



**UNIVERSITÄTS
KLINIKUM**
Jena

Institute of clinical chemistry and laboratory diagnostics

Integrated Biobank Jena

Lecture: Biobanking and Quality indicators

Quality indicators (QIs) in preanalytics of biospecimen
as a prerequisite for reliable findings in prospective
biomedical research

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Please contact me if you have any questions regarding this lecture or Biobanking/Preanalytics in general:

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Content

1. Biobanking and sample quality
2. Liquid sample heterogeneity
3. Critical preanalytics
4. Steps to high sample quality
5. Quality indicators (QIs)



Important

Lecture will be online

What is a biobank?



Cover Credit: Arthur Hochstein

“Think of it as an organic bank account. You put your biomaterial in and earn medical interest in the form of knowledge and therapies that grow out of that deposit – no monetary reward, just the potential that you might benefit from the accumulated data at some later date.” – Alice Park 2009

“The key to a powerful biobank is high-quality specimens from as wide a swath of the country's population as possible.”

What is a biobank?





Biorepository and Biobank – attempt of a definition

Biorepository

A facility that collects, catalogs, and stores samples of biological material, such as urine, blood, tissue, cells, DNA, RNA, and protein, from human, animals, or plants for laboratory research.

If the samples are from people, medical information may also be stored along with a written consent to use the samples in laboratory studies.

A biorepository facilitates the dissemination of specimens and the assurance of sample quality and related data.

Biobank

„...is a biorepository that accepts, processes, stores and distributes biospecimens and associated data for use in research and clinical care...“

Biospecimen – a quantity of tissue, blood, urine, or other biologically derived material.

Def. Biorepository – National Cancer Institute (NIH) – <https://biolincc.nhlbi.nih.gov/glossary>

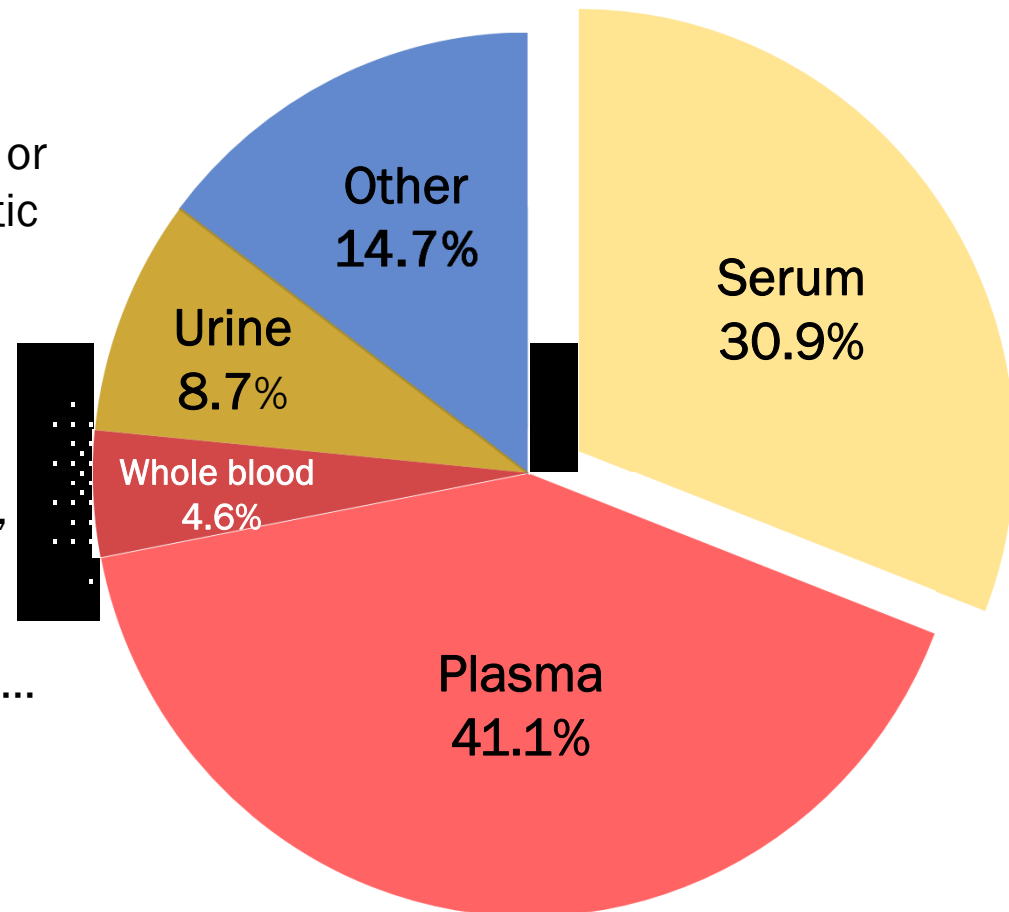
De Souza and Greenspan 2013 Biobanking past, present and future: responsibilities and benefits; doi:10.1097/QAD.0b013e32835c1244

Biospecimen in GBA (~ 16.94 Mio. „liquid“ samples)

Biobank samples originate from clinical/biomedical research studies or the clinical routine process (diagnostic laboratories)

Biospecimen stored in biobanks are diverse:
Blood (serum, plasma), Urine, Saliva, CSF, Sweat, Milk, Lacrimal, endometrial/peritoneal fluids, microdialysate, breath and volatiles ...

Tissue, cell cultures, DNA, RNA ...



<https://www.bbmri.de/ueber-gbn/german-biobank-alliance/>

Source: German Biobank Alliance 2020
~ 35 academic biobanks (2022)

What is most important for biobanks?



Quality of
Biospecimen



¹<https://www.freezerchallenge.org/fc-blog/blast-the-ice-jam1642359>

²<https://med.stanford.edu/news/all-news/2009/10/ice-age-over-sustainability-effort-targets-freezers.html>

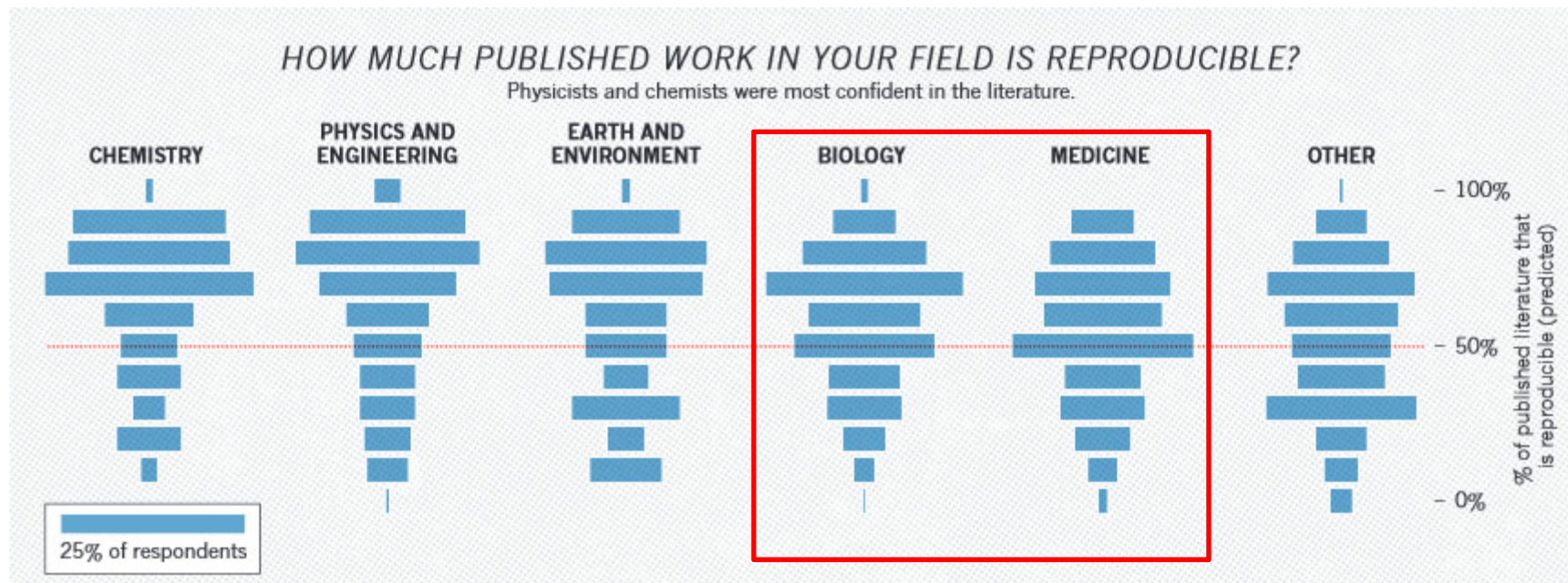
³<https://www.haus.de/leben/gefrierschrank-abtauen-22156>

⁴<https://freelims.org/blog/what-is-a-biobank.html>

⁵<https://www.biobanken-verstehen.de/was-sind-biobanken/>



Why do we need high-quality samples?



High-quality, well characterized human biological samples are crucial for **accurate diagnostics** in the clinical routine laboratory and for **reliable, conclusive, reproducible** biomedical research.

Baker, M.(2016), 1500 scientists lift the lid on reproducibility Nature volume 533, pages 452–454



What is a high-quality sample?

