SPIDIA Newsletter 10/2011

SPIDIA Homepage (www.SPIDIA.eu)

News about the SPIDIA project, including up-to-date lists of events where to meet us, downloads of SPIDIA posters and presentations, links to other organizations and related initiatives are posted regularly on our homepage. There you can also find more information about the background of the project and about the SPIDIA partners. If you have questions or ideas, you can also get into contact with us using the „Contact Us" form. Feel free to visit us at www.SPIDIA.eu

Contents

About Us

What is SPIDIA

SPIDIA (Standardisation and improvement of generic pre-analytical tools and procedures for *in vitro* diagnostics) is a four-year large-scale integrating research project that will work on the missing standardisation and improvement of pre-analytical procedures for *in vitro* diagnostics. SPIDIA's research and standardisation activities cover all steps from creation of evidence-based guidelines to creation of tools for the pre-analytical phase to testing and optimisation of these tools through the development of novel assays for sample quality biomarkers. The consortium is built by seven public research organisations, eight research companies and an official European standards organisation. SPIDIA's budget is € 13,000,000 with an EC contribution of € 9,000,000.

Why was SPIDIA initiated

In vitro diagnostics have enabled a significant progress in medicine. Further progress is expected by new technologies analysing cellular biomolecule profiles as nucleic acids, proteins, and metabolites. Studies have demonstrated that the profiles of these molecules can change drastically during transport and storage, thus making a reliable diagnostic or pharmaceutical research unreliable or even impossible. Therefore further progress is limited due to the lack of guidelines in sample collection, handling, stabilisation and storage of clinical samples and due to still missing new and improved sample technologies. The project SPIDIA aims to close this gap by providing guidelines, quality assurance schemes and innovative pre-analytical tools. These may also be of high importance for biobanking and biomedical research.

SPIDIA's approach

SPIDIA is organised around three activities. Each consists of multiple work packages. The first activity leads to pan-European quality assurance schemes and guidelines for the pre-analytical phase of *in vitro* diagnostics. Such documents will be based on evidence gathered during ring trials to be performed in order to elucidate problematic steps in pre-analytical procedures. These procedures will have a specific focus on DNA, RNA, protein, and metabolite targets isolated from tissue, tumour, whole blood, serum, and plasma samples. In addition, sample quality assurance biomarker(s) will be discovered to serve as indicators for artificial, post-collection changes of clinical and biological samples. Our second activity is dedicated to the discovery, development and integration of breakthrough technologies that strengthen weak steps and links in the pre-analytical phase of *in vitro* diagnostics. The results are intended to allow the association of classical and molecular diagnostics. This work includes the discovery of novel stabilisation technologies for tissues, blood, and non-invasive samples, such as swab samples to the integration of multiple pre-analytical steps into an automated workflow. Finally, our third activity focuses on management, ethics and spreading of excellence. This activity aims to perform training to disseminate information about discoveries and guidelines to the clinical, scientific and biobanking communities. It will also ensure ethical sensitivity and compliance.

SPIDIA's Project Progress

New Advances in Technologies for Developing Tissue-Based Diagnostics

Evaluation of a New Fixation and Stabilisation Technology

Within the first three years of SPIDIA, a new tissue fixation and stabilisation technology was developed, allowing the association of classical histopathological analysis with emerging molecular analyses within standardised protocols and biomedical tools. Different alcohols and acids were combined in a multitude of combinations with biomolecule preserving substances, identified in a large screening program, which included more than 1500 different compounds and mixtures. The final solution consists of a two-step process using a fixation and a stabilisation reagent in a sequential manner, so that the tissue is first fixed and then transferred to a stabilisation reagent, in which it can be stored and transported for at least seven days at room temperature or up to 8 weeks at 2-8°C. The new tissue preservation technology was called PAXgene Tissue System.

For direct comparison of current and novel tissue preservation techniques, tissue collection was started in a combined approach. Samples were freshly frozen in liquid nitrogen as well as fixed with formalin and the PAXgene Tissue System and paraffin-embedded. Several parameters were investigated: morphology, antigenicity, proteins, metabolites, DNA and (mi)RNA, including downstream applications. Outstanding advantages were recognised concerning RNA preservation in tissue samples processed with the PAXgene Tissue System. More than 3500 samples of different organs and diseases were collected and processed including different protocol variations representing critical parameters for sample quality in a routine clinical setting (e.g. warm/cold ischemia, tissue size, fixation times, storage conditions) at the participating pathology departments (Department of Pathology, Josephine Nefkens Institute, Erasmus MC, Rotterdam (EMC); Institute of Pathology, Medical University of Graz (MUG); Institute of Pathology, Technical University Munich (TUM)).

