## **Oral Communication Abstract – 3B.03**

## VARIABILITY OF TASTE AND SMELL GENES ALONG THE SILK ROAD

## PIRASTU N., D'ADAMO P., GIROTTO G., ROBINO A., ATHANASAKIS E., GASPARINI P.

Institute for Maternal and Child Health - IRCCS "Burlo Garofolo" – Trieste, University of Trieste (Italy)

## Silk Road, Population studies, genetics of taste, food preferences

Thanks to the scientific expedition Marcopolo2010 (www.marcopolo2010.it) we have studied approximately 20 different communities from Georgia to China. Their genomes have been analyzed with 700,000 genetic markers. All the data were then analyzed with PCA. Preliminary results demonstrate the similarity between the Kazakh populations (different populations are largely overlapping) and the extreme homogeneity' of those located in the Zerafshan Valley (Tajikistan). Additional data indicate that ethnically and linguistically isolated populations such as those of the Pamir, are now losing their uniqueness. As a matter of fact, they are characterized by a mixture of unique and peculiar individuals together with individuals close to those living in other regions of Tajikistan. Finally, surprising was the situation of the Uzbeks Quarshie, falling off sharply from all other populations examined. Apart from this general view, we tested phenotypes and genotypes related to taste, smell, hearing and vision. As regards taste we were able to demonstrate a gradient of distribution from west to east of supertaster for PROP/PTC bitter compounds. Moreover, food preferences are the main factor driving food intake and choice. Although taste has been widely studied especially in regards of pure tastes such as bitter or sweet perception, the relationship between taste related genes and food preferences has seldom been explored. The Silk Road has been the root through which spices and silk have come from the far east to Europe creating a particular mixture of population along it. However up to now no one has studied the way this populations are genetically related to each other. We have thus created a genetic map based on whole genome single nucleotide markers. We have used this knowledge to test 26 genes related to taste and how this genes influence food preferences. In particular we have found that TAS1R gene which encodes the sweet receptor is associated to alcohol related foods; PCLB2, a gene related to smell is associated to liking of hot tea; the capsaicin receptor TPRV1 is associated to white/red radish; and finally ITPR3 is associated to many foods including Lamb, Sheeps Cheese, Fava Beans and Watermelon significantly, but it shows to influence up to 35 more foods. These knowledge will help understand better the effect of admixture of this populations and will help clarify the genetic relationship between taste, smell and food preferences.