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CEBP Focus: Biomarkers and Biospecimens

Hypothesis/Commentary

Standard Preanalytical Coding for Biospecimens: Defining the Sample PREanalytical Code

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Abstract

Background: Management and traceability of biospecimen preanalytical variations are necessary to provide effective and efficient interconnectivity and interoperability between Biobanks.

Methods: Therefore, the International Society for Biological and Environmental Repositories Biospecimen Science Working Group developed a "Standard PREanalytical Code" (SPREC) that identifies the main preanalytical factors of clinical fluid and solid biospecimens and their simple derivatives.

Results: The SPREC is easy to implement and can be integrated into Biobank quality management systems and databases. It can also be extended to nonhuman biorepository areas. Its flexibility allows integration of new novel technological developments in future versions. SPREC version 01 is presented in this article.

Conclusions and Impact: Implementation of the SPREC is expected to facilitate and consolidate international multicenter biomarker identification research and biospecimen research in the clinical Biobank environment. *Cancer Epidemiol Biomarkers Prev; 19(4); 1004–11. ©2010 AACR.*

Introduction

A sample stored in a Biobank is a representation of and contains implicit information about the real world. The more precise the recording of processing variables throughout the sample's life span, the more accurate and extensive is the extraction of explicit information when this is required for clinical or research purposes.

The effect of preanalytical procedures on the biomolecular information extracted from specimens stored in research Biobanks is well recognized (1) and "biospecimen research" has emerged to clarify further the cellular and molecular alterations attributed to preanalytical processes (2). These are defined as those procedures that take place between specimen collection and experimental analysis. Understanding the effects of preanalytical factors on sample variation is critical, particularly for clinical research projects using biological specimens derived by more than one collection procedure or center (2). Standardization of biobanking procedures is challenging; however, the standardization of preanalytical processes within clinical settings presents equivalent, sometimes-overlooked challenges for which communication and harmonization tools are needed. The idea of "quality" with respect to biosamples cannot be uniquely defined because the processing conditions that optimize a specimen for use may vary according to the tests to be carried

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out. Managing samples to make them suitable for specific tests is a research goal that can be pursued only if these conditions are carefully traced. Therefore, harmonization of methods to trace preanalytical information is a necessary condition for the development of large-scale research involving samples from different settings.

It is envisaged that the application of a preanalytical sample code will facilitate a more effective interlaboratory and intralaboratory specimen use by scientists from different Biobanks supplying samples for common research (3) and validation exercises (4). This article presents for the first time a Sample PREanalytical Code (SPREC) that, akin to a "specimen barcode," provides details about preanalytical sample processing. It is envisaged that the SPREC will help researchers and biobankers identify and communicate the most important preanalytical variables associated with each specimen. The SPREC is intended to serve as a code that will become recognized internationally within the clinical biobanking sector; its wider application for nonclinical biospecimens is also discussed.

Standard Coding of Preanalytical Procedures

Presented here is the global SPREC code (Tables 1 and 2), a coding system based on the standard preanalytical options which have recently been published for biospecimen research purposes (2). Each biospecimen is assigned a seven-element-long code that corresponds to seven preanalytical variables and contains a string of 11 (for fluids) or 13 (for solid tissues) letters in a defined order, separated by six hyphens. Wherever possible, we make use of the existing Laboratory Data Management System (LDMS) codes (5) for the sample types and the primary container types. In contrast to the LDMS that mainly includes sample types and primary container types relevant to the clinical laboratory, the SPREC includes, not only the main sample and collection types encountered by biobanks, but also the sample processing types constituting the entire preanalytical chain. If the preanalytical option used is unknown or inconstant, the letter "X" is used. If the preanalytical option used is known but does not correspond to any of the standard options, the letter "Z" is used. Because this code is applied to a sample during the processing and labeling procedure and before freezing of the aliquots, information on the number of freeze-thaw cycles and storage duration is not provided. The code can be linked to all aliquots of the corresponding sample and it will allow immediate assessment of each preanalytical step. The SPREC is expected to have particular value for multipartner validation and quality control and the execution of multicenter projects (e.g., involving proteomic, genomic, and Barcode of Life studies).

