

Ibarguchi, G., Gaston, A. J. and Friesen, V. L. 2011. Philopatry, Morphological divergence, and kin groups: structuring in thick-billed murre *Uria lomvia* within a colony in Arctic Canada. – J. Avian Biol. 42: 134-150.

Appendix 1

Summary of spatial autocorrelation analyses.

Global colony-wide spatial autocorrelation analyses (200 m; example in Fig. A1-1) revealed a weak pattern of oscillating autocorrelation coefficients (R) along the distance axis. The number of significant R coefficients were overall few (and almost absent for females based on cytochrome b), similar for both sexes based on microsatellites, and for males based on cytochrome b (details not shown). The number of significant r coefficients tended to decrease with increasing distance class at these large scales.

Ledge-wide analyses (< 6 m) varied individually by ledge, sex, marker, and distance class size. Combined spatial analyses of the ten ledges (i.e. simultaneous analyses to detect patterns consistent among all ledges) for all birds, males, and females also varied. However, based on cytochrome b, trends were observed at several distance classes of some clusters of significant R at 180 cm for all birds and males, and at 300 cm for females (not shown). Within ledges, as distance class sizes increased, significant spatial autocorrelation was observed for males based on cytochrome b at larger distance classes approaching the average ledge size (e.g. combined within-ledge analyses in Fig. A1-2). However, negative spatial autocorrelation was observed for females at the smaller distance classes, although no R coefficients were significant. For microsatellites, a trend was observed of significant positive R coefficients for all birds at the 15 cm distance class size only (i.e. within breeding sites, between breeding partners).

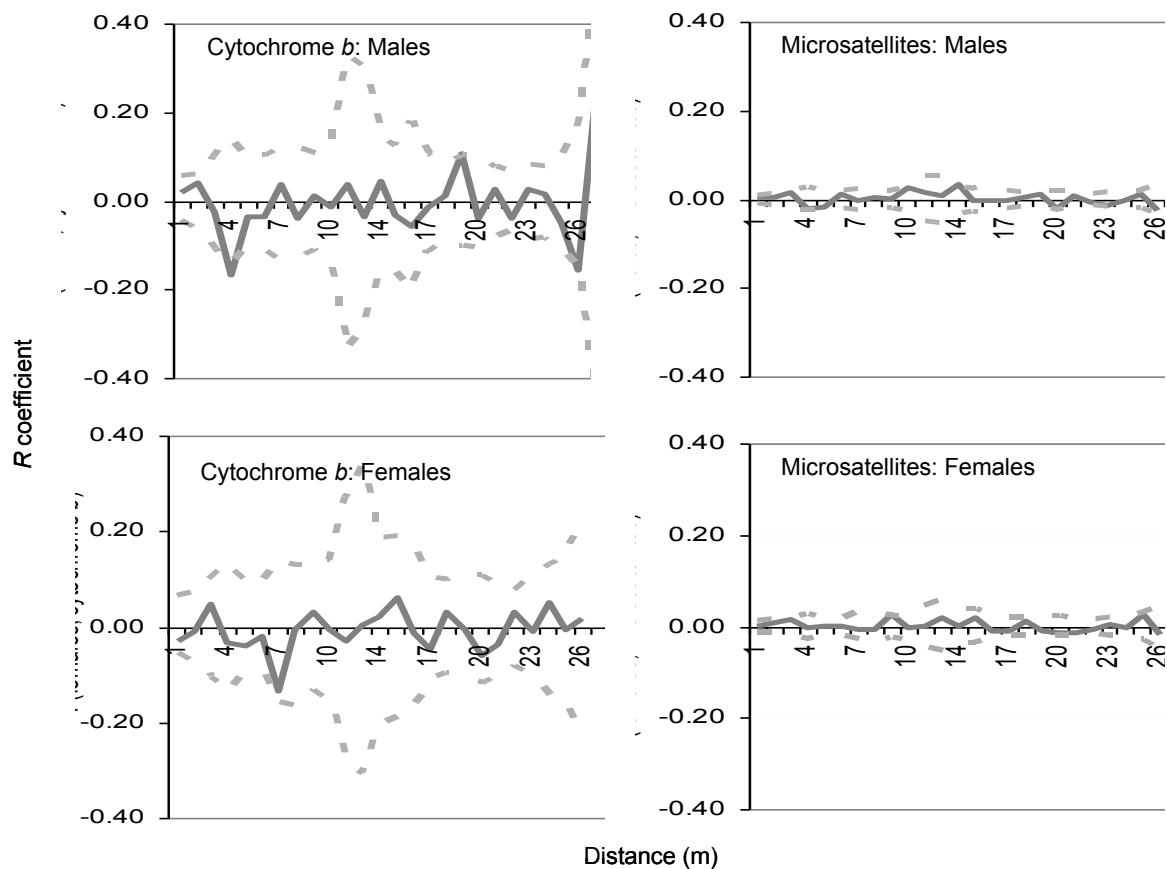
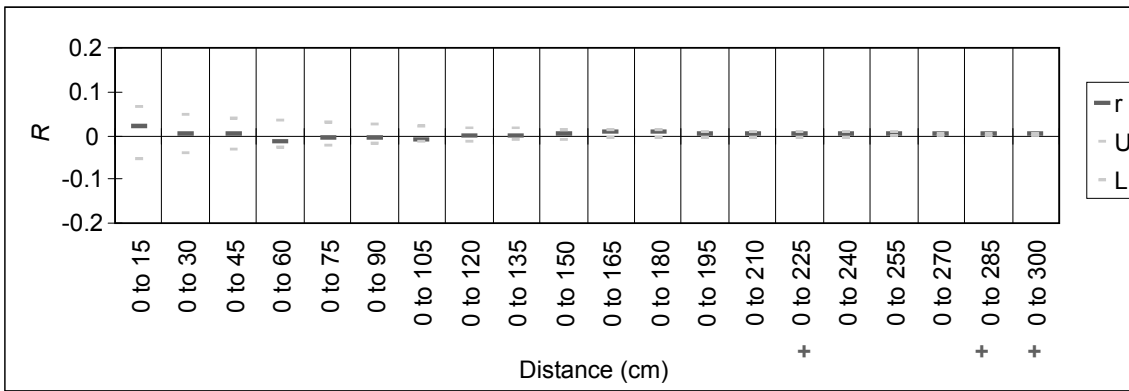
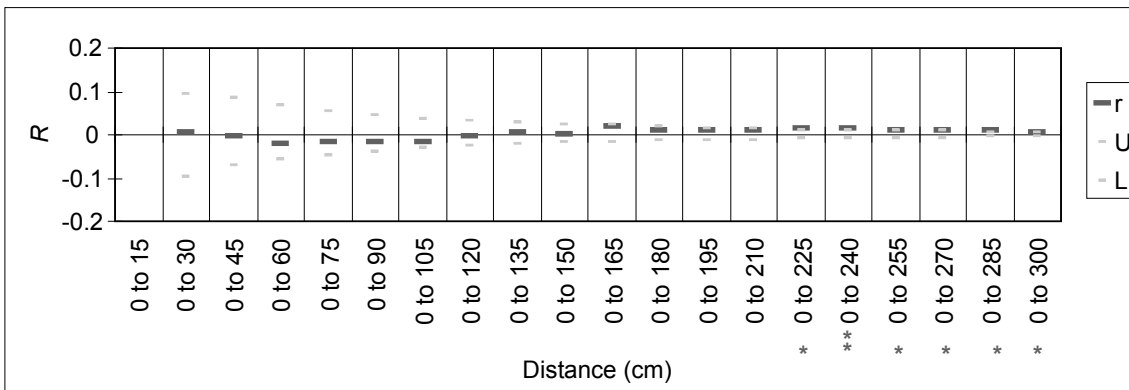


