



GeT

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<http://get.genotoul.fr>
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Who are we?

- ④ Genomics and Transcriptomics (GeT) core facility of Genotoul located on 5 sites
- ④ Regional node of National Infrastructure within the « France Génomique » PIA program
- ④ Labels :
 - IBISA Label
 - INRA strategic core-facility
- ④ Quality Certification :
 - ISO9001 (GeT-PlaGe, GeT-Biopuces)
 - NFX 50 900 (GeT-PlaGe)



Team and Expertise

④ A team of 30 people with:

- Technological Specialty and Scientific community by site
- Experts in Agronomy, Environment, Microbiology, Health
- Competence in biology, bioinformatics, biostatistics



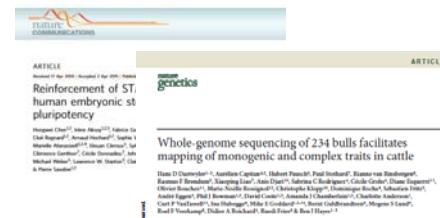
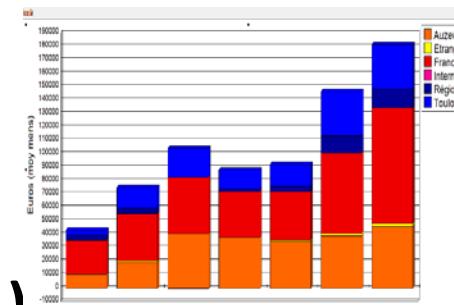
④ Partnership with Genotoul Bioinformatic core-facility (NG6) for:

- Data storage and management
- Data Quality analysis



Activity

- 15 R&D projects
 - Mate paired, chipseq, metylation, GBS, 3G NGS, capture, long fragments, HIC...
- More than 100 laboratories (INRA, CNRS, INSA, INSERM, CHU, CIRAD ...)
 - More than 160 research teams
 - More than 250 projects
 - 2M€ of activity
- 19 Research projects (ANR, INCA, H2020 ...)
- 46 Publications as co-author since 2012





What is NEW ?





Organization : The new GeT

- ⌚ NEW : From “a network of platforms” to
“a **ONE** multi-sites more integrated core facility”

