Honey contains DNA from many different organisms that are part of hive micro-environmental niches and honey bee pathospheres. In this study, we recovered and sequenced mite mitochondrial DNA (mtDNA) from honey from different locations around the world (Europe, Asia, Africa, North and South America). DNA extracted from 17 honey samples was amplified with eight primer pairs targeting three mite mtDNA genes, obtaining 88 amplicons that were sequenced with an Ion Torrent sequencing platform. A bioinformatic pipeline compared produced reads with Varroa spp. mtDNA sequence entries available in GenBank and assigned them to different mitotypes. In all honey samples, the highest percentage of reads was attributed to the K1 lineage, including a few variants derived from it, in addition to J1 reads observed in the two South American samples and C1-1 reads obtained from the Chinese honey. This study opens new possibilities to analyse mite lineages and variants and monitor their geographical and temporal distribution, simplifying surveillance against this damaging honey bee parasite.