Fig. A1-1. Example correlograms of global spatial autocorrelation analyses (across the colony; size class = 1 m) from GenAlEx v. 6 truncated here to 27 m to show weak oscillation pattern (i.e. approximating a random distribution or small patches of structure varying in size and space). Solid gray lines represent R coefficients; dashed lines are upper and lower 95% confidence intervals for R; coefficients crossing upper confidence intervals are significantly positive.

Cytochrome *b*- All birds pooled



Cytochrome *b*- Males



Cytochrome *b*- Females

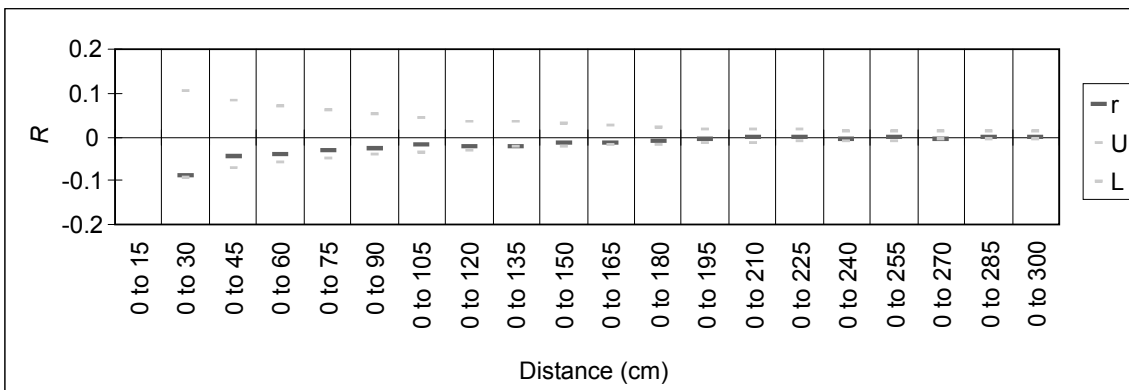


Fig. A1-2. Combined spatial autocorrelation analyses for 10 ledges for increasing distance classes, based on cytochrome *b*. Significant *R* coefficients for the combined ledges are indicated. (* = $P < 0.05$; ** = $P < 0.01$; + = $0.05 < P < 0.09$; trend, + = $0.05 < P < 0.09$; upper U and lower L 95% confidence intervals, gray thin lines). Note the negative *R* coefficients in females up to 195 cm.

Appendix 2
 Relatedness bins: comparing ledges and groups

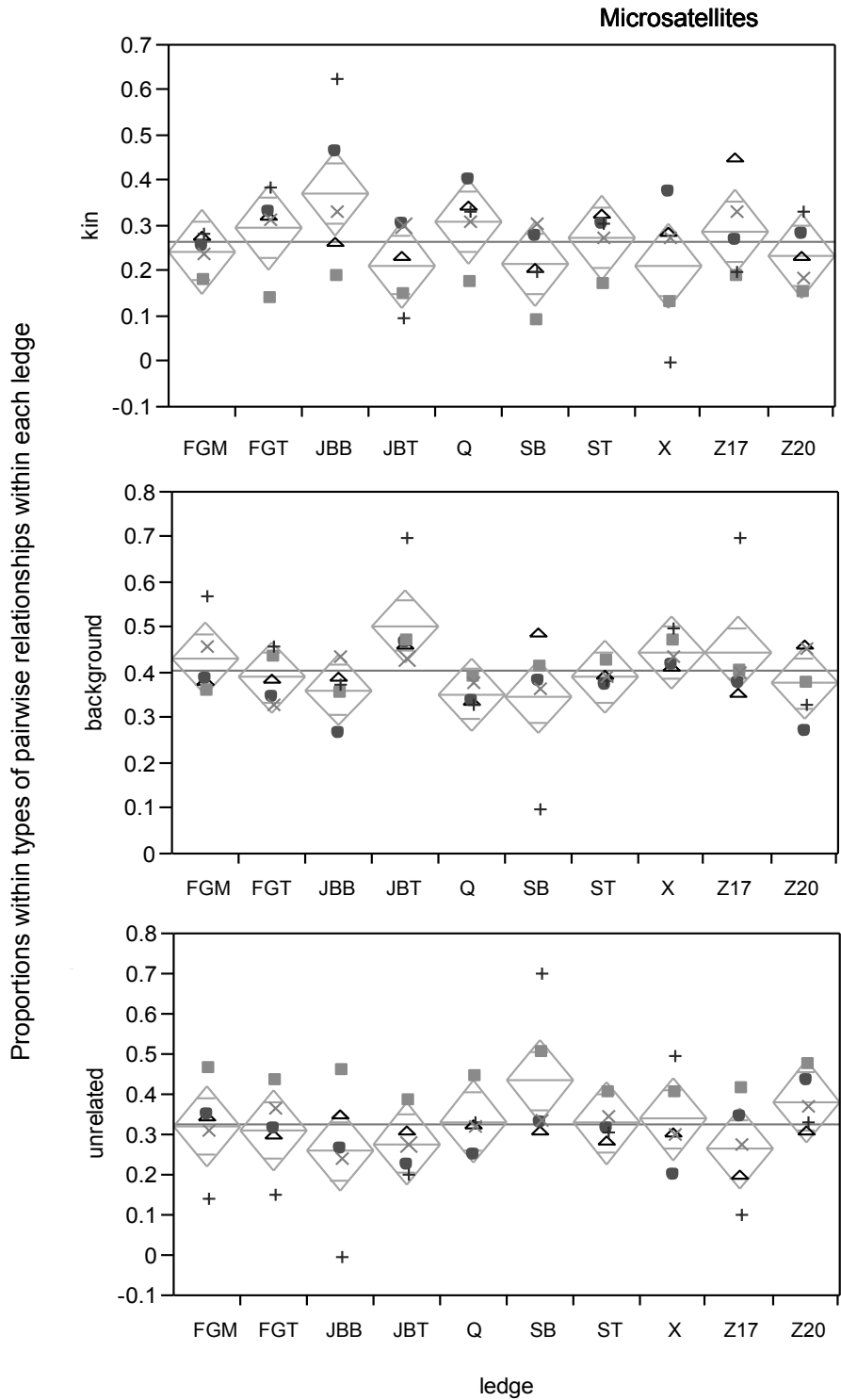


Fig. A2-1. Among-ledge and among-group comparisons of proportions of pairwise relatedness within each bin based on microsatellites: kin (top panel), background (middle), and highly unrelated proportions (bottom). Diamond plots are means with 95% CIs; global means are the solid gray lines in each panel. Groups: males, triangles; females, circles; all birds, squares; breeding partners, crosses; randomly generated birds, x's (Y-axes are not at the same scale).

