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## Erratum

## Erratum to “Extracellular polymeric substances in aerobic granular sludge under increasing salinity conditions” [Water Research (2026) 292/125313]

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The authors would like to inform readers that a sentence was inadvertently omitted from the ‘Abstract’ section during the production process.

The correct ‘Abstract’ section should read as follows:

### Abstract

The long-term effects of environmental conditions, such as seawater salinity, on the extracellular polymeric substances (EPS) of aerobic granular sludge (AGS) remain poorly understood. This study investigated EPS changes during a stepwise increase in salinity (0–4%), renewing over 90% of biomass at each condition. Stable granulation, complete anaerobic acetate uptake, and phosphate removal were maintained throughout. FT-IR of granules showed significant changes in glycans (1025 cm<sup>-1</sup>) and sialic acid (1730 cm<sup>-1</sup>), which were reflected in the EPS. Lectin microarray revealed that increasing salinity reduced glycan diversity in EPS glycoproteins, while increasing negatively charged groups, including sialic acids and sulfated groups. At 4%

salinity, EPS negative charge increased by 19.8% compared to 0%. Microbial community composition shifted from a diverse mix (Dechloromonas; 23%, “*Candidatus* Competibacter”; 13%, “*Candidatus* Accumulibacter”; 28%) at 0% to a dominant (69% – 75%) unclassified Accumulibacter clade I species at 1 - 4% salinity. Metaproteomic analysis showed strong upregulation of genes of “*Ca. Accumulibacter*” involved in monosaccharide, lipopolysaccharide, and peptidoglycan biosynthesis from 3% - 4% salinity, indicating its adaptation to salinity stress. Dechloromonas and “*Ca. Competibacter*” represented a minor or a non-significant fraction of those proteins related to glycan synthesis across the salinities. Despite that no glycoprotein biosynthesis pathways were identified in the metaproteomic data, three putative glycoproteins produced by “*Ca. Accumulibacter*” were detected across all conditions. They were downregulated as the salinity increased. These findings highlight how “*Ca. Accumulibacter*” dynamically adapts its EPS, particularly glycoprotein glycans, in response to increasing salinity, offering new insights into EPS adaptation under environmental stress.

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