Non-native species are often associated with substantial ecological and economic impacts. To understand potential ecological impacts of invasive species, implement appropriate control measures, and predict future invasions, it is important to identify the source(s) of invasion. Ants are one of the most ecologically important taxa, and introduced ants can substantially alter ecosystems and devastate native fauna. The tropical fire ant, *S. geminata*, natively inhabits areas in North, Central, and South America, but is emerging as a tramp species across the globe. In this study we used genetic data (45 microsatellite loci, and a 646 bp sequence of mitochondrial Cytochrome oxidase I) to identify source populations of tramp *S. geminata* by comparing ants collected in invaded areas (Australia, India, Madagascar and islands in the Indian Ocean, Philippines, Thailand, and Hawaii) to native populations in North, Central, South America and the Caribbean. We analyzed microsatellite allele frequencies using a Bayesian clustering technique to determine population structure in the native range; invasive samples were then assigned to a native population based on frequency of shared alleles. We constructed phylogenetic trees from CO1 using parsimony Bayesian methods to evaluate evolutionary relationships among native and invasive ants. We found a substantial amount of genetic diversity among native *S. geminata*, and very little among invasive ants. All invasive ants share a single CO1 haplotype; they also had a low frequency of shared alleles with native populations. Tramp populations were most closely related to specimens from Texas and northern Mexico. The single shared haplotype, and low genotypic diversity in the invasive ants suggest that movement of *S. geminata* across the globe has been recent, and may have originated in northern Mexico/Texas. However, the low frequency of shared alleles among invasive and non-invasive ants suggests that the true source population may not have been sampled.