

# Next Generation Sequencing for Food Authenticity, Traceability and Safety



Mario Gadanho<sup>1</sup>, Sandra Chaves<sup>1</sup>, Amanda Manolis<sup>2</sup>, Geoffrey Cottenet<sup>3</sup> <sup>1</sup>SGS Molecular, Lisboa, Portugal, <sup>2</sup>Thermo Fisher Scientific, Microbiology, Basingstoke, UK, <sup>3</sup> Nestlé Research Center, Lausanne, Switzerland



#### 1. INTRODUCTION

Food authenticity and fraud are topics of high interest in the food industry and highly controlled by authorities. The complexity of the food supply chain is challenging the abilities of analytical tools used for traceability of ingredients for food production. The most common method to verify species substitution and species identification is Real Time PCR. However, PCR testing is limited by the number of targets that can be simultaneously identified and differentiated. This can be critical, especially when testing highly processed and complex food that often contain multiple different species.

The introduction of Next Generation Sequencing (NGS) into the food sector revolutionizes food authenticity testing. NGS untargeted approach enables accurate detection and differentiation of thousands of different species in each sample using DNA sequencing that is recognized as the most reliable method for species identification.

In the present study an innovative NGS-based approach was tested for meat, fish and spices/herbs species identification.

Kudu

King quail

Crocodile

Pheasant

Cattle Yak

Donkey

Antilope

Daw

Weasel

Muskrat

Mallard duck

Crocodile

Pheasant

Partridge

Impala

Gnu

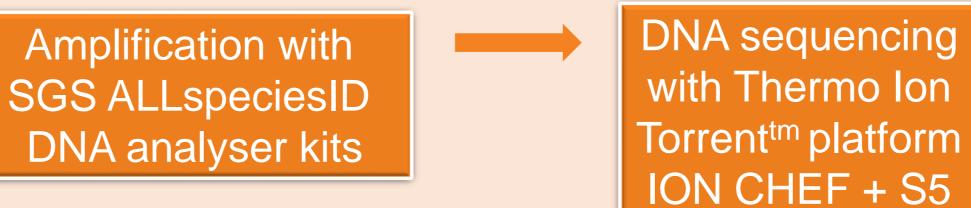
Oryx gazella

Buffalo

Camel

#### 2. WORKFLOW







Data analysis with SGS **ALL**speciesID software

- Short DNA fragments suitable for processed food
- 24-36h workflow
- Multiplex and meta-barcoding approach
- In silico analysis for DNA sequence comparison
- Curated Database with thousands of entries

#### 3. RESULTS

### 3.1 Meat species results

Number of samples tested: 148 Number of species tested: 49 Species mix: up to 3 Spiked level: 1%, 10%, 50%, 100%

