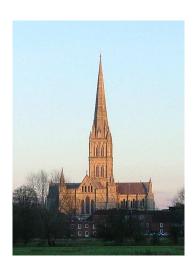


# The National Genetics Reference Lab (Wessex):

### who are we and what do we do?



Helen White, PhD Senior Scientist

NGRL (Wessex)





#### **UK National Genetics Reference Laboratories**

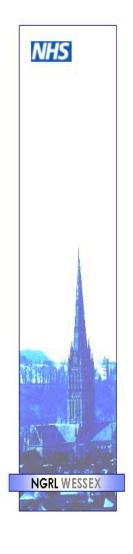


- Established in 2002 by the Department of Health as an initiative by the Department of Health to support the UK NHS genetic lab services
- Two laboratories based in Manchester and Salisbury (Wessex)



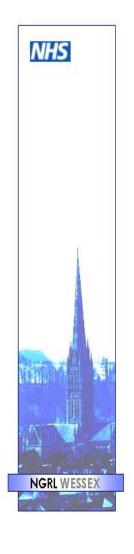
- NGRL (Wessex) is integrated with:
  - o Wessex Regional Genetics Laboratory in Salisbury and work closely with
    - o Human Genetics Division at the University of Southampton
    - o Wessex Clinical Genetics Service

#### **UK National Genetics Reference Laboratories**



- Our work encompasses cytogenetic, molecular cytogenetic and molecular genetic analysis
- Principal focus is on development, validation and quality assurance of genetic testing for constitutional and acquired abnormalities
- The specific remit of the laboratories includes:
  - o Technology development, assessment and validation
  - o Developing new quality management systems
  - o Developing reference and control reagents
  - o Developing information systems for genetics
  - o Providing advice to government and professional bodies
- Our current work programmes are overseen by a steering group

# Work programmes 2002 - 2007



Generally reflected genetics labs need to respond to targets set in the Genetics White Paper (2003)

"Our inheritance, our future: realising the potential of genetics in the NHS"

Dept of Health invested up to £18 million capital on upgrading NHS genetics laboratory facilities in England.

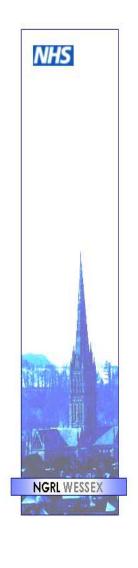
"As a result of this investment, by 2006 genetic testing times will be cut and the results should be available to the following standards:

o within 3 days where the result is urgent (eg. prenatal diagnosis)

o within 2 weeks where the genetic mutation is already known

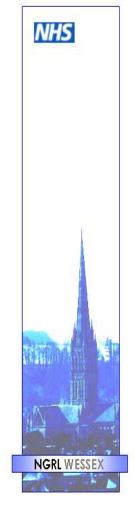
o within 8 weeks for unknown mutations in a large gene"

# Work programmes 2002 - 2007



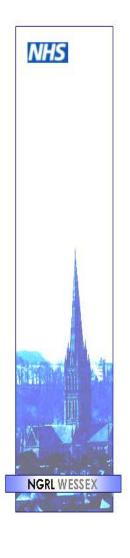
- Reference and Control Materials
- Technology Assessments & White Paper targets
- Genetic diversity and reference ranges
- Developments in cytogenetics and molecular cytogenetics
- Fluorescence in situ hybridisation reference service
- Advice, Training, Education and Horizon Scanning

# **Control Reagents for Genetic Testing**



- NHS genetic diagnostic laboratories in the UK (and labs worldwide)
   perform thousands of mutation detection assays every month using diverse technologies
- Laboratories generally use locally sourced controls as standards to confirm that an assay is working correctly
- Widespread variation in the number and type of controls used in different laboratories
- Can potentially compromise quality assurance