- What do you want to do with the samples? (**Fit-for-Purpose**, e.g. suitable sample for diagnostics or research)
- What **analysis/methodology** will you use? (Omic-Technologies, e.g. Next Generation Sequencing, Proteomics, Metabolomics; cell cultures still viable?)
- e.g. DNA extraction -> high yield of good-quality DNA from blood after 24 h storage at room temperature possible (1)
- e.g. for Metabolomics -> the metabolome at the time of extraction and analysis should reflect as closely as possible the original *in vivo* metabolome



It Depends!

(1) Lahiri DK, Schnabel B. DNA isolation by a rapid method from human blood samples: effects of MgCl₂, EDTA, storage time, and temperature on DNA yield and quality. *Biochem Genet* 1993;31:321- 8.

If it depends, how do we assess a high-quality sample?

What affects my samples/biospecimen?

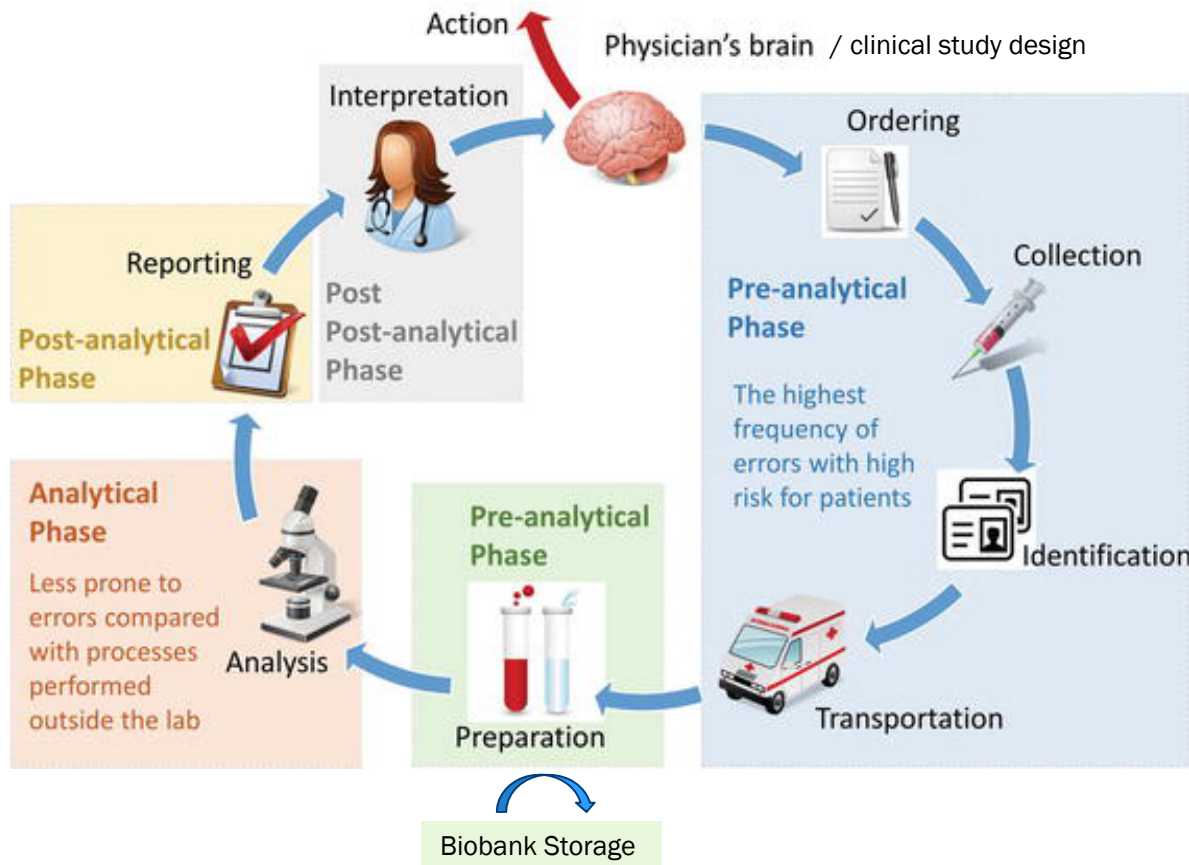


- Sample collection conditions
- Sample additives
- Transportation conditions
- Temperature
- Sample history

**Pre-analytical
Phase**



What is the Pre-analytical phase?



In the 70ies of the last century, the term “pre-analytical phase” was introduced in the literature.

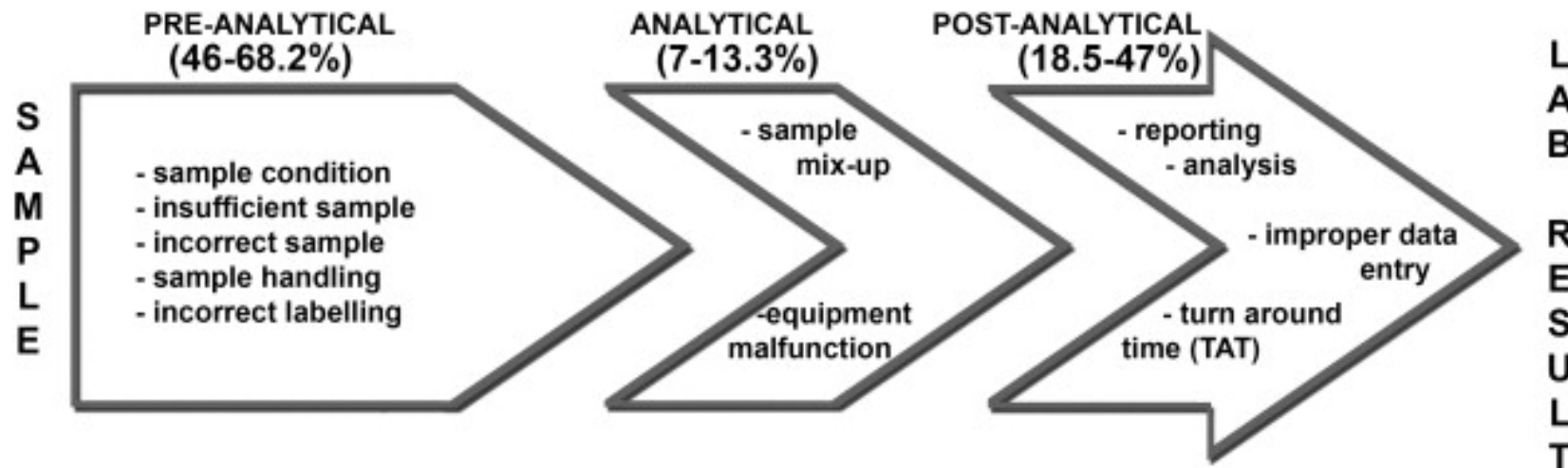
This term describes all **actions and aspects** of the “brain to brain circle” of the medical laboratory diagnostic procedure happening **before the analytical phase**.¹

Biobank samples originate from clinical/biomedical research studies or the clinical routine process (diagnostic laboratories).

¹Guder, W. G. (2014) **History of the preanalytical phase**: a personal view Biochem Med (Zagreb), 24(1): 25–30.

#Modified - Ramune Sepetiene, Raminta Sidlauskiene and Vaiva Patamsyte **Plasma for Laboratory Diagnostics (2018)** DOI: 10.5772/intechopen.76092

Errors in clinical studies and laboratory processes



- Diverse errors occur at every level of the health care system
- Pre-analytical variation constitutes the majority of laboratory errors
- Def. **Laboratory error**: ... is any defect from ordering tests to reporting results and appropriately interpreting and acting on these^{1,2}

¹Bonini PA, Plebani M, Ceriotti F, Francesca Rubboli F. Errors in laboratory medicine. Clin Chem 2002;48:691–8.

²ISO/WD TS 22367. Medical laboratories – reduction of error through risk management and continual improvement

Kalra, J. Kalra N., Baniak, N. (2013) Medical error, disclosure and patient safety: A global view of quality care. Clinical Biochemistry 46, 1161-1169

Errors in clinical studies and laboratory processes

Biological and Environmental variability

Collection

Venous blood collection - phlebotomy

Identification and Transport

Sample processing

Long-term storage



Errors in clinical studies and laboratory processes

| Step | Preanalytical variable | Recommendation |
|----------|---------------------------------|-------------------------------|
| Ordering | Ordering forgotten | Laboratory Information System |
| | Consent: none, improper, lost | Secure consent |
| | Typing error, improper labeling | Check Spelling |
| | Incorrect patient ID | Scan IDs, avoid manual typing |

- Errors have an impact on the quantity or quality of the biospecimens collected (e.g. sample can be incorrect, might be missed, collected in duplicate or even lost)
- Without / improper or lost consent can limit the analytical value of a sample



Preanalytics: Sources of sample heterogeneity

| | Study | A | B | C | D | E |
|-----------------|--|---|---|---|---|-------------------------------|
| Collection | <ul style="list-style-type: none"> - Subjects - Collection conditions | | | | | |
| Sample handling | <ul style="list-style-type: none"> - Temperature - Time Delays - Protocol variations - Transport | | | | | Pneumatic tube vs. |
| Storage | <ul style="list-style-type: none"> - Sample Count - Volume - Container type - Temperature | | | | | |