A dedicated work program was carried out to investigate the preservation of tissue morphology and antigenicity using the new fixative in comparison to neutral buffered formalin. H&E staining showed that the morphology was similar or to some extent even with better nuclei detail level for the PAXgene Tissue Fixative compared with formalin-fixated tissue. A thorough examination of antigenicity started, using 40 different antibodies.

Some of the tested antibodies are:

- CD2, CD3, CD5, CD10
- ERα, PR, Her2
- Cytokeratin 5/6, cytokeratin AE1/AE3, cytokeratin 7
- Ki67, S100, vimentin

At this point, all antibodies tested so far showed staining results in immunohistochemistry comparable to the golden standard formalin. In some cases it was necessary to modify the antigen retrieval step, e.g. using a retrieval buffer with a different pH or omitting the antigen retrieval completely. Enzymatic pretreatment was not necessary at all.

In conclusion, tissue fixated with the new PAXgene Tissue System showed comparable morphology to formalin in H&E stainings and also good antigenicity in IHC, but slight modification of standard staining protocols developed for FFPE tissue might be needed.

Publications of these comprehensive comparative studies concerning the preservation of nucleic acids, morphology and antigenicity are in preparation.

In addition, the applicability for different proteomic analyses was demonstrated and published by Ergin et al (J Proteome Res. 2010 Oct 1;9(10):5188-96). We could show that proteins are non-degraded and immunoreactive and most importantly post-translational modifications like the phosphorylation of proteins are preserved.

Improving the Tissue Collection and Standardising the Pre-Analytical Workflow for Tissue Samples

In order to further integrate and standardise the workflow of tissue collection/stabilisation and transport, a prototypical container was developed, into which the two new fixation/stabilisation solutions could be integrated. First prototypes were moulded on the basis of the most favoured design concept - a container with two separate chambers, into which the fixation- and the stabilisation reagent could be filled (Fig. 1). The volume capacities of the chambers were designed according to the fixation and stabilisation solution volume that is needed to fixate/stabilise tissue pieces, which fit into standardised histocassettes. A holder for a histocassette was integrated into the lid of the container, so that it can be easily transferred from the fixative into the stabiliser solution.

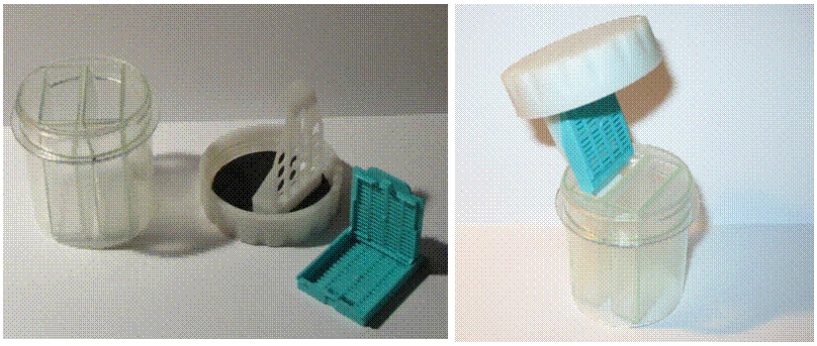


Fig. 1. Prototype container for the "Two chamber one closure concept"
Left hand side: Container concept with two chambers: The lid contains a holder for a standard histocassette. Each of the two chambers holds one of the two stabilisation components of the tissue stabilisation technology. Right hand side: Assembled tissue container.

A labelling concept and handling instructions address safety issues concerning transport and minimize possible human errors during handling. A standardised workflow for tissue fixation and stabilisation using the container device was established (Fig. 2). One aspect of the standardisation was the definition of the tissue size by using standardised tissue histocassettes. Another aspect was the definition of specific time frames for the fixation time and the evaluation of the maximum storage times of tissue in the stabiliser under different temperature conditions. It turned out that tissue was stable for up to 7 days at 25°C and up to 4 weeks at 2-8°C, with no negative impact on the tissue morphology or the nucleic acid stabilisation.

