



## From Sequence to Consequence: tools for the Exploitation of Livestock Genome

**The experience of managing cutting-edge  
science in Quantomics**

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## The Quantomics Consortium

1. Bioscience Network Ltd	GB
2. Aarhus Universitet	DK
3. Universitetet for Miljø og Biovitenskap	N
4. European Molecular Biology Laboratory	D
5. The University of Edinburgh	GB
6. Universitat Autònoma de Barcelona	E
7. Università degli Studi di Milano	I
8. Maa ja Elintarviketal Ouden Tutkimuskeskus	FIN
9. Universität Leipzig	D
10. Aviagen Ltd	GB
11. The Hebrew University of Jerusalem	IL
12. Aristotelio Panepistimio Thessalonikis	GR
13. Argentix Ltd	GB
14. Centre de Regulacio Genomica	E
15. Landbruk og Fødevarer	DK
16. Commonwealth Scientific and Industrial Research Organisation	AUS
17. Associazione Nazionale Allevatori Bovini della Razza Bruna	I

€8m project 17 Partners

[www.quantomics.eu](http://www.quantomics.eu)

June 1, 2009

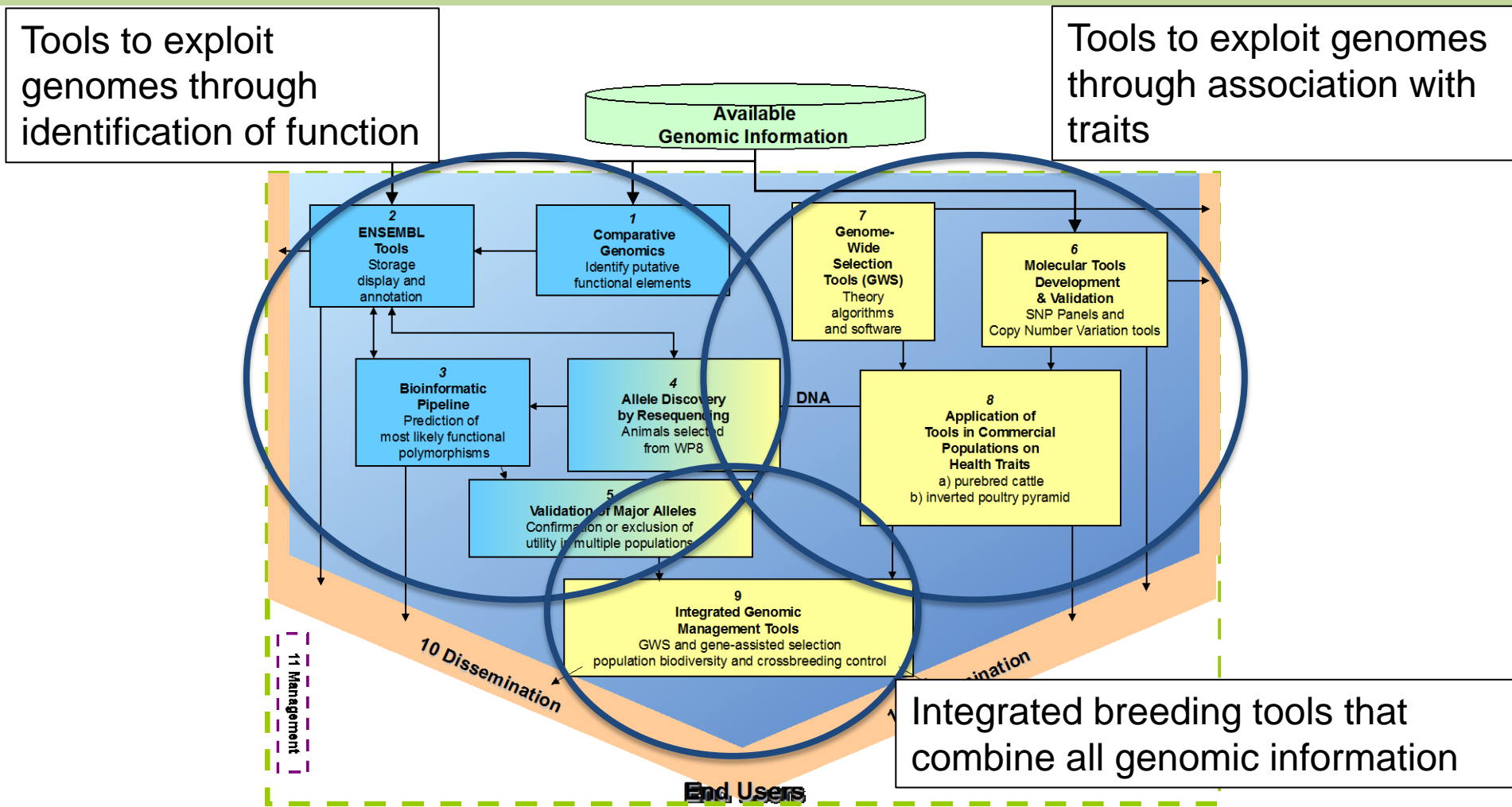
Nov 30, 2013



## Quantomics aims

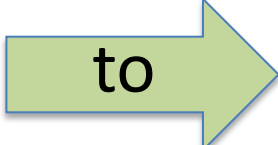
- Take advantage of cutting edge genomic information to:
  - Develop new tools for application in the project and by industry;
  - Extend these tools to deal with new type of information (e.g. CNV)
  - Provide new ways for managing biodiversity using molecular DNA

