NOTICE

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Adoption of ICH¹ Guidance: Definitions for Genomic Biomarkers, Pharmacogenomics, Pharmacogenetics, Genomic Data and Sample Coding Categories - ICH Topic E15

Health Canada is pleased to announce the adoption of the ICH guidance Definitions for Genomic Biomarkers, Pharmacogenomics, Pharmacogenetics, Genomic Data and Sample Coding Categories (E15).

This guidance has been developed by the appropriate ICH Expert Working Group and has been subject to consultation by the regulatory parties, in accordance with the ICH Process. The ICH Steering Committee has endorsed the final draft and recommended its adoption by the regulatory bodies of the European Union, Japan and USA.

In adopting this ICH guidance, Health Canada endorses the principles and practices described therein. This document should be read in conjunction with this accompanying notice and with the relevant sections of other applicable Health Canada guidances, including Health Canada’s guidance document, Submission of Pharmacogenomic Information.


It is recognized that the scope and subject matter of current Health Canada guidances may not be entirely consistent with those of the ICH guidances that are being introduced as part of our commitment to international harmonization and the ICH Process. In such circumstances, Health Canada adopted ICH guidances take precedence.

Health Canada is committed to eliminating such discrepancies through the implementation of a phased-in work plan that will examine the impact associated with the adoption of ICH guidances. This will result in the amendment or, depending on the extent of revisions required, withdrawal of some Health Canada guidances.

This and other Guidance documents are available on the Health Canada website.

1 International Conference on Harmonisation of Technical Requirements for the Registration of Pharmaceuticals for Human Use
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GUIDANCE DOCUMENT
Definitions for Genomic Biomarkers, Pharmacogenomics, Pharmacogenetics, Genomic Data and Sample Coding Categories
ICH Topic E15

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Health Products and Food Branch
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<tr>
<th>Our mission is to help the people of Canada maintain and improve their health.</th>
<th>HPFB’s Mandate is to take an integrated approach to managing the health-related risks and benefits of health products and food by:</th>
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<tr>
<td>Health Canada</td>
<td>• minimizing health risk factors to Canadians while maximizing the safety provided by the regulatory system for health products and food; and,</td>
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<td>• promoting conditions that enable Canadians to make healthy choices and providing information so that they can make informed decisions about their health.</td>
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Également disponible en français sous le titre: Définitions pour les biomarqueurs génomiques, la pharmacogénomique, la pharmacogénétique et les catégories pour le codage des échantillons et des données génomiques, ICH thème E15
FOREWORD

This guidance has been developed by the appropriate ICH Expert Working Group and has been subject to consultation by the regulatory parties, in accordance with the ICH Process. The ICH Steering Committee has endorsed the final draft and recommended its adoption by the regulatory bodies of the European Union, Japan and USA.

In adopting this ICH guidance, Health Canada endorses the principles and practices described therein. This document should be read in conjunction with the accompanying notice and the relevant sections of other applicable guidances.

Guidance documents are meant to provide assistance to industry and health care professionals on how to comply with the policies and governing statutes and regulations. They also serve to provide review and compliance guidance to staff, thereby ensuring that mandates are implemented in a fair, consistent and effective manner.

Guidance documents are administrative instruments not having force of law and, as such, allow for flexibility in approach. Alternate approaches to the principles and practices described in this document may be acceptable provided they are supported by adequate scientific justification. Alternate approaches should be discussed in advance with the relevant program area to avoid the possible finding that applicable statutory or regulatory requirements have not been met.

As a corollary to the above, it is equally important to note that Health Canada reserves the right to request information or material, or define conditions not specifically described in this guidance, in order to allow the Department to adequately assess the safety, efficacy or quality of a therapeutic product. Health Canada is committed to ensuring that such requests are justifiable and that decisions are clearly documented.
E15

Document History

<table>
<thead>
<tr>
<th>Code*</th>
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1. INTRODUCTION

1.1 Objective of this Guidance Document

In order to develop harmonised approaches to drug regulation, it is important to ensure that consistent definitions of terminology are being applied across all constituents of the International Conference on Harmonisation (ICH). An agreement on definitions will facilitate the integration of the discipline of pharmacogenomics and pharmacogenetics into global drug development and approval processes.

1.2 Background

Pharmacogenomics and pharmacogenetics have the potential to improve the discovery, development and use of medicines. Each of the ICH regions has published specific pharmacogenomic and pharmacogenetic guidelines, or concept papers, and is in the process of developing others. However, the lack of consistently applied definitions to commonly used terminology raises the potential for either conflicting use of terms in regulatory documentation and guidelines, or, inconsistent interpretation by regulatory authorities, ethics committees and sponsor companies.