# NGRL (Wessex) Reference Material 2002 - 2007



#### Plasmid based control material for mutation scanning

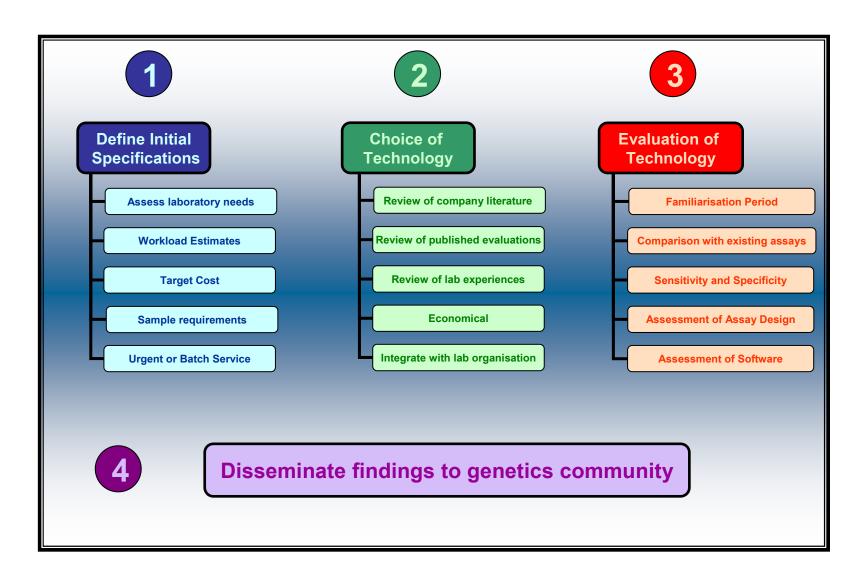
Generated sets of plasmid constructs that harbour defined sequence changes and which can be used as controls for a wide range of mutation assays

- Familial breast cancer and colorectal cancer (n=193)
- Generic controls for Mutation Scanning (n=52)

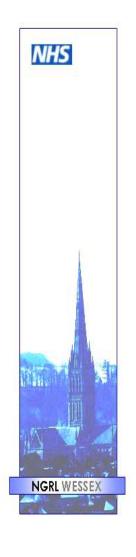
#### **Genomic DNA (lymphoblastoid cell lines)**

- Normal controls
- Myotonic dystrophy
- Friedreich ataxia

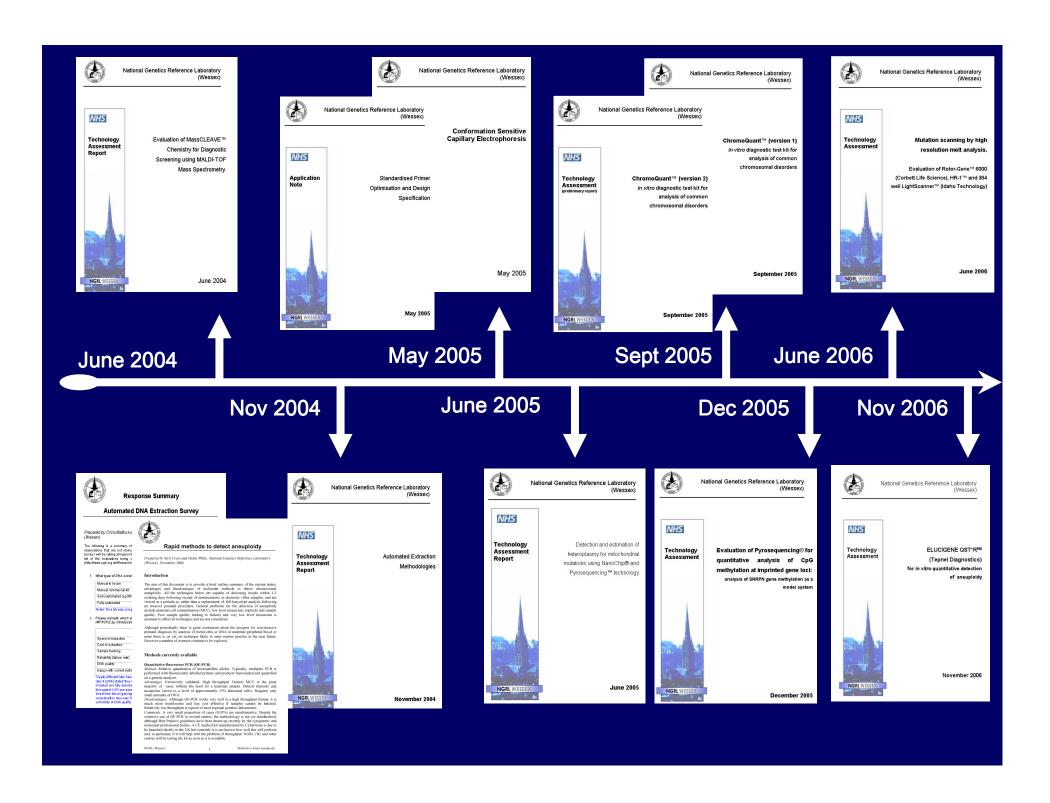
# NGRL (Wessex) Health Technology Assessment



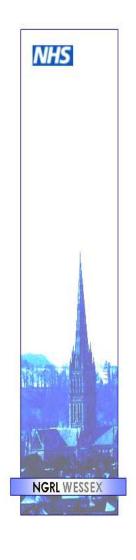
# Scope of Technology Assessments 2002 - 2007



- SNP / defined mutation detection
- Allele Quantification / Dosage
- Epigenetic analysis
- Meeting White Paper Targets
  - o Automated DNA extraction platforms
  - o Rapid mutation scanning
  - o Rapid aneuploidy detection