## Combining Two Strategies



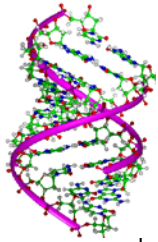


## Animal Genetics ↔ Bioinformatics

- Exchange of knowledge content
  - Bioinformatics => Animal Genetics
  - Animal Genetics => Bioinformatics
- Full exploitation of the potentiality of the integration of fields
  - Reversing the flow of genomic information  
from animal  to human
  - E.g. Long non coding RNA from RNAseq data  
Quantomics data in ENSEMBL



## Progress in Animal Genetics



1953  
Watson and  
Crick



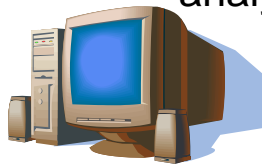
1977  
DNA  
sequenced

1991  
'Halothane'  
gene test

2001  
Genomic Sel.  
proposed

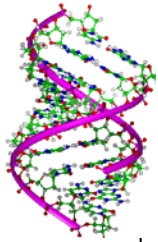
1920s and 30s  
Fisher, Lush  
and others  
Population  
Genetics

1970s +  
Advances in  
quantitative  
analysis





## Progress in Animal Genetics



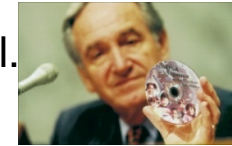
1953  
Watson and  
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1977  
DNA  
sequenced

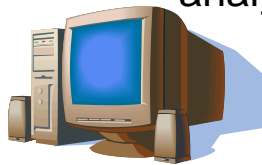
1991  
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gene test

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2003  
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sequenced

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Fisher, Lush  
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Population  
Genetics



