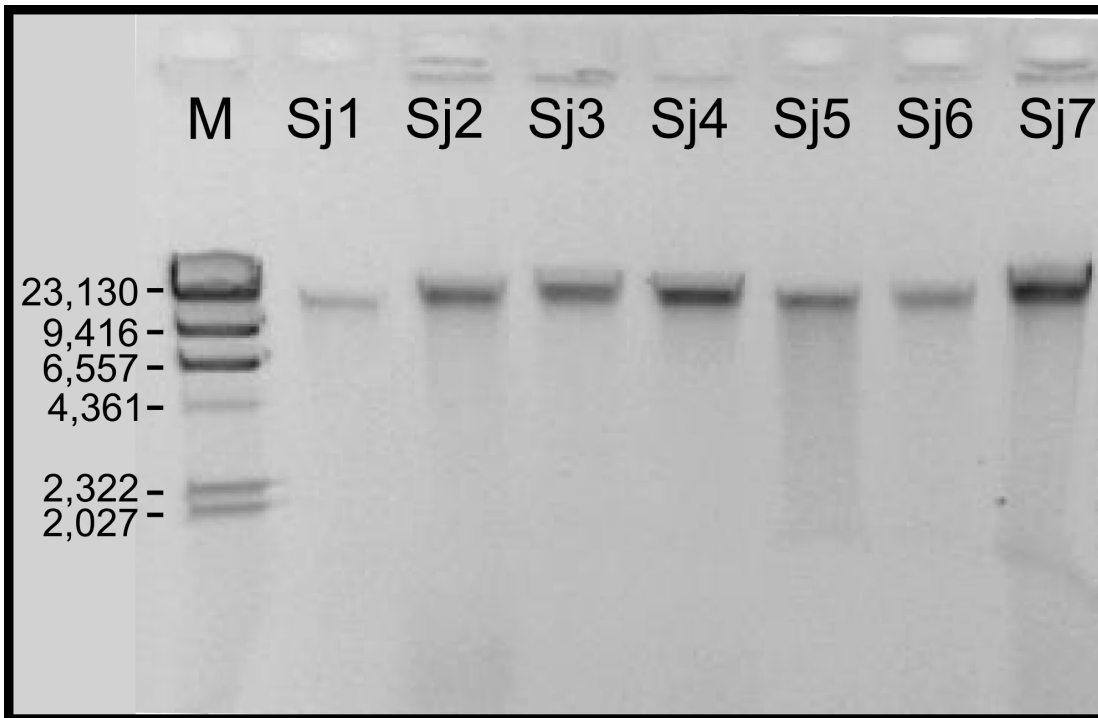


SUPPLEMENTARY FIGURES

Exploring molecular variation in *Schistosoma japonicum* in China

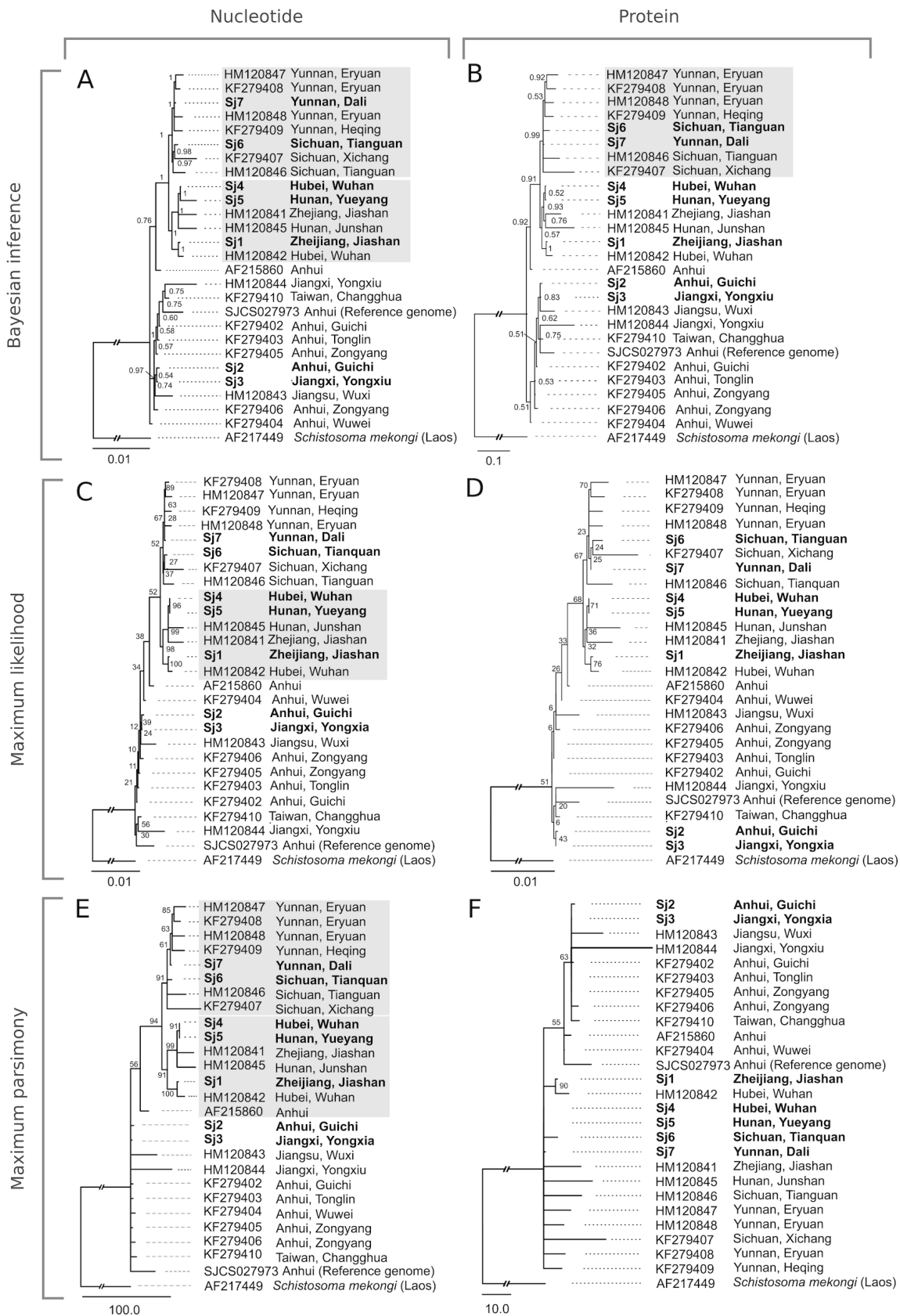
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Supplementary Figure 1 | Integrity of archived *Schistosoma japonicum* genomic DNA.

Genomic DNA was isolated from pooled adult *S. japonicum* (i.e. male and female *en copula*; $n = 10$ pairs) representing each of the populations Sj1 to Sj7. Genomic DNA samples were subjected to electrophoresis in an agarose gel (0.7%); Lambda DNA/*Hind*III was used as a molecular weight marker (M).



Supplementary Figure 2 | Phylogenetic relationships of *Schistosoma japonicum* populations based on analyses of data for 12 protein-encoding mitochondrial genes. The consensus trees from separate analyses of nucleotide (A, C and E) or amino acid (B, D and F) sequence data using the Bayesian inference (A and B), maximum likelihood (C and D) and maximum parsimony (E and F) tree-building methods. Posterior probabilities (pp) or nodal support values are indicated. Groups with strong nodal support are highlighted in grey. GenBank database accession numbers of individual gene sequences are at the ends of individual branches.