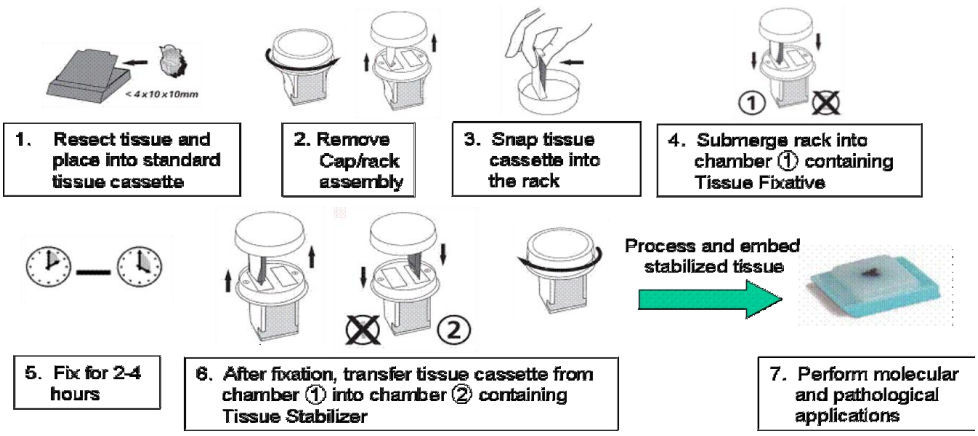


Fig. 2. Suggested workflow for tissue fixation and stabilisation using the prototype container device.

Tackling the Challenges of Metabolomic Studies Based on Tissue Material

In order to standardise the pre-analytical workflow for tissue-based metabolomics, SOPs for NMR sample preparation and spectral acquisition for metabolomic studies on tissue material were established and the effect of pre-analytical procedures such as ischemia, storage and preservation techniques on the metabolome was investigated.

In conclusion, our studies have demonstrated that pre-analytical parameters have a major impact on molecular tissue analysis and assay results. Consequently, the quality of tissue-based molecular analyses can only be defined in the

context of the pre-analytical procedures. Hence, the results generated within this SPIDIA work package will also serve as a baseline data set for the standardisation activity of SPIDIA.

Within a collaboration that SPIDIA initiated with the US National Cancer Institute (NCI), the PAXgene Tissue System was evaluated by the NIH Common Research Fund program GTEx (Genotype-Tissue Expression, www.commonfund.nih.gov/gtex/) for tissue collection from post-mortem cases. The evaluation showed a tissue morphology quality which was at least comparable to formalin fixation, resulting in further use of the PAXgene Tissue System within the consortium. It is planned to collect multiple tissues from 1,000 post-mortem donors during this project. For details please visit:

http://www.genome.gov/Pages/About/NACHGR/September2011AgendaDocs/NACHGR_Sep122011_%20GTExUpdate_Struewing.pdf

How to Improve and Standardise the Pre-analytical Phase of Molecular Diagnostics Based on Blood Samples

Molecular diagnostics have allowed a great progress in medicine, but their use can be limited by the lack of guidelines for collection, handling, stabilisation and storage of biological samples. SPIDIA intends to develop a panel of pan-European external quality assurance schemes (EQAs) specifically designated for blood-derived DNA, cell-free DNA from plasma, and blood-derived RNA. The development of evidence-based quality guidelines for blood and plasma samples requires the identification of critical steps in pre-analytical procedures that need further improvement.

To reach this goal, SPIDIA performed ring trials for analysing the status quo of pre-analytical workflow standardisation in Europe. With support of the EFCC (European Federation of Clinical Chemistry and Laboratory Medicine, http://www.efcclm.eu/), a total of 322 applications have been collected from 219 laboratories in 30 different European countries.

SPIDIA DNA and DNAplas Ring Trials

The participating laboratories received blood or plasma samples, respectively, and extracted DNA from these samples by using their standard DNA extraction procedure. After spectrophotometric measurement of the extracted DNA, the laboratories sent this sample to the SPIDIA laboratory (University of Florence). There we quantified the DNA samples again by spectrophotometry and by real-time PCR, measuring the quantity of the single copy gene RNase P. In order to evaluate the DNA integrity of the DNA samples, another SPIDIA laboratory (QIAGEN GmbH) performed pulsed field gel electrophoresis analysis. Integrity of DNA extracted from plasma was analysed applying the Isohelix™ Quality Check Kit and the Agilent® DNA Kit. As an additional DNA quality parameter, the presence of interferences in the extracted DNA was evaluated by kinetic analysis using Kineret™ Version 1.0.5 software (Labonnet Ltd.). Amplification data of individual samples were used to calculate their kinetics distance (KD) from a defined reference set of samples.