Tragelaphus strepsiceros

Felix catus

Rattus norvegicus

Coturnix japonica

Camelus dromedarius

Alcelaphus buselaphus

Tragelaphus scriptus

Mustela erminea

Ondatra zibethicus

Crocodylus siamensis

Phasianus colchicus

Aepyceros melampus

Alectoris chukar

Corvus macrorhynchos

Crocodylus niloticus

Lophura inornata

Oryx leucoryx

Bos grunniens

Equus asinus

Meles meles

Anas sp

Bubalus bubalis

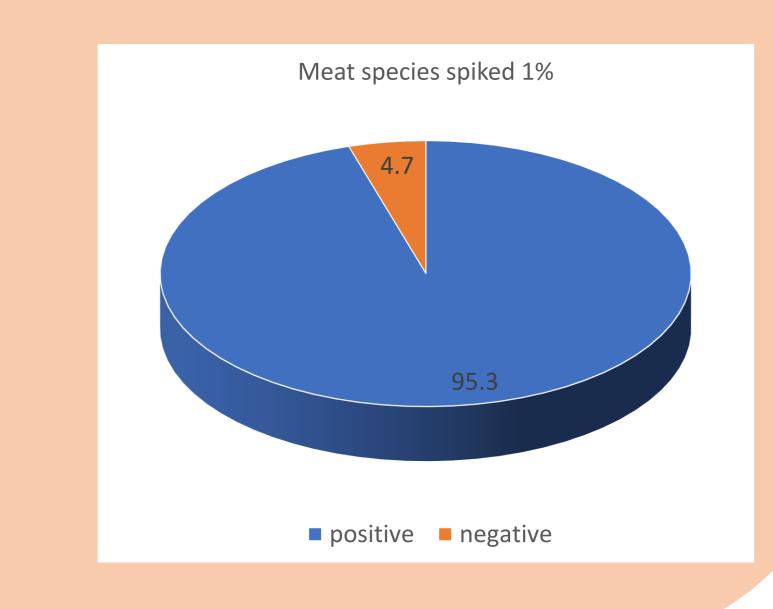
Vulpes vulpes

Alces alces

Ovis_aries	Sheep
Capra_hircus	Goat
Lepus_capensis	Hare
Oryctolagus_cuniculus	Rabbit
Macropus_rufus	Kangaroo
Capreolus_capreolus	Roe Deer
Cervus_elaphus	Red Deer
Rangifer_tarandus	Reindeer
Antidorcas_marsupialis	Springbok
Equus_hemionus	Zebra
Lama_glama	Lama
Gallus_gallus	Chicken
Canis_familiaris	Dog
Bison_bison	Bison
Cervus_dama	Fallow Deer
Equus_caballus	Horse
Sus_scrofa	Pork
Bos_taurus	Beef
Meleagris galopavo	Turkey
Cairina moscata	Duck
Alopochen aegptiacus	Goose
Struthio camelus	Ostrich
Columba livia	Pigeon
Numida meleagris	Guinea fowl
Dromaius novaehollandiae	Emu

