Terra Nova Genomics, Inc.

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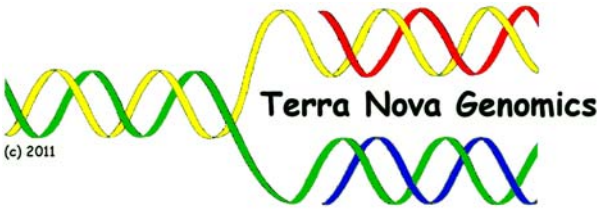
After providing forensic genetic services since 1998, **Terra Nova Genomics, Inc** was incorporated in 2011 to expand the range of traditional **genetic** testing to include state-of-the art **genomic** testing in **DNA forensics**.

We specialize in consultation, testing, and expert testimony on **questioned species identity of commercial products** and **forensic wildlife & fisheries material**. We have provided evidence and testimony for the federal **Department of Fisheries & Oceans**, **Canadian Wildlife Service**, **RCMP**, **Canadian Food Inspection Agency**, as well as **Sobeys** and other private companies. Our forensic investigations have been featured on ***CBC Radio & Television***, the ***Globe & Mail***, the ***St John's Telegram***, other national and international news media, and an invited review for ***Lab Focus***, a leading biotechnology trade journal.

Please see the links above for information about **technical details**, **services offered**, and **pricing**.

Please **Contact Us** for further information.



Terra Nova Genomics, Inc.

About Us

Dr Steve Carr and **Dr Dawn Marshall** between them have almost forty years experience in **applied genetics**, **genomics**, and **biotechnology**, including ground-breaking applications of **PCR**, **automated DNA Sequencing**, and **DNA microarray technology**. Their independent and joint research has been published in leading international peer-reviewed journals, including *Proceedings of the National Academy of Sciences*, *Evolution*, *Genetics*, *Molecular Biology & Evolution*, *Molecular Ecology*, *Genome*, *Forensic Science International, the Canadian Journal of Fisheries & Aquatic Science*, and the *Canadian Journal of Zoology*.

Dr. Steve Carr
President & Co-Founder

Dr. Carr received his PhD in Genetics from the University of California, Berkeley, and did post-doctoral work in Wildlife Genetics at Texas A&M. He is currently Professor of Biology, with a cross-appointment to the Faculty of Medicine, at Memorial University of Newfoundland. He has taught courses in Genetics, Evolution, Mammalogy, Vertebrate Biology, Biotechnology, and Human Population Genetics. He is on the Editorial Board of *Mitochondrial DNA*, and is a former Non-Government Member of the Committee on the Status of Endangered Wildlife in Canada (COSEWIC), which makes scientific recommendations under Canada's Species-At-Risk Act (SARA). He has more than 40 publications in genetics, genomics, and evolutionary biology of vertebrate species.

Dr. Carr can be contracted directly at steve.carr@terranovagenomics.com

Dr. H. Dawn Marshall
President & Co-Founder

Dr. Marshall received her PhD in Genetics from the Univerity of Toronto, and did post-doctoral research at the University of British Columbia. She is currently Assistant Professor of Biology at Memorial University of Newfoundland, where she teaches courses in Biotechnology and Evolution.

Dr. Marshall can be contacted at dawn.marshall@terranovagenomics.com

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Services

Forensics

We offer **DNA** sequence analysis of biological specimens of unknown or uncertain origin, for the purpose of identification to species. Examples include (1) **Identification of the species of origin** of fish remains seized in cases of suspected out-of-season poaching, (2) **Identification of species in mixed lots** of commercial fish products, where adulteration is suspected, (3) **Identification of blood to species**, where blood spoors may point to criminal activity, and (4) **Identification to species of wildlife or fisheries materials** where external identifiers (skin, scale, feathers, or hair) have been removed.

Genomics

New **biotechnologies** developed by us make it possible to identify distinct individuals within species, and to make unambiguous associations between fisheries or wildlife material left at a crime scene, and evidence seized elsewhere. For example, fish scales or guts at a poaching site can be identified with individual fillets seized elsewhere. Our method is much faster and more accurate than conventional microsatellite methods.

Biotechnology

- Development of academic **biotechnology** as applied **industrial** methods
- Development and licensing of **Intellectual Property (IP)** in new biotechnologies
- Development of **grants and contracts** to aid industry, government agency, and private business

Terra Nova Genomics, Inc.