The first element of the SPREC code corresponds to the biospecimen type. The SPREC can be applied to different types of primary samples and their simple derivatives. Primary samples are defined as specimens directly collected from the donor (e.g., whole blood, urine, and solid tissue). Simple derivatives are defined as the samples prepared through a simple laboratory manipulation (e.g., after centrifugation of collection tubes or mechanical disruption of tissues) without the addition of chemical substances by the laboratory technician and without cell disruption or cell selection as part of a multistep process. Although somewhat arbitrary, to keep the coding functional, those derivatives whose isolation requires usage of multiple steps and/or addition of chemical substances by the technician are defined as complex derivatives and are not covered by SPREC (e.g., nucleic acids, proteins, lipids, sorted cells, cultured cells, immortalized cells).

The SPREC elements applicable to fluid biospecimens (supernatants and/or fluid-derived cells) are the following (see Table 1):

First code element: type of sample
Second code element: type of primary container
Third code element: precentrifugation
Fourth code element: centrifugation
Fifth code element: second centrifugation
Sixth code element: postcentrifugation
Seventh code element: storage condition

The SPREC elements applicable to solid tissue or tissue-derived cytologic biospecimens are the following (see Table 2):

First code element: type of sample
Second code element: type of collection
Third code element: warm ischemia time
Fourth code element: cold ischemia time
Fifth code element: fixation type
Sixth code element: fixation time
Seventh code element: storage condition

Examples:

Based on the adoption of the SPREC, reference preanalytical processing methods can be recommended in the professional Guidelines or Best Practices (6). Examples of future potential reference preanalytical processing may be the following (see also, Table 3):

- Serum specimen
  SER-SST-A-E-N-A-G. This corresponds to a serum (SER) specimen that has been collected from a serum collection tube (SST), whose precentrifugation delay is <2 hours at room temperature (A); centrifugation has been done at ambient temperature at 3,000 to 6,000 g with braking (E). Only one centrifugation step was done (N) and the delay between centrifugation and freezing was <1 hour at 3°C to 7°C (A). Serum was stored in straws at a temperature between −85°C and −60°C (G).
- Plasma specimen
  PL2-SED-B-B-E-A-G. This corresponds to a double spun plasma (PL2) specimen that has been collected from a sodium EDTA vacutainer collection tube (SED), whose precentrifugation delay is

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Table 1. Preanalytical variables included in the SPREC (seven-element-long SPREC), version SPREC-01, applied to fluid samples. Codes in bold come from the LDMS

Type of sample	
Ascites fluid	ASC
Amniotic fluid	**AMN**
Bronchoalveolar lavage	**BAL**
Blood (whole)	**BLD**
Bone marrow aspirate	**BMA**
Breast milk	**BMK**
Buccal cells	**BUC**
Unficolled buffy coat, viable	**BUF**
Ficoll mononuclear cells, viable	**CEL**
Fresh cells from non blood specimen type	**CEN**
Cells from nonblood specimen type (e.g., disrupted tissue), viable	**CLN**
Cord blood	**CRD**
Cerebrospinal fluid	**CSF**
Nasal washing	**NAS**
Ficoll mononuclear cells, nonviable	**PEL**
Cells from nonblood specimen type (e.g., disrupted tissue), nonviable	**PEN**
Pleural fluid	**PFL**
Plasma, single spun	**PL1**
Plasma, double spun	**PL2**
Saliva	**SAL**
Semen	**SEM**
Serum	**SER**
Sputum	**SPT**
Stool	**STL**
Synovial fluid	SYN
Tears	**TER**
24-h urine	**U24**
Urine	**URN**
Other	ZZZ
Type of primary container	
Vacutainer acid citrate dextrose or equivalent	**ACD**
Vacutainer citrate phosphate dextrose or equivalent	**CPD**
Vacutainer lithium heparin or equivalent	**HEP**
Vacutainer hirudin or equivalent	HIR
Oragene collection container or equivalent	**ORG**
Paxgene blood RNA+	**PAX**
Vacutainer potassium EDTA or equivalent	**PED**
S8820 protease inhibitor tablets or equivalent	**PI1**
Protease inhibitors	PIX
Polypropylene tube sterile	PPS
Paxgene blood DNA	PXD
Paxgene bone marrow RNA	PXR
Vacutainer sodium citrate or equivalent	**SCI**
Vacutainer sodium EDTA or equivalent	**SED**
Vacutainer sodium fluoride/potassium oxalate or equivalent	**SPO**

