Annex 4

Guidelines on estimation of residual risk of HIV, HBV or HCV infections via cellular blood components and plasma

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Guidelines published by the World Health Organization (WHO) are intended to be scientific and advisory in nature. Each of the following sections constitutes guidance for national regulatory authorities (NRAs) and for manufacturers of biological products. If an NRA so desires, these WHO Guidelines may be adopted as definitive national requirements, or modifications may be justified and made by the NRA.
Abbreviations

anti-HBc antibodies to hepatitis B core protein
anti-HBs antibodies to hepatitis B surface antigen
CE Conformité Européenne (conforms to European requirements)
CLIA chemiluminescence immunoassay
EIA enzyme immunoassay
FDA Food and Drug Administration
HBsAg hepatitis B surface antigen
HBV hepatitis B virus
HCV hepatitis C virus
HIV human immunodeficiency virus
ID-NAT individual donation nucleic acid amplification technique
IDI interdonation interval
IU International Unit(s)
IVD in vitro diagnostic
MP-NAT minipool nucleic acid amplification technique
NAT nucleic acid amplification technique
OBI occult hepatitis B infection
P probability
PCR polymerase chain reaction
PDMP plasma-derived medicinal product
RDT rapid diagnostic test
RR residual risk (used in mathematical formulae)
vDWP viraemic phase of the diagnostic window period
1. Introduction

The course that a viral infection may take in an individual and the different phases of viral infections are described in the following sections – together with the advantages and limitations of using different blood-screening assays for the different infection phases. Blood-screening assays are differentiated by distinct categories. The residual risk of missing viral infections using any screening assay is mainly due to the viraemic phase of the diagnostic window period (vDWP) for each assay – the mean size of which varies between different assay categories. Another component of the residual risk is the virus epidemiology of the donor population (consisting of repeat and first-time donors) with the rate of new infections (incidence) in donors determining the probability of window-period donations. The residual risk per donation from the repeat-donor subpopulation may be used to extrapolate the respective risk for the first-time donor subpopulation, for which incidence data are often unavailable. The residual risk affects recipients of non-pathogen-inactivated blood components to whom viruses may be transmitted. It also determines the potential viral load of plasma pools used for the manufacturing of plasma-derived medicinal products (PDMPs); this potential contamination level needs to be assessed against the viral inactivation or reduction strategies in the manufacturing process.

2. Purpose and scope

These WHO Guidelines provide advice on estimating the residual risk of human immunodeficiency virus (HIV), hepatitis B virus (HBV) or hepatitis C virus (HCV) being present in cellular blood components and plasma. This estimation has implications for the safety of non- (or incompletely) pathogen-inactivated blood components or plasma products. There are large differences in the prevalence and incidence of viral infections in blood donors around the world. The impact of such epidemiological differences on blood safety needs to be assessed together with the sensitivity of the testing strategy applied. Such assessments may be used to guide strategic decisions on the choice of assays to detect virus-positive blood donations and as a basis for cost–benefit analysis of the different testing scenarios most suitable in the region. The factors influencing the risk of virus transmission by blood components are described, as well as simple mathematical formulae to calculate its probability. These estimates may also be used to counsel recipients on the risks of transfusion. Similarly, the probability and potential level of viral contamination of plasma pools used for the manufacture of PDMPs can be calculated. The infectivity risk of plasma products can then be estimated in relation to the inactivation and reduction capacity of the manufacturing process.
Currently, recovered plasma from whole blood donations is often not used for plasma fractionation because of perceived potential virus risks and quality concerns. This is true for (but not limited to) many blood establishments in low- and middle-income countries, where specific data (for example, on interdonation periods of individual donors) are often not available due to a lack of computerized systems. These WHO Guidelines therefore aim to enable the approximate estimation of residual risks based on limited data, while recognizing that more precise models have been published in the scientific literature. Nevertheless, it is hoped that this document can help in rationalizing decision-making on the use of plasma units for fractionation.

Since the performance of screening assays is one of the key elements in minimizing the residual risk of blood components and guaranteeing the safety of plasma products, these WHO Guidelines also contain advice on the assessment of in vitro diagnostics (IVDs) in studies using specimen panels from the region (Appendix 1). Such targeted performance evaluations for new assays may be performed prior to the acceptance of a new blood-screening assay in a country.

3. Terminology

The definitions given below apply to the terms as used in these WHO Guidelines. These terms may have different meanings in other contexts.

**Analytical sensitivity**: the smallest amount of the target marker that can be precisely detected by an IVD assay; it may be expressed as the limit of detection and is often determined by testing limiting dilutions of a biological reference preparation.

**Apheresis**: the process by which one or more blood components are selectively obtained from a donor by withdrawing whole blood, separating it by centrifugation and/or filtration into its components, and returning those not required to the donor. The term “plasmapheresis” is used for a procedure dedicated specifically to the collection of plasma.