SPIDIA RNA Ring Trial

In analogy to the DNA Ring Trials, the aims of the SPIDIA RNA Ring Trial were to determine the current status of the pre-analytical workflow for RNA-based analyses from blood samples, to discover problems within current workflows and to create evidence for the subsequent definition of guidelines, that improve the workflow for these blood samples. The participating laboratories received two blood samples collected in K_2EDTA or in PAXgene Blood RNA tubes carrying a cellular RNA profile stabilising solution, depending on the laboratories' standard practices. They were asked to extract RNA from this blood at different time points, following their internal procedures, and to send the RNA back to the SPIDIA laboratory

(University of Florence). There the RNA samples were analysed by pre-defined parameters to assess their quality: purity and total amount (by spectrophotometric measurement), integrity (by Agilent technology RIN evaluation), transcript levels of GAPDH, IL1 beta, IL8 and c-fos genes (by qPCR) and the presence of matrix interferences (by Kineret software).

Data Analysis and Next Steps

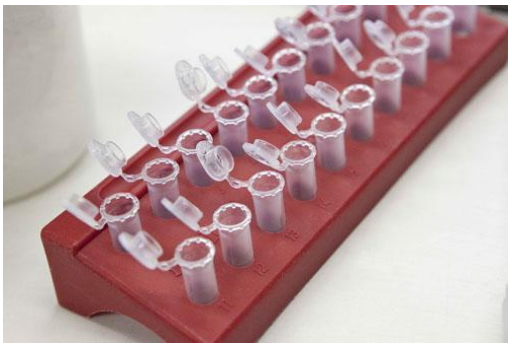
The data of all three ring trials were analysed correlating the pre-analytical variables, as e.g. storage temperature and used extraction methods, with the parameters associated to nucleic acid quality, as e.g. yield, purity, or integrity, in order to draw a first draft of evidence-based guidelines. Finally, we did a statistical evaluation of all gained data and generated a final report for the participants.

Based on the results of these SPIDIA Ring Trials, we are currently developing a first draft of evidence-based guidelines which will be included into a second set of Ring Trials, planned to test the improvement of the laboratory performance.

ANNOUNCEMENT: The second run of the three SPIDIA Ring Trials is now open for applications. Visit http://www.efcclm.eu/spidia/, where you can find more information and the application form. The participation is free. The deadline for applications is October 30, 2011.

Identification and Analysis of First Sample Quality Biomarker Sets Completed

RNA and Proteins in Tissue



One of the goals of SPIDIA is to find out which of the many pre-analytical factors during processing of clinical tissue specimen affects protein biomarkers most. Since the last newsletter, partners of SPIDIA have completed the analysis of a first set of tissues and applied targeted (reverse phase protein array) and non-targeted proteomic approaches (tandem mass spectrometry) to identify proteins and phosphoproteins that may change during tissue processing. The data are now ready to draft a manuscript for publication. Furthermore, Affymetrix® chip analysis was performed to analyse the stability of RNA during the pre-analytical phase. Regulated and stable RNA genes were identified and will be validated in the next months in order to identify possible sample RNA quality biomarkers to monitor the pre-analytical phase of tissue samples.

RNA in Blood

The primary objective for the blood quality biomarker group is to identify RNA biomarkers affected by pre-analytical variation in blood samples. We have identified and validated a set of biomarkers for monitoring pre-analytical variation of RNA in EDTA blood samples and in stabilized blood samples. Currently, we are planning an extended evaluation of the validity of the biomarkers in a large cohort of blood samples. Furthermore, to expand the number of biomarkers, additional candidates have been selected from a new microarray study and will be validated with qPCR in the next few months.

Metabolomics in Urine, Serum, Plasma, and Tissue

Low molecular weight molecules were identified that change most during the pre-analytical phase in freshly collected samples. The results will be used to put together metabolites into chemically coherent subsets, to assist interpretation of the undesired side-reactions occurring during tissue management within a clinical/biobank environment and provide input for the definition of reliable, validated and harmonized SOPs.