Table 1. Preanalytical variables included in the SPREC (seven-element-long SPREC), version SPREC-01, applied to fluid samples. Codes in bold come from the LDMS (Cont'd)

Type of primary container		
Vacutainer serum separator tube or equivalent		**SST**
Tempus tube		**TEM**
Vacutainer trace elements		TRC
Unknown		XXX
Other		ZZZ
Precentrifugation (delay between collection and processing)		
RT*	<2 h	A
3°C to 7°C	<2 h	B
RT	2-4 h	C
3°C to 7°C	2-4 h	D
RT	4-8 h	E
3°C to 7°C	4-8 h	F
RT	8-12 h	G
3°C to 7°C	8-12 h	H
RT	12-24 h	I
3°C to 7°C	12-24 h	J
RT	24-48 h	K
3°C to 7°C	24-48 h	L
RT	>48 h	M
3°C to 7°C	>48 h	N
35°C to 38°C	<2 h	O
Unknown		X
Other		Z
Centrifugation		
RT 10 min	<3,000 g no braking	A
RT 10 min	<3,000 g with braking	B
3°C to 7°C 10 min	<3,000 g no braking	C
3°C to 7°C 10 min	<3,000 g with braking	D
RT 10 min	3,000-6,000 g with braking	E
3°C to 7°C 10 min	3,000-6,000 g with braking	F
RT 10 min	6,000-10,000 g with braking	G
3°C to 7°C 10 min	6,000-10,000 g with braking	H
RT 10 min	>10,000 g with braking	I
3°C to 7°C 10 min	>10,000 g with braking	J
No centrifugation		N
Unknown		X
Other		Z
Second centrifugation		
RT 10 min	<3,000 g no braking	A
RT 10 min	<3,000 g with braking	B
3°C to 7°C 10 min	<3,000 g no braking	C
3°C to 7°C 10 min	<3,000 g with braking	D
RT 10 min	3,000-6,000 g with braking	E
3°C to 7°C 10 min	3,000-6,000 g with braking	F

(*Continued on the following page*)

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Table 1. Preanalytical variables included in the SPREC (seven-element-long SPREC), version SPREC-01, applied to fluid samples. Codes in bold come from the LDMS (Cont'd)

Second centrifugation		
RT 10 min	6,000-10,000g with braking	G
3-7°C 10 min	6,000-10,000 g with braking	H
RT 10 min	>10,000 g with braking	I
3°C to 7°C 10 min	>10,000 g with braking	J
No second centrifugation		N
Unknown		X
Other		Z
Postcentrifugation delay		
<1 h 3°C to 7°C		A
<1 h RT		B
1-2 h 3°C to 7°C		C
1-2 h RT		D
2-8 h 3°C to 7°C		E
2-8 h RT		F
8-24 h 3°C to 7°C		G
8-24 h RT		H
>24 h 3°C to 7°C		I
>24 h RT		J
Unknown		X
Other		Z
Long-term storage		
PP tube 0.5-2 mL†	−85°C to −60°C	A
PP tube 0.5-2 mL	−35°C to −18°C	B
Cryotube 1-2 mL	Liquid nitrogen‡	C
Cryotube 1-2 mL	−85°C to −60°C	D
Cryotube 1-2 mL	Programmable freezing to <−135°C	E
Straw	Liquid nitrogen	F
Straw	−85°C to −60°C	G
Straw	−35°C to −18°C	H
Straw	Programmable freezing to <−135°C	I
PP tube ≥5 mL	−85°C to −60°C	J
PP tube ≥5 mL	−35°C to −18°C	K
Microplate	−85°C to −60°C	L
Microplate	−35°C to −18°C	M
Paraffin block	RT	P
Unknown		X
Other		Z

*RT, room temperature: 18°C to 25°C.
†PP, polypropylene.
‡Liquid nitrogen refers to either vapor or liquid phase.