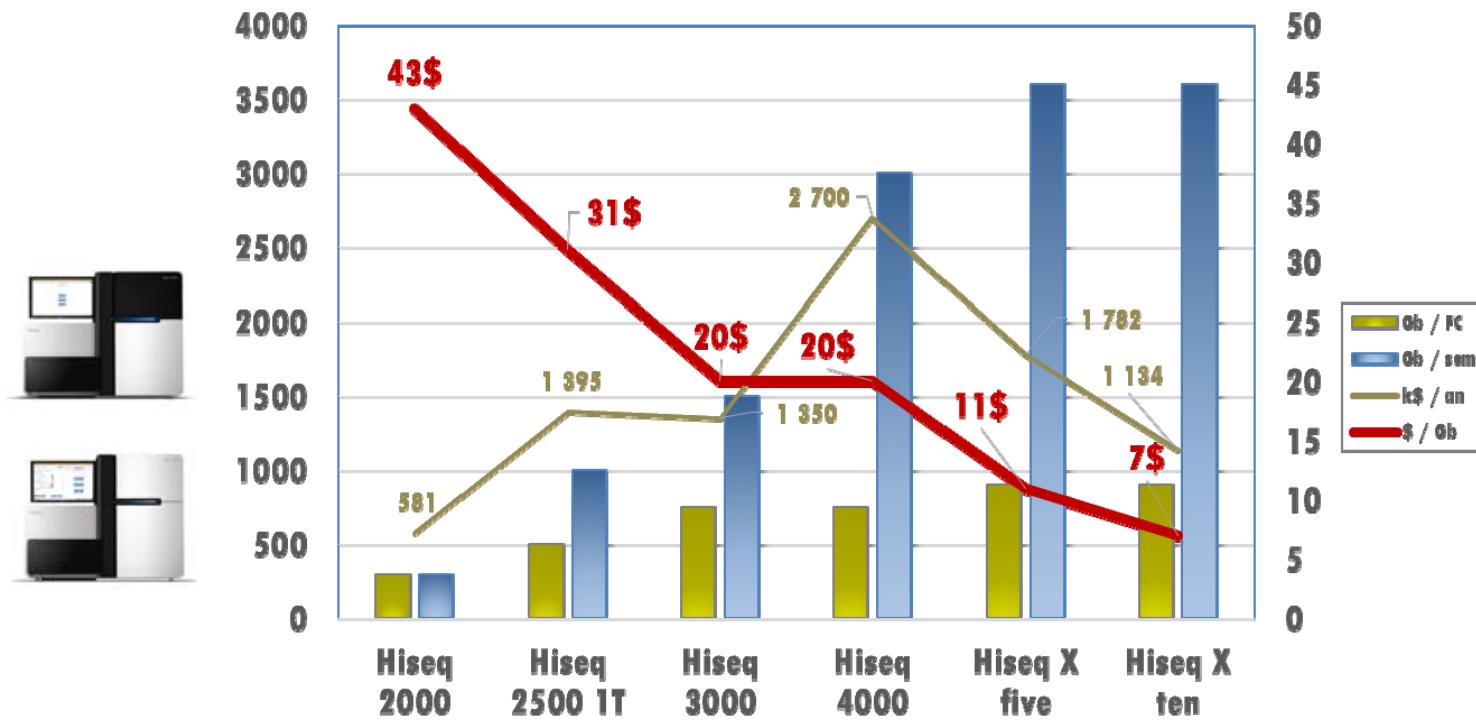
- ⌚ A closer management



- ⌚ GeT Ambassadors in the different scientific communities
- ⌚ GeT Engineers can work on different sites if needed



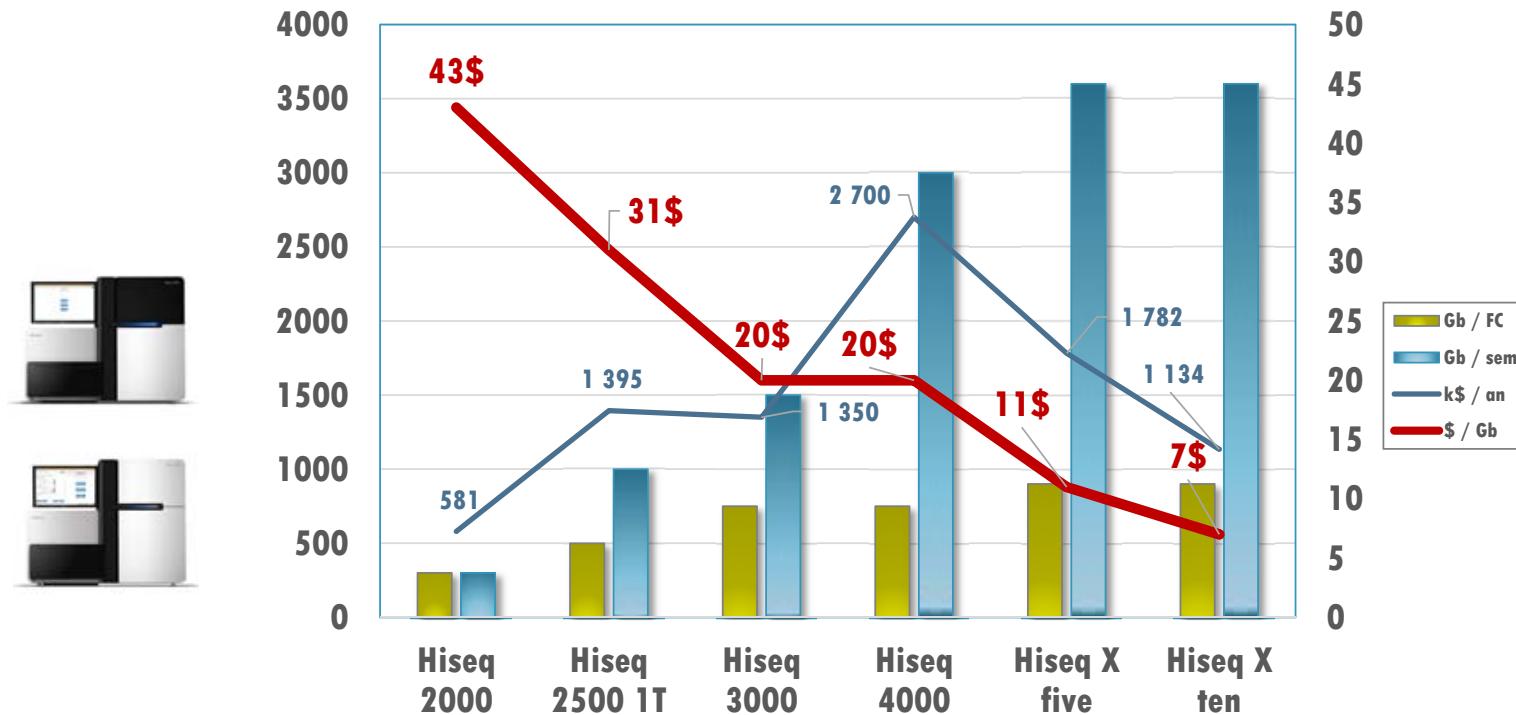
Evolution of Hiseq sequencers family



October 2015 : Non human DNA can be sequenced on Hiseq X (at 30x)
(sold by 5 or more)



Evolution of Hiseq sequencers family



October 2015 : Non human DNA can be sequenced on Hiseq X (at 30x)
(sold by 5 or more)



Evolution of Long Fragments sequencers



January 2015 :