**Blood collection**: a procedure whereby a single donation of blood is collected in a sterile receptacle containing anticoagulant and/or stabilizing solution, under conditions designed to minimize microbiological contamination, cellular damage and/or coagulation activation.

**Blood component**: a constituent of blood that can be used directly or after further processing for therapeutic applications. The main therapeutic blood components are red blood cell concentrates, platelet concentrates, plasma for transfusion and cryoprecipitate.

**Blood establishment**: any structure, facility or body that is responsible for any aspect of the collection, testing, processing, storage, release and/or distribution of human blood or blood components when intended for transfusion.
or further industrial manufacturing. It encompasses the terms “blood bank”, “blood centre”, “blood transfusion unit”, “blood service” and “blood transfusion service”. The definition of this term may differ between legislations.

**Blood product:** any therapeutic substance derived from human blood, including whole blood, blood components and PDMPs.

**Diagnostic sensitivity:** the probability that an assay gives a positive result in human specimens containing the target marker (that is, being true positive).

**Diagnostic window period:** the time interval from infection to the time point when a blood specimen from that infected person first yields a positive result in a diagnostic or screening assay for that agent (for example, for specific antibodies); in the context of residual risk this is often simply called the “diagnostic window” or “window period”. The diagnostic window period consists of two phases – the first period of viral replication in the target tissue without presence in peripheral blood is called the eclipse period; the eclipse period is then followed by the ramp-up phase during which the virus concentration increases exponentially in the blood (viraemic phase). Blood components prepared from a blood donation made during the viraemic phase of the diagnostic window period (vDWP) (the potentially infectious window period) can transmit infection to the transfusion recipient, or the respective plasma may contaminate the plasma pool used for manufacturing PDMPs.

**Donor:** a person in defined good health conditions who voluntarily donates blood or blood components.

**First-time (tested) donor:** a donor whose blood or plasma is tested for the first time for infectious disease markers in a blood establishment.

**Fractionation:** the (large-scale) process by which plasma is separated into individual protein fractions that are further purified for medicinal use. The term “fractionation” is usually used to describe a sequence of processes, including plasma protein separation steps (typically precipitation and/or chromatography) and purification steps (typically ion-exchange or affinity chromatography). These steps may also contribute to the inactivation or removal of bloodborne infectious agents (most specifically viruses and, possibly, prions).

**Hepatitis B virus (HBV):** an enveloped double-stranded DNA virus; causative agent of hepatitis B.

**Hepatitis C virus (HCV):** an enveloped single-stranded RNA virus; causative agent of hepatitis C.

**Human immunodeficiency virus (HIV):** an enveloped diploid single-stranded RNA virus; causative agent of acquired immunodeficiency syndrome (AIDS).

**Incidence:** the number of newly acquired infections per unit of time in a defined population.
**NAT conversion**: the time period during which specific nucleic acids (for example, viral nucleic acids after a recent virus infection) become detectable by a nucleic acid amplification technique.

**Nucleic acid amplification technique** (NAT): a testing method to detect the presence of a targeted area of a defined nucleic acid sequence (for example, viral genome) using amplification techniques such as polymerase chain reaction (PCR) or transcription mediated amplification (TMA).

**Plasma**: the liquid portion remaining after separation of the cellular elements from blood – collected in a receptacle containing an anticoagulant, or separated by the continuous filtration or centrifugation of anticoagulated blood.

**Plasma for fractionation**: plasma (from whole blood or apheresis) used for the production of PDMPs.

**Plasma for transfusion**: plasma (from whole blood or apheresis) used for direct infusion into patients without a prior fractionation step. It can be subjected to treatment for inactivating a broad range of pathogens.

**Plasma-derived medicinal products** (PDMPs): a range of medicinal products obtained by the fractionation of human plasma. Also called plasma derivatives, plasma products or fractionated plasma products.

**Plasmapheresis**: see “Apheresis” above.

**Prevalence**: the proportion of past infections identified over a specified period in a defined population.

**Recovered plasma**: plasma recovered from a whole blood donation and used for transfusion or for fractionation into PDMPs.

**Repeat donor**: a person who has donated blood/plasma previously in the blood establishment. The definition of this term may differ between legislations.

**Sensitivity**: see “Analytical sensitivity” and “Diagnostic sensitivity” above.

**Seroconversion**: the time period during which specific antibodies develop (for example, after a recent virus infection) and become detectable in the blood; this term is sometimes also used for the time period during which viral antigens, such as hepatitis B surface antigen (HBsAg), or viral nucleic acids become detectable in the blood after recent infection. See also “NAT conversion” above.