<2 hours at 3°C to 7°C (B); first centrifugation has been done at ambient temperature at <3,000 g with braking (B) and second centrifugation has been done at ambient temperature at 3,000 to 6,000 g with braking (E). The delay between centrifugation and freezing was <1 hour at 3-7°C (A). Plasma was stored in straws at a temperature between −85°C and −60°C (G).

- Urine specimen

  U24-PIX-B-A-N-A-J. This corresponds to a 24-hour urine (U24) specimen that has been collected in a collection tube with protease inhibitors (PIX), whose precentrifugation delay is <2 hours at 3°C to 7°C (B); centrifugation has been done at ambient temperature at <3,000 g without braking (A). Only one centrifugation step was done (N) and the delay between centrifugation and freezing was <1 hour at 3°C to 7°C (A). Urine was stored in >5-mL polypropylene tubes at a temperature between −85°C and −60°C (J).

- CSF Specimen

  CSF-PPS-B-C-N-A-A. This corresponds to a cerebrospinal fluid (CSF) specimen that has been collected in a sterile polypropylene collection tube (PPS), whose precentrifugation delay is <2 hours at 3°C to 7°C (B); centrifugation has been done at 3°C to 7°C at <3,000 g without braking (C). Only one centrifugation step was done (N) and the delay between centrifugation and freezing was <1 hour at 3°C to 7°C (A). CSF was stored in 0.5- to 2-mL polypropylene tubes at a temperature between −85°C and −60°C (A).

- Solid tissue or cytologic Specimen

  TIS-BPS-N-B-RNL-A-A. This corresponds to a solid tissue (TIS) specimen that has been collected as a biopsy (BPS), with no warm ischemia (N), with cold ischemia of <10 minutes (B), fixed in RLALater (RNL) for <15 minutes (A) and stored in a 0.5- to 2-mL polypropylene tube at a temperature between −85°C and −60°C (A). Biopsies, obtained either at time of traditional surgery, laparoscopy, or puncture, and cytologic specimens such as fine needle aspirates, are assigned the same SPREC.

The SPREC labeling system provides a generic format for specimen comparison and is intended to facilitate research collaborations across different laboratories and institutions handling similar specimens. This code could be incorporated into the ongoing biospecimen publication guidelines of the National Cancer Institute/Office of Biorepository and Biospecimen Research (OBBR) because those guidelines (7) address the need for more detailed information on the preanalytical conditions of specimens used for research activities.

Scope of the SPREC

The application of preanalytical barcodes such as SPREC will need to be delineated and defined with respect to "downstream" standard laboratory practices and operational procedures taking into account sample type and utility. The SPREC has been specifically devised for primary samples (at the point of collection) and simple derivatives (e.g., plasma, buffy coat) and is not

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Table 2. Preanalytical variables included in the SPREC (seven-element-long SPREC), version SPREC-01, applied to solid samples. Codes in bold come from the LDMS

Type of sample	
Fresh cells from nonblood specimen type	**CEN**
Cells from nonblood specimen type (e.g., disrupted tissue), viable	**CLN**
Cells from fine needle aspirate	FNA
Hair	**HAR**
Cells from laser capture microdissected tissue	LCM
Cells from nonblood specimen type (e.g., disrupted tissue), nonviable	**PEN**
Solid tissue	**TIS**
Cells from disrupted tissue	LCM
Other	ZZZ
Type of collection	
Autopsy <6 h postmortem	A06
Autopsy 6-12 h postmortem	A12
Autopsy 12-24 h postmortem	A24
Autopsy 24-48 h postmortem	A48
Autopsy 48-72 h postmortem	A72
Biopsy	**BPS**
Fine needle aspirate	FNA
Punction	PUN
Surgical excision	SRG
Swab	**SWB**
Other	ZZZ
Warm ischemia time	
<2 min	A
2-10 min	B
10-20 min	C
20-30 min	D
30-60 min	E
>60 min	F
Unknown	X
Not applicable (e.g., biopsy)	N
Other	Z
Cold ischemia time	
<2 min	A
2-10 min	B
10-20 min	C
20-30 min	D
30-60 min	E
>60 min	F
Unknown	X
Not applicable (e.g., autopsy)	N
Other	Z
Fixation type	
Nonaldehyde with acetic acid	ACA
Aldehyde based	ALD
Alcohol based	ETH
Nonbuffered formalin	FOR
Snap freezing	**SNP**
Nonaldehyde without acetic acid	**NAA**
Neutral buffered formalin	**NBF**