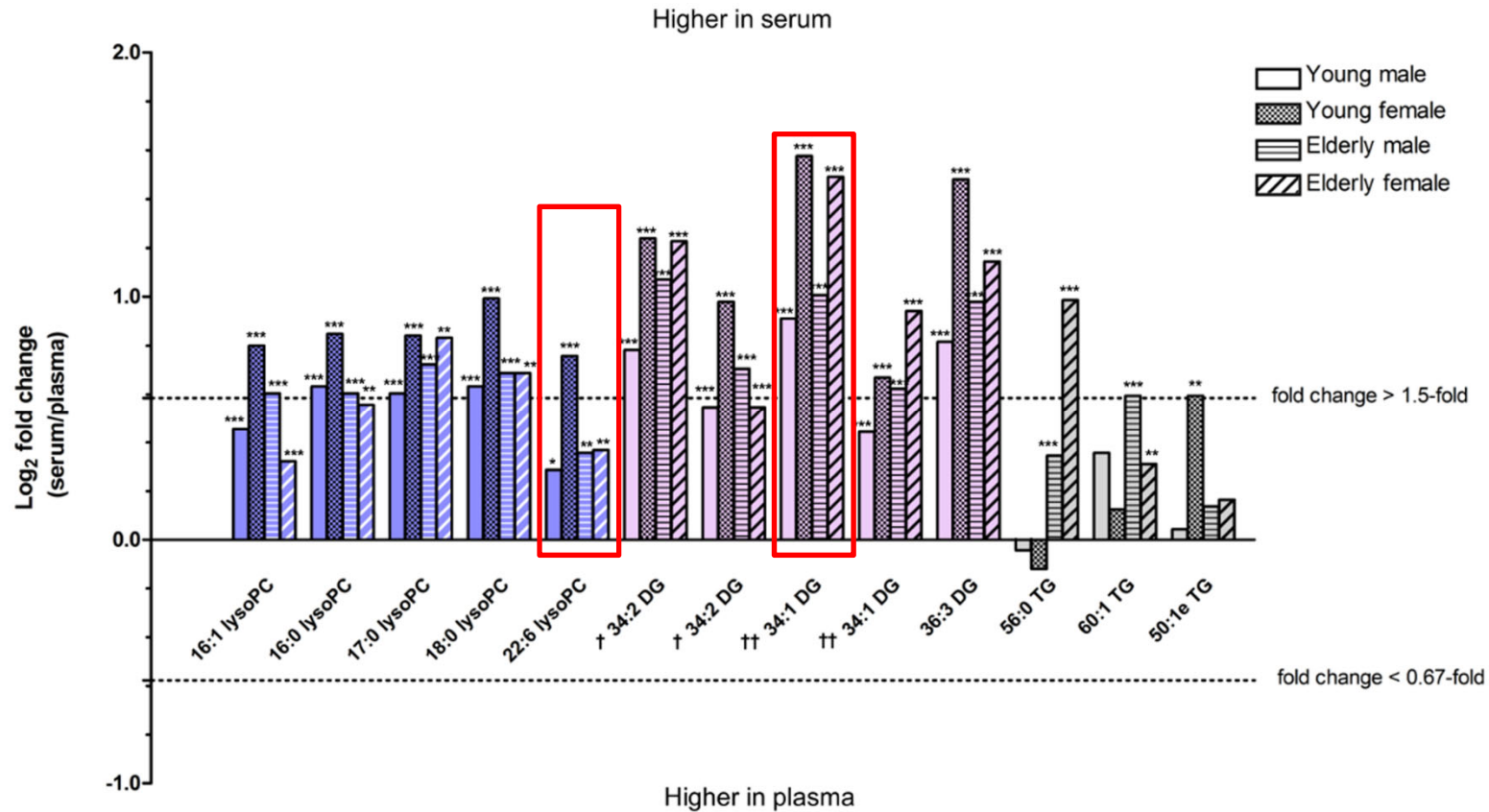


Biological and Environmental variability

| Factor | Preanalytical variable |
|---------------------------|--|
| Biological variability | Age, Sex, Ethnicity, Body mass index (BMI), Circadian and Diurnal rhythms |
| | Hormone status, Menstrual cycle, Pregnancy, Lactation, |
| | Circadian and Diurnal rhythms |
| | Fasting/Feeding, Diet, Drugs (Alcohol, Caffeine, etc.) Smoking, Hydration Status |
| Environmental variability | Seasonal changes, Temperature, Humidity, Moisture, Geographic location, Altitude, Sunlight |

¹Ellervik, C. *et al.* (2015) Preanalytical variables affecting the Integrity of human biospecimens in biobanking, *Clinical Chemistry* 61:7, 914-934

AGE

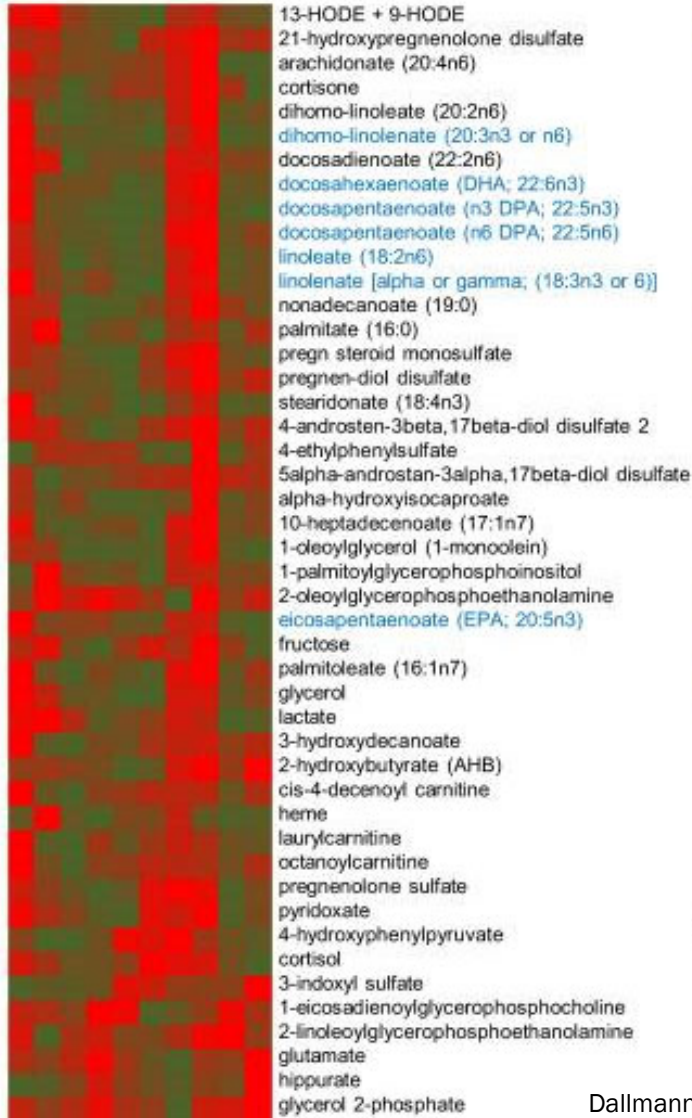


Differences in lipid metabolite levels in human blood samples between plasma and serum.

e.g. 22:6 lysoPC – altered in young females compared to young male, elderly males/females; 34:1 DG male/female

Time awake

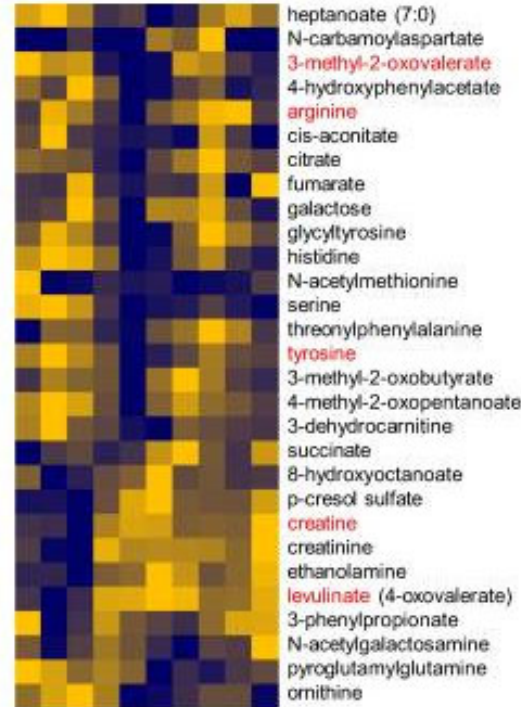
1 12 24 36 h



Plasma

Time awake

1 12 24 36 h



Saliva



Diurnal rhythm

The levels of nearly all lipid products were highest at midmorning to noon and were significantly lower at other times of the day.¹

- In plasma several lipids show a strong diurnal rhythm
- In saliva, largest group with diurnal rhythm were amino acids e.g. Arginine or Tyrosine

Dallmann, R. et al. (2012) The human circadian metabolome, Proc Natl Acad Sci U S A. 109(7): 2625–2629.



