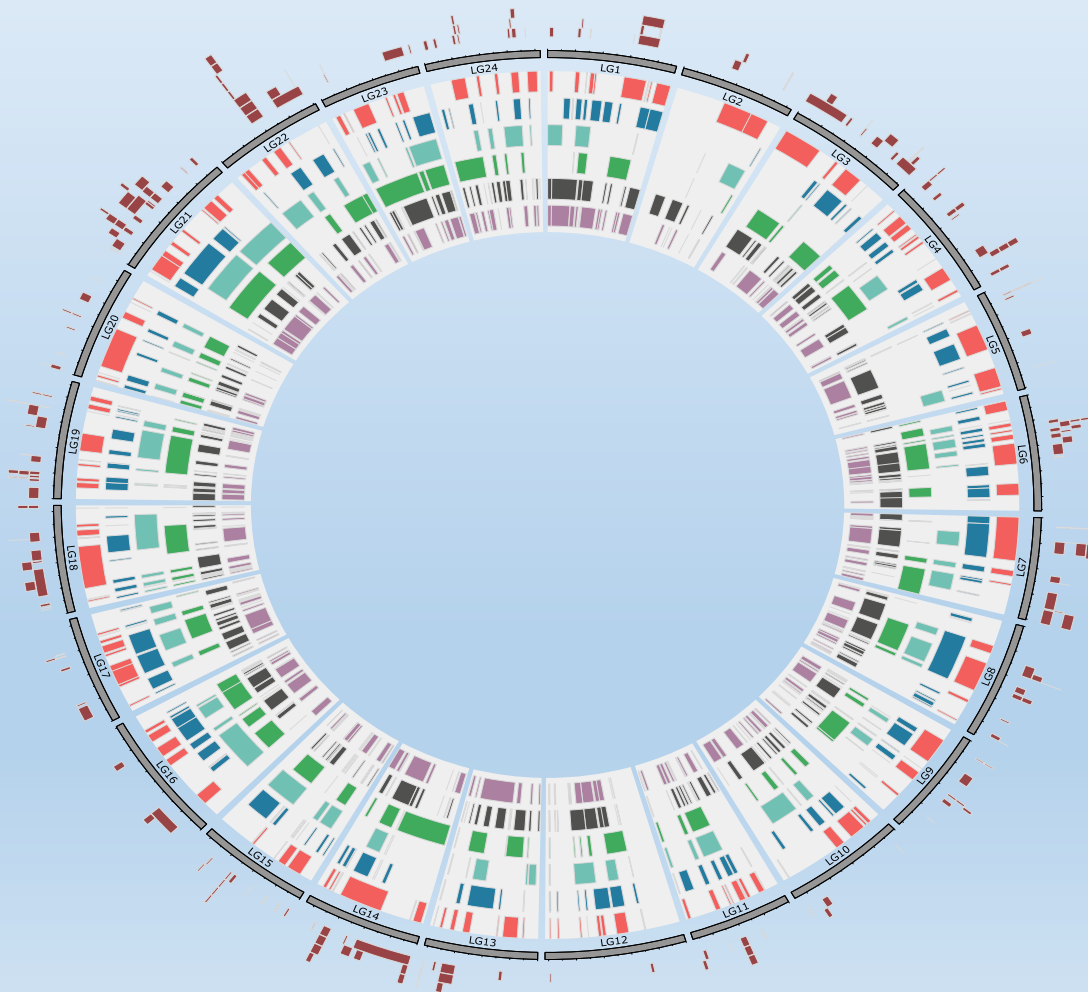


# Omics approaches to Understanding Impacts of Oil Spills on Macroorganisms



# Omic

## Vast improvement in technology