Table 2. Preanalytical variables included in the SPREC (seven-element-long SPREC), version SPREC-01, applied to solid samples. Codes in bold come from the LDMS (Cont'd)

Fixation type		
Optimum cutting temperature medium		**OCT**
RNA Later		**RNL**
Unknown		XXX
Other		ZZZ
Fixation time		
<15 min		A
15 min to 1 h		B
1-4 h		C
4-8 h		D
8-24 h		E
24-48 h		F
48-72 h		G
Unknown		X
Other		Z
Long-term storage		
PP tube 0.5-2 mL*	−85°C to −60°C	A
PP tube 0.5-2 mL	−35°C to −18)°C	B
Cryotube 1-2 mL	Liquid nitrogen†	C
Cryotube 1-2 mL	−85°C to −60°C	D
Cryotube 1-2 mL	Programmable freezing to <−135°C	E
Straw	Liquid nitrogen	F
Straw	−85°C to −60°C	G
Straw	−35°C to −18°C	H
Straw	Programmable freezing to <−135°C	I
PP tube ≥5 mL	−85°C to −60°C	J
PP tube ≥5 mL	−35°C to −18°C	K
Microplate	−85°C to −60°C	L
Microplate	−35°C to −18°C	M
Paraffin block	RT	P
Unknown		X
Other		Z

NOTE: RT, room temperature: 18°C to 25°C.
*PP, polypropylene.
†Liquid nitrogen refers to either vapor or liquid phase.

applicable to complex derivatives, such as extracted nucleic acids or proteins and already established cell lines and microbial strains. More complex derivatives and protocols are sensitive to sample type, equipment, laboratory environment, technical proficiency, and skills that are not easily and consistently captured between laboratories before sample labeling. Extensive technical manipulations are necessary for the production of complex derivatives and, inherently, these will introduce preanalytical variables that differ between laboratories, operators, and applications. For instance, variation can depend upon extraction method (e.g., salting out or silica

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based) and brand of commercial kit. The SPREC does not include very rare biospecimen types for which LDMS can be consulted.

Integration of the SPREC in Biobank Quality Management and Databases

Preanalytical processes are critical to the resulting quality of the banked samples. Adoption of a standard preanalytical coding system such as the SPREC by a Biobank compels the gathering of the required information during the sample collection phase. Increasing accuracy in each step increases the quality of individual specimens, which is an asset for the Biobank, and the documentation of such quality records provides intrinsic value to the samples, which is easily shared with other researchers. The SPREC coding makes it immediately recognizable that biospecimens have been processed by a laboratory with strict quality control of processing conditions and shows the capacity of the Biobank to collect such information. This rewards quality management investments in Biobank laboratories implementing them.

Potentially, the SPREC can be incorporated into preexisting Biobank Quality Management Systems and tracking databases so that the SPREC code populates the same record and is linked to all aliquots of the parent sample and to all other data. Thus, the SPREC can be considered as a new data point attached to the sample and entered as a new parameter into biorepository database systems. This approach will validate and record permanently all sample treatment from primary specimen procurement through simple processing and sample storage, thereby contributing to quality standards (4, 8).

Many Biobanks are associated with pathology and diagnostic laboratories equipped with a Laboratory Information Management System, and in many cases, much of the information required for SPREC coding may be extracted from the database. This may make the collection of preanalytical information by the Biobank economically and practically more sustainable. Diagnostic practices impose strict operating procedures for the collection and handling of biological samples. This is advantageous to SPREC coding because it reduces the likelihood of erroneous handling of specimens.

