

CORRECTION

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Correction: Independent divergences of the Aquaporins across different genera highlight the distinct adaptation mechanisms within mytilida

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Following publication of the original article it was reported that Figs. 6 and 7 were transposed and therefore did not match their captions.

The correct figures with their captions are given in this Correction and the original article has been updated.

The original article can be found online at <https://doi.org/10.1186/s12864-025-12345-8>.

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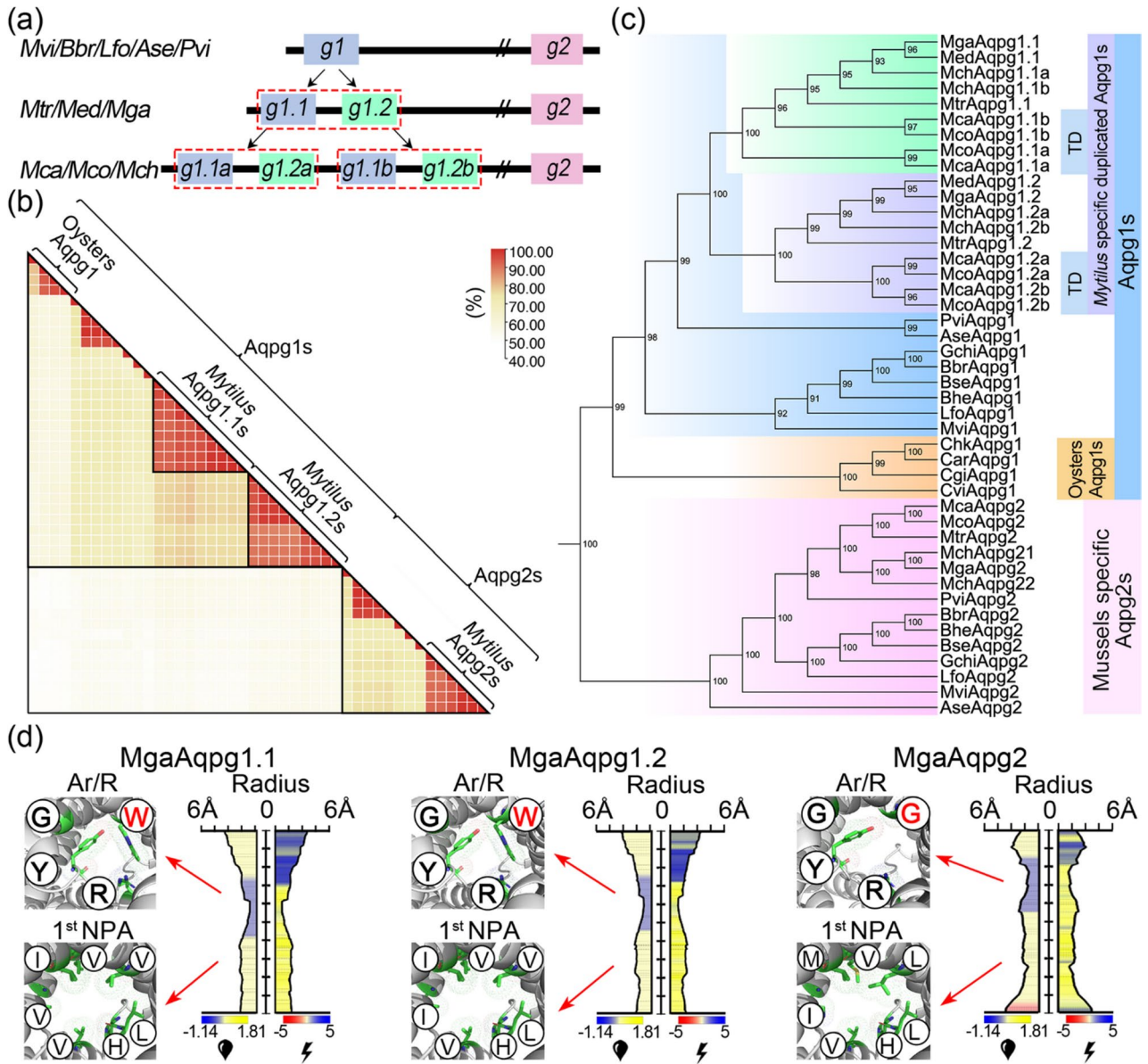


Fig. 6 Multiple duplications and diversification of the AQGP subfamily in mussels. **a** Duplication patterns of the expanded AQGP orthologs in mussels. Double slashes “//” between Aqpg1 and Aqpg2 orthologs indicate that these two orthologs are not adjacent on the chromosome. **b** Heatmap showing CDS identity among duplicated AQGP orthologs in oysters and mussels. **c** Phylogenetic distribution of AQGP genes in oysters and mussels. Paralogous originating from tandem duplication events are marked with colour-coded rectangles, emphasizing their evolutionary relationships. **d** Non-cytoplasm side view of the enlarged Ar/R selective region and NPA motif in duplicated AQGP orthologs. The amino acids composed these regions are highlighted by elements (Figure S1b). The right plots depict the inner surface properties of the duplicated AQGP orthologs including charge level (thunderbolt symbol) and hydrophobicity (droplet symbol) throughout the channel. The y-axis corresponds to the channel coordinate

