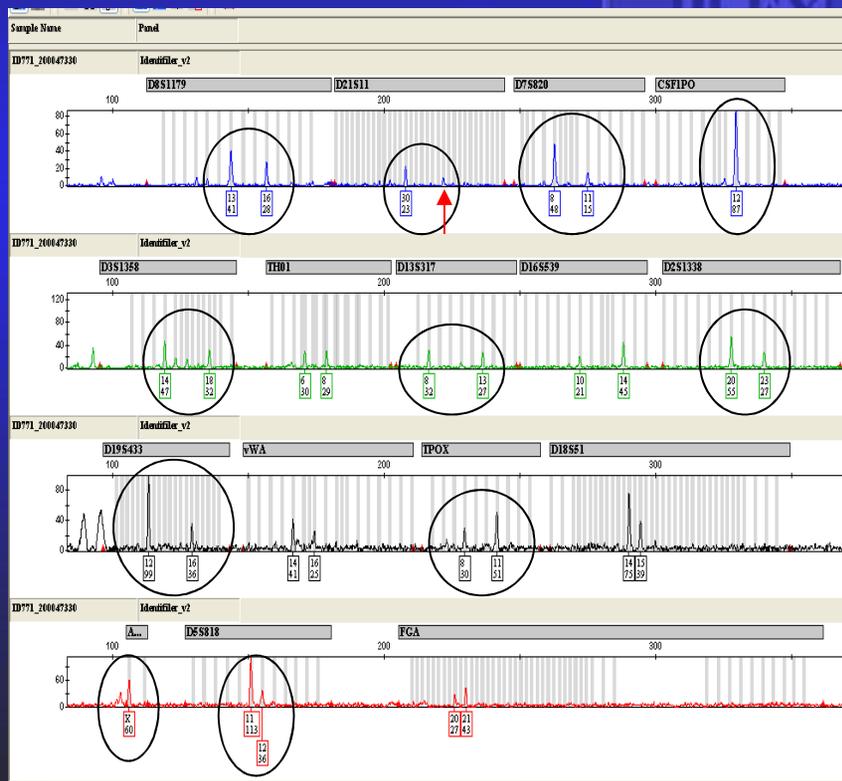


Approfondimento alcuni risultati biologici più significativi

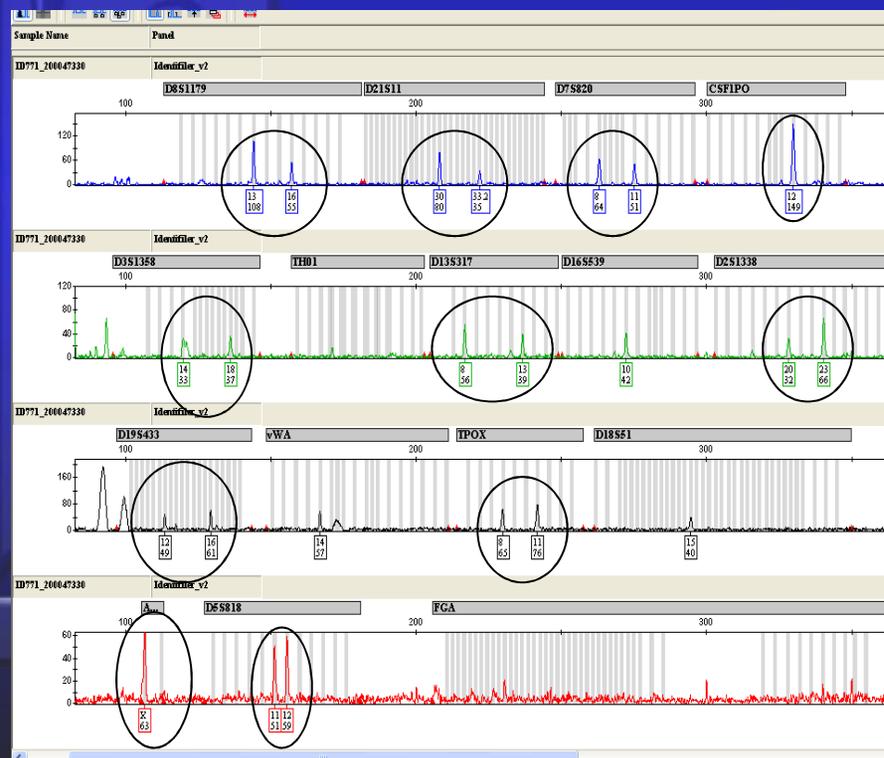
Rep.36 traccia B: coltello lungo 31 cm con manico nero