**Source plasma**: plasma obtained by apheresis for further fractionation into PDMPs.

**Viraemic phase of the diagnostic window period** (vDWP): the part of the diagnostic window period during which viruses are present in the blood; the beginning of the viraemic phase is defined by the putative presence of one virus particle in a blood component (20 mL plasma for packed red blood cells) and can be extrapolated using viral replication kinetics (viral doubling time).

**Window period**: see “Diagnostic window period” above.
4. Course of HIV, HBV and HCV infections

The course of infection in humans differs for HIV, HBV and HCV depending on the biological features of the virus and on the individual immunological response to the infection. In principle, chronically persistent virus infections can be distinguished from infection courses leading to clearance of the virus. Both courses have in common an acute phase which is associated with viral replication, detectable viraemia and sometimes with clinical symptoms. A chronically persisting infection without viral clearance almost always occurs with HIV, frequently with HCV and sometimes with HBV.

4.1 Acute infection

The acute viraemic phase of infection is followed by the humoral and cellular immune responses, resulting in seroconversion and potential clearance of the virus. For some infections the immunity also protects against reinfection. The acute viraemic phase of virus infection in blood donors may be detected by antigen assays or, more sensitively, by assays based upon the nucleic acid amplification technique (NAT). Antibody assays are not useful for the detection of acute infections, but have long been used for the detection of persistent infection (HIV, HCV). Usually there is an overlap of immunoglobulin detection (for example, of immunoglobulin M) and the declining phase of viraemia.

For HBV, both acute resolving and chronic persistent infection courses occur. The frequencies of either are dependent upon different factors (such as the age of the individual becoming infected). It has been estimated that in 70% of HBV-infected donors hepatitis B surface antigen (HBsAg) may be detected transiently in blood, 5% develop chronic HBV infection with continuous antigaemia and 25% do not show detectable antigaemia. In principle the marker HBV DNA follows the same transient pattern as HBsAg but the median length of viraemia detection is longer. The transient nature of these HBV blood-screening markers requires the use of an adjustment factor when calculating rates of new infections (1).

4.2 Chronic persistent infection

HIV causes persistent infection in almost all infected individuals, while HCV infection becomes chronic in approximately 70% of cases (2). A minority of HBV-infected adults (around 5%) become chronic carriers, depending on the age and immune status of the infected subjects. These chronic infections of HIV, HBV and HCV are usually lifelong active infections associated with viral replication characterized by continuous or reappearing (undulating) phases of viraemia, despite the presence of specific antibodies.
Persistent viraemic infections are usually detectable by both serology and NAT-based assays. An exception is HBV where low-level HBV-DNA-positive carriers (HBsAg negative; antibodies to hepatitis B core protein (anti-HBc) positive) have been associated with so-called occult hepatitis B infection (OBI) (3, 4). In some low-prevalence countries the potential OBI transmission risk has been greatly reduced by the introduction of anti-HBc testing. However, in large parts of the world where HBV is endemic, screening for this marker would lead to the loss of an unacceptable proportion of donors. Blood components from donors with OBI have transmitted HBV at a low frequency (approximately 3%), while the presence of detectable levels of antibody against HBsAg (anti-HBs) has been found to protect against infection, with few exceptions (5–9). The OBI-associated risk for HBV transmission via cellular blood components may be reduced by sensitive NAT-based screening assays. The OBI-associated input of HBV into plasma pools used for the manufacture of PDMPs appears negligible when compared to the potential viral loads in diagnostic window period donations.

5. Residual risk origins

Predominantly, the residual risk of HIV, HBV or HCV infections in blood or plasma donations is defined as the probability of collecting a donation from an asymptomatic viraemic donor infected with one of these bloodborne viruses, and this not being detected by the routine screening assays.

Such an undetected blood donation may transmit the infection to a recipient if the blood components are not pathogen inactivated. If the pathogen inactivation and removal capacity of the production process is not sufficient an infectious unit of plasma may also contaminate a manufacturing plasma pool and pose a risk to the recipients of the plasma-derived products.

The non-detection of virus infection in blood or plasma donors may be caused by assay failures or by donors being in the diagnostic window period.

5.1 Assay failures

Assay failures in blood screening can occur due to viral variants escaping detection (for example by oligonucleotide mismatches in NAT-based methods, monoclonal antibodies not detecting the antigen of a mutant virus, or recombinant antigens/peptides not detecting antiviral antibodies) (10–12). The contribution of assay failures to the residual risk is considered negligible for “state-of-the-art” assays and will not be factored into the residual risk calculation suggested by these Guidelines. Nevertheless, it is important to continuously survey the quality features of screening assays and to identify potential causes of false test results. Post-marketing surveillance of assay safety,
quality and performance is a mechanism for detecting, investigating and acting on any issues and failures identified, and for addressing the need for continuous assay improvement (13).