Resources

The publications below include **forensic, fisheries, and wildlife applications of genetics and genomics**, and provide technical detail on our methods.

Links to Articles on Our Site

Pope AM, SM Carr, KN Smith, & HD Marshall. 2011. **Mitogenomic and microsatellite variation in descendants of the founder population of Newfoundland: high genetic diversity in an historically isolated population.** *Genome*, 54,110-119. [PDF]

SM Carr, AT Duggan, & HD Marshall. 2009. **Iterative DNA sequencing on microarrays: a high-throughput NextGen technology for ecological and evolutionary mitogenomics**. *Laboratory Focus* 13, 8-12. [PDF]

HD Marshall, MW Coulson, & SM Carr. 2008. **Near neutrality, rate heterogeneity, and linkage govern mitochondrial genome evolution in Atlantic Cod (*Gadus morhua*) and other gadine fish**. *Molecular Biology & Evolution* 26, 579-589. [PDF]

SM Carr & HD Marshall. 2008. **Phylogeographic analysis of complete mtDNA genomes from Walleye pollock (*Gadus chalcogrammus* Pallas, 1811) shows an ancient origin of genetic biodiversity.** *Mitochondrial DNA* 19, 490-496. [PDF]

SM Carr & HD Marshall. 2008. **Intraspecific phylogeographic genomics from multiple complete mtDNA genomes in Atlantic Cod (*Gadus morhua*): Origins of the "*Codmother*," trans-Atlantic vicariance, and mid-glacial population expansion**. *Genetics* 108, 381-389. [PDF]

SM Carr, HD Marshall, AT Duggan, SMC Flynn, KA Johnstone, AMPope, & CD Wilkerson. 2008. **Phylogeographic genomics of mitochondrial DNA: patterns of intraspecific evolution and a multi-species, microarray-based DNA sequencing strategy for biodiversity studies.** *Comparative Biochemistry and Physiology, D: Genomics and Proteomics* 3,1-11. [PDF]

SMC Flynn & SM Carr. 2007. **Interspecies hybridization on DNA resequencing microarrays: efficiency of sequence recovery and accuracy of SNP detection in human, ape, and codfish mitochondrial DNA genomes sequenced on a human-specific MitoChip.** *BMC Genomics* 8, 339. [PDF]

KA Johnstone, HD Marshall, & SM Carr. 2007. **Biodiversity genomics for Species At Risk: patterns of DNA sequence variation within and among complete mitochondrial DNA genomes of three species of Wolffish (*Anarhichas* spp.).** *Canadian Journal of Zoology* 85,151-158. [PDF]

HD Marshall, KA Johnstone, & SM Carr. 2006. **Species-specific oligonucleotides and multiplex PCR for forensic discrimination of two species of scallops, *Placopecten magellanicus* and *Chlamys islandica*.** *Forensic Science International* 167,1-7. [PDF]

MW Coulson, HD Marshall, P Pepin & SM Carr. 2006. **Mitochondrial phylogeographic genomics of gadine fish: Implications for taxonomy and biogeographic origins.** *Genome* 49,1115-1130. [PDF]

SM Carr, HD Marshall, KA Johnstone, LM Pynn, and GB Stenson. 2002. **How to tell a sea monster: Molecular discrimination of large marine animals of the North Atlantic.** *The Biological Bulletin* 202,1-5. [PDF]

Useful Web Links

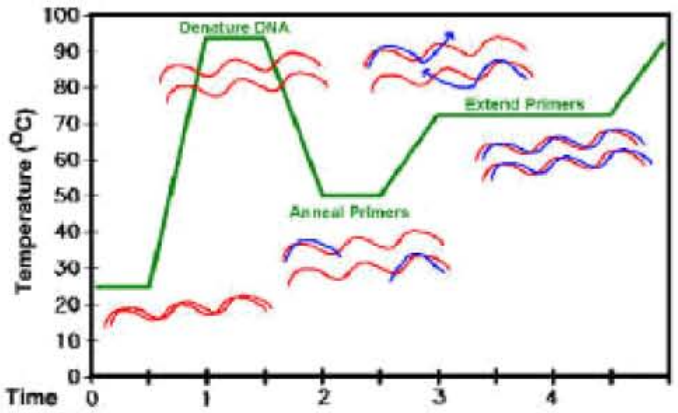
Biol2250 - Principles of Genetics
On-line notes for Dr Carr's Principles of Genetics course at Memorial University.
Provides useful background on classical and molecular genetics

Biol3950 - Principles of Genetic Biotechnology
On-line notes for Dr Marshall's course in DNA Biotechnology.
A prime source for in-depth discussion of DNA as a forensic tool.

