

## Effect of Climate Change on the Genomics of Invasiveness of the Whitefly *Bemisia tabaci* Species Complex by Estimating the Effective Population Size via a Coalescent Method

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**Abstract :** Invasive species represent an increasing threat to food biosecurity, causing significant economic losses in agricultural systems. An example is the sweet potato whitefly, *Bemisia tabaci*, which is a complex of morphologically indistinguishable species causing average annual global damage estimated at US\$2.4 billion. The *Bemisia* complex represents an interesting model for evolutionary studies because of their extensive distribution and potential for invasiveness and population expansion. Within this complex, two species, Middle East-Asia Minor 1 (MEAM1) and Mediterranean (MED) have invaded well beyond their home ranges whereas others, such as Indian Ocean (IO) and Australia (AUS), have not. In order to understand why some *Bemisia* species have become invasive, genome-wide sequence scans were used to estimate population dynamics over time and relate these to climate. The Bayesian Skyline Plot (BSP) method as implemented in BEAST was used to infer the historical effective population size. In order to overcome sampling bias, the populations were combined based on geographical origin. The datasets used for this particular analysis are genome-wide SNPs (single nucleotide polymorphisms) called separately in each of the following groups: Sub-Saharan Africa (Burkina Faso), Europe (Spain, France, Greece and Croatia), USA (Arizona), Mediterranean-Middle East (Israel, Italy), Middle East-Central Asia (Turkmenistan, Iran) and Reunion Island. The non-invasive 'AUS' species endemic to Australia was used as an outgroup. The main findings of this study show that the BSP for the Sub-Saharan African MED population is different from that observed in MED populations from the Mediterranean Basin, suggesting evolution under a different set of environmental conditions. For MED, the effective size of the African (Burkina Faso) population showed a rapid expansion  $\approx 250,000$ -310,000 years ago (YA), preceded by a period of slower growth. The European MED populations (i.e., Spain, France, Croatia, and Greece) showed a single burst of expansion at  $\approx 160,000$ -200,000 YA. The MEAM1 populations from Israel and Italy and the ones from Iran and Turkmenistan are similar as they both show the earlier expansion at  $\approx 250,000$ -300,000 YA. The single IO population lacked the latter expansion but had the earlier one. This pattern is shared with the Sub-Saharan African (Burkina Faso) MED, suggesting IO also faced a similar history of environmental change, which seems plausible given their relatively close geographical distributions. In conclusion, populations within the invasive species MED and MEAM1 exhibited signatures of population expansion lacking in non-invasive species (IO and AUS) during the Pleistocene, a geological epoch marked by repeated climatic oscillations with cycles of glacial and interglacial periods. These expansions strongly suggested the potential of some *Bemisia* species' genomes to affect their adaptability and invasiveness.

**Keywords :** whitefly, RADseq, invasive species, SNP, climate change

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