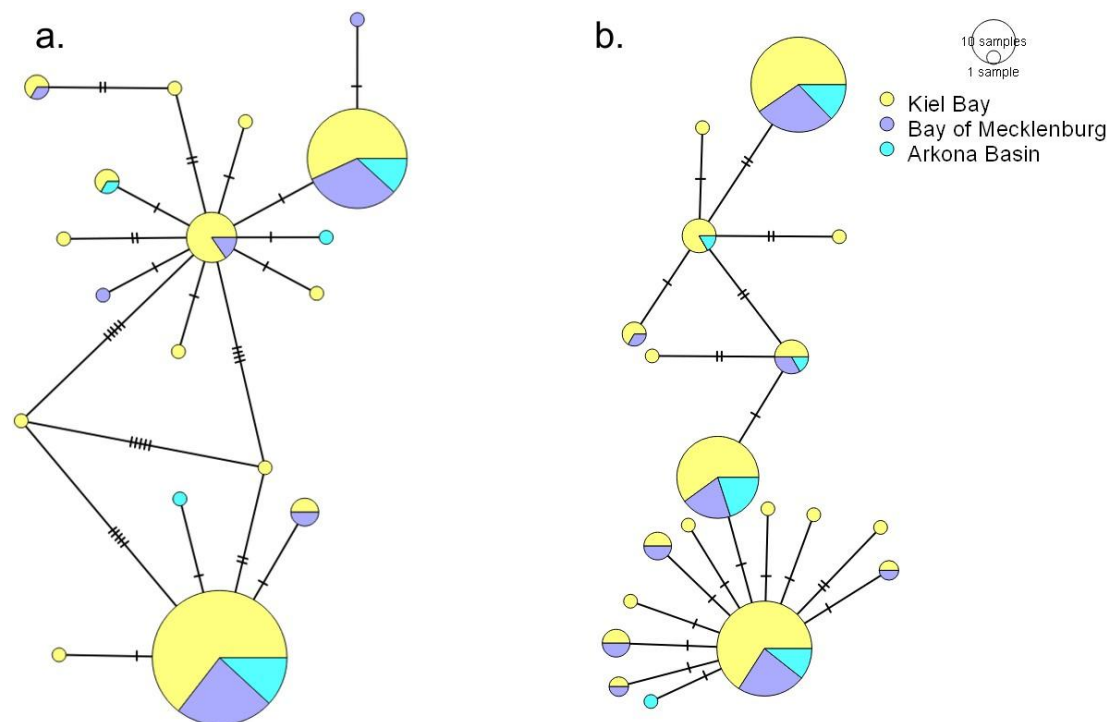


## Supplementary Information

### Single-marker analyses of mitochondrial COI and CytB datasets

COI sequences (up to 614 bp) were obtained from 174 *Arctica islandica* individuals, whereas CytB sequences (up to 398 bp) were recovered from 161 individuals across the investigated regions (Supplementary Data 1). For both markers, the majority of specimens originated from Kiel Bay (COI:  $n = 109$ ; CytB:  $n = 100$ ). Haplotype network analyses revealed similar patterns of extensive haplotype sharing among regions, short mutational distances between haplotypes, and low overall sequence divergence (Fig. S1). The most frequent haplotypes were distributed throughout the study area, and no evidence of geographic clustering was detected.



**Fig. S1** | Mitochondrial haplotype networks of *Arctica islandica* populations from the German waters of the Baltic Sea. Minimum spanning networks are shown for (a) COI sequences ( $n = 174$ ) and (b) CytB sequences ( $n = 161$ ). Circle size is proportional to haplotype frequency, and pie-chart segments indicate haplotype distribution among sampling regions. Hash marks on branches represent mutational steps between neighbouring haplotypes.

Across regions, both mitochondrial markers exhibited high haplotype diversity combined with moderate nucleotide diversity (Table S1). Diversity estimates were consistently higher for CytB than for COI. Kiel Bay showed the highest haplotype richness and number of polymorphic sites for both markers, likely reflecting the comparatively larger sample size relative to the Bay of Mecklenburg and Arkona Basin.