We will be updating these links frequently so be sure to check back often.

Basic Steps in a Forensic DNA Analysis

DNA is present in a variety of living or once-living sources, including hair, feathers, and scales, blood, tissue or body fluid samples, as well as food items such as fresh meat, fish, or shellfish, or dried, canned, smoked, or otherwise preserved food, etc. The small size of many forensic samples and the very small quantity of **DNA** present means that it is first necessary to increased the number of **DNA** copies present.

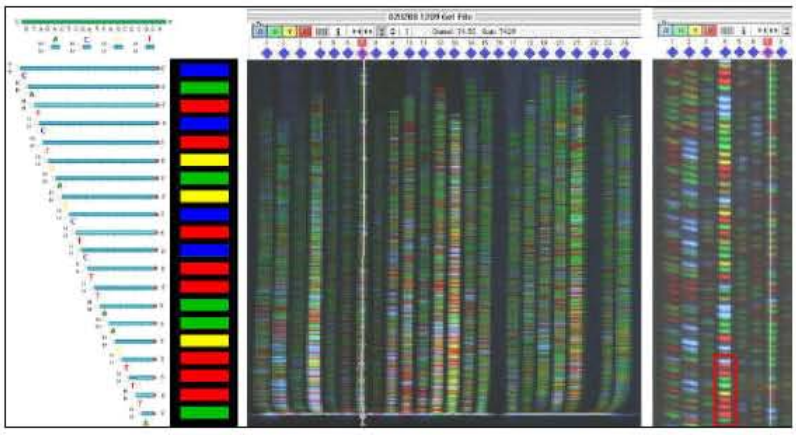


"*DNA Xeroxing*" by the PCR

The **polymerase chain reaction** (**PCR**) is a method of '***DNA xeroxing***' that amplifies the small amount of a particular **DNA** sequence present in a sample to usable quantities. The **PCR** experiment includes a **DNA** source, a pair of short **DNA primers** that flank the **DNA** region to be amplified, a heat-resistant **DNA** copying enzyme (***Taq***), and a pool of the four **DNA** building-block (**dNTPs**). The reaction is carried out in a computer-regulated heating block (a **thermal cycler**). **PCR** includes three stages: the reaction is first heated to melt the **DNA** strands, cooled so that the primers can find the **DNA** targets and stick to them, and finally heated again to allow the ***Taq*** enzyme to copy the **DNA**. Each **PCR** cycle *doubles* the amount of the **DNA** of interest: ten doublings produce 1,000 copies, and 30 cycles yields 2^{30} copies for a billion-fold amplification. This produces a sufficient quantity of the gene region of interest for **DNA** sequencing.

"*False Colour*" automated DNA sequencing

After **PCR**, a sequencing reaction is set up that synthesizes multiple copies of both **DNA** strands by incorporating a set of fluorescently-labeled **DNA** bases, A C G & T, into the new **DNA** [left]. The **DNA** sequence of each strand can then be read as the successive '*rungs*' in the sequencing '*ladder*'. The gel image on the automated DNA sequencer [middle] builds a "*false colour*" composite representation of 24 different **DNA** sequences. In the magnified view at right, each lane shows a different **DNA** sequence as a "*ladder*". For example, in the fourth lane, the first few bases will be read as ATTTGAATTC . **Terra Nova Genomics** uses instruments that can sequence 96 reactions simultaneously.