Collection

| Factor | Preanalytical variable | Recommendations |
|------------|--|---|
| Collection | Biological and Environmental variability | Follow evidence-based literature and guidelines for standardization; Study design |
| | e.g. Diurnal Rhythm | Fixed time of sample collection |
| | Incorrect collection (e.g. phlebotomy, puncture) | Educate and train staff and patients (training and E-learning) |
| | Collection device, Collection device age, Anatomical location of collection, Contamination of specimen, | Use the same tubes Check expiration date Sterile collection |
| | Tube material, additives | Correct tube for target analysis |
| | Sample Volume, Filling volume tubes | Proper for analysis According to manufacturer information |

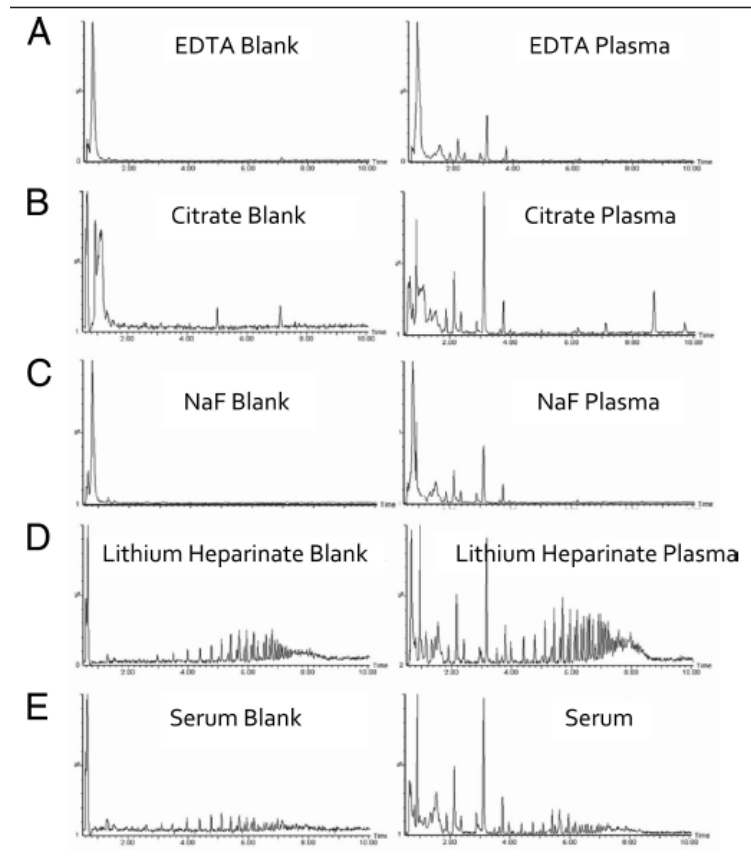


Fig. 1. Investigation of chemical noise arising from different blood collection tubes.

The blanks (50 g/L human albumin in normal saline) and blood samples were collected in commercial blood collection tubes with the following additives: (A), K⁺-EDTA; (B), Na⁺-citrate; (C), Na⁺-fluoride (NaF); (D), lithium-heparinate and (E), kaolin to enhance the generation of serum. (F), Mass spectra of chemical noise [(-CH₂CH₂O-)_n] detected in lithium-heparinate plasma, which exhibits typical polyethylene glycol clusters (38). Typical total ion chromatograms of blanks, plasma, and serum are given.

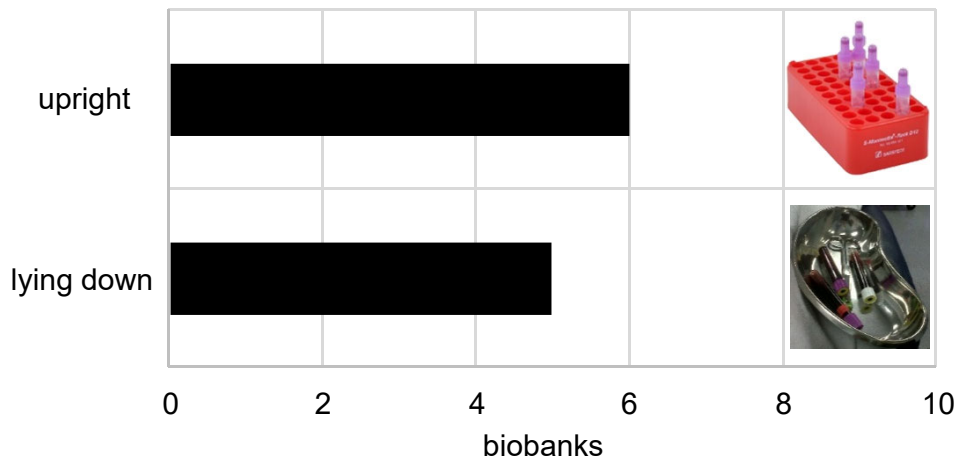
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Impact of Collection tube on Mass spectrometry

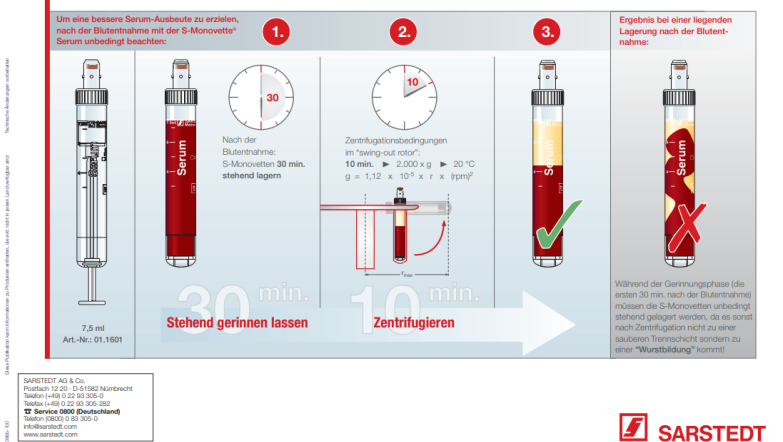
- Chemical background (in mass spectrometry) of blanks (50g/L human albumin in saline solution) and blood in different sample containers.
- Contaminants present in the blood collection tubes may affect the ionization process during an LC-MS run, thereby suppressing metabolite ionization and/or introducing interfering peaks

Improper handling of serum

Sample transport within locations



Produktinformation S-Monovette® Serum



Um eine bessere Serum-Ausbeute zu erzielen, nach der Blutentnahme mit der S-Monovette® Serum unbedingt beachten:

- 1.** Nach der Blutentnahme: S-Monovetten 30 min. stehend lagern. **30 min. Stehend gerinnen lassen**
- 2.** Zentrifugationsbedingungen im "swing-out rotor": 10 min. \rightarrow 2.000 x g \rightarrow 20 °C $g = 1,12 \times 10^{-5} \times r \times \text{rpm}^2$. **10 min. Zentrifugieren**
- 3.** Ergebnis bei einer liegenden Lagerung nach der Blutentnahme: **Während der Gerinnungsphase (die ersten 30 min. nach der Blutentnahme) müssen die S-Monovetten unbedingt stehend gelagert werden, da es sonst nach Zentrifugation nicht zu einer sauberen Trennschicht sondern zu einer "Wurstbildung" kommt!**

7,5 ml
Art.-Nr.: 01.1601

SARSTEDT

- Serum monovette should be stored upright, otherwise no clean phase separation occurs - "sausage formation" (danger: less yield, unclean collection of serum)



Venous blood collection - phlebotomy

| Preanalytical variable |
|--|
| Position of the patient (sitting or laying down) |
| Technical error such as placement of the tourniquet |
| Choice of container type and additive |
| Order of blood withdrawel to reduce carry-over effects |
| Filling volume of collection container, appropriate mixing |



Recommended order of draw







| According to Gurr ¹⁰ : | | | According to CLSI ¹¹ : | | |
|-----------------------------------|---------------|---------------------------------|-----------------------------------|---------------|---------------------------------|
| Based on BS 4851 (EU Code) | ISO 6710:2017 | | Based on BS 4851 (EU Code) | ISO 6710:2017 | |
| | | Blood culture | | | Blood culture |
| | | Serum/serum-gel blood | | | Citrate blood |
| | | Citrate blood | | | Serum/serum-gel blood |
| | | Heparin/heparin-gel blood | | | Heparin/heparin-gel blood |
| | | EDTA blood | | | EDTA blood |
| | | Fluoride/citrate-fluoride blood | | | Fluoride/citrate-fluoride blood |

¹⁰ Gurr et al.: Musterstandardarbeitsanweisung Präanalytik. J Lab Med 2011
¹¹ CLSI Procedures for the Collection of Diagnostic Blood Specimens by Venipuncture, Approved Standard 2007, 6th edition GP 41-A6 (former H3-A6), 27 (26)

Filling volume

S-Monovette® Wichtige Information zur Handhabung

Hinweis zum Füllvolumen

| | |
|---|---|
|  <p>Mischungsverhältnis von 1:10 beeinflusst unmittelbar das Analyseergebnis und muss eingehalten werden!</p> |  <p>Nennvolumen muss eingehalten werden, da sonst die erhöhte Fluoridkonzentration zu Hämolyse führt!</p> |
|  <p>Füllvolumen sollte mindestens 80% betragen gemäß ISO 6710 (1,2-2,0 mg EDTA/ml Blut!)</p> |  <p>Nennvolumen muss eingehalten werden, da das Mischungsverhältnis auf Grund der Flüssigkeitsmenge das Analyseergebnis beeinflusst!</p> |
|  <p>Mischungsverhältnis von 1:5 beeinflusst unmittelbar das Analyseergebnis und muss eingehalten werden!</p> |  <p>Mischungsverhältnis nicht wichtig, jedoch sollte das Volumen ausreichend für die Anforderungen sein, da sonst eine zweite S-Monovette® erforderlich wird!</p> |

Hinweis: Sorgfältig über Kopf schwenken

S-Monovetten **unmittelbar nach der Blutentnahme sorgfältig über Kopf schwenken!**


EDTA Citrat 1:10
Fluorid/Citrat-Fluorid BSG

Hinweis zur Lagerung

Die S-Monovetten Serum und Serum-Gel müssen während der Gerinnungsphase (die ersten 30 min. nach der Blutentnahme) **unbedingt stehend gelagert werden**, da es sonst nach Zentrifugation nicht zu einer sauberen Trennschicht, sondern zu einer „Wurstbildung“ kommt.