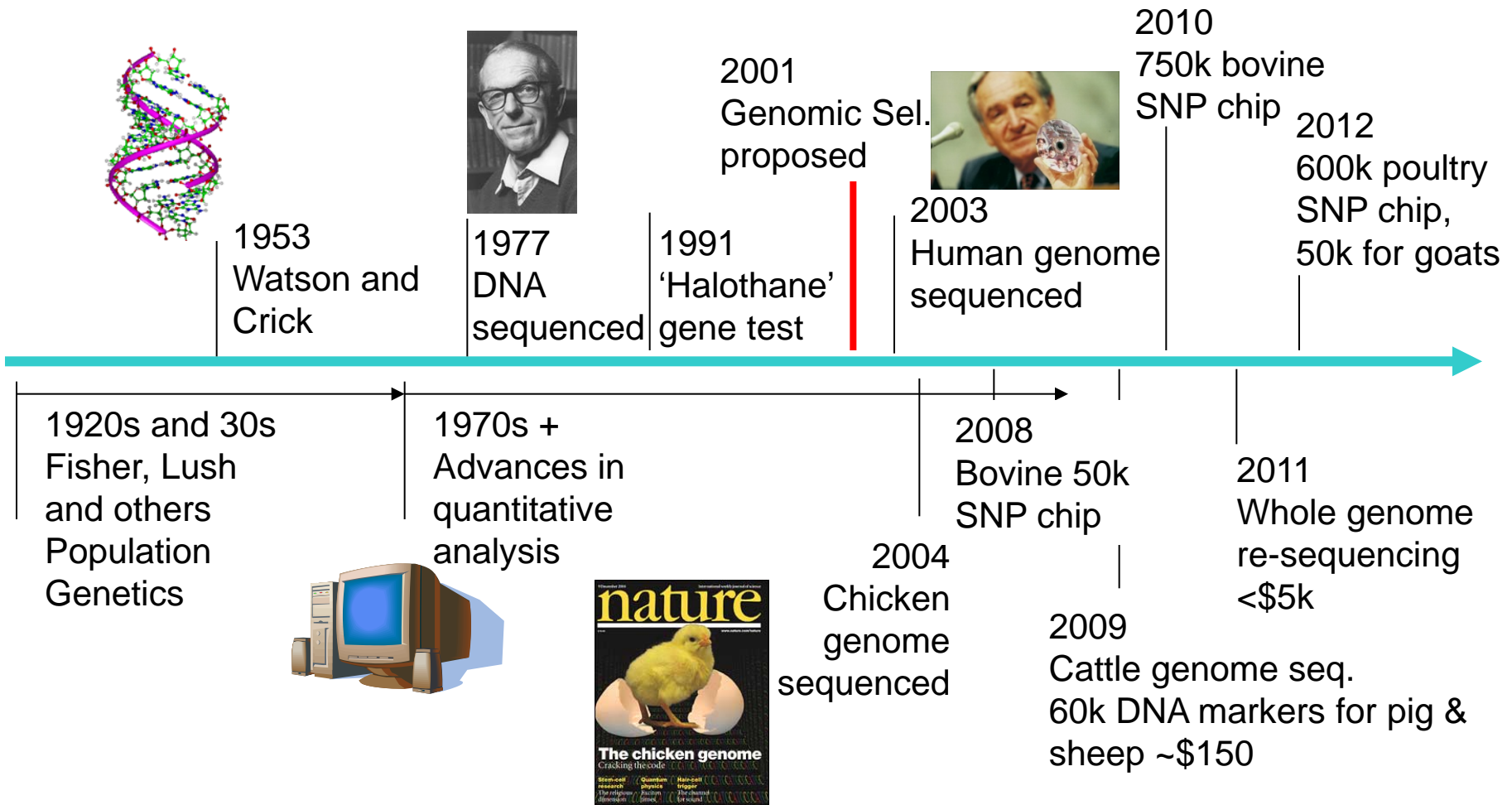
1970s +  
Advances in  
quantitative  
analysis



