Since January 2020 Elsevier has created a COVID-19 resource centre with free information in English and Mandarin on the novel coronavirus COVID-19. The COVID-19 resource centre is hosted on Elsevier Connect, the company's public news and information website.

Elsevier hereby grants permission to make all its COVID-19-related research that is available on the COVID-19 resource centre - including this research content - immediately available in PubMed Central and other publicly funded repositories, such as the WHO COVID database with rights for unrestricted research re-use and analyses in any form or by any means with acknowledgement of the original source. These permissions are granted for free by Elsevier for as long as the COVID-19 resource centre remains active.
features that roughly reflect the progression of the disease: placen-
titis, oligohydramnios, hyperechogenic bowel, hepatosplenomegaly,
IUGR, ventriculomegaly, intracerebral hyperechogenic foci or micro-
cophaly. These primary markers can lead to the diagnosis of more
complex associations of both systemic and CNS abnormalities in up
to 20% of the cases.

Early experience with treatment of intrauterine cytomegalovirus
infection appears promising following two approaches. Therapeutic
Valganciclovir concentrations were achieved in maternal and fetal
blood with maternal oral administration of this drug in cases of
symptomatic infection. Maternal administration of hyper-immune
immunoglobulins may help re-routing some of the early and acute
effects of the infection on the placenta and the fetus. A combination
of these two approaches should be evaluated in a randomized
controlled trial.

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R3 Paediatric clinical disease registers and ECCI
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For many clinical conditions disease registers are now available, with
considerable benefits and pitfalls associated with their use. A number
of disease registers in complex childhood infection are already
underway usually collecting clinical, laboratory and treatment data.
These cohort studies allow clinical and treatment outcome data to
be collected and analysed for rare conditions. Examples include the
European Collaborative Study and the European Paediatric Hepati-
tis C Register. Such studies can evaluate issues around perinatal
transmission, factors influencing disease progression and patterns of
clinical disease outcome. Cohort collaborations are not randomised
clinical trials and treatment outcomes have to be analysed with cau-
tion. A rapidly increasing use of cohort studies is post licensing drug
surveillance. Many new drugs are licensed or used in paediatrics on
the basis of very limited data. There is often short clinical phase II
studies, with short follow up. Other common problems include very
limited pharmacokinetic data in infants and adolescents, and poor
long term toxicity data, which may be different in paediatrics in
comparison to adult studies. In the UK cohort studies in paediat-
ric HIV infection have provided useful information on drug dosing
and disease management strategies with the aim of standardising
and improving clinical care (www.chipscohort.ac.uk). International
information allows the possibility of linking disease registers to
improve power for analysis of outcome studies. Cohort also can
provide a useful starting point to develop clinical networks for future
trials in rare diseases. Generally data from a smaller number of
committed centres, with clear reasons for starting the register and
understanding of potential bias are the best prognostic factors for
the success of a register. Clear clinical and financial plans for the
long term outcome of the register and its ultimate goal are also vital
for its success. Web based registers now simply data collection,
but lead to complex questions of consent, which vary across the EU.
ECCI could develop a simple disease register across the EU and
the possible role and use for such a register will be discussed.

Abbott Molecular Symposium

S1 Real-time PCR based hepatitis and retrovirus assays in
laboratory routine use: insights from a European user
A.M. Geretti 1, A. Garcia-Diaz, C.L. Booth, W. Labett, N. McAllister,
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Detection and quantification of plasma RNA load plays a key role
in the evaluation and clinical management of infection with HIV-1
and hepatitis C virus (HCV). In the era of highly active antiretroviral
therapy, HIV-1 plasma RNA load continues to play an import prog-
nostic role as a determinant of the rate of CD4 count decline and an
indicator of the risk of transmission. Most importantly, plasma viral
load suppression to below the lower limit of detection is the indicator
of successful antiretroviral therapy and main surrogate marker for
immunological and clinical success. Detection of HCV RNA has
become increasingly important in the diagnosis and management of
hepatitis C infection. Absolute viral load and the early log decline af-
after starting treatment are clinically useful in predicting sustained viro-
logical responses and guiding therapy should be continued. Based on
these considerations, the availability of reliable assays for
HIV-1 and HCV RNA detection and quantification is critical in the
routine diagnostic settings. At the Royal Free Hospital, over 2000
samples have been tested by the Abbott Real-time HIV-1 and HCV
quantitative assays. The assays offer several advantages, including
(a) availability of automated nucleic acid extraction; (b) turn-around
time of 2 hours; and (c) wide dynamic ranges of quantification. Their
use in clinical practice has demonstrated a low risk of carry-over,
contamination, high intra-assay and inter-assay reproducibility, good
performance with a variety of HIV-1 subtypes and HCV genotypes,
and strong correlation with results obtained by other assays in
comparative studies (r > 0.9).