Another potential root cause of assay failure is an inadequate quality management system in place within the testing laboratory. Quality assurance aspects include: (a) participation in external quality assessment (proficiency testing and on-site supervision); (b) the conduct of process (quality) control; (c) maintaining adequate documentation (through standard operating procedures) and record-keeping (testing logbooks, registers); (d) maintaining proper inventory and purchasing systems; (e) equipment maintenance; (f) safe facilities; (g) appropriate organization; and (h) measures to ensure adequately trained and competent testing personnel.

5.2 Diagnostic window periods

Historically, the phase elapsing between the time point of infection and the point of first detectability of the viral marker by the screening assay has been called the diagnostic window period. All types of screening assays are associated with a diagnostic window, the length of which is dependent upon the screening marker, the screening assay category, the sensitivity of the assay used and the replication kinetics of the virus during early infection.

The diagnostic window of HIV, HBV and HCV infections begins with the eclipse phase during which the virus is not yet detectable in blood (even by highly sensitive NAT-based assays). This non-viraemic phase is followed by the viraemic ramp-up phase during which virus concentration in the plasma increases in an exponential fashion. For each of the three bloodborne viruses covered in these Guidelines (HIV, HBV and HCV) a specific constant replication rate is apparent until a peak or plateau phase of maximal viral concentration is reached.

In the context of blood safety, the viraemic phase within the diagnostic window period is relevant. The start of the potentially infectious window period during the early ramp-up phase of viraemia can be defined as the point at which one virus particle is present in a blood component. A generally accepted worst-case assumption for cellular components is to define the start of the infectious window period as the point at which the concentration reaches one virus particle in 20 mL of plasma (the volume co-transfused with a red blood cell unit suspended in additive solution) (14). Viral replication characteristics in the early phase of infection are rather consistent among recently infected individuals. This phenomenon results in characteristic doubling times of plasma viral concentration for HIV, HBV and HCV. By knowing the viral replication kinetics of HIV, HBV or HCV in the early infection phase, along with the diagnostic sensitivity of the screening assay, the length of the viraemic phase can be extrapolated for each screening assay.
5.2.1  **HIV**

HIV replicates with an average doubling time of 20 hours (0.83 days) to reach a peak level of viraemia of up to $10^7$ IU HIV RNA/mL (15). This virus concentration decreases in parallel with the development of specific antibodies detectable by anti-HIV assays. The currently most sensitive antigen assays can detect HIV p24 antigen at a level corresponding to $10^4$ IU HIV RNA/mL. Most HIV antigen-antibody combination (“combo”) assays are less sensitive in their detection of p24 antigen when compared to antigen assays – with the corresponding HIV RNA concentration for detection by state-of-the-art combo assays being around $10^5$ IU/mL (15, 16). Attention should be paid to donors having taken early antiretroviral treatment or pre-exposure antiretroviral treatment which could reverse seroconversion and lower viral load (17).

5.2.2  **HBV**

The replication rate of HBV in the early infection phase as determined by the increase in viraemia is significantly lower when compared to HIV or HCV, with an HBV average doubling time of 2.6 days (18, 19). HBV viraemia in the early infection phase is detected earlier by NAT-based assays than by HBsAg assays. In the absence of NAT-based assays the use of HBsAg assays with a high analytical sensitivity is key for the detection of early infection.

5.2.3  **HCV**

For HCV an average doubling time of 10.8 hours (0.45 days) during the ramp-up phase has been determined, followed by an anti-HCV-negative plateau phase of several weeks characterized by high-level viraemia of up to $10^8$ IU HCV RNA/mL (20, 21). HCV core antigen appears to be detectable by core antigen assays during the major part of this anti-HCV-negative phase, namely the entire plateau phase and the last part of the ramp-up phase. Similar to HIV, the antigen detection efficiency of current HCV combo assays is less than that of the antigen assays. Combo assays have an overall detection rate of approximately 40% of anti-HCV-negative window period specimens, and preferentially detect those with virus concentrations above $10^6$ IU HCV RNA/mL (22).

6. Screening assay categories and diagnostic window periods

6.1  **Screening assay categories**

In these Guidelines screening assays are discussed according to the following categories:

- NAT-based
While antibody assays are designed to detect both recent and chronic persistent infections, the additional benefit of antigen or viral genome detection lies mainly in further reducing the diagnostic window period. The length of the diagnostic window period varies greatly between the different assay categories.