2004  
Chicken  
genome  
sequenced



## Progress in Animal Genetics





## New Genomic Tools and Reducing Costs Provide More Options

e.g. Cattle

Whole genome re-sequence



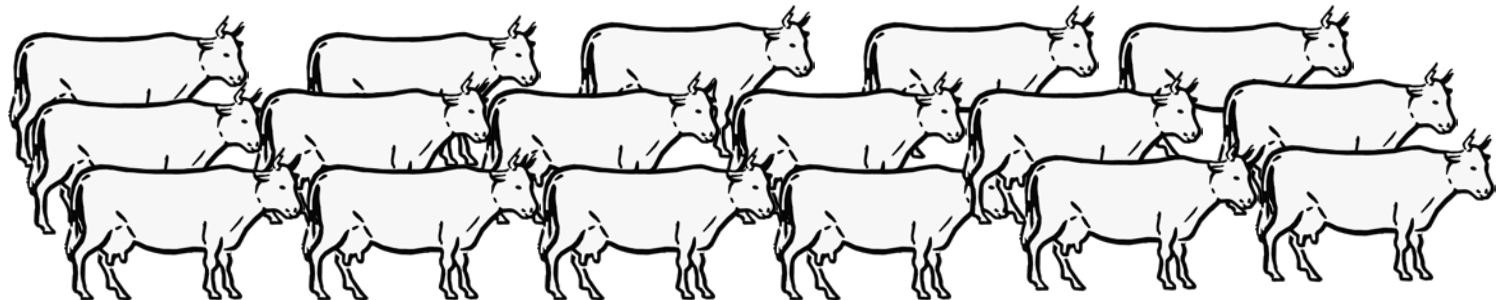
~750k SNPs



50k SNPs

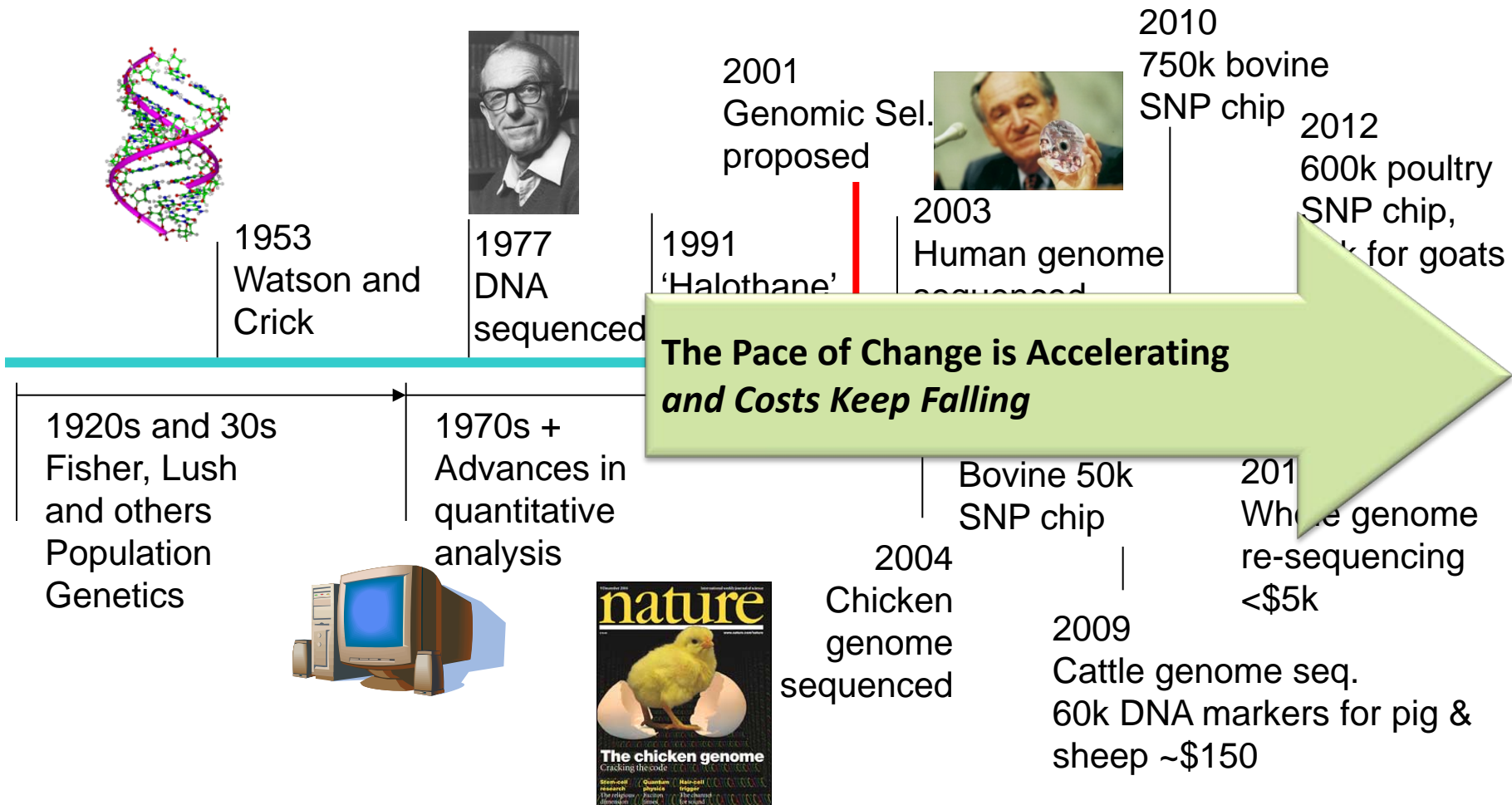


Phenotypes  
3-10k SNPs  
(targeted for  
imputation)