S2 Characteristics of a new automated real time PCR assay
for monitoring HBV patients
J.A. Rhoads 1, K.S. Riesing 2, E.K. Pabich 2, S. Thamm 2,
F. Zoulim 3, V. Thibaut 4, C.R. Muller 1, 1Abbott Molecular, 
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unit 271 and liver department, University Lyon, France, 4Hotel de la
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Genetic diversity among the various subtypes and genotypes of
human Hepatitis B Virus (HBV) is known to exist. This diversity
presents a challenge in designing a real time PCR assay that
accurately quantitates HBV samples with a high degree of sensitivity.
To accomplish this, a sequence alignment was performed which
encompassed representative sequences for the various subtypes
and genotypes of HBV. Next, a search for three conserved regions
in close proximity to each other resulted in the identification of
a highly conserved area in the HBV surface gene upstream from
known HBsAg and Pol mutations. Putative PCR primer and probe
sequences designed within this region were compared to all known
HBV isolates to ensure that these sequences were optimal.

Due to the high degree of conservation within the primer and
probe regions selected, the PCR annealing and read steps can be
performed at high temperature. Using high temperature anneal/read
favors the formation of specific amplification product while also
maintaining the ability of the assay to detect and quantitate diverse
HBV genotypes. Studies were performed on the Abbott m2000
system to evaluate the RealTime HBV assay sensitivity, specificity
and quantification of patient specimens with HBV genotypes A through
H. In addition, specimens containing known Pre-Core, Core
and drug resistance mutations were tested in a blinded study and were
compared to results from a comparator assay.

The resulting assay detects below 50 copies/ML up to at least
1E9 copies/ML on HBV serum or plasma specimens using
automated sample preparation and covers genotypes A–H with excellent
specificity.

S3 CMV DNA quantification in plasma using an automated
real-time PCR assay
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Background: Sensitive quantification of cytomegalovirus (CMV)
DNA is required for the diagnosis of CMV infection or reactivation
and the monitoring of transplanted patients. We have previously
validated a highly sensitive assay (US Cobas CMV, Roche) for the
quantification of CMV DNA viremia in organ transplanted patients.

Objectives: We evaluated a new sensitive PCR assay coupled
with an automated extraction system (CMV real-time PCR, Abbott)
by direct comparison with the US Cobas.

Results: Using limiting dilutions of CMV DNA positive plasma,
the two assays had a similar detection threshold of 20–40 copies/ML.
Coefficient of variations of CMV real-time PCR assay varied from 1 to 12% for CMV DNA levels ranging between 4.0 to 1.3 log copies/ml. Comparative studies using 179 routine samples showed a concordance of 89%: 18 samples positive by CMV real-time PCR only and 2 samples positive by US Cobas. Discrepancies were only observed for samples with less than 300 copies/ml. The two assays showed high correlation ($R = 0.93$), and on average values obtained by CMV real-time PCR were 0.4 log higher than those of US Cobas. Successive samples of transplanted patients with evidence of CMV infection or reactivation revealed that CMV real-time PCR assay was positive earlier and for longer period of time after treatment initiation.

**Conclusion:** Both assays had similar analytical performances, however the CMV real-time PCR assay has the advantages of automated extraction and higher dynamic range. On clinical samples there is a clear trend for a higher sensitivity of the CMV real-time PCR assay.

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**Exhibitors Symposium**

**S4** The innovative qiaSymphony system from Qiagen takes ease of use to a new level

M.N. Kraak*. Qiagen Instruments, Switzerland

Efficient purification of nucleic acids is critical for reliable results in downstream analyses. To address these needs, we are developing an innovative, modular system for medium-throughput sample prep and assay setup. The aim of this work is to provide an initial evaluation of the performance characteristics of the new QiaSymphony sample prep module for fully automated purification of pathogen nucleic acids from a range of samples.

The QiaSymphony sample prep module takes ease of use to a new level and can be operated by anyone – from the novice to the expert. Using proven magnetic-particle technology, a wide range of primary or secondary samples with input volumes up to 1 ml can be processed. You can perform all your molecular biology applications with one hardware configuration. Sample prep is even more economical since all your automated applications can be covered with just a few kits.