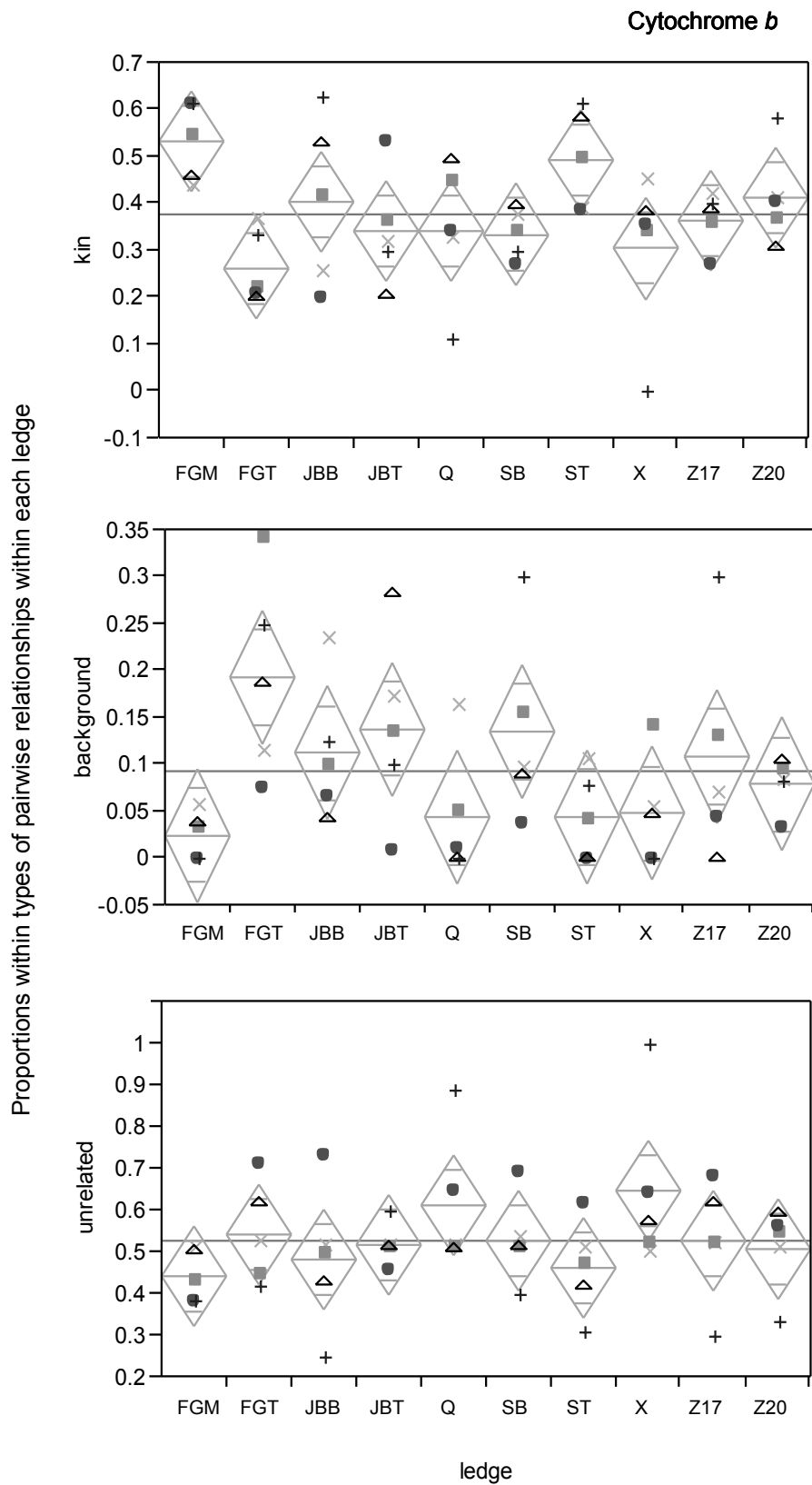


Fig. A2-2. Among-ledge and among-group comparisons of proportions within each relatedness bin based on cytochrome *b*: kin (top panel), background (middle), and highly unrelated proportions (bottom). Diamond plots show means with 95% CIs; global means are the solid gray lines in each panel. Groups: males, triangles; females, circles; all birds, squares; breeding partners, crosses; randomly generated birds, x's. (Y-axes are not at the same scale).