# Work programmes 2007 - 2012

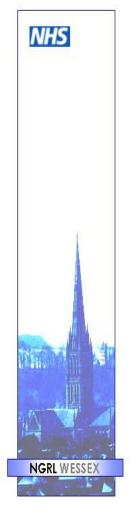


More focused on development of technologies that are likely to have a major impact on genetic testing in the future

- Reference Reagents (Prof Nick Cross & Dr Helen White)
- New generation sequencing (Chris Mattocks)
- Non invasive prenatal diagnosis (Dr Helen White)
- Array CGH (Dr John Crolla)
- Cytogenetics Resources (Dr John Barber)
- Meeting and Workshops

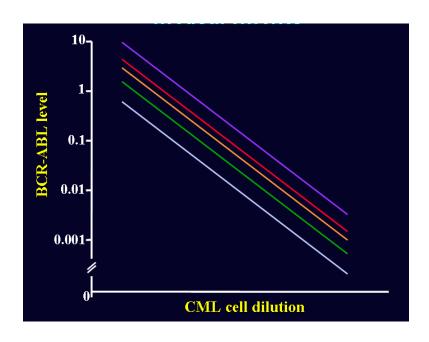
# Reference reagents

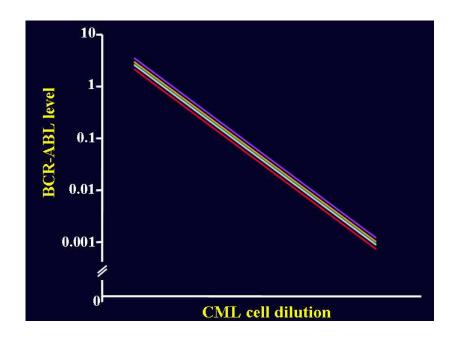
# Real time Quantitative PCR analysis of the BCR-ABL fusion transcript



- RQPCR is routinely used to quantify levels of BCR-ABL mRNA transcripts from chronic myeloid leukaemia patients
- Accurately determines the response to treatment and is particularly valuable for patients who have achieved complete chromosomal remission.
- Despite efforts to establish standardised protocols for BCR-ABL fusion transcript quantitation there is still substantial variation in the way in which RQ-PCR for BCR-ABL is carried out and how results are reported indifferent laboratories worldwide

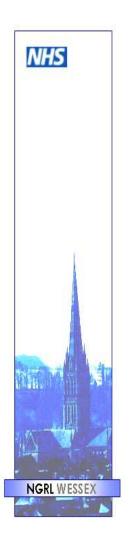
- An international scale (IS) has recently been established recently that is anchored to two key points defined in the IRIS trial: a common baseline (100% BCR-ABL<sub>IS</sub>) and major molecular response (0.1% BCR-ABL<sub>IS</sub>)
- Definition of the IS currently relies on relating results directly or indirectly to the Adelaide international reference laboratory
- A more robust definition of the IS requires the development of internationally accredited reference reagents





# Reference reagents

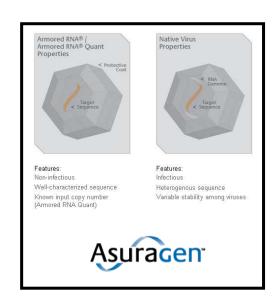
#### Real time Quantitative PCR analysis of BCR-ABL



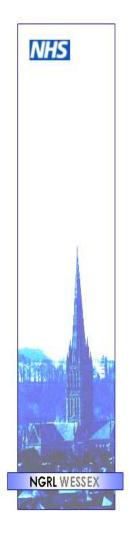
NGRL (Wessex) in collaboration with the National Institute of Biological Standards and Control and Asuragen have developed the following prototype reference materials which were field trialled in 2007.

- Freeze dried cell lines
- Armored RNA constructs

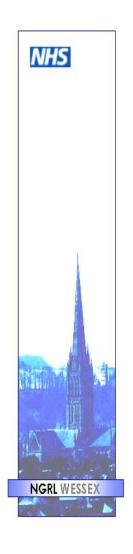




#### International field trials



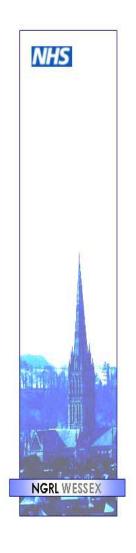
- The performance of the freeze dried cells was assessed by 14 labs (7 EU, 4 USA, 3 Asia/Australasia) using 7 different protocols and 9 different RQ-PCR platforms.
- The performance of the aRNA samples was assessed by 29 labs (22 EU, 3 USA, 4 Asia/Australasia) analysing 3 different control genes on 14 different RQ-PCR platforms.
- Both freeze dried cells and aRNAs performed well and appear to be suitable for the development of *BCR-ABL* reference reagents
- Large scale production of the freeze dried cell lines took place in Sept
- Reagents to be used as 'higher order' internationally accredited primary reference materials field trial due early 2009
- The aRNA constructs will undergo a further round of field trial evaluation with the aim of establishing them as secondary reference reagents.