High process safety is assured through automated bar code reading of samples and reagents, and a fully automated load check helps to prevent human error. For increased convenience and flexibility, the system allows in-process sample loading, enabling immediate processing of urgent samples.

The QiaSymphony system will be available in 2007. The QiaSymphony system is under development and planned for general laboratory use. No claim or representation is intended for its use to provide information for the diagnosis, prevention, or treatment of a disease.

**S5** Performance evaluation of real-time PCR based assays for the detection and quantitation of hepatitis B virus DNA

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Viral load determination for hepatitis B virus (HBV) is an essential marker for introducing and monitoring efficient therapy. **artus** HBV PCR Kits are real-time PCR based assays specifically developed for the use with the LightCycler® (Roche), the Rotor-Gene 3000 (Corbett Research), and the ABI Prism Instruments (Applied Biosystems). The goal of this work was to evaluate the performance of **artus** HBV PCR Kits in combination with highly efficient viral DNA isolation systems: the silica membrane based QIAamp DSP Virus Kit and automated, magnetic-particle technology based BioRobot® Workstations (QIAGEN).

Serial dilutions of plasma samples spiked with the HBV DNA 1st International Standard (WHO 97/746) were extracted using the QIAamp DSP Virus Kit and different BioRobot Workstations (QIAGEN). For the determination of the viral load the eluates were analyzed using **artus** HBV PCR Kits for the LightCycler® (Roche), the Rotor-Gene 3000 (Corbett Research) and the ABI Prism Instruments (Applied Biosystems).

Clinical sensitivity and specificity were evaluated and quantitative results were correlated by analyzing clinical samples using the **artus** HBV Kits in comparison with a reference method.

The specificity of the **artus** HBV assays has been proven by testing the HBV Genotype Panel (Teragenix), in-house genotyped clinical samples, precore mutation (Teragenix) and seroconversion panels (Boston Biodemica Inc.).

All viral DNA isolation systems showed highly sensitive and reliable results in combination with **artus** HBV PCR Kits for detection and quantitation of HBV. Quantitative results correlated strongly with a diagnostic reference method and all members of the HBV genotype panel were detected with comparable sensitivity.

The combination of sample preparation using the QIAamp DSP Virus Kit or BioRobot® Workstations (QIAGEN) and **artus** HBV real-time PCR assays enables sensitive and highly reliable results for the detection and quantitation of HBV.

**S6** New sensations in molecular diagnostics – NucliSens easyMAG extraction platform and NucliSens EasyQ assays

A. Troesch*. Director R&D Molecular Biology bioMérieux, Grenoble, France

bioMérieux, through its NucliSens range, offers a complete molecular diagnostic platform for extraction, amplification and real-time detection. This presentation will explain the proprietary core technologies as well as highlight some key products from the NucliSens range.

NucliSens extraction is based on BOOM® technology, which is recognized as the Gold Standard in nucleic acid isolation. In the new platforms the technology has been further enhanced by the introduction of magnetic silica particles. Two systems are available for magnetic extraction, i.e. NucliSens easyMAG, the automated platform and NucliSens miniMAG, a more manual system ideally suited for lower throughput labs.

NucliSens amplification and detection is based on real-time NASBA® technology, which enables fast and accurate amplification and real-time detection using molecular beacons. This specific, isothermal method of nucleic acid amplification can be used for the amplification of RNA and DNA and is carried out on the NucliSens EasyQ Analyzer.

bioMérieux is at the forefront of offering more sensitive molecular-based tests to respond to this major public health concern. An example is NucliSens EasyQ HIV-1 v1.2, an established HIV-1 viral load assay that recently has been combined with the NucliSens easyMAG for maximum user convenience. Furthermore assays have been developed in the range of lower respiratory tract infections (LRTI), like NucliSens EasyQ RSV A+B, NucliSens EasyQ hMPV, NucliSens EasyQ SARS-CoV, NucliSens EasyQ Influenza H5 & N1, and CNS infections like NucliSens EasyQ Enterovirus and NucliSens EasyQ HSV 1/2. Other assays that will complement those panels are under development.

**S7** Bayer Molecular: viral load testing today and tomorrow

A.J. Uzgiris*. Bayer HealthCare LLC, Diagnostics Division, USA

Viral load testing is an important component of patient management for those with HIV or hepatitis infection. Bayer HealthCare offers comprehensive viral testing solutions including VERSANT® HIV-1, HCV, and HBV viral load assays. The VERSANT™ 440 Molecular System will perform existing bDNA assays with walkaway automation providing greater laboratory efficiency. The first new assay for this system, an increased sensitivity HCV test, is in development.