USE OF GENETICS IN VERIFICATION OF SPECIES IDENTIFICATION AND LEGAL ORIGIN DURING TRADE OF SOUTHERN BLUEFIN TUNA

Dr James Findlay Bureau of Rural Sciences

<u>Abstract</u>

Genetics offers a powerful tool to complement other Monitoring, Control and Surveillance (MCS) techniques as it allows reliable species identification at any stage of the supply chain. It may also be used to discriminate legal and illegal SBT.

遺伝子技術

遺伝学はそのほかのモニタリング・コントロール及び監視 (MCS)の技術を補完 する強力なツールである。さらに、合法的・非合法的 SBT を区別することにも 使用できる。

Introduction

- 1. There are two key questions that must be answered in order to effectively monitor the trade of Southern Bluefin Tuna (SBT) from the point of capture through to the point of sale to consumers. These are:
 - a) Is it SBT?; and
 - b) Was it legally caught?
- 2. Modern genetic techniques have the potential to cost-effectively answer both of the questions and when combined with appropriate audit trails and inspections it can provide a powerful tool in a reliable monitoring and compliance scheme.
- 3. Genetic testing is already a requirement in the Australian SBT quota management arrangements (see below) and has been considered by other regional fisheries management organisations as a tool for monitoring catch of tuna species

Is it SBT?

- 4. Most experienced fishers and trained fisheries officers can discriminate between unprocessed SBT (*Thunnus maccoyii*) and most other species of tuna except Atlantic bluefin, *Thunnus thynnus* and Pacific bluefin *Thunnus orientalis*. Bluefin tuna in excess of 300kg can be identified as being either Atlantic or Pacific bluefin (i.e. not SBT) as such fish would exceed the maximum recorded size of SBT.
- 5. Experienced fish biologists can morphologically discriminate between the three species of bluefin tuna at all sizes (with some uncertainty) while fish are unprocessed

(i.e. whole with gut and gills *in situ*). However, once the fish is processed, species identification becomes increasingly uncertain as the level of processing progresses. For example, two of the key features used to discriminate SBT from the other bluefin tuna species are the colour patterns of the liver and the number of gill rakers. Once these are removed (e.g. when a fish is gutted and gilled), species discrimination becomes much more uncertain. Species discrimination without the use of genetics is almost impossible from loins and fillets.

6. Modern genetic techniques, using species-specific markers and probes, are powerful and cost-effective tools in the reliable identification of SBT. At present in Australia, all bluefin are considered SBT for the purposes of compliance with individually transferable quotas unless genetic tests are undertaken (at the expense of the fisher) to verify that fact that the fish is not an SBT (i.e. quota is decremented for all bluefin unless the genetic test shows that the specimen is not an SBT).

Was it caught legally?

7. Beyond discriminating between species, forensic genetic techniques have the ability to discriminate between individuals of the same species. Hence, it may be feasible to use forensic genetics to discriminate between legal and illegal SBT at any point between capture and retail sale by taking samples from all legally caught SBT and using these as a basis for genetic 'finger-print' comparisons to samples collected from elsewhere in the supply chain. This could be done on either an audit basis or 'saturated' basis.

How much would it cost?

8. At this stage, we have not attempted to design a genetic sampling and testing system for the CCSBT. The specific design should be part of an integrated MCS approach. Until there is further development of the MCS system for the CCSBT it would be impossible to cost a genetic component. Specific genetic probes to identify SBT and northern bluefin have been developed and used by CSIRO.

Additional Benefits

9. In addition to providing a powerful component within a broader monitoring and compliance framework, genetic sampling provides considerable potential as a scientific tool for the estimation of fishing mortality rates and population size both alone and in conjunction with conventional tagging studies. Hence, such applications with further improve the cost-effectiveness of genetic approaches to MCS.