

Patterns of mtDNA diversity in North Atlantic populations of the mussel *Mytilus edulis*

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The post-colonization direction of gene flow in Fig. 5 was reversed. Although this mistake alters some conclusions regarding post-colonization gene flow (p. 405), *IM*-derived estimates of population splitting (s) and divergence times are correct as reported and these data form the basis for the major conclusions regarding routes of colonization. The recombinant haplotype from Mahone NS is 677 not 667.

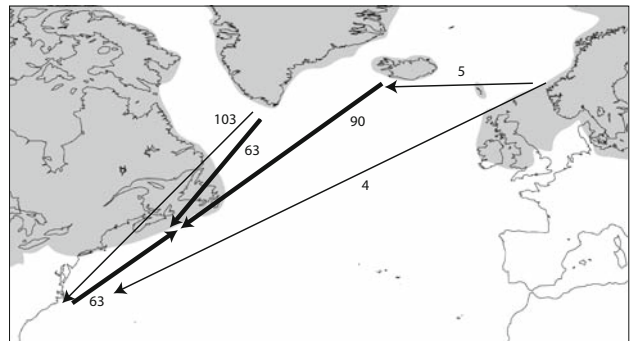


Fig. 5 Post-colonization gene flow. Arrows show all cases where the highest posterior probability of migration was greater than 0 (in models that included migration). **Bold arrows** show the instances where these probabilities were statistically significant ($P < 0.05$). **Numbers** are the point estimates of the number of migrants (Nm or gene flow) per generation

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