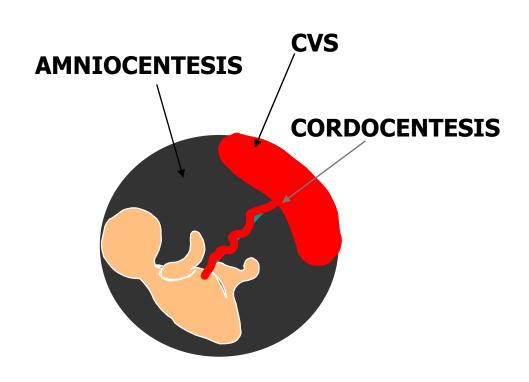




Non invasive pre natal diagnosis of Down Synrome (trisomy 21)

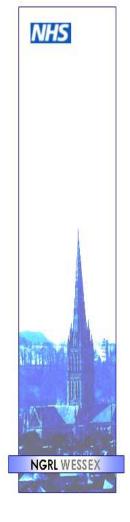
# **Current prenatal diagnosis requires invasive procedures**





1% risk of miscarriage
Not possible before 11 weeks' gestation

# Down syndrome screening in the UK



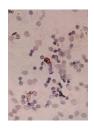
- The invasive approach to obtaining fetal tissue and DNA is currently the gold standard for prenatal diagnosis
- Many women are reluctant to undergo invasive testing, either due to the small but significant risk to the pregnancy, or because they would not terminate the pregnancy irrespective of the results.
- Of the approximately 700,000 pregnant women per year in the UK, around 30,000 amniocentesis tests and 8,000 CVS tests were conducted in the period 2002/03 (Human Genetics Commission, 2004), potentially causing around 460 miscarriages.
- A reliable and convenient method for non-invasive prenatal diagnosis (NIPD) has therefore long been sought to reduce this risk of miscarriage and allow earlier diagnosis.

# Other sources of fetal tissue for non-invasive prenatal diagnosis



## **Fetal cells** in maternal circulation

erythroblasts trophoblastic cells leucocytes

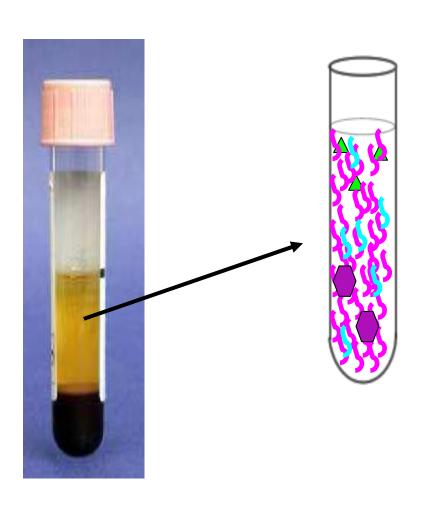






Difficult to isolate and persist for years after pregnancy

# Extraction of cell free fetal nucleic acids from maternal plasma



- Cell free maternal DNA (96.6%)
- ▲ Cell free fetal DNA (3.4%)

Amount of cf fetal DNA extracted is equivalent to 25 genomes / ml plasma

- **Cell free maternal RNA**
- Cell free fetal RNA

Detectable from 5 weeks' gestation and cleared from circulation within 30 minutes of delivery

# How can cell free fetal nucleic acids be used for non-invasive Down syndrome testing?

#### Major technical challenge

Background of cell free maternal **DNA** means direct quantification of fetal chromosome copy number is problematic and technically demanding

Ideally need:

targets that are free from maternal background interference

and / or

technologies that enable extremely accurate copy number 'counting'