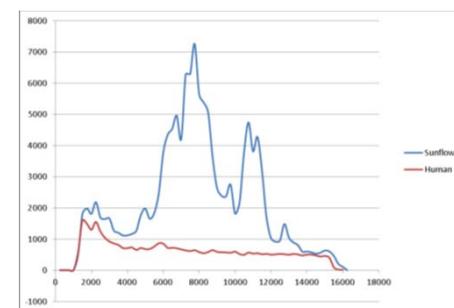
- P6/C4 chemistry of PacBio permits sequencing of longer fragments (at the same error rate)
- Oxford Nanopore is ever in development



Investment in a PacBio RSII with Region MP/FEDER funding, at first for plant genomes



Sunflower : 30 % of repeated sequences (LTR)
Human : 8.8 % of repeated sequences



libraugen



From NGS short reads to long reads

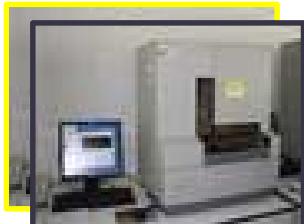
- ④ First PACBIO installed in France

- ④ SUNRISE project to acquire expertise
 - To validate quality of DNA
 - To improve library preparation
 - To increase the number of reads
 - To increase the length of reads

- ④ More projects to develop new applications :
 - Whole genome sequencing on different species
 - Targeted sequencing
 - Complex population
 - RNA sequencing
 - Epigenetic



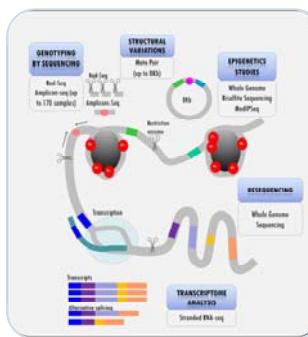
A complete portfolio of sequencers at GeT



400 pb
1Gb



200 pb
13 Gb



15 000 pb
1.2 Gb (6h)



25 000 pb
7 Gb (48h)



2x 300 pb
15 Gb

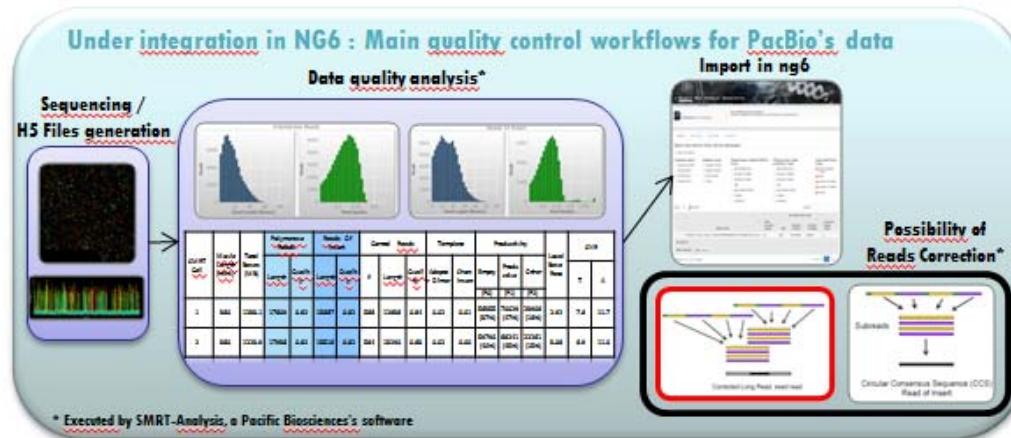


2x150 pb
700 Gb



LIMS development

- ④ Current integration in **NG6** : Main quality control workflows for PacBio's data



- ④ Upcoming : A new LIMS for NGS samples, sequencing and analysis tracking



<http://get.genotoul.fr>



Communication

Website

The screenshot shows the GeT website homepage. At the top, there's a navigation bar with links like "Accueil", "Ateliers", "Réservation", "Actualités", "Qualité", and "Contact". Below the navigation is a section titled "ACTUALITÉS" with four news items. Under "GET EN QUELQUES MOTS", it describes GeT as a platform for genomics and transcriptomics. It lists services like sequencing, genotyping, transcriptomics, and bioinformatics. A "NOS APPAREILS" section shows images of sequencing machines. At the bottom, there's a "RESTER EN CONTACT PAR E-MAIL" section and a "genoIBSA" logo.

Twitter account :@GeT_Genotoul

The screenshot shows the GeT_Genotoul Twitter profile. It has 85 tweets, 40 followers, 100 following, and 1 favorite. The bio states: "GeT is a core facility expert in genomics and transcriptomics, engaged in agronomical, environmental, microbiological and medical projects." It also mentions "Toulouse, France" and the URL "get.genotoul.fr". The timeline includes a tweet about capturing 1300 cells from 80 kreads per cell, along with several sequencing-related figures and diagrams.



GeT in a mapmind