Barcode-Etikettierung

richtig *falsch*

 Füllvolumen sollte **mindestens 80%** betragen gemäß ISO 6710 (1,2-2,0 mg EDTA/ml Blut!)

According to ISO 6710 – filling volume should be **at least 80%**

Excerpt SOP – sampling location:

3. Sample processing

Per patient: 2 serum and EDTA monovettes full and 3 serum or EDTA monovettes half-full are collected and processed in the laboratory.

- Allow blood collection tubes to rest for 30 min after blood collection (make sure serum is clotted).

- Additive K-EDTA is present in twice the concentration
- Shear forces are greater with less volume -> risk of hemolysis (17% hemolytic samples)



Identification and Transport

| Factor | Preamerical variable | Recommendations |
|----------------|--|--|
| Identification | Correct assignment of the samples to the patients | Laboratory Information and Management System (LIMS) |
| | Correct assignment of the samples history | LIMS + accompanying documents |
| Transport | Environmental exposure Temperature Shear Force in pneumatic tubes | Fast, secure transport in suitable packaging to the laboratory/biobank Samples cooled? Track temperature Reduce transportation speed |

Unexpected high urine amylase activity¹

“In the 1960s, before operating a case with acute abdominal pain surgeons ordered to measure amylase in urine in order to exclude pancreatitis as a possible cause of the abdominal pain. After the amylase was increased, the operation was postponed, until continuous symptoms forced to operate. The surgeon said “When looking into the pancreas, there was no sign of pancreatitis, hence the amylase result must be wrong!”. Having no explanation, we asked the nurses to send several patient’s urine having no symptoms. Although most cases exhibited normal amylase activity, some again exhibited increased values. Having asked all persons involved in sampling and transport, it turned out that the nurses collecting and transferring the samples, sometimes held discussions close to the open vessels containing the urine that had to be delivered to laboratory. During this discussions, quite often drops of nurse’s spittle came into contact with the patient’s samples thus contaminating them with amylase from the nurse’s saliva!”

¹Guder, W. G. (2014) **History of the preanalytical phase:** a personal view Biochem Med (Zagreb), 24(1): 25–30.



Sample processing

| Factor | Preanalytical variable | Recommendations |
|------------|---|--|
| Processing | Processing Duration | Process rapidly, document date and time of processing |
| | Time from blood collection to centrifugation (TTC), Time from centrifugation to freezing (TTF) | Important for blood-based samples – document date and time of processing |
| | Centrifugation speed/force, time and temperature | According to manufacturers recommendations |
| | Temperature | temperature controlled laboratory |
| | Aliquotation (volume) in barcoded tubes | Aliquot to secondary tubes, multiple small volume aliquots instead of one large volume aliquot (readable unique 2D coded cryostable tubes) |



Long-term storage

| Factor | Preanalytical variable | Recommendations |
|-------------------|---|--|
| Long-term storage | Storage duration, temperature, facility | Store at -80°C or in the vapour phase of liquid nitrogen |
| | Freeze-thaw cycles | Avoid multiple freeze-thaw cycles, single-use aliquots only |
| | Cryotubes, labeling | Barcoded cryotubes suitable for ultra-low temperatures |

Pre-analytical phase - how do we assess a high-quality sample?



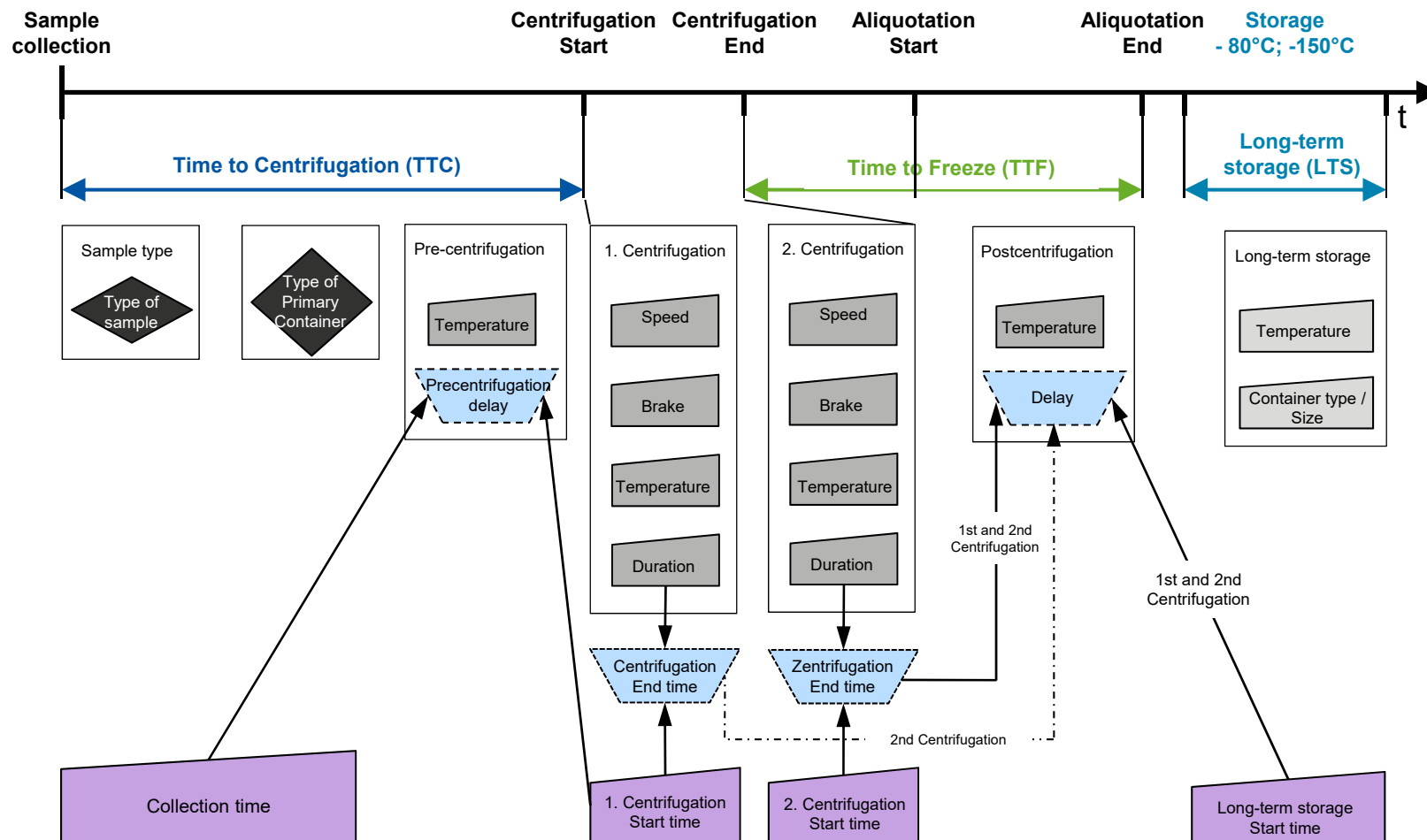
What would you do?