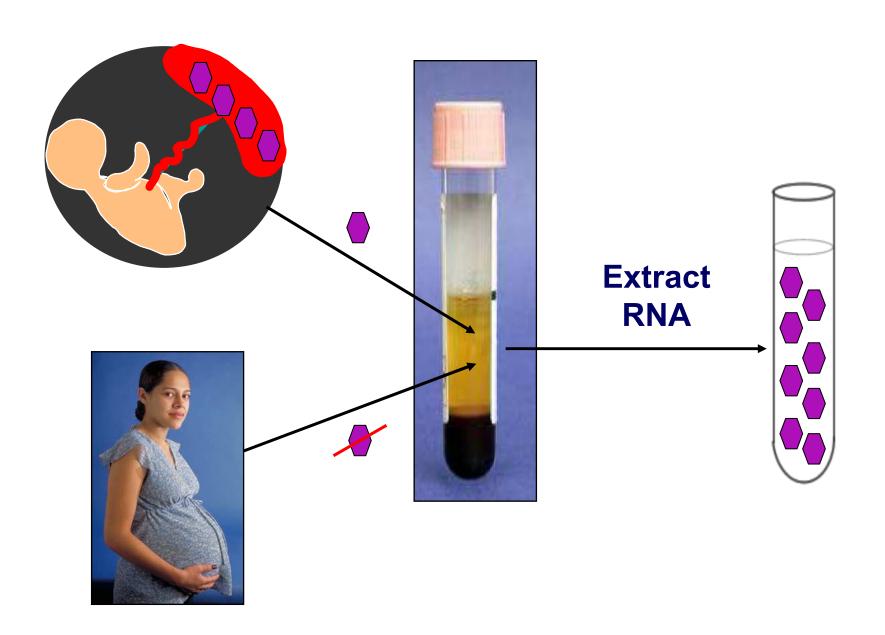
#### Recent major breakthroughs

Quantitative analysis of Single Nucleotide Polymorphisms in fetal specific mRNAs

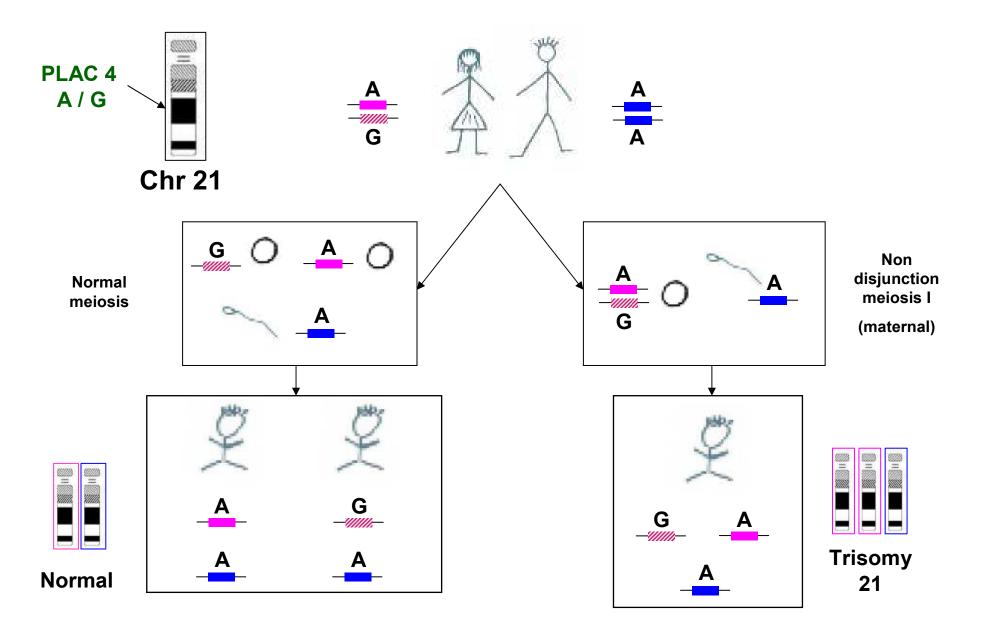
Digital PCR of cfRNA and cfDNA

Shotgun sequencing of cfDNA

# Quantitative analysis of SNPs in fetal specific mRNA

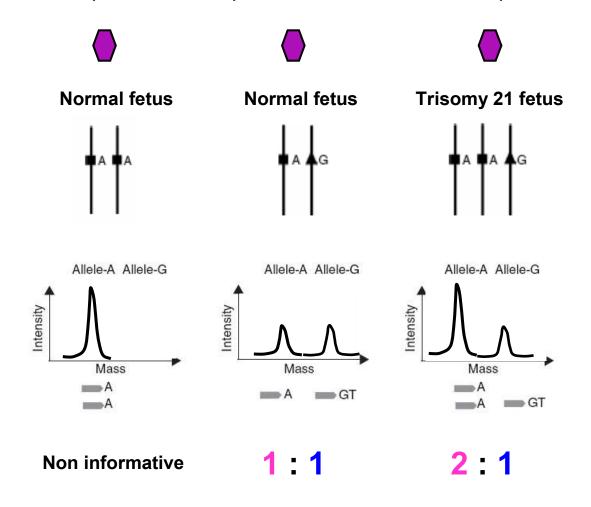


# Quantitative analysis of SNPs in fetal specific mRNA

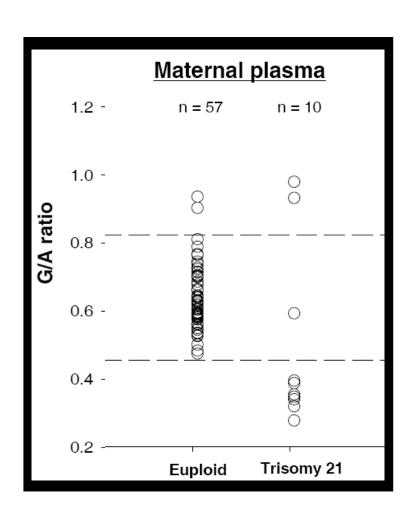


# Quantitative analysis of SNPs in fetal specific mRNA Analysis by MALDI-TOF (mass spectrometry)

- PLAC4 mRNA ( ) is derived exclusively from fetal chromosome 21
- PLAC4 mRNA expressed in the placenta and is found in the plasma of pregnant women

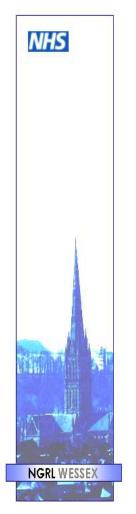


# Quantitative analysis of SNPs in fetal specific mRNA Analysis by MALDI-TOF (mass spectrometry)



- •Correctly diagnosed fetal trisomy 21 in **90%** of +21 cases (n=10)
- •Excluded diagnosis of trisomy 21 in **96.5%** of normal controls (n=57)
- Sensitivity: 90%
- Specificity: 96.5%

# RAPID : Reliable Accurate Prenatal non-Invasive Diagnosis - an integrated project to refine and implement safer antenatal testing



NIHR programme grant (2008 - 2013) co-ordinated by Dr Lyn Chitty:

#### October 2007

Submission of outline proposal (John Crolla and Helen White: co-applicants)

#### December 2007

NIHR outline proposal successful. Full submission invited

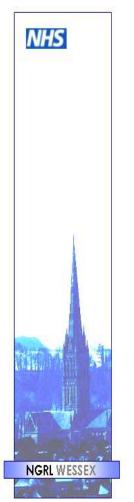
#### March 2008

Submission of full application (John Crolla and Helen White: co-applicants).

#### **Nov 2008**

£2 million awarded

# RAPID: Reliable Accurate Prenatal non-Invasive Diagnosis - an integrated project to refine and implement safer antenatal testing



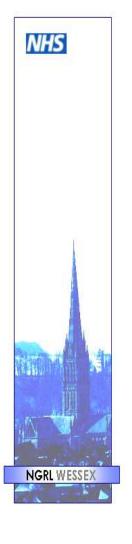
(£2 million NIHR Programme Grant – awarded Oct 2008)