6.1.1 **NAT-based assays**

NAT-based assays detect viral nucleic acids after in vitro amplification of a target region of the viral genome. Such assays are performed on individual donations (ID-NAT) or in small minipools of donations (MP-NAT). A true infection may not be detectable by NAT-based assays if the concentration of viral genomes is below the detection limit of the assay. Without virus-enrichment steps (for example, ultracentrifugation) in pooled specimens the length of the window period increases with the minipool size and is shortest with ID-NAT. At low virus concentrations in the early ramp-up phase of the window period the amount of virus in a defined volume follows a Poisson distribution, with higher virus concentrations associated with increasing detection probabilities by NAT-based assay. The concentration range between a 5% and a 95% probability of detection may be 100-fold, and this complicates the estimation of window-period reduction that can be achieved by the use of NAT-based assays. In these WHO Guidelines the three-fold concentration of the 95% detection probability has been taken as worst-case assumption for reliable NAT detection for estimating virus concentration in a potentially contaminated plasma pool (Table A4.1; normal font). However, NAT-based assay window periods may be significantly shorter at the lower bound of uncertainty range. The vDWP corresponding to the 50% NAT-detection probability is considered a more accurate estimate for virus transmission risk by blood components without pathogen inactivation (Table A4.1; bold italic font) (23, 24).

6.1.2 **Antigen assays**

Antigen assays have been optimized for the detection of viral proteins (antigens), which are part of the virus particle, such as viral capsids (for example, HIV p24 or HCV core) or virus envelopes; or are subviral particles (for example, HBsAg). For recently infected individuals, non-reactive test results using antigen assays are caused by an absence of viral proteins, the presence of mutated antigen or the presence of antigens with concentrations below the detection limit of the assay.
6.1.3 **Combo assays**

Combo assays are designed to simultaneously detect specific antibodies and viral proteins; non-reactive combo assay test results for a true infection may be caused by the absence (or too low a concentration) of antibodies and/or viral antigens in the test sample, or by hidden epitopes in the immune complexes. The antigen-detection potency of combo assays is often lower than that of assays optimized for exclusive antigen detection.

6.1.4 **Antibody assays**

Antibody assays report infection through the detection of specific antibodies against the pathogen; for recently infected individuals, non-reactive test results using antibody assays can be caused by the absence of specific antibodies, an antibody concentration that is insufficient for obtaining a signal in the immunoassay or low binding strength (avidity) of antibodies. The design of the antibody assay determines its sensitivity and capacity to detect low-avidity antibodies.

6.1.5 **RDTs**

RDTs are diagnostic devices of simple design, often based on immunochromatographic (lateral flow) or immunofiltration (flow-through) technologies. RDTs do not require complex equipment and provide the test result within a short time (15–30 minutes). Although often not claimed by the manufacturer a suitable for use in blood screening, these devices are sometimes used for blood-safety testing in resource-limited settings or in emergency situations. RDT technology is associated with a lower sensitivity than that of more sophisticated immunoassays developed specifically for blood screening (25, 26).

6.2 **Diagnostic window periods**

NAT-based assays are generally able to detect a recent infection sooner than antigen assays, followed by combo assays and antibody assays. These differential capacities for detecting recent infections result in different lengths of the diagnostic window period for different assay categories. Within each of the assay categories, individual assays from different manufacturers may have different sensitivities. These differences sometimes result in overlapping diagnostic sensitivities in detecting early infection when less sensitive assays of one category are compared with the more sensitive assays in another category. For example, currently the most sensitive HIV1/2 antibody assay provides a shorter diagnostic window period than the least sensitive HIV1/2 combo assay. This is true both for assays prequalified by WHO and for CE-marked assays. Furthermore, assays may...
have differing sensitivities for different viral genotypes and/or for viral subtypes. The vast majority of commercial seroconversion panels used for diagnostic sensitivity studies originate from regular plasma donors, and mainly represent viral genotypes and subtypes prevalent in Europe and the United States (namely HIV subtype B, HCV genotypes 1–3 and HBV genotype A). However, the sensitivity of assays observed with these seroconversion panels may not always be representative for early infection with viral genotypes prevalent elsewhere in the world (27). Further details on this and other considerations in the evaluation of new blood-screening assays are provided in Appendix 1.

Mean estimates of the length of the vDWP for so-called state-of-the-art assays are presented by assay category in Table A4.1. These estimates should be used for risk calculation unless more detailed information is available on the sensitivity and corresponding window period of the assay used for blood screening. Hence, if comparative data obtained with multiple seroconversion panels indicate that the sensitivity of a specific assay is clearly different from the mean value shown in Table A4.1, the more accurate data for this assay should be used for the estimation of residual risk.
Table A4.1
Length of the vDWP for different assay categories (days)\(^a\)