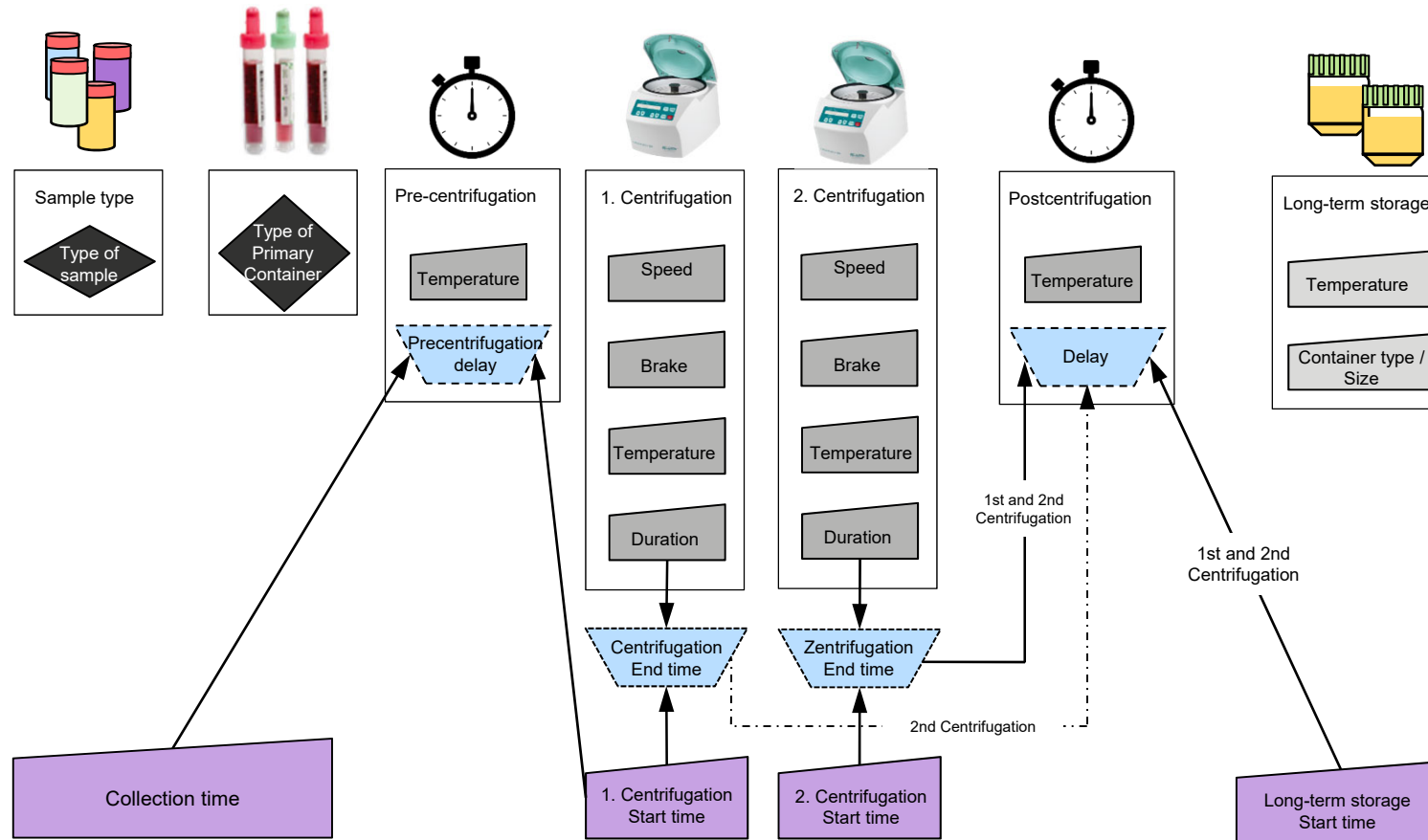
Steps to high sample quality

- Establishment of **standard operating procedures (SOPs)** for sample processing
- **Training of staff** in pre-analytical precautions during sample handling and implementation of SOPs
- Implementation of technical approaches in pre-analytical procedures – **electronic sample tracking**, electronic patient/study participant ID, **electronic time tracking** of pre-analytical processes
- **Synchronizing** of pre-analytical structures and processes between biobanks and clinics
- Mapping and documentation of sample history. Main pre-analytical parameters were included in a labeling system for sample collections in biobanks (**SPREC**),

SPREC – Sample PREanalytical Coding for biospecimen – an attempt to improve sample quality registration



SPREC – Sample PREanalytical Coding for biospecimen – an attempt to improve sample quality registration



SPREC2.0 for liquid samples (7 characters), example

SER-SST-A-A-N-B-A



SPREC – Sample PREanalytical Coding for biospecimen – an attempt to improve sample quality registration

SER-SST-A-A-N-B-A

Ser= Serum; SST = Serum separator tube with clot activator

TABLE 1. (CONTINUED)

| Type of sample | |
|--|-----|
| Density-gradient-centrifugation-separated mononuclear cells, viable | CEL |
| Fresh cells from nonblood specimen type | CEN |
| Cells from nonblood specimen type (e.g., ascites, amniotic), viable | CLN |
| Cord blood | CRD |
| Cerebrospinal fluid | CSF |
| Enriched (physicochemically) circulating tumor cells | CTC |
| Dried whole blood (e.g., Guthrie cards) | DWB |
| Nasal washing | NAS |
| Density-gradient-centrifugation-separated mononuclear cells, nonviable | PEL |
| Cells from nonblood specimen type (e.g., ascites, amniotic), nonviable | PEN |
| Pleural fluid | PFL |
| Dental pulp | PLP |
| Plasma, single spun | PL1 |
| Plasma, double spun | PL2 |
| Red blood cells | RBC |
| Saliva | SAL |
| Semen | SEM |
| Serum | SER |
| Sputum | SPT |
| Stool | STL |
| Synovial fluid | SYN |
| Tears | TER |
| 24 h urine | U24 |
| Urine, random ("spot") | URN |
| Urine, first morning | URM |
| Urine, timed | URT |
| Other | ZZZ |

TABLE 1. (CONTINUED)

| Type of primary container | |
|--|-----|
| Nonaldehyde-based stabilizer for cell-free nucleic acids | SCK |
| Sodium EDTA | SED |
| Sodium heparin | SHP |
| Sodium citrate | SND |
| Serum separator tube with clot activator | SST |
| Tempus® tube | TEM |
| Trace elements tube | TRC |
| Unknown | XXX |
| Other | ZZZ |

| Precentrifugation (delay between collection and processing) | | | |
|---|---------------------------|---|--|
| RT | <30 min | A | |
| 2°C–10°C | <2h | A | |
| 2°C–10°C | <2h | B | |
| RT | 2–4h | C | |
| 2°C–10°C | 2–4h | D | |
| RT | 4–8h | E | |
| 2°C–10°C | 4–8h | F | |
| RT | 8–12h | G | |
| 2°C–10°C | 8–12h | H | |
| RT | 12–24h | I | |
| 2°C–10°C | 12–24h | J | |
| RT | 24–48h | K | |
| 2°C–10°C | 24–48h | L | |
| RT | >48h | M | |
| 2°C–10°C | >48h | N | |
| >35°C | >2h | O | |
| Unknown | | X | |
| Other | | Z | |
| Centrifugation | | | |
| RT 10–15 min | <3000 g no braking | A | |
| RT 10–15 min | <3000 g with braking | B | |
| 2°C–10°C 10–15 min | <3000 g no braking | C | |
| 2°C–10°C 10–15 min | <3000 g with braking | D | |
| RT 10–15 min | 3000–6000 g with braking | E | |
| 2°C–10°C 10–15 min | 3000–6000 g with braking | F | |
| RT 10–15 min | 6000–10000 g with braking | G | |
| 2°C–10°C 10–15 min | 6000–10000 g with braking | H | |
| RT 10–15 min | >10000 g with braking | I | |
| 2°C–10°C 10–15 min | >10000 g with braking | J | |
| RT 30 min | <1000 g no braking | M | |
| No centrifugation | | N | |
| Unknown | | X | |
| Other | | Z | |
| Second centrifugation | | | |
| RT 10–15 min | <3000 g no braking | A | |
| RT 10–15 min | <3000 g with braking | B | |
| 2°C–10°C 10–15 min | <3000 g no braking | C | |
| 2°C–10°C 10–15 min | <3000 g with braking | D | |
| RT 10–15 min | 3000–6000 g with braking | E | |
| 2°C–10°C 10–15 min | 3000–6000 g with braking | F | |
| RT 10–15 min | 6000–10000 g with braking | G | |
| 2°C–10°C 10–15 min | 6000–10000 g with braking | H | |
| RT 10–15 min | >10000 g with braking | I | |
| 2°C–10°C 10–15 min | >10000 g with braking | J | |
| No centrifugation | | N | |

| Postcentrifugation delay | | | |
|----------------------------|-----------------------|---|--|
| <1 h 2°C–10°C | | A | |
| <1 h RT | | B | |
| 1–2 h 2°C–10°C | | C | |
| 1–2 h RT | | D | |
| 2–8 h 2°C–10°C | | E | |
| 2–8 h RT | | F | |
| 8–24 h 2°C–10°C | | G | |
| 8–24 h RT | | H | |
| 24–48 h 2°C–10°C | | I | |
| 24–48 h RT | | J | |
| >48 h RT | | M | |
| Not applicable | | N | |
| Unknown | | X | |
| Other | | Z | |
| Long-term storage | | | |
| PP tube 0.5–2 mL | (–85) to (–60)°C | A | |
| PP tube 0.5–2 mL | (–85) to (–135)°C | B | |
| PP tube 0.5–2 mL | <–135°C | V | |
| Cryotube® 1–2 mL | LN | C | |
| Cryotube® 1–2 mL | (–85) to (–60)°C | D | |
| Cryotube® 1–2 mL | Programmable freezing | E | |
| | to <–135°C | | |
| Plastic cryo straw | LN | F | |
| Straw | (–85) to (–60)°C | G | |
| Straw | (–35) to (–18)°C | H | |
| Straw | Programmable freezing | I | |
| | to <–135°C | | |
| PP tube ≥5 mL | (–85) to (–60)°C | J | |
| PP tube ≥5 mL | (–35) to (–18)°C | K | |
| Microplate well | (–85) to (–60)°C | L | |
| Microplate well | (–35) to (–18)°C | M | |
| Cryotube® 1–2 mL | LN after temporary | N | |
| | (–85) to (–60)°C | | |
| Plastic cryo straw | LN after temporary | O | |
| | (–85) to (–60)°C | | |
| Paraffin block | RT or 2–10°C | P | |
| Paraffin block | (–35) to (–18)°C | U | |
| Bag | LN | Q | |
| Dry technology medium | RT | R | |
| PP tube 40–500 µL | (–85) to (–60)°C | S | |
| PP tube 40–500 µL | (–35) to (–18)°C | T | |
| PP tube 40–500 µL | <–135°C | W | |
| Original primary container | (–35) to (–18)°C or | Y | |
| | (–85) to (–60)°C | | |
| Unknown | | X | |
| Other | | Z | |