Loci genici confermati nelle due corse elettroforetiche

I° corsa elettroforetica



II° corsa elettroforetica

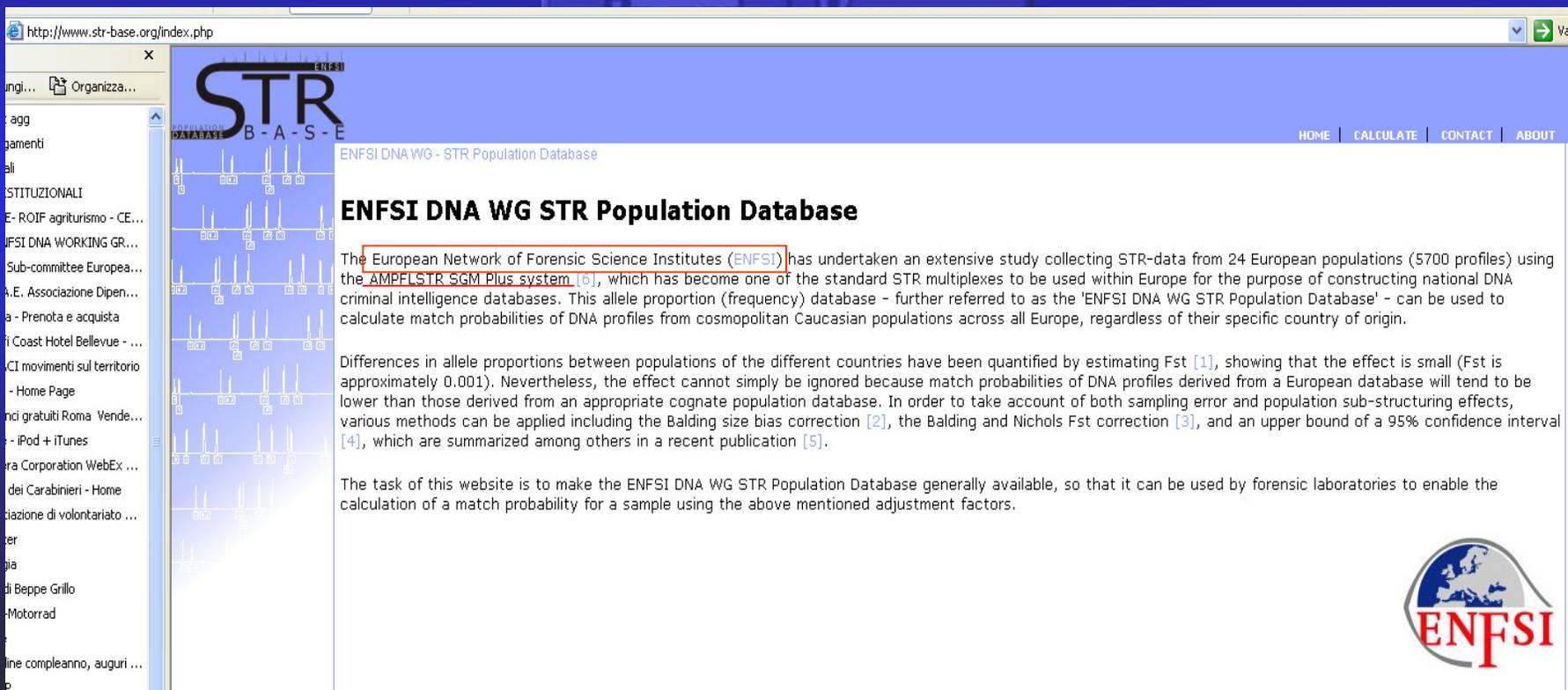


Approfondimento

alcuni risultati biologici più significativi

Rep.36 traccia B: coltello lungo 31 cm con manico nero

Quanto è raro questo profilo di Dna?



The screenshot shows a web browser window displaying the ENFSI DNA WG STR Population Database website. The address bar shows the URL <http://www.str-base.org/index.php>. The page features a navigation menu on the left with various links, a main content area with the title "ENFSI DNA WG STR Population Database", and a logo in the bottom right corner. The main content area includes a paragraph about the database's purpose and a paragraph about the genetic differences between populations.