Development of an Integrated Workflow for the Processing of Human Blood Samples

Current workflows for processing of blood samples show a clear cut between the pre-analytical steps and the analytical steps of the *in vitro* diagnostic process. Pre-analytical systems typically integrate collection/transport, storage and extraction of the target biomolecules for the downstream analytical assay. There was no system available that integrates the pre-analytical steps and also the analytical assay. The aim of one of the SPIDIA work packages was to develop an integrated robotic system based on magnetic bead technology for low and medium throughput extraction of RNA from stabilised blood samples, which further integrates also the reaction setup for nucleic acids based assays into the pre-analytic workflow in order to standardize the whole process from sample collection to analysis.

Based on the existing QIAsymphony SP robotic sample preparation platform, QIAGEN developed a fully automated protocol for isolation of total RNA including miRNA from stabilized blood samples. The workflow requests only minimal human interaction and thus further standardises the pre-analytical sample handling for blood samples. The developed protocol generates ready to use RNA including miRNA for transcript analyses from stabilized blood samples. The next step in the workflow is the setup of the RT-PCR assay, which uses this RNA. Based on the new developed QIAsymphony AS robotic system, QIAGEN generated a reaction setup protocol that takes the isolated RNA and generates a complete mastermix for quantitative RT-PCR reactions.

Test of New Pre-analytical Tools and Guidelines in Biomarker Discovery Programs

Another SPIDIA work package aims at demonstrating the applicability of the standardised pre-analytical tools and procedures developed in the other work packages in biomarker discovery programs. Selected case examples include: *i*) the validation of the gene expression signature of Alzheimer's disease in whole blood, *ii*) the ability to distinguish Alzheimer's disease from other clinically overlapping forms of dementia and *iii*) the identification of a possible gene, microRNA expression and metabolic signature of colorectal cancer.

Within this frame, we used proton nuclear magnetic resonance (^{1}H-NMR) to profile the serum metabolome of 155 metastatic colorectal cancer (mCRC) patients and 139 healthy subjects from three Danish hospitals. Our findings establish that ^{1}H-NMR profiling of patient serum can provide a strong metabolomic signature of mCRC. The metabolomic signature derived from patients with mCRC predicts overall survival and provides insight into potential new biomarkers that can be used to predict disease progression and personalise treatment.

This work resulted so far in two publications:

Bernini P, Bertini I, Luchinat C, Nincheri P, Staderini S, Turano P. Standard operating procedures for pre-analytical handling of blood and urine for metabolomic studies and biobanks. J Biomol NMR. 2011 Apr;49(3-4):231-43.

Bertini I, Cacciatore S, Jensen BV, Schou JV, Johansen JS, Kruhøffer M, Luchinat C, Nielsen DL, Turano P. Metabolomic NMR fingerprinting to identify and predict survival of patients with metastatic colorectal cancer. *submitted*.

Development of Guidelines and Further Activities in Order to Harmonize Pre-Analytical Workflows

The advances achieved within the different work packages have enabled SPIDIA to start with the development of evidence-based guidelines. SPIDIA partner CEN (European Committee for Standardization in Brussels) has organised first international working group meetings in order to develop a European standard working draft document for the molecular *in-vitro* diagnostic pre-analytical phase.

SPIDIA also cooperates with organisations outside the diagnostic segment as the European Research Infrastructure BBBMRI (Biobanking and Biomolecular Resources Research Infrastructure, www.bbmri.eu).

In order to also evaluate possbilities of harmonizing pre-analytical workflows on a broader international level including regions outside Europe, SPIDIA cooperates with the US CLSI (Clinical and Laboratory Standards Institute, www.clsi.org), as well as with the US OBBR (Office of Biorepositories and Biospecimen Research, www.biospecimens.cancer.gov) within its caHUB (cancer Human Biobank) and BRN (Biospecimen Research Network) initiatives, e.g the NIH Common Fund program GTEx (Genotype Tissue Expression, www.commonfund.nih.gov/gtex/).