1.3 Scope of this Guidance Document

This guidance document contains definitions of key terms in the discipline of pharmacogenomics and pharmacogenetics, namely genomic biomarkers, pharmacogenomics, pharmacogenetics and genomic data and sample coding categories. The validation and qualification processes for genomic biomarkers, evidence for their intended use and acceptance criteria across ICH regions are outside of the scope of this guidance. As new scientific knowledge in the discipline of pharmacogenomics and pharmacogenetics emerges, the current guidance will be reviewed and expanded if appropriate.

2. GUIDANCE

Definitions of a genomic biomarker, pharmacogenomics, pharmacogenetics, and genomic data and sample coding categories are detailed below. The definition of what constitutes a genomic biomarker is key to understanding the definitions of pharmacogenomics and pharmacogenetics and is therefore introduced in this guidance first. Additional information useful to an understanding of aspects covered by each of the definitions is also provided. Some of the principles described in this guidance might be applicable to proteomics, metabalomics and other related disciplines.
2.1 Genomic Biomarker

2.1.1 Definition

A genomic biomarker is defined as follows:
A measurable DNA and/or RNA characteristic that is an indicator of normal biologic processes, pathogenic processes, and/or response to therapeutic or other interventions.

2.1.2 Additional Information

1. A genomic biomarker could, for example, be a measurement of:
   • The expression of a gene;
   • The function of a gene;
   • The regulation of a gene.

2. A genomic biomarker can consist of one or more deoxyribonucleic acid (DNA) and/or ribonucleic acid (RNA) characteristics.

3. DNA characteristics include, but are not limited to:
   • Single nucleotide polymorphisms (SNPs);
   • Variability of short sequence repeats;
   • Haplotypes;
   • DNA modifications, e.g., methylation;
   • Deletions or insertions of (a) single nucleotide(s);
   • Copy number variations;
   • Cytogenetic rearrangements, e.g., translocations, duplications, deletions or inversions.

4. RNA characteristics include, but are not limited to:
   • RNA sequences;
   • RNA expression levels;
   • RNA processing, e.g., splicing and editing;
   • microRNA levels.
5. The definition of a genomic biomarker is not limited to human samples, but includes samples from viruses and infectious agents as well as animal samples, i.e., for the application of genomic biomarkers to non-clinical and/or toxicological studies.

6. The definition of a genomic biomarker does not include the measurement and characterisation of proteins or low molecular weight metabolites.

2.2 Pharmacogenomics and Pharmacogenetics

2.2.1 Definitions

2.2.1.1 Pharmacogenomics

Pharmacogenomics (PGx) is defined as:
The study of variations of DNA and RNA characteristics as related to drug response.

2.2.1.2 Pharmacogenetics

Pharmacogenetics (PGt) is a subset of pharmacogenomics (PGx) and is defined as:
The study of variations in DNA sequence as related to drug response.

2.2.2 Additional Information

1 The term drug should be considered synonymous with investigational (medicinal) product, medicinal product, medicine and pharmaceutical product (including vaccines and other biological products).

2 PGx and PGt are applicable to activities such as drug discovery, drug development, and clinical practice.

3 Drug response includes the processes of drug absorption and disposition (e.g., pharmacokinetics, (PK)), and drug effects (e.g., pharmacodynamics (PD), drug efficacy and adverse effects of drugs).

4 The definitions of PGx and PGt do not include other disciplines such as proteomics and metabolomics.
2.3 Categories for Genomic Data and Samples Coding

PGx and PGt research depends on the use of biological samples to generate data. A harmonised definition for the coding of these samples and their associated data will facilitate use in research and development of new medicines.

There are four general categories of coding: identified, coded, anonymised and anonymous. Coded data or samples can be single or double coded.

The implications of using a specific data and sample coding category should be considered in the design of PGx and PGt research studies.

Some implications are highlighted in this section and summarised in Table 1.

2.3.1 Identified Data and Samples

Identified data and samples are labelled with personal identifiers such as name or identification numbers (e.g., social security or national insurance number). As the samples and associated data are directly traceable back to the subject, it is possible to undertake actions such as sample withdrawal or the return of individual results in accordance with the subject’s request. The use of identified data and samples allows for clinical monitoring, subject follow-up and the addition of new data from the subject. Identified data and samples offer privacy protection comparable to that of general healthcare confidentiality in everyday medical practice. Identified data and samples are generally not considered appropriate for purposes of clinical trials in drug development.

2.3.2 Coded Data and Samples

Coded data and samples are labelled with at least one specific code and do not carry any personal identifiers.

2.3.2.1 Single Coded Data and Samples

Single coded data and samples are usually labelled with a single specific code and do not carry any personal identifiers. It is possible to trace the data or samples back to a given individual with the use of a single coding key. In general, the clinical investigator is responsible for maintaining the coding key. As the samples and associated data are indirectly traceable back to the subject via the coding key, it is possible to undertake actions such as sample withdrawal, or the return of individual results in accordance with the subject’s request. The use of
single coded data and samples allows for clinical monitoring, subject follow-up or the addition of new data from the subject. Single coding is the current standard used in clinical research and offers additional safeguards to the subject’s identifiers compared to the general healthcare confidentiality and privacy protection in everyday medical practice.