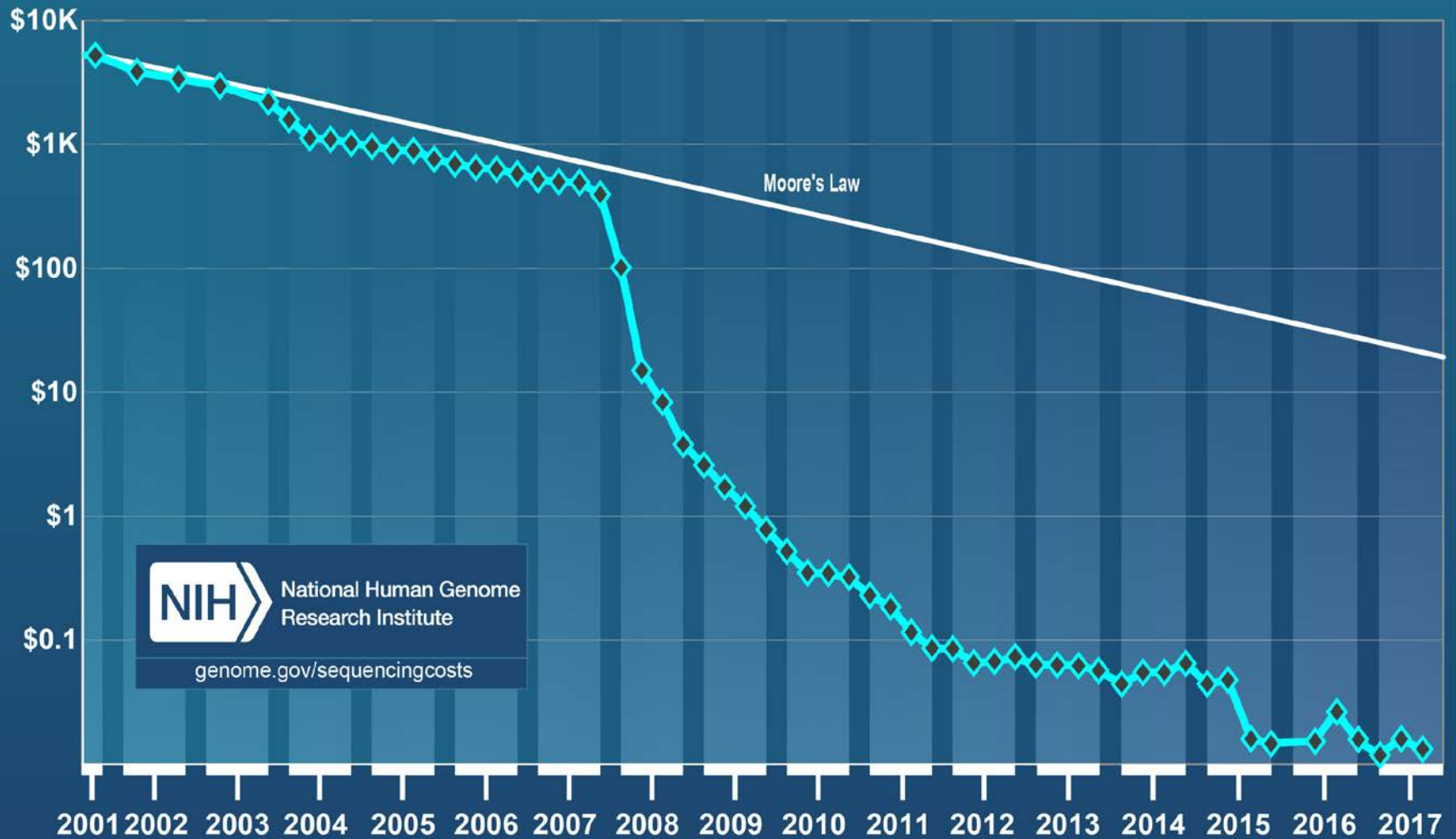
96 wells of Sanger sequencing (~600 bp) = 57,600 bp

4,000 SNP-loci (125 bp –paired) = 1,000,000 bp (per individual)

