Ant species of the *Cataglyphis altisquamis* group are characterized by a hybridogenetic mode of reproduction. Two distinct genetic lineages co-occur in each population and queens mate with males originating from the alternative lineage than their own. Queens use sexual reproduction to produce an inter-lineage hybrid worker force, but they use asexual reproduction (parthenogenesis) for the production reproductive offspring. Thus, sterile workers systematically arise from the hybridization of two genetic lineages, whereas the sexual forms belong all to the queen lineage. Recently, it has been shown that new reproductive queens are occasionally produced by gynogenesis. In gynogenetic species, sperm cells are required to trigger embryogenesis but usually do not transmit their genome to the zygote. However, this mode of reproduction provides an opportunity for incidental leakage of sperm DNA into clonal queen-destined eggs (Schlupp 2005). Using both mitochondrial and nuclear genes, we examined phylogeographic patterns of 3 species belonging to the *Cataglyphis altisquamis* group where hybridogenesis and gynogenesis co-occur. Our results reveal three important insights. (1) For each species, a single pair of nuclear lineages exists across all populations sampled. Reproductives from each genetic lineage interbreed to produce sterile workers; by contrast, new queens and males are asexually produced. (2) Remarkably, genetic analyses reveal strong incongruences between mitochondrial and nuclear variations: variation at mtDNA shows a geographic structure independent of nuclear lineages segregation. This indicates a substantial mitochondrial gene flow between the two divergent nuclear lineages. (3) Consistent with these results, we found a higher mitochondrial diversity within species than between species. Such uncommon pattern of mitochondrial distribution most likely stems from recombination events between mitochondrial genomes from distinct lineages. Overall, this study shows how alternative reproductive strategies can shape complex phylogeographic patterns.