**Meat Species** 

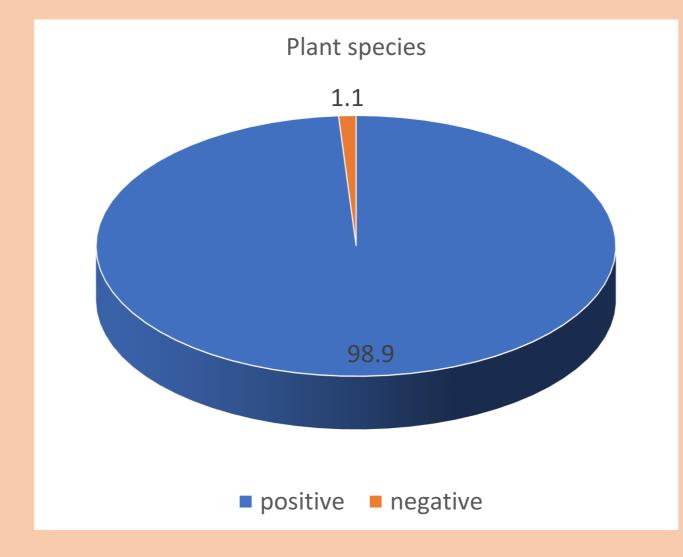
positve negative

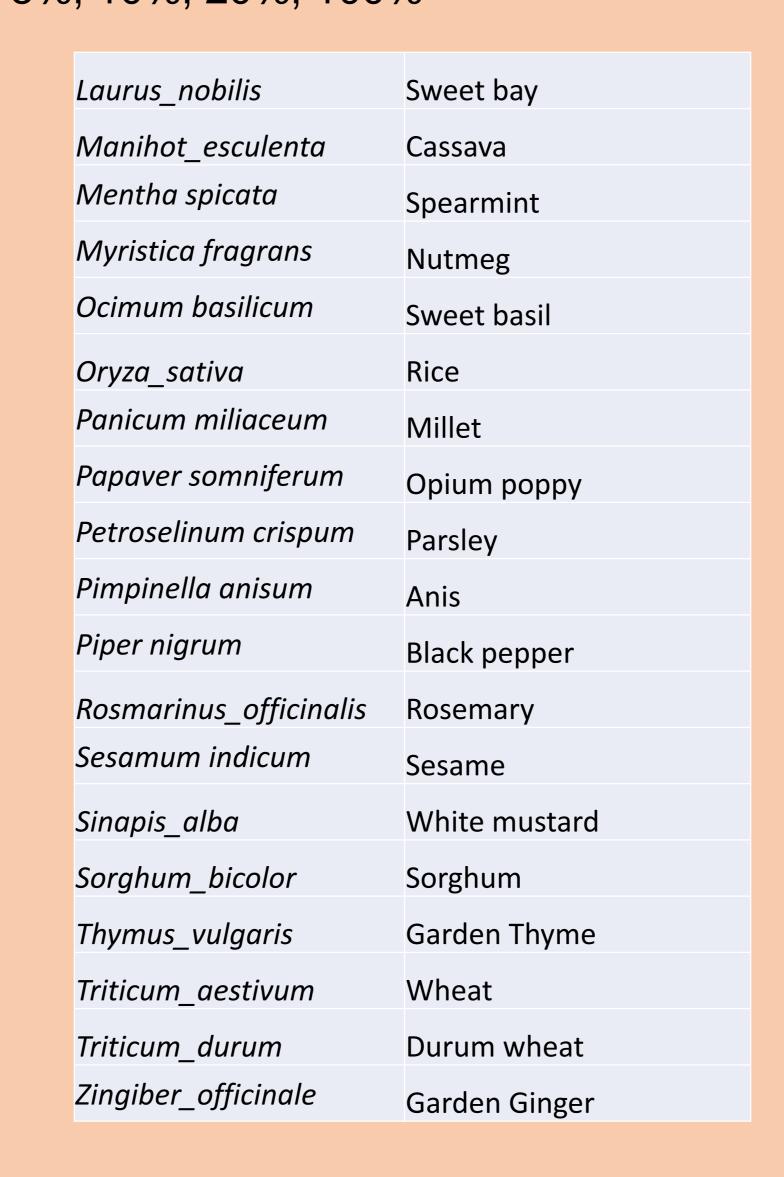


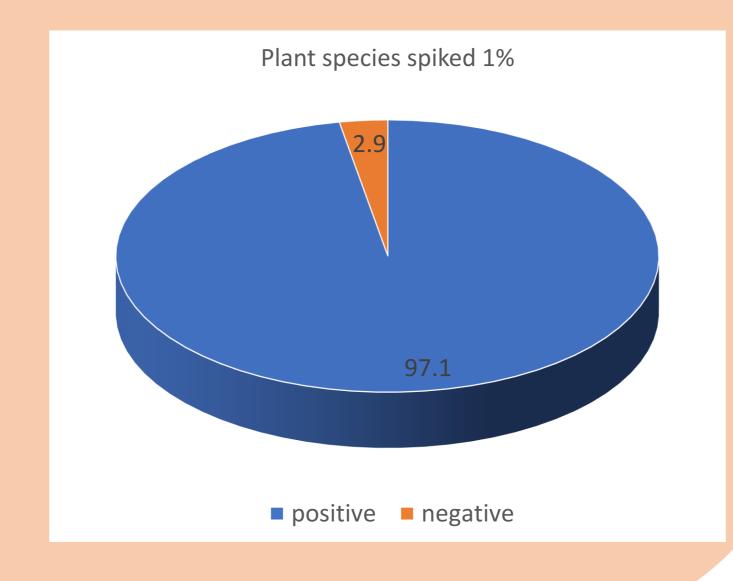
### 3.2 Plants species (spices/cereals) results

Number of samples tested: 347 Number of species tested: 39 Species mix: up to 5 Spiked level: 1%, 5%, 10%, 20%, 100%