ENFSI DNA WG STR Population Database

The European Network of Forensic Science Institutes (ENFSI) has undertaken an extensive study collecting STR-data from 24 European populations (5700 profiles) using the **AMPFLSTR SGM Plus system** [6], which has become one of the standard STR multiplexes to be used within Europe for the purpose of constructing national DNA criminal intelligence databases. This allele proportion (frequency) database - further referred to as the 'ENFSI DNA WG STR Population Database' - can be used to calculate match probabilities of DNA profiles from cosmopolitan Caucasian populations across all Europe, regardless of their specific country of origin.

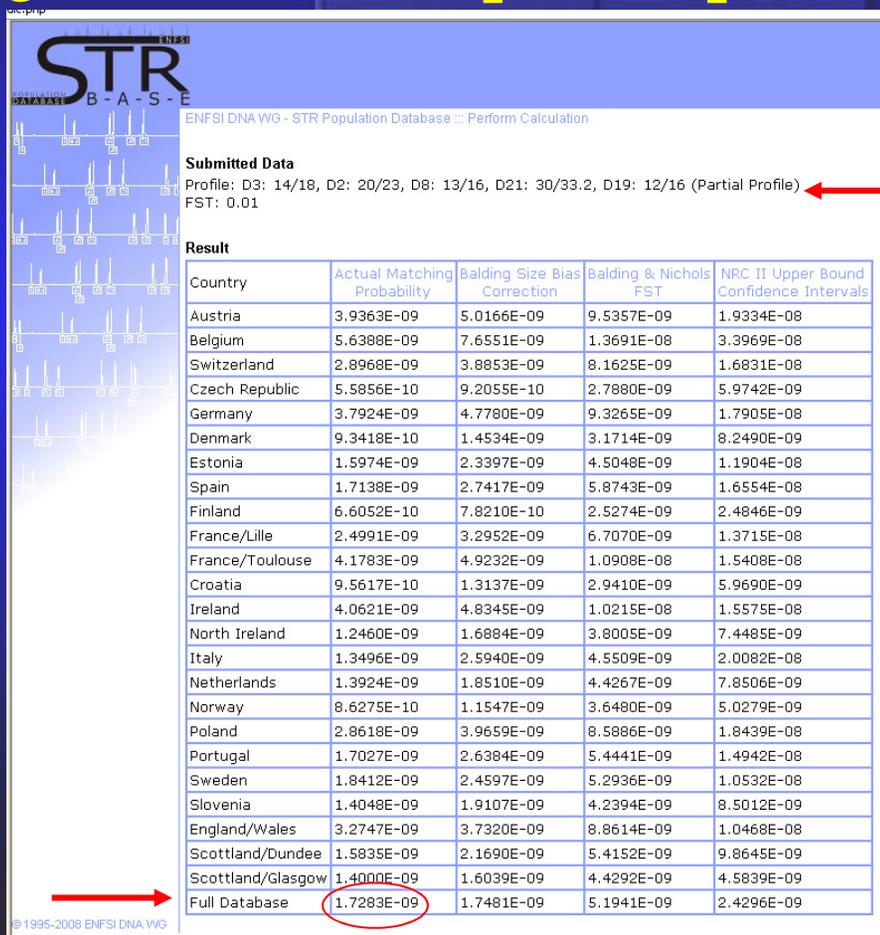
Differences in allele proportions between populations of the different countries have been quantified by estimating F_{st} [1], showing that the effect is small (F_{st} is approximately 0.001). Nevertheless, the effect cannot simply be ignored because match probabilities of DNA profiles derived from a European database will tend to be lower than those derived from an appropriate cognate population database. In order to take account of both sampling error and population sub-structuring effects, various methods can be applied including the Balding size bias correction [2], the Balding and Nichols F_{st} correction [3], and an upper bound of a 95% confidence interval [4], which are summarized among others in a recent publication [5].

The task of this website is to make the ENFSI DNA WG STR Population Database generally available, so that it can be used by forensic laboratories to enable the calculation of a match probability for a sample using the above mentioned adjustment factors.



Approfondimento

alcuni risultati biologici più significativi
Rep.36 traccia B: coltello l. 31 cm con manico nero
Quanto è raro questo profilo di Dna?



5 loci genici

1 individuo su
 1,7283 miliardi
 di individui