Lots of SPIDIA News Presented at the qPCR Symposium in Prague, June 13-17, 2011

The qPCR Symposium "Developments in Real-time PCR – From Preanalytics to Molecular Diagnostics" (http://www.qpcrsymposium.eu/) was arranged by SPIDIA partner TATAA during June 13–17 in Prague, Czech Republic. The event started with one day of workshops, including "SPIDIA: Towards the standardization of the preanalytical phase", followed by two days of seminars and two more days of workshops. The seminars were organized into two major tracts, "Circulating Tumor Cells – CTCs" and "Preanalytics and Standardization" that included several speakers from the SPIDIA consortium. The last two days of workshops included "SPIDIA: Sample preparation and quality control, Blood samples", "SPIDIA: Sample preparation and quality control, Tissue and other samples" and "SPIDIA: Invited speakers course" given by lecturers from the SPIDIA consortium. The symposium was very successful with more than 250 attendants from all over the world, and highly appreciated by both speakers and audience.

Talks given by SPIDIA partners during the symposium:

Uwe Oelmueller: Generic Pre-analytical Workflows: Challenges and Solutions

Mario Pazzagli: The Pre-analytical Phase for Molecular Methods in Blood Samples

Christian Viertler: The Impact of Tissue Pre-analytics on Molecular Analysis

Marcel Kap: How to Work with Biobanked Samples: The Possibilities and Impossibilities

Claudio Orlando: Altered Expression of MicroRNAs in Human Cancer: The Influence of Genetic and Epigenetic Factors
Ales Tichopad: Error in qPCR Quantification
Mikael Kubista: Single Cell Expression Profiling

Workshop "SPIDIA: Towards the Standardisation of the Preanalytical Phase"
On June 13, 2011, during the qPCR Symposium, SPIDIA partners met the laboratories participating in the DNA, DNAplas and RNA ring trials (see separate article above). SPIDIA speakers showed the results about the main procedures used by participant laboratories, described the aim of these three SPIDIA ring trials, the main pre-analytical variables and the parameters used to analyse the samples, and underlined the critical points concerning the first ring trials and sample analysis. Explanations were given about all details concerning the preparation of the SPIDIA-RNA, DNA and DNAplas shipping boxes, the procedures used to analyse the nucleic acid samples sent back from the participant laboratories, and set up of the SOPs for the Agilent RIN evaluation and spectrophotometric measurements. SPIDIA proposed a second ring trial to the participants to test the laboratories' improvements and to help SPIDIA to draw the definitive evidence-based guidelines.

SPIDIA Ethical, Legal and Social Topics

A dedicated SPIDIA work package takes care of the regulatory aspects and ethical topics involved in the exchange of human material for health care research purposes in the SPIDIA project. In addition, the work package is making the participating scientists more aware of the different ethical developments around research involving human materials. Therefore, the Project Ethical Committee (PEC) was set up consisting of one representative per participant in the SPIDIA project working with human and or animal material for research and the two international leading external specialists Ruth Chadwick (Cardiff University) and Anne Cambon-Thompson (INSERM).

Official documents were copied and sent to the PEC to monitor the official local rules are followed. Exchange of samples between the participants is performed on the OECI-TuBaFrost Code of Conduct (www.tubafrost.org). Next to that the PEC also created the SPIDIA ethical legal and social topics web page on http://www.spidia.eu to be transparent to the general public with the use of human and animal material for research.

In order to address the scientists awareness of the ethical developments, internal workshops on ethics were given for the SPIDIA consortium on the several occasions of the annual SPIDIA meetings involving our external advisors as experts, whereas also questionnaires were launched and participants documents concerning the SPIDIA projects ethics were further collected including the documents for the animal experiments.

The annual SPIDIA meeting in Prague contained a PEC workshop with the title "Ethics discovery discussions: Meet your neighbor". In this session several distinctive relationships with society, biobanking and regulation in which context the material is used were discussed. It became very clear for the attendees that regulatory issues were not the same as ethics. It is obligatory to follow the regulations, but not the ethics. The ethics, however, is not to be forgotten, including for instance transparency, which can enormously contribute to a positive attitude from the public. This positive attitude results in governments seeing no need to regulate the field stricter.

Where to meet us

SPIDIA Partners give regularly presentations about the project and their results on various congresses.