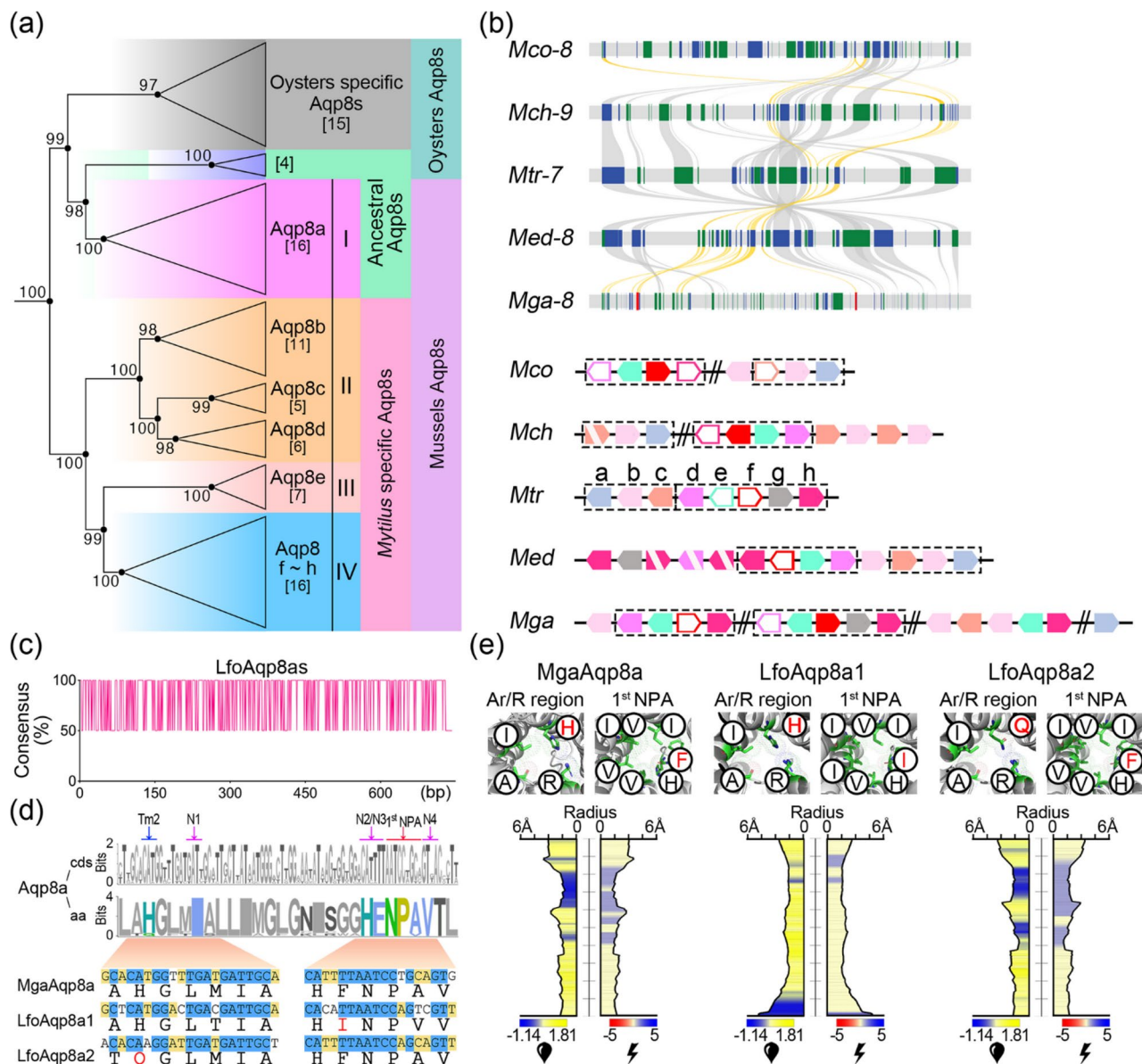


Fig. 7 Multiple duplications and diversification of AQP8 orthologs in mussels. **a** Phylogenetic distribution of diversified AQP8 orthologs in oysters and mussels. Each subgroup is highlighted in a different colour and marked I to IV, respectively. Orthologs within each subgroup are labeled a to h. **b** Multiple micro-synteny analysis of the genomic region encoding multiple duplicated AQP8 orthologs among species within the genus *Mytilus*. Yellow linking curves indicate collinearity among Aqp8 paralogs. Blue rectangles represent genes on the plus strand, and green rectangles on the minus strand. The corresponding distribution pattern of Aqp8 paralogs is shown below the synteny panel. The number following the species abbreviation indicates the chromosome ID. **c** Sequence consensus showing conservation between the independently duplicated Aqp8a paralogs in the golden mussel (*Lfo*). **d** Substitutions of the codons and amino acids in the selective filters among the independently duplicated Aqp8a paralogs in *Lfo*. Sequence logos, derived from multiple sequence alignments, depict conservation at key sites, which are highlighted in distinct colours and labeled. All other positions are shown in grey. The height of each nucleotide or amino acid symbol reflects its frequency at that position. **e** Structural comparison of duplicated Aqp8a paralogs in *Lfo*, focusing on the selectivity filter regions. The amino acids composed these regions are highlighted by elements (Figure S1b). Inner surface properties of the independently duplicated Aqp8a paralogs including charge and hydrophobicity level throughout the channel. The droplet symbolizes hydrophobicity, while the thunderbolt represents the charge level. The y-axis corresponds to the channel coordinate.