Clinical Research Applications of SPREC

Once the SPREC has been implemented, it will prove invaluable in biospecimen research (2). For example, a laboratory wishing to study the effect of centrifugation force (g) on urine will be able to define a baseline preanalytical procedure corresponding to code URN-PPT-B-D-N-A-J for which the only type of preanalytical variation will be the "centrifugation force" factor. The comparison will thus take place between URN-PPT-B-D-N-A-J and URN-PPT-B-F-N-A-J, and URN-PPT-B-H-N-A-J and URN-PPT-B-J-N-A-J.

Another example is provided by the biospecimen research laboratory studying the effect of delay between collection and the centrifugation of cerebrospinal fluid samples. In this case, if the repository applies processing methods corresponding to the SPREC CSF-PPT-B-F-N-A-A, then it will be able to study precentrifugation delays of <2, 4 to 8, 8 to 12, 12 to 24, and 24 to 48 hours at 3°C to 7°C. The preanalytical factors thus correspond to the codes CSF-PPT-B-F-N-A-A, CSF-PPT-F-F-N-A-A, CSF-PPT-H-F-N-A-A, CSF-PPT-J-F-N-A-A, and CSF-PPT-L-F-N-A-A.

SPREC also has potential utility in interlaboratory and intralaboratory research collaborations by facilitating researchers who wish to compare experimental specimen conditions and thus need to determine whether their research studies are comparable from the biospecimen standpoint. Collaborating researchers can similarly predetermine the exact specimen conditions required so that only qualifying specimens are obtained from respective biorepositories.

SPREC can advantageously complement existing reporting recommendations for tumor marker prognostic studies (REMARK). The goal of these guidelines is to encourage complete reporting of all relevant information on biomarker studies. The REMARK required information on specimen characteristics is "*type of biological material used (including control samples) and methods of preservation and storage*" (9). Advancing the REMARK further and zooming on the REMARK Materials and Methods section, the SPREC focuses on reporting detailed specimen characteristics in a standardized manner.

Clinical laboratories may also apply the SPREC in method validation studies, as part of the CLIA or ISO15189 accreditation process.

Environmental and Biodiversity (Nonclinical) Applications of the SPREC

The SPREC has been designed for clinical/human health care setting, but could be extended to all types of mammal and animal biospecimens to which common biobanking best practices apply. For nonclinical applications, it will be necessary to evaluate how best to dovetail preanalytical data with sample identification "passport" and processing information. This usually comprises technical, scientific, and logistic data, collated for each sample, e.g., collector/isolator, provenance, origin, taxonomy, sample processing, accession designation, sample clean-up, toxicologic, pathologic and sanitary status, mode of nonaxenic/axenic culture, and storage.

Nonclinical Biobanks service highly diverse communities for which it will be constructive to prospect adapting and adopting the SPREC approach for the full spectrum of biodiversity. This can be represented by the conservation of primary (viable/nonviable) samples of environmental, microbial, protistan, plant, and animal origin, as well as their complex molecular, cellular, and biotechnological derivatives. Primary samples of nonclinical

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bioresources can also comprise assemblages of axenic and nonaxenic strains, and cultures as well as symbiotic and parasitic associations. Different types of "base" (long term) and "working" (active) collections hold agronomic, scientific, and environmental bioresources in Biological Resources Centres, seedbanks, genebanks, field banks, natural history museums, botanical gardens, arboreta, and zoos (10). However, it will be prudent to balance the benefits of preanalytical barcoding with the risk of producing overcomplicated tools with limited application across different biorepositories.

Developing a generic preanalytical code for such diverse nonclinical collections will be challenging, particularly for long-established biorepositories that comprise biodiversity holdings sampled from different provenances. As preanalytical variation applies to all types of biological resources, it is important and timely to stimulate debate about the utility of the SPREC for nonclinical Biobank communities. In these cases, the preanalytical variables influencing the primary samples might also include specimen collection and transit methods, provenance (e.g., geographic location, environment), source (e.g., freshwater, soil), and habitat (11). How primary samples are collected, stabilized, and transported to the Biobank is particularly relevant for samples collected from distant, remote, and extreme locations. Information about the genetic and epigenetic stability of primary samples recovered from storage needs also pertinent preanalytical information (12).