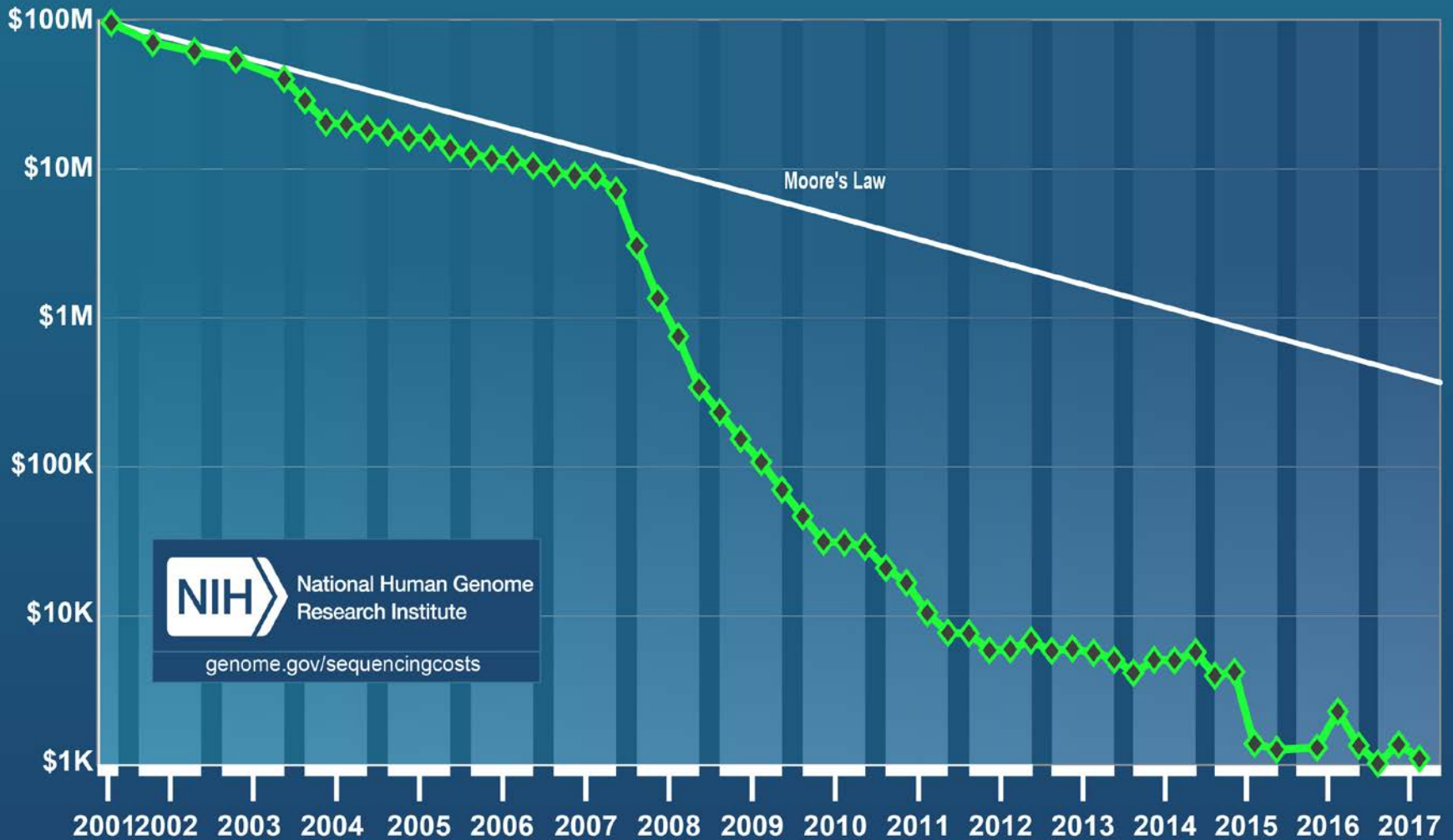
Whole-genome sequence ~ 1,000,000,000 bp

