

Figure 1: Edges with IBD between 0 and 100% (non inclusive) are white, while those with 100% IBD are coloured by haplotype labels. Edges with IBD < 50% are dashed, while those with IBD > 50% are solid.

Deep-dive into Buenaventura and Tumaco

We see a lot of genetic relatedness within and between sites and want to know if there is A) ongoing or one-time gene flow and B) two-way or source to sink gene flow.

Assuming travel between cities Tumaco and Buenaventura is symmetrical (try to confirm with expert knowledge / maritime traffic data), the site with higher incidence (Tumaco) is the most likely source.

Vertical lines are compatible with a transmission event, but could also arise due to similar haplotypes being detected at the same time across sites. Diagonal lines are not compatible with direct travel.

The fact that there are multiple repeat haplotypes suggests gene flow was not a one-time event. The fact that each site has some private repeat haplotypes suggests that there is potential for two-way flow.

Assuming Tumaco to be the source, Figure 1 suggests haplotypes 5 and 7 were transmitted from Tumaco to Buenaventura sometime after haplotypes 1 and 12 (circa years 2005 and 2003, respectively). Haplotype 2 was not detected in either site before 2005, we thus speculate that it was transmitted across sites sometime around 2005. Upon inspection of Figure 1 it is important to note however that absence of evidence is not evidence of absence due to non-exhaustive sampling of infections (e.g. all haplotypes could have been present in either site prior to their detection due to unsampled infections).

The number of differently coloured repeat haplotypes might give a false impression of the number of independent pieces of information, however. A network of relatedness between the repeat haplotypes (white edge IBD = 0.001, darkest edge IBD = 0.83) was thus plotted (Figure 2).

Of the haplotypes shared across Buenaventura and Tumaco, haplotypes 5, 7 and 12 are all highly related to one another, so might originate from a single parasite. On the contrary, haplotypes 1 and 2 are not highly related to the above cluster nor one-another. Together these results suggest three travel events.

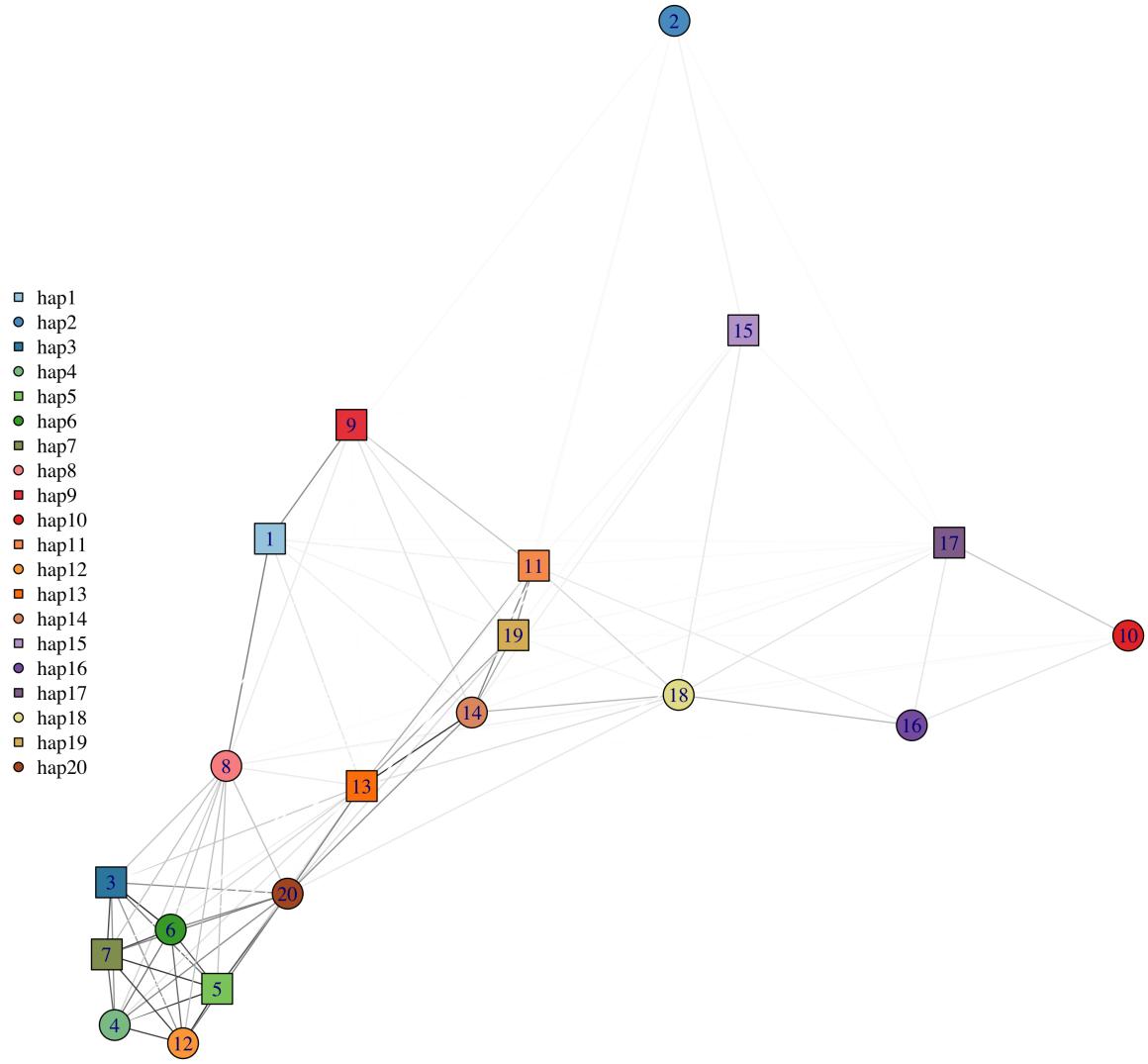


Figure 2: Relatedness across repeat haplotypes.