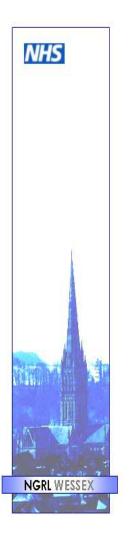
To improve the quality of NHS prenatal diagnostic services by evaluating early non-invasive prenatal diagnosis based on cell free fetal DNA and RNA extracted from maternal plasma.

- 1) Confirm laboratory standards for NIPD for:
  - Fetal sex determination
  - Single gene disorders
  - Down's syndrome (DS)
- 2) Evaluate NIPD for those indications using the ACCE framework (Analytic and Clinical validity, Clinical utility, and Ethical, legal and social aspects)
  - Evaluating cost effectiveness
  - Determining couples' choices, preferences and needs
  - Considering wider ethical, legal and social issues
  - Developing competences for health professionals
- 3) Develop an implementation plan for use by commissioners to establish NIPD as an NHS service

## RAPID: Role of NGRL (Wessex)

- Define Down Syndrome (DS) test sensitivity and specificity and evaluate new polymorphic markers (300 DS and 300 normal controls)
- Undertake pilot feasibility studies for DS testing
  - mass spectrometry (in collaboration with Sequenom)
  - digital PCR (in collaboration with Fluidigm)
  - targeted new generation sequencing
- Undertake population based feasibility study of NIPD for DS testing
  - Salisbury
  - King's College London Hospital
  - University College London Hospital
- Produce or (co-ordinate production) of prototype reference materials in collaboration with National Institute of Biological Standards and Control and NGRL (M)
- Produce standardised protocols and co-ordinate dissemination in collaboration with Great Ormand Street Hospital and NGRL (M)
- Participate in a model-based economic evaluation to assess incremental cost-effectiveness of NIPD versus current methods





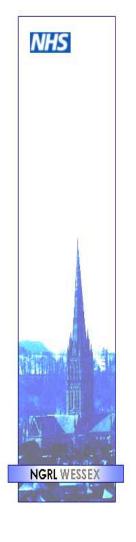
# Diagnostic application of next generation sequencing technologies