<table>
<thead>
<tr>
<th></th>
<th>ID-NAT(^b)</th>
<th>MP16-NAT(^b,c)</th>
<th>Antigen EIA/CLIA(^d)</th>
<th>Combo EIA/CLIA(^d)</th>
<th>Antibody EIA/CLIA(^d)</th>
<th>Antigen RDT(^e)</th>
<th>Combo RDT(^e)</th>
<th>Antibody RDT(^e)</th>
</tr>
</thead>
<tbody>
<tr>
<td>HIV</td>
<td>8</td>
<td>11</td>
<td>14</td>
<td>16</td>
<td>21</td>
<td>-</td>
<td>20</td>
<td>28</td>
</tr>
<tr>
<td></td>
<td>4</td>
<td>7</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>HBV</td>
<td>27</td>
<td>37</td>
<td>42</td>
<td>-</td>
<td>-</td>
<td>55</td>
<td>-</td>
<td>-</td>
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<td>17</td>
<td>27</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>HCV</td>
<td>5</td>
<td>7</td>
<td>9</td>
<td>38</td>
<td>60</td>
<td>-</td>
<td>-</td>
<td>80</td>
</tr>
<tr>
<td></td>
<td>3</td>
<td>5</td>
<td></td>
<td></td>
<td></td>
<td></td>
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<td></td>
</tr>
</tbody>
</table>

\(^a\) vDWP: defined here as the period with a virus concentration of \(\geq 1\) virus particle in 20 mL plasma. 1 virus particle has been assumed to correspond to 1 (HCV, HBV) or 2 (HIV) viral genome copies. 1 IU HCV RNA has been assumed to correspond to 4 genome copies HCV RNA; 1 IU HBV DNA to 5 genome copies HBV DNA; and 1 IU HIV-1 RNA to 0.5 genome copies HIV-1 RNA.

\(^b\) NAT-based assays: to date, only a limited number of NAT-based assays claiming blood screening as an intended use have been CE-marked or approved by the United States Food and Drug Administration (FDA). For a worst-case scenario, diagnostic window periods of less sensitive NAT-based assay versions have been taken as examples in Table A4.1.

Plasma pool contamination: for estimating the maximal virus concentration in a contaminated plasma pool the three-fold concentration of the 95% detection probability has been taken as a worst-case assumption for reliable and consistent (“100%”) NAT detection. This approach is analogous to the determination of the whole system failure rate in the European Commission’s common technical specifications for in vitro diagnostic medical devices (28). The respective sizes of the vDWPs in days are indicated in normal font.

Transmission risk by non-pathogen-inactivated blood components: the Poisson distribution property of analyte detection by NAT-based assay is considered suitable for more accurate estimation of virus transmission risk by blood components without pathogen inactivation. NAT-based assay window periods may be significantly shorter at lower bound of uncertainty range. The probability of 50% detection in the early ramp-up phase of viraemia may be taken as the basis for the respective vDWPs (indicated in bold italic font) (23, 24).

\(^c\) MP16-NAT = MP-NAT of 16 donations.

\(^d\) EIA/CLIA: for these assay types United States FDA-approved, CE-marked and/or WHO-prequalified assays of medium sensitivity have been selected as examples (20, 22, 25, 26, 29, 30).

\(^e\) RDT: there is a wide range of sensitivity among different RDT assays; values for medium-sensitivity RDTs have been used for Table A4.1 (25, 26).
7. Virus concentrations during diagnostic window period

For risk modelling of plasma pool contamination the maximal virus concentrations that can be found during the respective window period are relevant. Viral loads in viraemic plasma units undetected by screening assays define the extent of initial contamination of the plasma pool. Other parameters for calculation of potential contamination of plasma pools are the number of viraemic donations expected per pool and the individual plasma unit volume relative to the pool size. The maximal viral loads of window-period donations are listed in Table A4.2 as worst-case scenarios for each of the different assay categories correspondingly shown in Table A4.1.

Table A4.2
Maximal concentration of viral genomes in the vDWP (IU/mL)\(^a\)

<table>
<thead>
<tr>
<th></th>
<th>ID-NAT</th>
<th>MP16-NAT</th>
<th>Antigen EIA/CLIA</th>
<th>Combo EIA/CLIA</th>
<th>Antibody EIA/CLIA</th>
<th>Antigen RDT</th>
<th>Combo RDT</th>
<th>Antibody RDT</th>
</tr>
</thead>
<tbody>
<tr>
<td>HIV</td>
<td>150</td>
<td>2400</td>
<td>(2 \times 10^4)</td>
<td>(10^5)</td>
<td>(10^7)</td>
<td>(10^7)</td>
<td>(10^7)</td>
<td></td>
</tr>
<tr>
<td>HBV</td>
<td>24</td>
<td>384</td>
<td>(10^3)</td>
<td></td>
<td>(3 \times 10^4)</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>HCV</td>
<td>30</td>
<td>480</td>
<td>(10^4)</td>
<td>(5 \times 10^6)</td>
<td>(10^8)</td>
<td></td>
<td></td>
<td>(10^8)</td>
</tr>
</tbody>
</table>

\(^a\) IU/mL = International Units per millilitre

8. Confirmation of reactive screening results

The residual risk estimations rely on reactive screening assay results representing true infection events. Initially reactive screening results obtained by antibody or antigen tests should be checked by repeat testing in duplicate in the same assay. Even when reactivity is repeatedly obtained in the routine screening assay, the test result should still be checked by a confirmation strategy (31).