**Table S1** | Mitochondrial diversity indices based on single-marker gene sequences (COI and CytB) of *Arctica islandica* from the German waters of the Baltic Sea. Abbreviations: KB, Kiel Bay; MB, Bay of Mecklenburg; AB, Arkona Basin; n, number of sequences; K, number of haplotypes; S, number of polymorphic sites; Hd, haplotype diversity;  $\pi$ , length-normalised nucleotide diversity.

| Marker | Region | n   | K  | S  | Hd   | $\pi$ (norm) [%] |
|--------|--------|-----|----|----|------|------------------|
| COI    | KB     | 109 | 14 | 20 | 0.66 | 0.62             |
|        | MB     | 45  | 7  | 14 | 0.64 | 0.65             |
|        | AB     | 20  | 5  | 10 | 0.63 | 0.63             |
| CytB   | KB     | 100 | 19 | 19 | 0.80 | 0.89             |
|        | MB     | 40  | 8  | 10 | 0.78 | 0.90             |
|        | AB     | 21  | 6  | 8  | 0.78 | 0.84             |

Mismatch distribution analyses based on both mitochondrial markers supported a scenario of historical population expansion (Table S2). Under the sudden expansion model, estimates of  $\theta_0$  were close to zero, whereas  $\theta_1$  values were substantially higher across all regions, consistent with expansion from a small ancestral population.

Model fit under the sudden expansion model showed minor differences between markers (Table S2). For COI, SSD and Harpending's raggedness indices indicated significant deviations despite low absolute values, suggesting that a strict sudden expansion model may not fully explain the observed patterns. In contrast, CytB showed low and non-significant SSD and raggedness values.

Spatial expansion models yielded broadly consistent results for both markers, with similar estimates of expansion time and moderate migration parameters across regions. Under this model, SSD and raggedness were uniformly low and non-significant, supporting a demographic expansion scenario with spatial structure.

Neutrality tests supported a history of population expansion for both mitochondrial markers (Table S2). Fu's  $F_s$  values were strongly negative and highly significant across all regions, indicating an excess of rare haplotypes consistent with population growth. Tajima's D values were non-significant for both markers, suggesting no strong deviation from neutral expectations.

AMOVA analyses revealed no significant genetic structure among sampling regions. For both COI and CytB, the majority of genetic variation was partitioned within rather than among regions, with slightly negative and non-significant fixation indices (COI:  $F_{ST} = -0.016$ ,  $p = 0.86$ ; CytB:  $F_{ST} = -0.018$ ,  $p = 0.95$ ). Pairwise  $F_{ST}$  values and average pairwise sequence divergence ( $\pi_{XY}$ ) were consistently low and non-significant, further supporting a lack of detectable mitochondrial differentiation across the investigated regions.

42 **Table S2** | Demographic expansion and neutrality test results for *Arctica islandica* from the German waters of the Baltic Sea based on individual mitochondrial COI and CytB  
 43 sequences. Significance levels for the sum of squared deviations (SSD), Harpending’s raggedness index (r), and Fu’s  $F_s$  is indicated by asterisks: \*  $p \leq 0.05$ , \*\*  $p \leq 0.01$ .  
 44 Abbreviations:  $\tau$ , time since expansion;  $\theta_0 / \theta_1$ , population size before/after expansion; M, migration parameter.

|                         | COI      |          |          | CytB     |          |          |
|-------------------------|----------|----------|----------|----------|----------|----------|
|                         | KB       | MB       | AB       | KB       | MB       | AB       |
| sudden expansion model  |          |          |          |          |          |          |
| $\tau$                  | 7.87     | 8.16     | 8.27     | 7.53     | 8.01     | 7.65     |
| $\theta_0$              | 0.00     | 0.00     | 0.00     | 0.00     | 0.00     | 0.00     |
| $\theta_1$              | 4.31     | 4.04     | 4.47     | 5.04     | 4.97     | 4.32     |
| SSD                     | 0.12*    | 0.17**   | 0.20**   | 0.03     | 0.04     | 0.04     |
| r                       | 0.19*    | 0.30*    | 0.39*    | 0.04     | 0.06     | 0.07     |
| spatial expansion model |          |          |          |          |          |          |
| $\tau$                  | 6.40     | 6.83     | 7.48     | 5.01     | 5.87     | 5.33     |
| $\theta$                | 0.56     | 0.49     | 0.24     | 2.40     | 1.68     | 2.16     |
| M                       | 1.50     | 1.41     | 1.69     | 1.22     | 1.40     | 1.04     |
| SSD                     | 0.06     | 0.10     | 0.12     | 0.03     | 0.03     | 0.04     |
| r                       | 0.19     | 0.30     | 0.39     | 0.04     | 0.06     | 0.07     |
| neutrality tests        |          |          |          |          |          |          |
| Tajima’s D              | −0.03    | 0.66     | 1.13     | −0.12    | 1.49     | 1.52     |
| Fu’s $F_s$              | −25.99** | −25.93** | −22.92** | −26.14** | −26.06** | −25.80** |