Past Events

- **2011 BRN Symposium:**
  March 28-29, 2011
  Bethesda, Maryland, USA
  Oral presentations:
  - Uwe Oelmüller: EU Project SPIDIA Update - Standardisation and Improvement of Generic Pre-analytical Tools and Procedures for *In Vitro* Diagnostics
  - Sibylle Gündisch: Investigating the Impact of Pre-Analytical Variables on Protein Quality of Human Tissue Samples

  Poster presentation:
  - Daniel Grölz: PAXgene Tissue: A New Tissue Fixation Technology for Simultaneous Preservation of Morphology and Nucleic Acids

  http://www.brnsymposium.com/

- **7th Symposium on Molecular Pathology and (Histo)Cytochemistry:**
  April 29-30, 2011
  Olomouc, Czech Republic
  Oral presentation:
  - Peter Riegman: Tissue Banking in Morphological and Molecular Diagnostics

  http://lmp.upol.cz/workshop2011/abstrakta_patologie.pdf

- **ISBER 2011 Annual Meeting&Exhibits:**
  May 15-18, 2011
  Arlington, Virginia, USA
  Oral presentation:
  - Marcel Kap: PAXgene Tissue System in Routine Pathology: Increase Biobanking Opportunities of the Pathology Archive

  http://www.isber.org/mtgs/2011/

- **IFCC-WorldLab Meeting:**
  May 15-19, 2011
  Berlin, Germany
  Oral presentations:
  - Uwe Oelmüller: EU Project SPIDIA - Standardisation and Improvement of Generic Pre-analytical Tools and Procedures for *In Vitro* Diagnostics
  - Kurt Zatloukal: Pre-Analytical Parameters Impacting on Tissue-Based Biomarkers
  - Mario Pazzagli: Evidence-based Quality Guidelines for the Pre-analytical Phase of Blood Samples

  http://www.berlin2011.org/

- **TIDES Conference 2011:**
  May 22-25, 2011
  Boston, Massachusetts, USA
  Oral presentations:
  - Uwe Oelmüller: Standardisation and Improvement of Generic Pre-analytical Workflows for Human Samples

  http://www.ibclifesciences.com/TIDES/overview.xml

- **German Society of Pathology (DGP) Annual Meeting 2011:**
  June 16-19, 2011
  Leipzig, Germany
  Oral presentation:
  - Sibylle Gündisch: Evaluation of PAXgene-fixed, Paraffin-embedded Tissues for Proteomic Applications

  http://www.pathologen-kongress.de/

- **23rd European Congress of Pathology (ECP 2011):**
  August 27-September 01, 2011
  Helsinki, Finland
  Poster presentations:
  - Christian Viertler: A New Technology for Simultaneous Preservation of Biomolecules and Morphology in Tissues
  - Marcel Kap: Implementation of the PAXgene Tissue System in Routine Pathology
  - Sibylle Gündisch: Impact of Delayed Fixation on Protein Profiles in Clinical Tissue Samples

  http://www.esp-congress.org/

- **MipTec Conference 2011:**
  September 19-22, 2011
  Basel, Switzerland
  Oral presentation:
  - Uwe Oelmüller: The SPIDIA Consortium on Preanalytical Sample Treatment

  http://www.miptec.ch/

- **Reverse Phase Protein Array Global Workshop:**
  October 10-11, 2011
  Houston, Texas, USA
  Poster presentations:
  - Sibylle Gündisch: Impact of Delayed Fixation on Protein Profiles in Clinical Tissue Specimen
  - Sibylle Gündisch: A Novel Fixative Allows Morphological and Molecular Analysis from the Same Clinical Tissue Specimen

  http://www.mdanderson.org/education-and-research/education-and-training/schools-and-programs/cme-conference-management/conferences/cme/conference-management-reverse-phase-protein-array-global-workshop.html

- **53rd Symposium of the Society for Histochemistry:**
  October 12-15, 2011
  Munich, Germany
  Oral presentation:
  - Sibylle Gündisch: Evaluation of PAXgene-fixed, Paraffin-embedded Tissues for Morphological and Molecular Analysis

  http://www.helmholtz-muenchen.de/histochemistry2011

Upcoming Events

- **ESBB Inaugural Conference:**
  November 16-19, 2011
  Marseille, France
  Oral presentation:
  - Uwe Oelmüller: EU Project SPIDIA - Standardisation and Improvement of Generic Preanalytical Tools and Procedures

  http://www.esbb.org/nov2011/

Fig. 3. SPIDIA Partners at the last SPIDIA meeting in April 2011 in Rotterdam, Netherlands.

Colophon
SPIDIA, QIAGEN GmbH - QIAGEN Strasse 1 - 40724 Hilden - Germany