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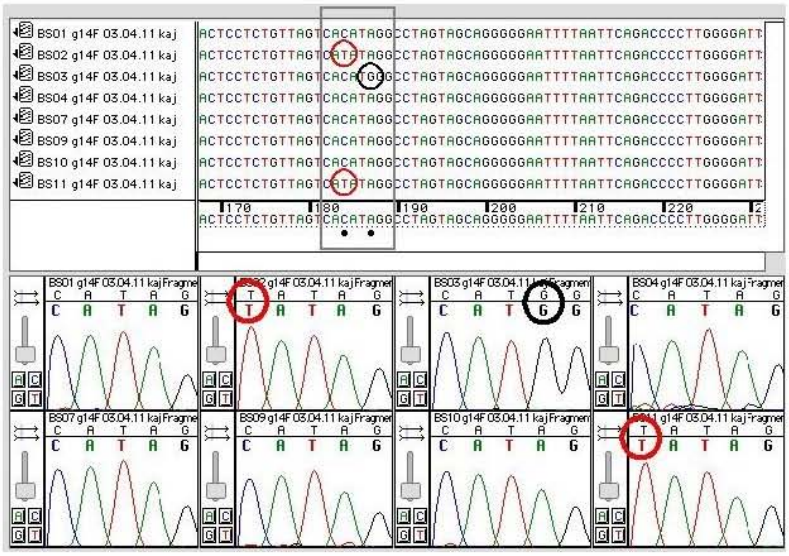
How It Works

DNA sequence Chromatogram

Each channel is scanned by the computer from bottom to top [white line in the 7th channel]. The scan is converted to a **chromatogram**, in which each band corresponds to a coloured peak: the order of peaks gives the **DNA** sequence.

Detection of DNA sequence variation ("*SNPs*")

Differences among **DNA** sequences of individuals and species arise from mutations that alter the four-letter code. Such single-letter changes are called **single-nucleotide polymorphisms** (**SNPs**). The top window shows an 80-letter stretch of **DNA** from eight Atlantic Cod. The black dots flag two **SNP** positions where individuals differ. As seen in the lower window, most individuals have the sequence **CATAG**: individuals *BS02* & *BS11* share a **C↔T SNP** variant at the third position (**TATAG**); individual *BS03* has a unique **A↔G SNP** at the sixth position (**CATGG**). Identification of such genetic differences permits inferences about relationships among individuals within species (genealogy), in time and space (phylogeography), and the evolutionary relationships (phylogeny) of related species.



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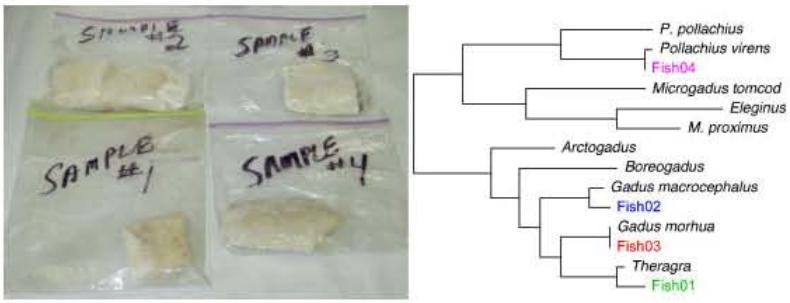
How It Works

"The Case of the Falsified Fillets"
DNA Forensics for Commercial Food Fisheries

The species identity of fish products that has been skinned, cleaned, filleted, cooked, frozen, dried, and / or salted can be difficult to determine. Questions may arise as to the origin of a commercial product: Is the catch in a boat's hold properly reported? Is the label on a package is accurate. A product may be physically altered to pass as another, for example by bleaching of fillets. Although physical identification may be impossible once skin and scales are gone, **DNA** survives processing in sufficient quantities to provide a reliable test.

In the forensic test shown here, the identity of salt-cured fish fillets in a commercial batch of "Cod" was questioned. **Terra Nova Genomics** compared the **DNA** sequences from fillet to a data base of known cod, pollock, and hake species. The analysis produces a "*family tree*", which shows that each of the four fillets belongs to a different commercial species: **Alaska pollock**, **Atlantic cod**, **Pacific cod**, and **pollock**.