### 2.3.2.2 Double Coded Data and Samples

Double coded data and samples are initially labelled with a single specific code and do not carry any personal identifiers. The data and samples are then relabelled with a second code, which is linked to the first code via a second coding key. It is possible to trace the data or samples back to the individual by the use of both coding keys. In general, the clinical investigator is responsible for maintaining the first coding key and does not have access to the second coding key. As the samples and associated data can very indirectly be traced back to the subject via the use of both coding keys, it may be possible to undertake actions such as sample withdrawal, or the return of individual results in accordance with the subject’s request. However additional electronic or technical processes may be added to further limit the ability to trace back from a genotype result to an individual subject. For example, a specific computer process that allows new subject data to be added but prevents the reconnection of the genotype data back to the individual subject identifier. The use of double coded data and samples allows for clinical monitoring, subject follow-up or the addition of new data from the subject. The use of the second code provides additional confidentiality and privacy protection for subjects over the use of a single code. Access to both coding keys is needed to link any data or samples back to a subject identifier.

### 2.3.3 Anonymised Data and Samples

Anonymised data and samples are initially single or double coded but where the link between the subjects’ identifiers and the unique code(s) is subsequently deleted. Once the link has been deleted it is no longer possible to trace the data and samples back to individual subjects through the coding key(s). Anonymisation is intended to prevent subject re-identification. As anonymised samples and associated data are not traceable back to the subject, it is not possible to undertake actions such as sample withdrawal, or the return of individual results, even at the subject’s request. The use of anonymised data and samples does not allow for clinical monitoring, subject follow-up or the addition of new data from the subject. The deletion of the coding key(s) linking the data and samples to a given subject’s identifiers provides additional confidentiality and privacy protection over coded data and samples, as it prevents subject re-identification through
the use of the coding key(s).

2.3.4 Anonymous Data and Samples

Anonymous data and samples are never labelled with personal identifiers when originally collected, neither is a coding key generated. Therefore there is no potential to trace back genomic data and samples to individual subjects. In some instances only limited clinical data can be associated with anonymous samples (e.g., samples from subjects with diabetes, male, age 50-55, cholesterol>240 mg/dl). As anonymous samples and associated data are not traceable back to subjects, it is not possible to undertake actions such as sample withdrawal, or the return of individual results, even at the subject’s request. The use of anonymous data and samples does not allow for clinical monitoring, subject follow-up, or the addition of new data.

2.3.5 Additional Information

The use of a specific coding category in relation to obtaining informed consent from subjects is not within the focus of this guidance and is not addressed herein.

The conditions under which the genomic data can be linked back to a subject’s personal identifiers for any purpose, including the return of genomic data to the subject, should be described in research related documents, e.g., the informed consent document.
Table 1: Summary of Genomic Data and Sample Coding Categories

<table>
<thead>
<tr>
<th>Sample Coding Category</th>
<th>Link Between Subject’s Personal Identifiers and Genomic Biomarker Data</th>
<th>Traceability Back to the Subject (Actions possible, including e.g. sample withdrawal or return of individual genomic results at subject’s request)</th>
<th>Ability to Perform Clinical Monitoring, Subject Follow-up, or Addition of New Data</th>
<th>Extent of Subject’s Confidentiality and Privacy Protection</th>
</tr>
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<tbody>
<tr>
<td>Identified</td>
<td>Yes (direct) Allows for subjects to be identified</td>
<td>Yes</td>
<td>Yes</td>
<td>Similar to general healthcare confidentiality and privacy</td>
</tr>
<tr>
<td>Coded</td>
<td>Single</td>
<td>Yes (indirectly) Allows for subjects to be identified (via single, specific coding key)</td>
<td>Yes</td>
<td>Standard for clinical research</td>
</tr>
<tr>
<td></td>
<td>Double</td>
<td>Yes (very indirectly) Allows for subjects to be identified (via the two specific coding keys)</td>
<td>Yes</td>
<td>Added privacy and confidentiality protection over single code</td>
</tr>
<tr>
<td>Anonymised</td>
<td>No</td>
<td>Does not allow for subjects to be re-identified as coding key(s) have been deleted</td>
<td>No</td>
<td>Genomic data and samples no longer linked to subject as coding key(s) have been deleted</td>
</tr>
<tr>
<td>Anonymous</td>
<td>No</td>
<td>Identifiers never collected and coding keys never applied Does not allow for subjects to be identified</td>
<td>No</td>
<td>Genomic data and samples never linked to subject</td>
</tr>
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