Much less expensive per base

# Cost per Raw Megabase of DNA Sequence



# Cost per Genome



# Red Drum Genome

## Basic Stats:

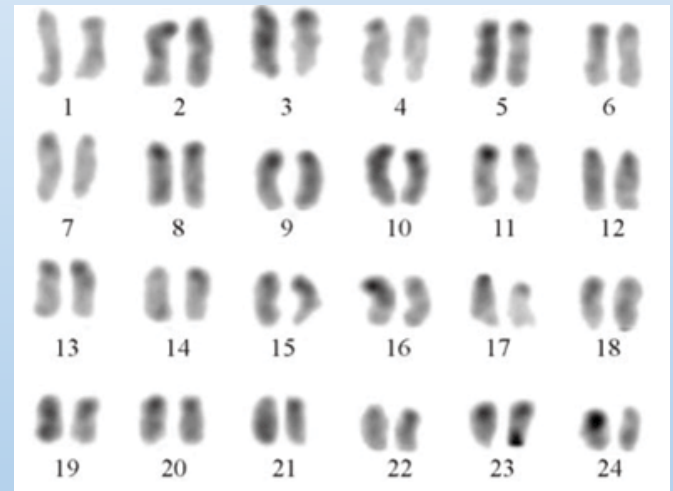
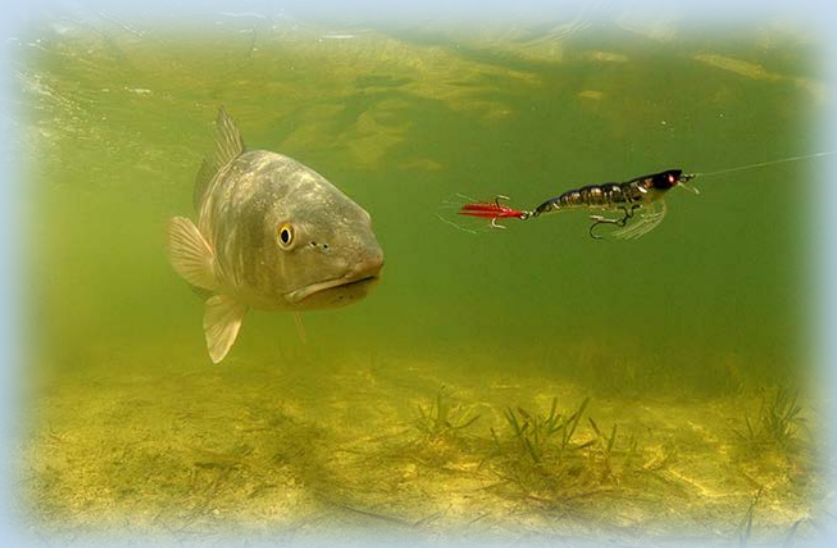
31 SMRT Cells

1 HiSeq

3,389 contigs

0.68 Gb of assembled sequence

Average coverage 50X



(*L. synagris*; Rocha and Molina 2008)

**Bottom line ~ \$20,000**

Genome size ~ 0.8 Gb

# Organismal Impacts (non-lethal)



## Laboratory setting

- Controlled
- Manipulation possible
- Measure of individual effects

## Wild populations

- Noisy
- Lots of extrinsic factors
- Measure of population effects



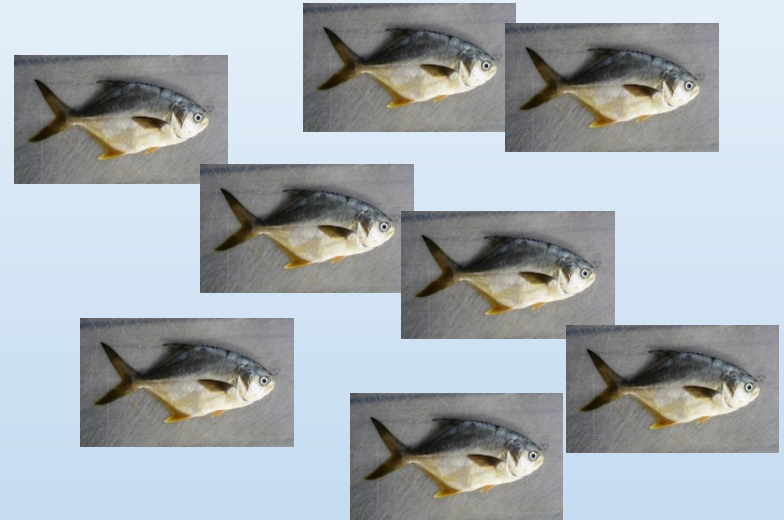
**Making connections is vital**

# Organismal Impacts (non-lethal)

## Current generation



## Next generation



## Selection

- Adult condition
- Feeding ecology
- Biological response

## Fitness

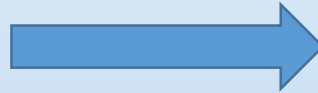
- Reproduction
- Adult fecundity
- Offspring survival
- Gene Expression

## Heritable change

- Epigenetic gene regulation
- Anthropogenic evolution

# Approaches

**Current generation**



**Next Generation**



## OMICS

- **Transcriptomics – gene expression**
- **Methylomics – gene regulation**
- **Genomics – gene frequency change**



# Needs and Direction



**Acute exposure: fairly easy to detect**

**Variation in response by species and environment**

**Need for laboratory verified assays**

**Challenge with “non-model” species**

# Needs and Direction



**Chronic exposure and impairment: more difficult**

**Research limited to few species**

**Need for laboratory verified assays**

**Often from “high-pollution” environments**

# Needs and Direction



**Anthropogenic evolution: permanent genetic change**

**Less information**

**Presents restoration challenge**