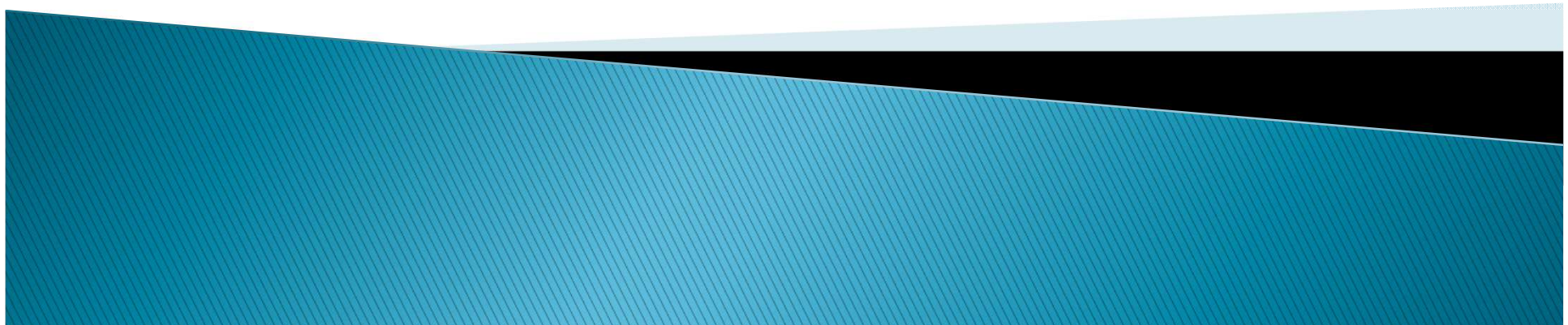


# TECHNIQUES FOR AUTHENTICATING COUNTRY OF ORIGIN LABELLING

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# WHAT DO WE MEAN BY 'COUNTRY OF ORIGIN'?

- ▶ For animals it could be where born, where raised or where slaughtered.
- ▶ According to EU legislation, country of origin is defined as '*the country where goods were wholly obtained or produced or, if produced in more than one country, where they last underwent substantial change*'.
- ▶ What is '*substantial change*'?



# THE OBVIOUS METHODS.....

Analysis of paper trails...

Stable isotope ratio analysis +/- trace elements

Isoscapes

A KEY ISSUE IS  
CREATION AND  
CURATION OF  
DATABASES AND  
ACCESS TO THEM

# THE LESS OBVIOUS METHODS

DNA speciation

SNP genotyping

Proteomics

Metabolomics

Metagenomics



# DNA SPECIATION (1)

- ▶ Ideal for determining if meat from a particular species of animal is present in a product.
- ▶ This method does not give any information about country of origin.
- ▶ Absence of a declared species or presence of an undeclared species would raise doubts about the claimed provenance of the product.
- ▶ The method could be used for honey from particular plant species (e.g. Manuka honey should contain *Leptospermum* DNA).



# DNA SPECIATION (2)



European cattle (*Bos taurus*)



Zebu cattle (*Bos indicus*)



# SNP GENOTYPING (1)

SNP genotyping has been used to determine if meat comes from premium breeds of cattle or pigs, e.g. Hereford cattle or Gloucester Old Spot pigs.

Premium cured meats are made by artisanal methods using animals from selected breeds, e.g. Serrano ham (Landrace pigs), Iberico ham (Iberico pigs) and Vitellone dell' Appennino Centrale (Chianina, Romagnola or Marchigiana cattle).

If certain breeds restricted to certain regions, SNP genotyping could be used to determine the origin of the meat.

**YOU CAN ASK QUESTIONS ABOUT BREED IN TWO WAYS: 'IS THIS BREED X' OR 'WHICH BREED IS THIS?'**

# SNP GENOTYPING (2)

SNP genotyping has shown that Traditional Hereford cattle are different from Hereford cattle. The latter were out-crossed in the US and then re-introduced to the UK.

SNP genotyping has shown that distinct populations of non-migratory fish exist.

SNP genotyping could be used to differentiate populations that are geographically distinct because of topography, e.g. islands (UK/ British Isles), mountain ranges (Pyrenees) or urbanisation.



# SNP GENOTYPING (3)

- ▶ The EU funded a project to determine if DNA typing could be used to identify the regional source of premium olive oils.
- ▶ The method failed because olive trees are out-breeding plants.
- ▶ The concept was ill-conceived because olive trees have been moved from region to region.
- ▶ Nevertheless, SNP genotyping could play a role in determining country or region of origin.



# PROTEOMICS

- ▶ Quantitative protein mass spectrometry now becoming routine and can be done with relatively unsophisticated instruments.
- ▶ Dried/ cured hams will have particular proteolysis profiles if produced by artisanal methods.
- ▶ Creatine kinase, myosin light chain and titin are the source of unique peptides in Spanish cured hams.



# METABOLOMICS

Metabolomics now well established as a technique and has been used to identify changes in GM crops, to compare crops grown in different regions and to identify markers of dietary intake.

The group at Royal Holloway have used metabolomics to distinguish tomatoes of the same variety grown in different locations.

Metabolomics coupled with pigment analysis and/or SNP genotyping *might* be a powerful combination.

# METAGENOMICS

Metagenomics is a technique whereby one can get a profile of the total microbial flora in a sample – even if many of these microorganisms cannot be cultivated.

Since the microbial flora associated with a sample will reflect the environment from which it comes metagenomics MAY be useful for verifying COOL.

A key issue will be showing consistency of metagenomic profile throughout a year and between years.

# DATABASES

- ▶ Genotypes are stable over long periods of time and it is relatively easy to detect introgression.
- ▶ The use of metabolomics and metagenomics will require databases to be established.
- ▶ As with stable isotopes, these databases will need to be developed and actively curated.
- ▶ Accessibility to databases will be crucial.



# KEY POINTS

- ▶ Stable isotope ratio analysis +/- trace element analysis will be the backbone of methods used to verify country of origin claims *but* databases will be a problem.
- ▶ Other methods will have a more limited role and may be restricted to products with PDO, PGI or TQA status.
- ▶ It will be a long time before we have the methodology to match the legislation.



QUESTIONS?