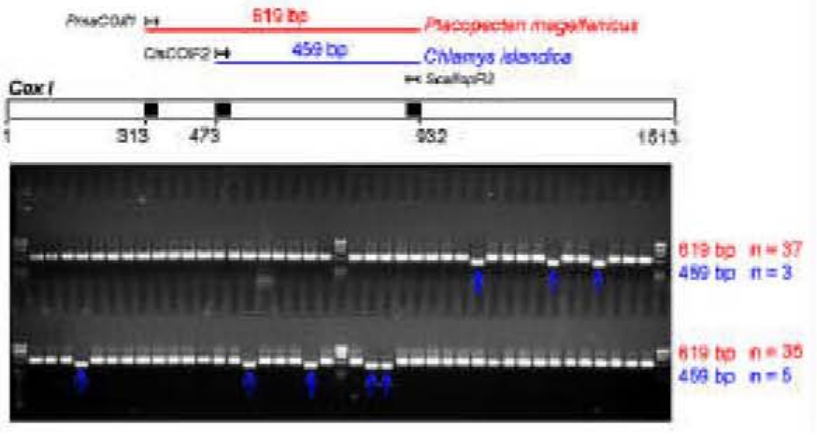


"The Case of the Scurrilous Scallops"
Species-Specific Oligonucleotides (SSOs) as a forensic DNA test

In some forensic cases, the cost of direct sequence analysis of large numbers of individuals is prohibitive. The case illustrates the development of a **novel industrial DNA forensic method** by **Terra Nova Genomics**.

The **DNA** sequences of a particular gene (*COI*) are known for many species of scallops, including two found in the Northwest Atlantic, Sea Scallops (*Placopecten*) and Icelandic Scallops (*Chlamys*). We combined an **PCR** primer (an "*oligo*") for a **DNA** sequence identical in both species (*ScallopR2*) with oligos specific for either species (*PmaCOIF1* and *CisCOIF2*). The sizes of the **PCR** amplification product expected from either species are different, longer in *Placopecten* and shorter in *Chlamys*. Use of **species-specific oligonucleotides** (**SSOs**) thus identifies species directly from the sizes of the **PCR** fragments, without the need for sequencing. The same procedure can be adapted for any species

A fisherman had a hold full of scallops that he claimed were from the open fishery for Icelandic Scallops, but which **DFO Enforcement** officers suspected they from the closed fishery for Sea Scallops. Since a small proportion of bycatch from the closed fishery might be considered acceptable, the legal question was: What fraction of the total catch was from the prohibited species? We extracted **DNA** from more than 900 individual scallops and applied the **SSO** test to each. Of the 80 scallops in the test below, all but eight (blue arrows) show the larger **DNA** fragment, which indicates that 90% are Sea Scallops, the closed fishery. In the complete series from two vessels, almost two-thirds were Sea Scallops. This evidence resulted in conviction, confiscation of the vessel, and heavy fine.



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How It Works

DNA Microarrays: the *ArkChip* for multi-species fisheries and forensics

A **DNA re-sequencing microarray** allows a sequence of 30~300,000 ACGTs to be determined in a single experiment. The microrarray is designed from a known reference sequence for the species of interest, and allows the same sequence to be read repeatedly from additional individuals. This is particularly well-suited to population genomics, where the collection of sequences from multiple individuals is called "*iterative sequencing*".

The example shows a complete **15,452bp human mtDNA genome** sequence arranged on microarray pattern. Each nucleotide position is represented in a vertical block of 4 cells in 5 rows (ACGT + a blank). In each block, the cell with the strongest **DNA** binding identifies the base present at that position. In the magnified insert view, the sequence of bases in each of four blocks is easily read by computer as the left-to-right order of successive brightest squares.

In an important biotechnological breakthrough, **Terra Nova Genomics** has shown that it is possible to use a **multi-species *ArkChip*** microarray to sequence the **mtDNA** genomes from several different species simultaneously, without interference ("*cross-talk*") among species. The larger figure shows a larger microarray that includes reference genomes from seven species, on which complete **mtDNA** genome sequences have been sequenced from four species (**Atlantic Cod**, **Atlantic Wolffish**, **Newfoundland Caribou**, and **Harp Seal**). Because the design, manufacture, and processing of the microarray is a fixed cost, the added cost of sequencing multiple species is limited to extraction and amplification of **DNA**.

Terra Nova Genomics has received funding for a second-generation ***ArkChip 2.0*** that will include ~20 different species. This converts an academic research design to an industrial tool for large-scale, long term monitoring of multiple commercial fishery stocks. Also, because **mtDNA** genome sequences of individuals within species are typically unique, it allows **forensic identification** and discrimination of individuals within species.