Origanum sp.	Origanum
Allium schoenoprasum	Wild chives
Allium_sativum	Garlic
Anethum graveolens	Dill
Argemone sp	Prickly poppy
Avena sativa	Oat
Brassica napus	Rape
Capsicum annuum	Cayenne pepper
Carum carvi	Caraway
Ceratonia siliqua	St John's bread
Conium maculatum	Poison henlock
Coriandrum sativum	Coriander
Crocus sativus	Saffron
Cuminum_cyminum	Cumin
Curcuma longa	Turmeric
Elettaria cardamomum	Cardamom
Foeniculum vulgare	Sweet fennel
Glycine max	Soybean
Hordeum vulgare	Barley
luniperus_communis	Juniper







## 3.3. Fish species results

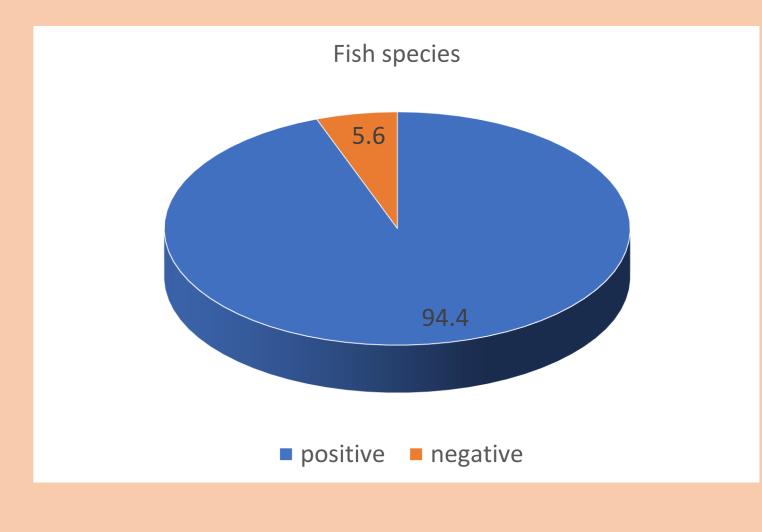
Number of samples tested: 78 Number of species tested: 26 Species mix: up to 2 Spiked level: 1%, 2%, 5%, !0%, 100%

Salmo salar Atlantic Salmon Yellowfin tuna Thunnus albacares Atlantic cod Gadus morhua Hippoglossus hippoglossus Pacific halibut Limanda limanda Common dab Merluccius merluccius European hake Melanogrammus aeglefinus Haddock Skipjack tuna Katsuwonus pelamis Albacore Thunnus alalunga Pleuronectes platessa Molva molva Ling Pike-perch Sander lucioperca Pollack Pollachius pollachius

European plaice Thunnus obesus

Trisopterus luscus Norway pout Witch flounder Cynoglossus senegalensis Oncorhynchus chrysogastei Pink salmon Angler Lophius piscatorius Oncorhynchus nerka Sockeye salmon Pangasianodon hypophthalmus Silver carp Scomber scombrus Atlantic mackerel Pink salmon Oncorhynchus gorbuscha Merluccius hubbsi Argentine hake North Pacific hake Merluccius productus Patagonian Macruronus magellanicus grenadier Merluccius gayi South Pacific hake

Bigeye tuna



# 4. CONCLUSIONS

- The NGS workflow could enable to identify all the species tested individually
- Identification of pure material at spiked levels higher than 5% was successfully obtained for more than 94% of the samples tested. A few negative results were obtained for some highly processed food products and mostly for fish-based samples.
- At the level of 1% spiking, more that 95% of the samples were correctly assigned to the species name.
- When combined, all targets could be analyzed simultaneously in a single NGS run which reduce significantly the NGS costs
- Based on these invitro analysis and on the in silico analysis of DNA sequences a database containing thousands of species was created.
- Extension of the databases is an on-going activity to include additional species

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