°C for 10 min. The mixture was quickly centrifuged at 3200 rpm for 30 seconds before 5 μ L 50 mM DTT was added (5mM final concentration) and incubated for 15 min at 56°C . After cooling the sample to room temperature, proteins were carbamidomethylated with 5 μ L 0.1M iodoacetamide (freshly made) for 30 min in the dark. Proteins were then digested overnight with chymotrypsin (Promega Ltd., UK) at a ratio of 1:100.

 Chymotrypsin, Sequencing Grade, 25ug **Promega Catalog #V1061**

 17:00:00 h

 Iodoacetamide, 15mg **Promega Catalog #VB1010**

 00:30:00 min - in the dark

Mass spectrometry for the identification of peptides

- 6 Peptides were concentrated by rotary evaporation to a final volume of 10 μ L and desalted using C18 Zip-Tips(Millipore). C18 Zip Tips were first pre-wetted with 2×10 μ L 100 % (v/v) acetonitrile and then pre-equilibrated with 2×10 μ L 0.1% (w/v) TFA in water. The peptides were loaded on the Zip Tip, the loading was repeated 7 to 8 times to ensure binding. The Zip Tip was washed with 10 μ L 0.1% (w/v) TFA. Finally, the peptides were eluted with 2 μ L of 5mg/mL α -cyano-4-hydroxycinnamic acid (CHCA, > 99% purity, Sigma) in 50:50 acetonitrile/water + 1%TFA, straight onto a 96 spot MALDI (matrix-assisted laser desorption/ionisation) target plate.



Analyses were performed on the instrument Synapt G2-Si (Waters, Manchester, UK) with MALDI source equipped with a frequency tripled Nd:YAG UV laser ($\lambda = 355$ nm), operating at 1 kHz. The spectrum acquisition time was 120 seconds, with 1 second scan rates, laser energy of 150 Au. The MS spectra were extracted by MASSLYNX v.4.1 (Waters, Manchester, UK) with the spectrum range from 500 Da to 4000 Da. The spectra were then processed using automatic peak detection including background subtraction.