454 GS FLX Life Sciences (Roche) Genetic Analyzer Solexa (Illumina) SOLID sequencing (Applied Biosystems)





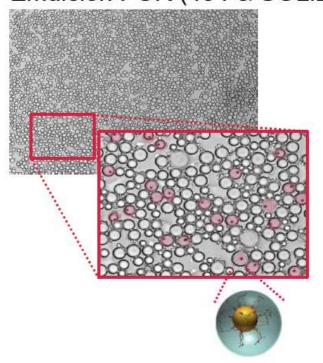


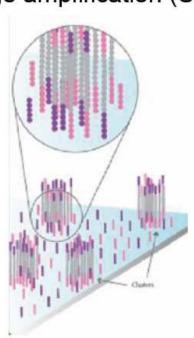


- Research is uncovering the genetic causes of multi-factorial diseases where many genes may be implicated
- Implementation of diagnostic tests for such disorders will demand ever increasing capacity to sequence multiple genes for each referral.
- Over the past two years a new generation of sequencing technologies has become commercially available.
- Very high throughputs have been achieved by massively increasing the density of analyses that can be performed in a single run.
- With conventional Sanger sequencing by capillary electrophoresis up to 384 sequences (more usually 96) can be generated in a single run.
- The new, or "next", generation sequencing technologies can deliver capacities several orders of magnitude greater than is possible by capillary sequencing.

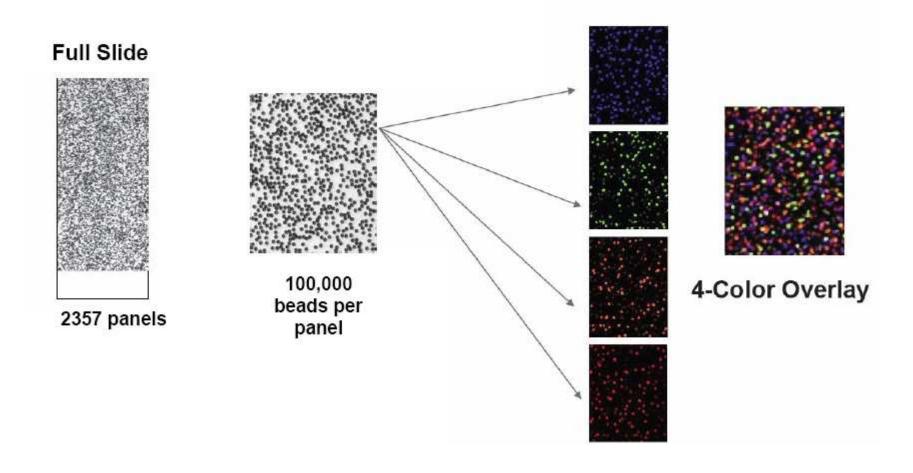
In situ amplification of single DNA molecule

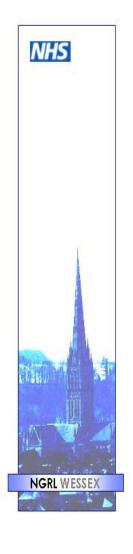
Emulsion PCR (454 & SOLiD) Bridge amplification (Solexa)



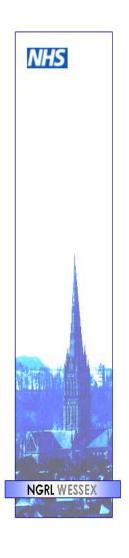


Massively parallel sequencing





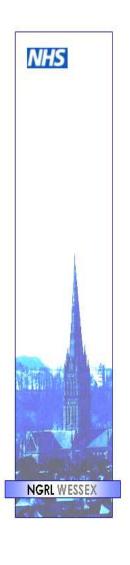
- Application of these technologies has mainly focused on large scale, genome wide, research applications
- But they have potential to profoundly impact on the scope and scale of genetic diagnostics
- Significant innovations are required to utilise these technologies in the diagnostic setting:
  - o The ability to target regions / gene of clinical interest
  - o The ability to ID tag samples to enable multiple tests to run in parallel
  - o IT infrastructure and knowledge to enable analysis of the data



#### **Aims**

- Co-ordinate efforts of early users within the NHS via an advisory group and the CMGS NGS interest group
- Develop protocols for sample preparation for a range of applications applicable to diagnostic use.
- Ongoing evaluation of the different platforms
- Provide timely feedback to companies
- Monitor development of existing and new technologies

# **Next generation sequencing: specific projects**



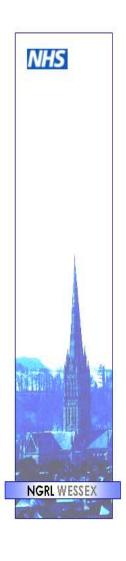
#### Three main applications

- o mutation scanning DNA / RNA
- o quantitative analysis
- o genome architecture

### The key areas of interest will be:

- o Enabling analysis of different samples / tests on one instrument run.
- o Rationalising the sample preparation workflow.
- o Interaction with NGRL(M) regarding data analysis and IT issues.