A= Precentrifugation delay < 2 h RT
 A= 1st Centrifugation RT 10 – 15 min < 3000 g, no braking
 N= no 2nd Centrifugation
 B= Postcentrifugation time < 1 h RT
 A= long-term storage in PP (polypropylen) tube 0.5 – 2 mL (–85 °C –60 °C)

Lehmann et al. 2012 Biopreservation and Biobanking, DOI:10.1089/bio.201200012

Betsou et al. 2018 Standard PREanalytical Code Version 3.0 BIOPRESERVATION AND BIOBANKING 16, DOI: 10.1089/bio.2017.0109



SPREC – Sample PREanalytical Coding for biospecimen – an attempt to improve sample quality registration

- SPREC system was established to increase transparency of sample history
- Contributes to a consistent sample coding and documentation in biobanks
- It forms the basis for the establishment of standard operating procedures (SOPs) for sample handling processes in laboratories and/or biobanks
- Two different SPREC codes – liquid and solid samples

Are all samples now of high quality?

What about older samples?



What should we do with?



- Biospecimens from pre-existing collection
- Rare biospecimens from patients with rare diseases
- Biospecimen with an insufficient sample history

Retrospective analysis



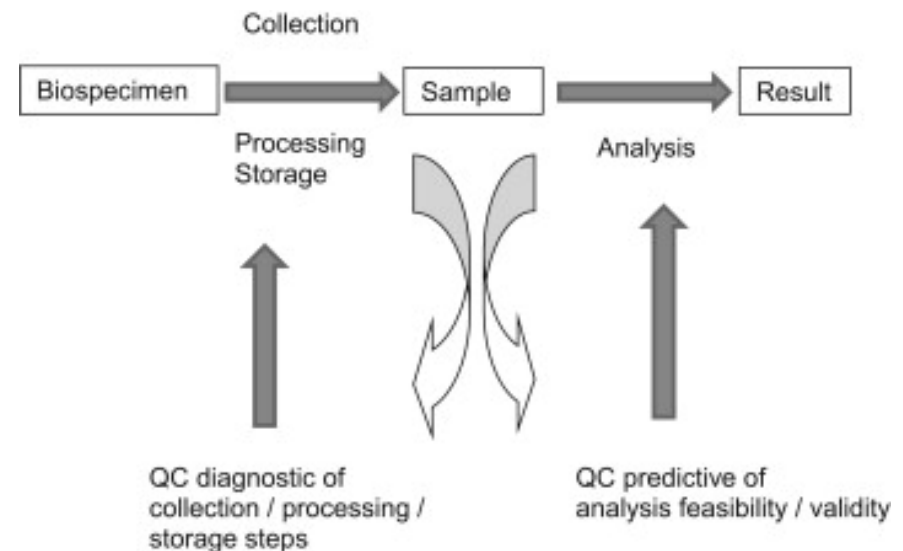
Quality indicators (QI) for biospecimen

Def. QIs are biomolecules used as tools for quality assessment of biospecimen

Categories:

Diagnostic: assess the processing steps of the biospecimen, such as delay of processing or storage conditions

Predictive: assess the feasibility and/or reliability of the downstream analysis (successful method performance)





Selection of Quality Indicators: Challenges/Criteria

- QIs should be characteristic for **one specific pre-analytical** condition
 - e.g. pre-analytical time delay, handling temperature, freeze-thaw cycles, long-term storage, ambient handling/storage temperature
- monitoring the most important common pre-analytical variations
- QIs should be **unaffected by confounders** such as
 - sample additives
 - certain disease states and/or
 - clinical conditions and/or
 - therapeutic interventions and/or
 - other confounders
- **Precise, robust, reproducible**
- QIs should be quantified at **moderate costs** and **require only minimal sample volume**

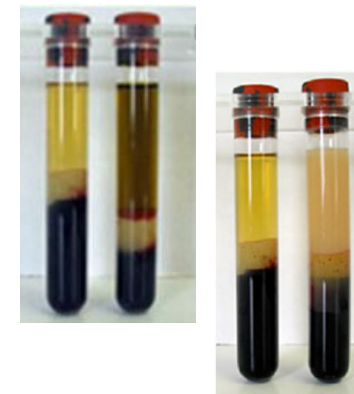
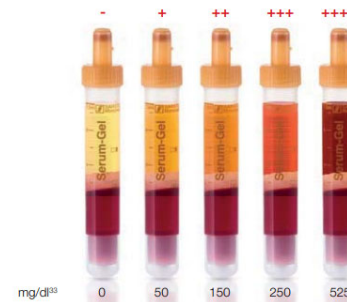


HIL-index: quality assessment in routine laboratory applications

HIL-index (Hemolysis, Icterus (Hyperbilirubinemia), Lipemia-Index) in human liquid biospecimens

Causes of HIL-positive samples:

- Hemolytic:* long application tourniquet, mechanical stress on erythrocytes...
- Icteric:* increased bilirubin concentration (yellow/brown sample)
- Lipemic:* high triglyceride concentration (white haze)



Consequences of HIL-positive samples: Biases in clinical diagnosis, interference with other assays

Analysis: quantification of hemoglobin, bilirubin and triglyceride concentration by automated absorption measurement (absorption spectrum: 500-804 nm)

Metabolomics as resource for quality indicators

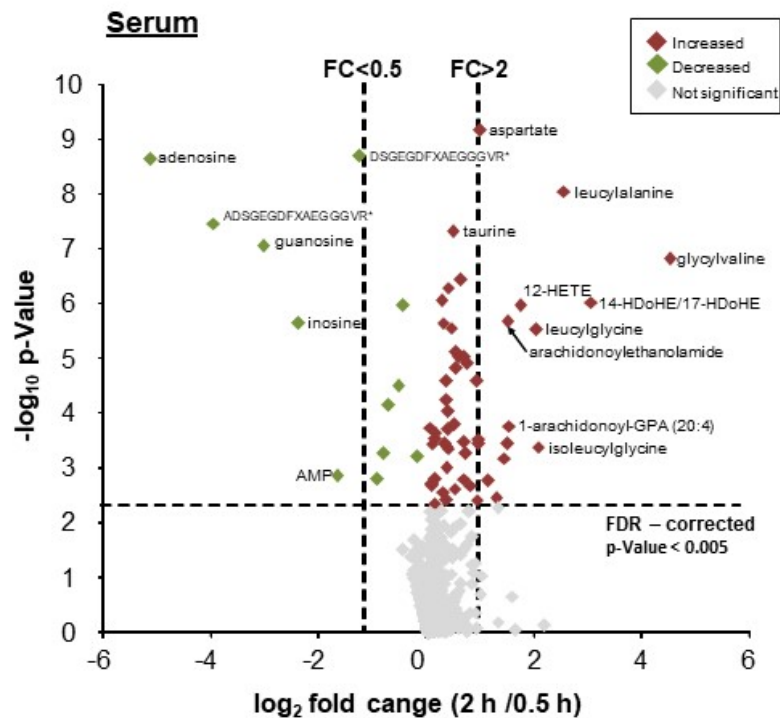
- Metabolomics = basis for establishment of individual phenotypes (biomarkers indicating diseases, nutritional status ...)
- Metabolome mirrors variations within the human body
- Concentration changes of metabolites are mainly due to cellular activities of blood cells and these changes reflect pre-analytical variation in biospecimens
- Several metabolites were identified as QI candidates for the discrimination of individual sample quality
- Need for consistent sample quality and storage conditions in Biobanks for reliable metabolomics analyses/biomarker identification

Obstacles:

