RULES FOR PARTICIPATING IN GEP-EMPOP

Labs interested in participating in this project must comply with the following requirements:

1.- To have succeeded the last GEP quality control (2008). As the samples that are in EMPOP are reference samples, to have passed the paternity section (samples M1 to M4) will be enough.

2.- To have data of HVS1 and HVS2 (16024-16365 & 72-340). If some lab can contribute with additional data of the control region (complete, HVS3) or have data of coding SNPs (phylogenetically significant), these data will also be welcome.

It is important to state the best possible geographical affiliation of the samples (region/city/population) as this is important for the import in EMPOP

3.- To send your data in an excel table.

4.- Haplotypes that contain length heteroplasmies must not be omitted. If these haplotypes were omitted due to a poor quality and difficult reading of the electros we would be biasing the number of occurrences of some haplotypes. In these cases, the correct way to proceed is to re-analyze the samples by using internal primers in order to obtain double readings of each sample.

5.- Please send your table to the following email address: [lourditasmt@ya.com](mailto:lourditasmt@ya.com). In a different message let me know that you have sent your data. You will have a reply informing you that the data were correctly received.

6.- The advisors of this collaboration are labs that sent their data previously and, therefore, are experienced in it. They are the following:

Instituto de Toxicología y Ciencias Forenses de Barcelona

Instituto de Toxicología y Ciencias Forenses de Madrid

Universidad de Buenos Aires

If there was any lab that had also sent their data, please get in touch with me in order to take it into account.

In the case of forensic data (second phase, probably) it is essential to follow the next additional recommendations:

1.- You must send electronic raw data (electros) of each sample (see EMPOP requirements document). All samples must have sequences from forward and reverese strands. In case of HVS1 length heteroplasmy, the lab must supply sequences that were generated from internal primers or double forward and reverse sequencing, in order to maintain forensic standards (double reading of each reported haplotype).

2.- In addition to electros, a summary table containing the readings (haplotypes) of all samples should be sent. (format identical to literature data)

3.- Samples from quality controls or collaborative exercises must not be included. If all of us include these haplotypes, we would be overestimating the frequency of those haplotypes.

4.- Send your data (electros and table) on a CD to the following address:

A/At Lourdes Prieto Solla

Comisaría General de Policía Científica

Laboratorio de ADN

C/ Julián González Segador s/nº

28043 Madrid

At the same time, send me and email ([lourditasmt@ya.com](mailto:lourditasmt@ya.com)) to report that you sent me your data. When I verify that the content of the CD could be read, you will receive a replay confirming the reception.