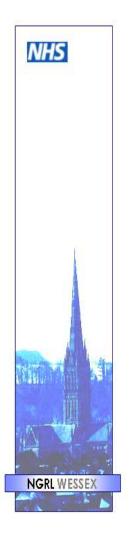
# **Next Generation Sequencing: In the pipeline**



### **NEAT** grant application:

- This application will allow us to expand the scope of our work on NGS technologies – Should the application not be successful we will continue with plans outlined in the proposal but the scale of work will be reduced
- Funding decision expected By 28th November 2008

# Johan den Dunnen Head of Centre Leiden Genome Technology Centre



#### **Future ahead:**

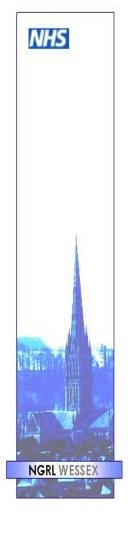
"Soon we will be able to sequence a complete human genome"

but if we can not make sense out of the variants detected, as to whether they are "pathogenic or not", this information is useless and misinterpretation...."

#### **Summary:**

"As clinical lab, do not buy a system yet, use that of your colleague, but start saving money, in 3-5 years you need it...!!"

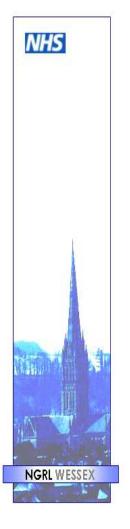
# **Array CGH**



- <u>Aim:</u> To develop a robust, cost effective, validated targeted oligonucleotide array CGH platform to detect common microdeletions and microduplications
- We have designed and validated a customised 4x44K Agilent array for constitutional aCGH:
  - o designed to provide the maximum genome wide resolution with the probes available
  - o Focuses specifically on the known micro-deletion and duplication syndromes.
- ■Design currently being upgraded to the new 4x180K format to provide better genome wide coverage



## **Cytogenetic Resources**



#### **Chromosome Anomaly Collection**

Catalogue of unbalanced structural chromosome abnormalities without phenotypic effect.

### **Chromosome Microdeletion / duplication syndrome**

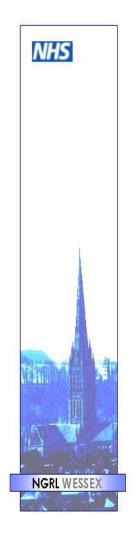
This collection was compiled by searching:

- o OMIM and PubMed databases using "microdeletion syndrome", "monosomy syndrome" and "microduplication syndrome"
- o Data from current published microarray series
- o Tests currently offered by the Key Locus Service of the NGRL (Wessex)

#### **Subtelomeric collection**

Catalogue of sub-telomeric deletions, duplications and rearrangements that may have no phenotypic consequences

# **Cytogenetic Resources**



#### Probe bank and key locus service

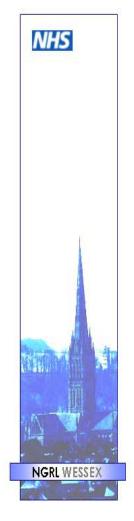
Utilise the molecular cytogenetics resources of the Wessex Regional Genetics Laboratory by obtaining probes from:

- o Human Genome Mapping Project Resources
- o Research Collaborators
- o Web-based FISH probe resources

Within the resources of the NGRL we are able to:

- o Interrogate the www databases to identify locus specific probes
- o Order BACs, PACs, cosmids etc from genome resource centres
- o Prepare the selected probes for FISH
- o Validate the FISH probes
- o Store glycerol stocks
- o Store genomic and labelled DNA from all probes

# **Meetings and Communication**



#### **Meetings**

New and Developing technologies meeting: Salisbury, July 2010

BCR-ABL meeting: London, 27<sup>th</sup> Nov

CMGS NGS Interest group meeting: Leeds, 15<sup>th</sup> Dec

#### **Conferences:**

CMGS Exeter March 2009

**BSHG Warwick August 2009** 

#### More information:

Website: www.ngrl.org.uk/Wessex

E Bulletin: LISTSERV@LISTSERV.MANCHESTER.AC.UK



ngrl.org.uk/Wessex

#### **Director**:

**Prof Nick Cross** 

#### **Co-directors**:

Dr John Barber Dr John Harvey Dr John Crolla Dr David Robinson Dr Tony Herbert

#### **Scientific and Technical staff:**

Dr. Helen White Chris Mattocks Dr. Shuwen Huang Gemma Watkins Victoria Hall Jan Mitchell