Confirmation strategies may include the use of more specific assays (for example, HIV Western blot or immunoblot, HCV immunoblot and HBsAg neutralization assay) or another screening or diagnostic assay for the same marker, but of different design.

NAT results should be checked by testing an independent aliquot of the donation to exclude contamination and/or by testing replicates to overcome potential Poisson distribution of the analyte present at low concentration. Follow-up investigations of the donor may further assist in differentiating false-positive from true-positive test results.
Only reactive screening test results subsequently confirmed as true positive should be taken for the estimation of residual risk. If no confirmation is performed, residual risk estimations based on reactive test results represent a worst-case scenario and may considerably overestimate the risks.

9. Virus epidemiology of donor populations

Donor populations consist of first-time donors (individuals donating for the first time) and repeat donors (donors with previous donation(s) having tested negative). Blood systems aim towards having an established population of repeat donors undergoing constant selection for absence of infectious markers.

9.1 First-time donors

Positive screening test results in first-time donors may be an indication of infections that occurred either a longer time ago (prevalent infections) or more recently (incident infections). Prevalent infections in first-time donors are expected to be easily detected by high-quality screening assay(s) without assay failures; in contrast, incident infections represent the major contribution to the residual risk of window-period infections. Making the distinction between prevalent and incident infections will require more detailed investigation – recently infected donors may be identified by NAT-only or antigen-only positive results. Furthermore, for antibody-positive donors, modified antibody assays (“detuned” or “recency” assays) can be used to determine the antibody binding strength (avidity). As antibody avidity increases with maturation of the humoral immune response it is possible to differentiate first-time donors with more recent (incident) infections (low-avidity antibodies) from donors with past (prevalent) infections (high-avidity antibodies) and thus determine the specific incidence of infection in this subpopulation (14, 32). If results from these investigations are not available for a specific first-time donor population, the incidence of infection in these donors can be derived from the rate among repeat donors by applying an adjustment factor. A number of scientific studies on HIV, HBV and HCV infections in different donor populations have investigated their incidence among both first-time and repeat donors. Although some of these studies found a two- to three-fold higher rate of recent infections among first-time donors (compared to the corresponding repeat donors) other studies have not found such a difference between the two donor subpopulations (33–38). In the absence of incidence data specific to the first-time donor population, one option is to assume a three-fold higher incidence of virus infections as the worst-case scenario for this subpopulation when compared to the corresponding repeat-donor subpopulation of the same blood establishment. This factor will be referred to as the “first-time donor incidence adjustment factor”. 
First-time donor incidence (and corresponding adjustment factor) does not have to be calculated for blood establishments in which newly registered donors are routinely tested for bloodborne infections prior to their first donation of blood or blood components.

9.2 Repeat donors

For repeat donors any confirmed positive screening test result indicates a new infection, which is likely to have occurred during the interdonation interval (IDI) – defined as the time period between the most recent donation (which in this case will have tested positive) and the previous donation (which will have tested negative). However, it is also possible that the previous donation (tested negative) was drawn during the diagnostic window period of the screening assay. The relative frequency of this possibility depends on the length of the IDI, with shorter IDIs increasing the probability of a vDWP donation that tested negative in the screening assay.

10. Estimation of incidence and window period modelling of risks

10.1 Incidence

The rate of new infections of repeat donors (incidence) is defined as the number of NAT conversions or seroconversions (number of infected donors) divided by the total number of person years of observation of all donors during the study period (14, 39, 40). Determining the person years of observation requires a computer system that records the follow-up periods for each individual donation. This kind of information management system is often not available in resource-limited blood establishments.

For the purpose of these Guidelines, both the estimation of incidence and the estimation of the residual risk per blood donation are derived from data from the repeat-donor population for the period of one calendar year (365 days). Incidence is calculated by dividing the number of newly infected repeat donors by the total number of repeat donors, usually expressed as the number of new infection cases per 100 000 repeat donors. If one calendar year is taken as the observation period then the incidence is expressed as per 100 000 person years. This simplification assumes that each repeat donor has been followed for one year during the calendar year and that differences in follow-up periods for individual donors will average out at one person year of observation per donor.

In low-incidence regions the number of positive donors may show strong year-to-year variation. For these situations longer periods may be chosen for the calculation of residual risks.
Screening-positive donations that were excluded for other reasons (for example, donor self-exclusion) may be excluded from the calculation (adjusted incidence).