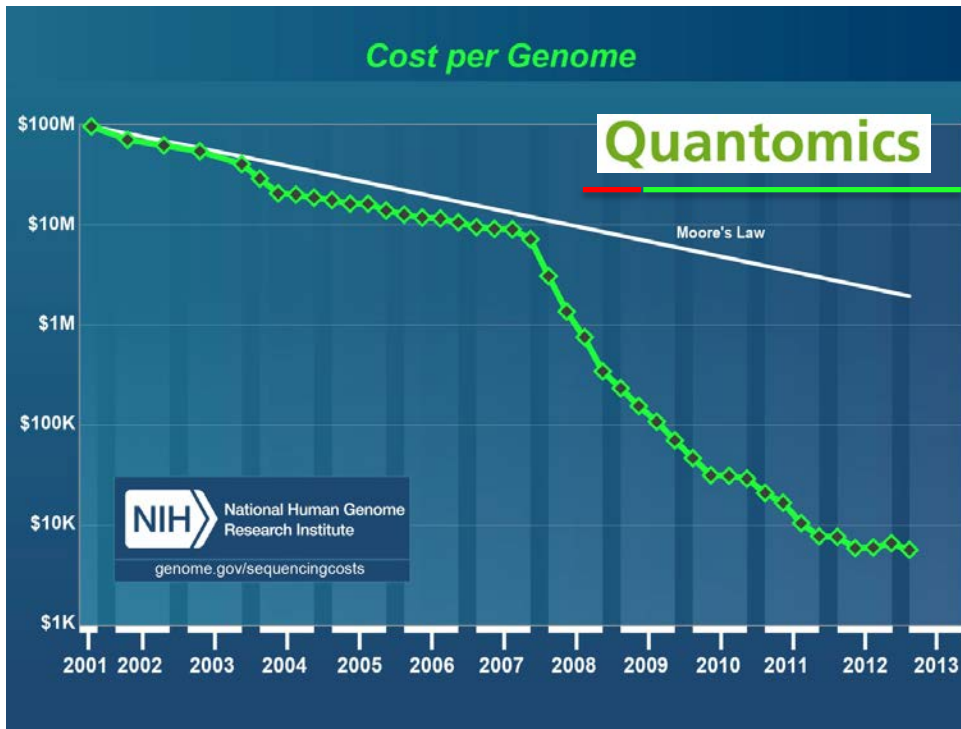


## Progress in Animal Genetics





## Pace of change



- Production costs of an assembled, human-sized (~3000Mb) genome.

**2017: < \$100**

Source: Wetterstrand KA. DNA Sequencing Costs: Data from the NHGRI Genome Sequencing Program (GSP) Available at: [www.genome.gov/sequencingcosts](http://www.genome.gov/sequencingcosts). Accessed 11 June 2013.



## Beyond the project boundaries

- Revision of strategies
  - genome sequencing , SNP calling and CNV mapping in cattle;
  - whole genome analysis in cattle;
  - validation steps.
  - Third parties and other collaborative projects
    - Collaboration and availability of information
      - (whether EC- or otherwise funded, completed or ongoing) (i.e “SABRE”, “1000 bull genome project”)
- Leveraged the financial investment and extended scientific excellence beyond the project boundaries



## Beyond the original plan

- Support by the EC in adopting a strategy which includes
  - cutting-edge science
    - Data production and data analysis;
  - to extend beyond the originally envisaged deliverables
    - Reduction in costs and collaboration with third parties



## External Collaborations

- Third party collaboration
  - Aiming to minimise investment for research and industry figures through a win-win collaboration
  - Viking Genetics (DK); Braunvieh Schweiz (CH)
  - Data and samples from HyLine USA
  - Data from research institutions around the world (e.g. RNAseq Data + poultry data Iowa USA)
- Data to 1000 bull genome project
- Management of IP issues
- Property of data and their usage in research / industrial application



## Data ownership - Research and Industry

- In cattle phenotype and genomic data from several sources:
  - Research consortia
  - Industry
- Collaborative data sharing
  - Avoidance of doubling efforts in data production
  - Obligation towards research consortia
  - Obligation towards industry
  - IP rights



## Pace of Change

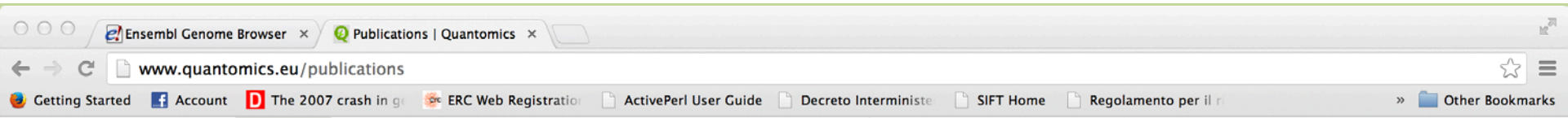
- In genomics data production
  - e.g. sequencing
- In informatic tools
  - e.g. performance / storage capacity
- Project as ambitious as to consider potentiality of deliverable according to the Pace of Change





