



FIGURE 7.14. X-alignments. (A) Schematic model of symmetric genome inversions. The model shows an initial speciation event, followed by a series of inversions in the different lineages (A and B). Inversions occur between the asterisks (*). Numbers on the chromosome refer to hypothetical genes 1–32. At time point 1, the genomes of the two species are still colinear (as indicated in the scatterplot of A1 vs. B1). Between time point 1 and time point 2, each species (A and B) undergoes a large inversion about the terminus (as indicated in the scatterplots of A1 vs. A2 and B1 vs. B2). This results in the between-species scatterplot looking as if there have been two nested inversions (A2 vs. B2). Between time point 2 and time point 3, each species undergoes an additional inversion (as indicated in the scatterplots of B2 vs. B3 and A2 vs. A3). This results in the between-species scatterplots beginning to resemble an X-alignment. (B) X-like alignment in dotplot of the main chromosomes of *Vibrio cholerae* (x-axis) and *Vibrio parahaemolyticus* (y-axis). (C) A weak X-like pattern exists even when comparing more distantly related species, in this case *V. cholerae* and *E. coli*. An X-like pattern indicates that the distance of a gene from the origin is conserved, but the side of the origin on which it is located is not conserved.

7.14A,B,C, redrawn from Eisen J.A. et al., 2000. *Genome Biol.* 1: research0011.1–0011.9, © 2000 BioMed Central Ltd