**Adnan et al (The heart of Silk Road “Xinjiang”)**

**Supplementary text 1**

**Comparison between Chinese and Asian population**

**3.5.2- China**

Genetic distances among the HAN population and other thirty-one populations from China were calculated using Nei’s standard formula and are summarized in **Supplementary Table 4B.** According to Nei’s genetic distance, the Han population (0.0016) from Liaoning showed the closest distance with our newly sampled HAN in Xinjiang, followed by the Han population (0.0022) from Central China, while the Mongol population (1.2981) from Inner Mongolia, China showed the most distant relationship with HAN in Xinjiang, followed by Kazakh population (1.1693) from Xinjiang. These Nei’s genetic distance values were used to build a neighbor-joining tree (N-J tree) between Xinjiang Han and 31 other populations **(Supplementary Figure 1A).** The first three components of PCA (PC1= 53.72%, PC2= 17.13%, PC3= 7.92%, extracted 78.77% genetic variation and showed that Turkic-speaking populations were closely linked **(Supplementary Figure 1C)**. A heat map was developedusing the genetic distances matrix and observed two clusters **(Supplementary Figure 1B)**. In the first cluster Manchu, Kyrgyz, Uzbek, Kazakh, and East Mongolian populations from China were clustered while the second was further dived into two clusters. In the second A cluster there were only two populations (Kazakh and Uyghur-2) while in second B rest of the populations were tightly clustered. These results were consistent with the PCA and Nei’s genetic distance results.

**3.5.3- Asia**

Genetic distances among the HAN population and fifty-eight other populations from Asia were calculated using Nei’s standard formula and are summarized in **Supplementary Table 4C.** After excluding Chinese populations, we found the populations from East Asia (Korean and Japanese) showed an affinity with the HAN population from Xinjiang, while the Mongol population from Mongolia was the most distant population from Asian populations with HAN followed by the Kadazan population from Malaysia, being distant from Asian populations. These Nei’s genetic distance values were used to build a neighbor-joining tree (N-J tree) for Xinjiang Han and 58 other populations from Asia **(Figure 5A).** Uyghur and Kazakh populations showed more association with Central Asian and South Asian populations. The first ten components of PCA (PC1= 36.26%, PC2= 14.78%, PC3= 9.75%, PC4= 8.25%, PC5= 6.51%, PC6= 4.72%, PC7= 3.02%, PC8= 1.96%, PC9= 1.53% and PC10= 1.4%) extracted 88.22% of genetic variation **(Figure 5C)**. All Chinese populations were placed on the left side of the plot except for few Xinjiang populations which shows the affinity between Chinese minorities or genetic differences among Xinjiang Muslim populations and the Han population. A heat map of the genetic distances matrix was also generated **(Figure 5B)** and observed two clusters. In the first cluster, again Manchu, Kyrgyz, Uzbek, Kazakh, and East Mongolian populations from China were clustered while the second cluster was further divided into two clusters. In the second A cluster all populations from East Asia (China, Korea, and Malaysia) clustered tightly while in second B cluster populations from Central Asia, South West Asia, and West Asia ( Central Asian Muslims living in China, Pakistan, India, Iran, Turkey, Azerbaijan, and Afghanistan) were clustered tightly. These results were consistent with the PCA and Nei’s genetic distance results.