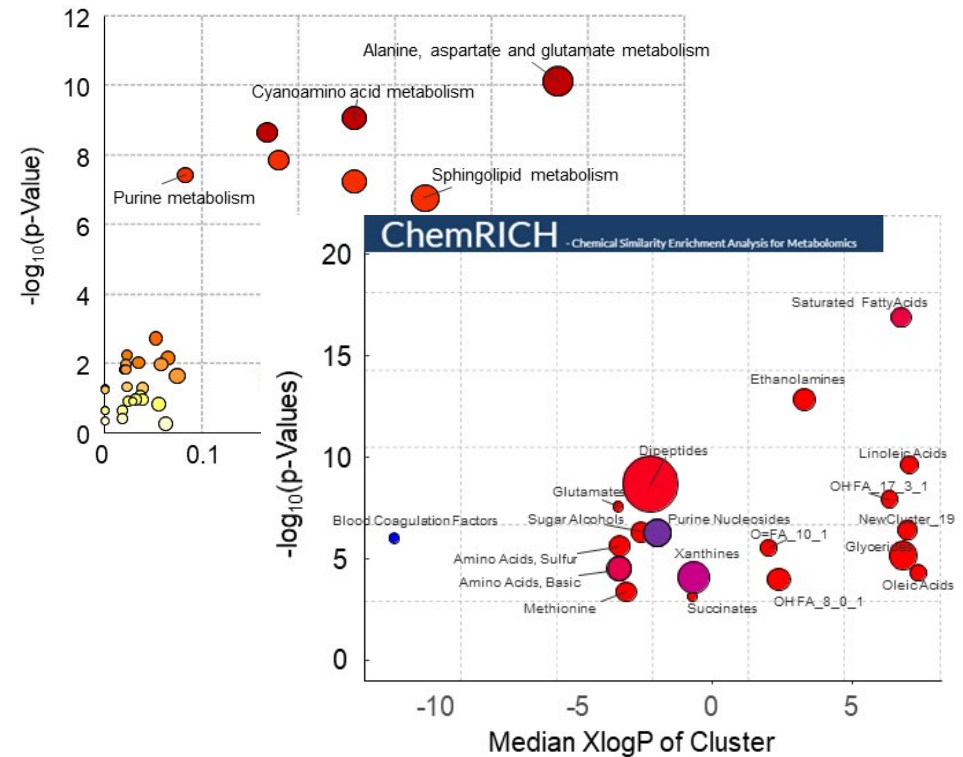
- Heterogeneous sampling and biobanking processes
- Not all biospecimen are well studied (saliva, feaces)

Metabolomics as resource for quality indicators

Metabolite profiling of human serum



Level of significance is $p < 0.05$ (paired T-test). FDR correction was applied using the Benjamini and Hochberg method*. Asterisks indicate putatively identified metabolites. (N=10)



- Metabolites were used for Pathway Enrichment and Chemical Similarity Enrichment Analysis to map individual altered pathways and cluster compounds based on chemical similarity to identify potential quality markers

Metabolomics as resource for quality indicators

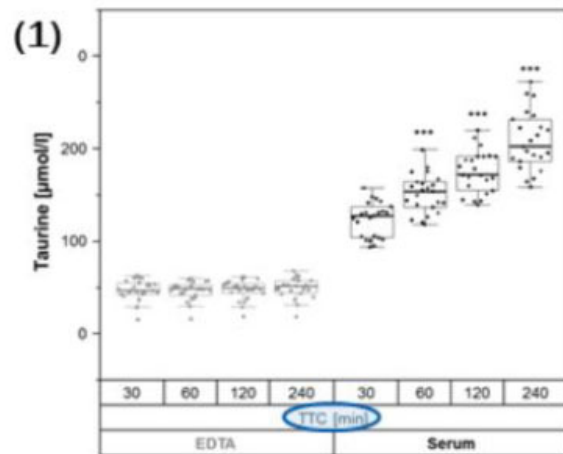
Table 3. Proposed QIs to be considered for further investigation in serum and EDTA plasma.

| Potential QIs in Serum | Median Opt. Cutoff | Specificity n+/n > 1 h | Sensitivity 1-(n-/n) < 1 h |
|------------------------------|--------------------|------------------------|----------------------------|
| HG-ratio | 1.41 | 79% (11/14) | 85% (22/26) |
| XI-ratio | 2.06 | 100% (14/14) | 73% (19/26) |
| | | Specificity n+/n > 2 h | Sensitivity 1-(n-/n) < 2 h |
| Tetranor-12(S)-HETE | 0.45 ng/mL | 92% (12/13) | 100% (7/7) |
| 12(S)-HEPE | 8.17 ng/mL | 100% (13/13) | 86% (6/7) |
| 8(S)-HETE | 2.22 ng/mL | 100% (13/13) | 86% (6/7) |
| 12-HETE | 15.14 ng/mL | 92% (12/13) | 86% (6/7) |
| 12-oxo-EETE | 2.62 ng/mL | 100% (13/13) | 86% (6/7) |
| Potential QIs in EDTA Plasma | Median Opt. Cutoff | Specificity n+/n > 1 h | Sensitivity 1-(n-/n) < 1 h |
| HI-ratio | 1.54 | 85% (11/13) | 81% (22/27) |

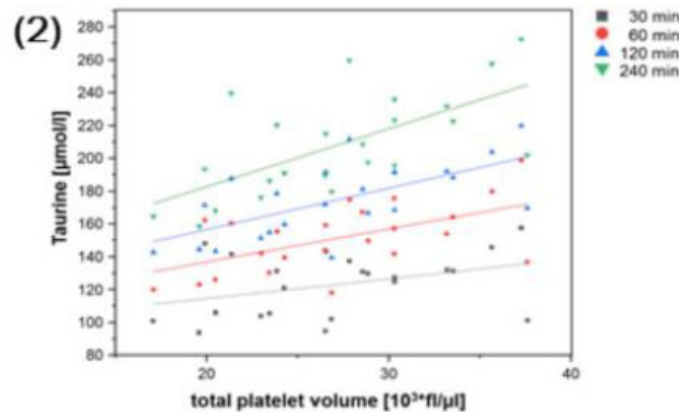
The table displays the calculated median optimal cutoffs for all considered QIs in validation sample 1 and 2 in serum and EDTA plasma and applies them in validation sample 3 and 4. n+, measurements with a positive test result; n-, measurements with a negative test result; n > 1 h, 2 h measurements with a TTC > 1 or 2 h; n < 1 h, 2 h, measurements with a TTC < 1 or 2 h.

- HG (hypoxanthine/guanosine)-ratio and XI (xanthine/inosine)-ratio were identified to discriminate with high sensitivity and specificity a TTC > 1 h in serum
- Several eicosanoids were identified to discriminate with high sensitivity and specificity a TTC > 2 h in serum

Taurine as serum specific indicator of TTC delay



- concentration increase during serum sample storage (1)
- correlation between individual platelet count and volume (MPV) and Taurine (2)
- Taurine quantification via LC-MS/MS, ion-exchange chromatography



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Metabolome: source for potential Quality indicators – a current selection from the literature

| Serum (tested pre-analytical conditions) | EDTA-Plasma (tested pre-analytical conditions) |
|---|---|
| Amino acids/derivatives/amino acid-scores | |
| Arginine (TTF ¹) | Arginine (TTF ¹ , Temperature ¹) |
| Ornithine (TTF ¹) | Ornithine (TTC ² , TTF ¹ , Temperature ¹) |
| Aspartate (TTC ^{2,3,4} , TTF ¹) | Aspartate (TTF ^{1,4} , Temperature ¹) |
| Glycine (TTF ¹) | 5-Oxo-proline (TTC ¹¹) |
| Taurine (TTC ³) | |
| other metabolites | |
| Glucose (TTC ⁴ , TTF ⁷) | Glucose (TTC ⁴ , TTF ^{5,7}) |
| Pyruvate (TTC ⁴) | Lactate (TTC ⁴ , TTF ⁵ , Temperature ^{5,6}) |
| LysoPC C18:0 (TTF ⁹ , Temperature ⁹) | LysoPC C18:0 (TTF ^{1,2,8} , Temperature ^{1,2,8}) |
| LysoPC C18:1 (TTF ⁹ , Temperature ⁹) | Ascorbate/Ascorbic Acid (TTC ¹² , Temperature ⁶) |
| α-Ketoglutarate (TTC ⁴) | α-Ketoglutarate (TTC ⁴) |

References: next slide

Literatur additions

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²Kamlage et al., 2014, Clinical Chemistry 60:2, DOI: 10.1373/clinchem.2013.211979

³Kamlage et al., 2018, Metabolites, 8, 6, doi:10.3390/metabo8010006

⁴Liu et al., 2010, Analytical Biochemistry, 406, doi:10.1016/j.ab.2010.07.015

⁵Malm et al., 2016, Biobanking and Biopreservation, Vol. 14, No. 5, DOI: 10.1089/bio.2015.0092

⁶Trezzi et al., 2016, Metabolomics, 12:96, DOI 10.1007/s11306-016-1038-1

⁷Boyanton et al., 2002, Clinical Chemistry, 48:12

⁸Yang et al., 2013, Analytical Chemistry, 85, DOI 10.1007/s11306-016-1038-1

⁹Anton et al., 2015, Plos One, doi:10.1371/journal.pone.0121495

¹⁰Betsou et al., 2013, JMD Vol.15, No. 1; <http://dx.doi.org/10.1016/j.jmoldx.2012.06.008>

¹¹Jain et al., 2017, Clinica Chimica Acta, 466, <http://dx.doi.org/10.1016/j.cca.2017.01.005>

¹²Karlsen et al., 2007, European Journal of Clinical Nutrition, 61

Educational objectives

1. What is biobanking and why is it important?
2. Sample quality
3. Preanalytical Source of Errors?
4. SPREC? Function and Components of SPREC
5. Steps to a high sample quality
6. Quality indicators: Definition, Requirements/confounding factors, examples