Supporting Information (SI)

Bio-oxidation of elemental mercury to mercury sulfide and humic acid bound mercury by sulfate reduction for Hg\textsuperscript{0} removal in flue gas

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Mercury thermorelease curves of biofilm samples in Phase I after sequential extraction of WS-Hg, IE-Hg, MeHg, HA-Hg and Hg-SR, respectively; (f) Mercury thermo-release curves of reference mercuric compounds;

Figure S6. Qualitative analysis of mercury speciation in biofilm by Hg-TPD: (a-e)

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Mercury thermorelease curves of biofilm samples in Phase II after sequential extraction of WS-Hg, IE-Hg, MeHg, HA-Hg and Hg-SR, respectively;

Figure S7. Qualitative analysis of mercury speciation in biofilm by Hg-TPD: (a-e)

Mercury thermo-release curves of biofilm samples in Phase III after sequential extraction of WS-Hg, IE-Hg, MeHg, HA-Hg and Hg-SR, respectively;
Procedures of Sequential Extraction Processes

(1) Total mercury (Tot-Hg): 2.5 g biofilm sample was digested with 16 mL aqua regia at 160 °C hotplate for 3 h; (2) WS-Hg: 20 g biofilm was sampled, air-dried overnight and weighted. 50 mL DDI water was added to 20 g biofilm sample and the mixture was shaken by vortex at 200 rpm for 2 h then centrifuged at 10000 rpm for 3 min. Sediment was subject to secondary extraction and the supernatants were collected. 10 mL evenly mixed supernatant was digested with 4 mL aqua regia at 100 °C water bath for 1 h; (3) IE-Hg: 50 mL 1 M NH₄Ac (aq) was added to the residue in (2) followed by procedures in (2); (4) MeHg: 20 mL 2 % HCl-10 % ethanol solution was added to residue in (3). The mixture was shaken by vortex at 200 rpm for 20 min, sonicated at 60 ± 2 °C for 20 min, centrifuged at 5000 rpm for 10 min and digested as per procedures in (2); (5) HA/FA-Hg: 50 mL 1 M NH₃·H₂O was added to residue in (4) followed by procedures in (2). 10 mL evenly mixed supernatant was digested with 10 mL concentrated HCl and 10 mL 30 % H₂O₂ at 85 °C water bath for 2 h; (6) Hg-SR: The residue (4) was first digested with 10 mL 0.02 M HNO₃ at 85 °C water bath for 2 h and subsequently with 16 mL 30 % H₂O₂ at 85 °C water bath for 1 h. 50 mL 1 M NH₄Ac-6 % HNO₃ solution was added to the digest followed by procedures in (2); (7) HgS: residue in (6) was repeatedly rinsed with DDI water for 2 h and air-dried overnight. 2.5 g residue was digested as per procedures in (1).
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Figure S3. Functional genes classified into sulfur metabolism
Figure S4. Biological Hg\textsuperscript{0} removal in the sulfate-reducing MBfR during days 91-124:

(a) Performance of Hg\textsuperscript{0} removal; (b) Hg\textsuperscript{2+} concentration in recirculating medium
Figure S5. Qualitative analysis of mercury speciation in biofilm by Hg-TPD: (a)-(e) Mercury thermo-release curves of biofilm samples in Phase I after sequential extraction of WS-Hg, IE-Hg, MeHg, HA-Hg and Hg-SR, respectively; (f) Mercury thermo-release curves of reference mercuric compounds.
Figure S6. Qualitative analysis of mercury speciation in biofilm by Hg-TPD: (a)-(e) Mercury thermo-release curves of biofilm samples in Phase II after sequential extraction of WS-Hg, IE-Hg, MeHg, HA-Hg and Hg-SR, respectively; (f) Mercury thermo-release curves of reference mercuric compounds.
**Figure S7.** Qualitative analysis of mercury speciation in biofilm by Hg-TPD: (a)-(e) Mercury thermo-release curves of biofilm samples in Phase III after sequential extraction of WS-Hg, IE-Hg, MeHg, HA-Hg and Hg-SR, respectively; (f) Mercury thermo-release curves of reference mercuric compounds.