Cognizance of preanalytical factors can be built into the management of new Biobanks at the onset of specimen procurement and curation. For established Biobanks, it may be better to bring preanalytical measures on line for new accessions by targeting those with a high requirement for robust quality control measures. This is opportune because nonclinical biorepositories are increasingly tasked to meet the stringent expectations of clients involved in biodiversity-biotechnology, bioinformatics, and molecular-knowledge economies. Similar levels of expectation are demanded from Biological Resources Centres servicing environmental monitoring, endangered species conservation, and climate change research. In all these scenarios, developing nonclinical SPRECs could be useful, not least because they can facilitate quality control and specimen risk management. It is envisaged that preanalytical barcodes could be applied to primary specimens, their simple derivatives, and newly initiated cultures, for example: reference strains, strain standards, type collections/cultures, environmental indicators/biomarkers, and samples used in taxonomic, molecular, genomic, and proteomics research, and for strain deposition.

Engaging the SPREC in nonclinical settings will clearly require careful harmonization with existing procedures, databases, documentation, and storage protocols (8, 12). However, identification of preanalytical variables is in line with the need to enhance international-level Quality Management Systems across all types of biorepository (8, 13). It is anticipated that the SPREC will become increasingly relevant to repositories conserving "global public goods," which comprise socioeconomic, internationally significant genetic and environmental resources. Preanalytical barcodes also have relevance for Biobanks holding biodiversity secured from high-risk environments seriously affected by climate change and for which a recording of preanalytical variables at

Table 3. Biospecimen description examples according to SPREC-01

Fluid specimens	Serum	Plasma	Urine	Cerebrospinal fluid
Sample type	SER	PL2	U24	CSF
Type of container	SST	SED	PIX	PPT
Precentrifugation	A	B	B	B
Centrifugation	E	B	A	C
Second centrifugation	N	E	N	N
Postcentrifugation	A	A	A	A
Storage	G	G	J	A

Solid specimens	Solid tissue
Sample type	TIS
Type of collection	BPS
Warm ischemia	N
Cold ischemia	B
Fixation type	RNL
Fixation time	A
Storage	A

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the point of collection will be critical for restoration and reintroductions.

Although many core practices are generic across biorepository sectors (13), differences inevitably exist; therefore, concerted action will be required in the future to design appropriate preanalytical barcodes for Biobanks working outside the clinical and health care sectors. This will need a commitment to collaborate across different biobanking communities. One way forward might be to create "virtual" pilot projects specifically designed to test and harmonize generic version(s) of SPREC-01 across and within different biorepository sectors.

Conclusion

This article presents the first version of the clinical SPREC (designated SPREC-01) and its purpose is to support evidence-based biobanking and foster efficient interconnectivity between Biobanks. A fine-grained characterization of preanalytical quality features of the specimens maximizes the value of a Biobank: a shared standard, such as SPREC, promotes quality practices and allows peer institutions to exchange resources with maximum benefits and with minimum associated costs. The SPREC's optimal use will require adjustments and timely reviews to keep the criteria in line with future technological developments as new assays and techniques are developed (e.g., nanotechnology, Da Vinci robot–assisted laparoscopy). Importantly, clinical and nonclinical SPRECs will need to take into account differences in preanalytical parameters in different geographic and international settings (e.g., tropical, ambient, and polar temperatures). The SPREC presented herein is simple, straightforward, and easy to implement, even for Biobanks in developing countries and those with limited resources because it can be handwritten or incorporated into a linear or two-dimensional barcode. The SPREC is flexible, making it possible to add new elements and/or new preanalytical options and corresponding coding characters. The value of SPREC-01 has also been proposed for use in nonclinical sectors with a view to encouraging a wider debate about its value across different thematic biobanking sectors.

Disclosure of Potential Conflicts of Interest

No potential conflicts of interest were disclosed.

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Standard Preanalytical Coding for Biospecimens: Defining the Sample PREanalytical Code

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