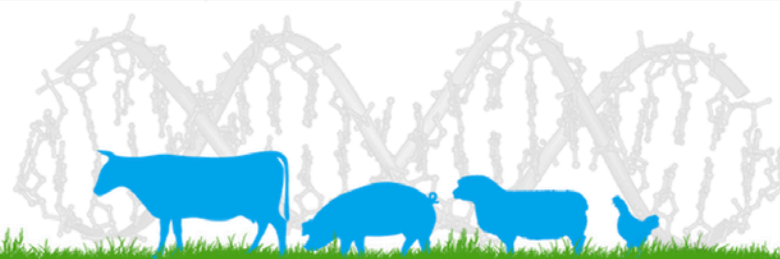
## Outcomes and implications

- Two general breakthroughs for breeders
  - Short to medium term:
    - an unbiased one step genomic evaluation procedure is available for breeders and industry.
    - Improved understanding of the genetics underlying health traits
  - Medium to long-term
    - bioinformatics annotation of the genomes, will help in improving efficiency of selection process



## Quantomics

From Sequence to Consequence :  
Tools for the Exploitation of Livestock Genomes



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## Publications

### [Multi-platform next-generation sequencing of the domestic turkey \(Meleagris gallopavo\): genome assembly and analysis.](#)

Dalloul RA, Long JA, Zimin AV, Aslam L, Beal K, Ann Blomberg L, Bouffard P, Burt DW, Crasta O, Crooijmans RP, Cooper K, Coulombe RA, De S, Delany ME, Dodgson JB, Dong JJ, Evans C, Frederickson KM, Flicek P, Florea L, Folkerts O, Groenen MA, Harkins TT, Herrero J, Hoffmann S, Megens HJ, Jiang A, de Jong P, Kaiser P, Kim H, Kim KW, Kim S, Langenberger D, Lee MK, Lee T, Mane S, Marçais G, Marz M, McElroy AP, Modise T, Nefedov M, Notredame C, Paton IR, Payne WS, Perlea G, Prickett D, Puiu D, Qioa D, Raineri E, Ruffier M, Salzberg SL, Schatz MC, Scheuring C, Schmidt CJ, Schroeder S, Searle SM, Smith EJ, Smith J, Sonstegard TS, Stadler PF, Tafer H, Tu ZJ, Van Tassell CP, Vilella AJ, Williams KP, Yorke JA, Zhang L, Zhang HB, Zhang X, Zhang Y, Reed KM

*PLoS Biol.* (2010) 8:e1000475

Europe PubMed Central: [20838655](#) NCBI PubMed: [20838655](#)

### [eHive: an artificial intelligence workflow system for genomic analysis.](#)

Severin J, Beal K, Vilella AJ, Fitzgerald S, Schuster M, Gordon L, Ureta-Vidal A, Flicek P, Herrero J

*BMC Bioinformatics* (2010) 11:240

Europe PubMed Central: [20459813](#) NCBI PubMed: [20459813](#)

### [RNAZ 2.0: IMPROVED NONCODING RNA DETECTION.](#)

Gruber AR, Findeiß S, Washietl S, Hofacker IL, Stadler PF

*Pac Symp Biocomput* (2010) 15:69-79

Europe PubMed Central: [19908359](#) NCBI PubMed: [19908359](#)

### [PLEXY: efficient target prediction for box C/D snoRNAs.](#)

Kehr S, Bartschat S, Stadler PF, Tafer H

*Bioinformatics* (2011) 27:279-80

Europe PubMed Central: [21076148](#) NCBI PubMed: [21076148](#)

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## Conclusions

- Future projects will need, during the advance of the project, great flexibility
  - in the use of technologies, tools and resources
  - in the composition of its consortium and in interaction with industries.
- Flexibility to rapidly adapt to “Pace of change” is crucial for having a world leading scientific community
  - By Project management
  - By project funders

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    - Johanna Vilkki
    - Dave Burt
    - Theo Meuwissen
    - John Woolliams
- External collaborators