**Formula 1: Incidence (per 100 000 person years)**

\[
\text{Incidence} = \frac{\text{number of repeat donors tested positive during one year}}{\text{total number of repeat donors in the year}} \times 100 000
\]

10.2 **Residual risk per blood donation in repeat donors**

For calculating the probability that a blood donation has been collected during the vDWP different factors are involved:

- the rate of new infections (incidence) in the repeat-donor population
- the length of the vDWP for the assay used (Table A4.1).

The residual risk of a blood donation from a repeat donor having been collected during the vDWP of the screening assay used can be calculated as follows:

**Formula 2: Residual risk (RR) per donation**

\[
\text{RR per donation} = \text{vDWP} \times \text{incidence}
\]

RR is usually expressed as per million donations (for which one has to multiply the RR figure calculated above by 1 million.

Formula 2 can be directly used to calculate RR for HIV and HCV infections in repeat donors; for HBV infections RR calculated by this formula has to be multiplied by an HBV incidence adjustment factor.

10.2.1 **HBV incidence adjustment factor**

An adjustment factor of ≥ 1 is necessary because HBV (sero)conversions in repeat donors may be missed due to the transient nature of viraemia and antigenaemia in HBV infections that resolve after the acute phase. Such a transient infection course is seen in adults for the majority of HBV infections (95%) while 5% become chronic carriers. The probability of missing transiently detectable HBsAg or HBV DNA in repeat donors by respective screening assays depends on the length of the IDIs and on assay sensitivity. The donation frequency of repeat donors (average number of donations per repeat donor) determines the average length of the IDI. The average IDI (in days) can be calculated by dividing the observation period of one calendar year (365 days) by the average number of donations per repeat donor. For each assay category
a mean detection period for the transient HBV marker (HBsAg or HBV DNA) can be factored into the adjustment. Further contributions to the adjustment factor originate from HBV infections without detectable antigaemria (assumed to be 25%; transiently picked up by sensitive HBV NAT-based assays) (1). The scientific literature provides several different estimates for the length of transient antigaemia (1, 19, 41). The differences observed between the underlying studies may be explained by different infection routes, different inoculum, different HBV genotypes, and HBsAg or HBV-DNA assays of different sensitivity.

The lengths of the HBV marker detection periods have been estimated from the available data for the different assay categories and are listed in Table A4.3.

<table>
<thead>
<tr>
<th></th>
<th>NAT ID</th>
<th>MP16-NAT</th>
<th>HBsAg EIA/CLIA</th>
<th>HBsAg RDT</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>90</td>
<td>70</td>
<td>60</td>
<td>44</td>
</tr>
</tbody>
</table>

The probability $P$ (in %) of detection by HBsAg assays (Table A4.3) may be calculated as:

$$P = 70\% \times \frac{\text{HBsAg detection period}}{\text{IDI}} + 5\%$$

The probability $P$ (in %) of detection by NAT-based testing (Table A4.3) may be calculated as:

$$P = 95\% \times \frac{\text{HBV DNA detection period}}{\text{IDI}} + 5\%$$

The HBV incidence adjustment factor is calculated as $100/P$. For results where $P \geq 100\%$ no adjustment is necessary.

To determine the RR per donation for HBV infection, the figure obtained for HBV using Formula 2 in section 10.2 above is then multiplied by the adjustment factor for the specific assay category used.

### 10.2.2 Adjustment for IDIs

The incidence/window period modelling of residual risk, as described above, assumes that donation behaviour with regard to donation timing and frequency is the same for both infected and non-infected donors. However, evidence can be found in the scientific literature indicating that seroconverting or
NAT-converting donors sometimes delay their return to blood donation, and therefore have larger average IDIs than non-infected donors, resulting in a lower residual risk (42). Mathematical models are available to reflect this difference in donor behaviour (43). For high-incidence settings (that is, settings in which a higher number of repeat donors have tested positive (seroconverters or NAT converters) for HIV, HBV or HCV infection) the harmonic mean of individual IDIs (in days) of the converting repeat donors (that is, the period between the last negative donation and the first positive donation after infection with the respective virus) may be compared with the mean IDI of non-infected repeat donors (36). Respective functions for calculating mean or harmonic mean values are part of commonly used statistical software (for example, Excel). The residual risk calculation may then include the IDI adjustment factor $S$.

$$
S = \frac{\text{mean IDI of all donors}}{\text{harmonic mean IDI of converters for virus X}}
$$

If, however, only a few acute infections are found it is advised to take the average IDI of all repeat donors.

### 10.2.3 First-time donor incidence adjustment factor

In the absence of specific incidence data for first-time donors, a three-fold higher residual risk may be assumed for blood donations from such donors when compared to repeat donors of the same donor population.

Accordingly, the residual risk of a blood donation from a first-time donor having been collected during the vDWP of the screening assay may be assumed to be three-fold higher than the risk calculated for a blood donation obtained from the corresponding repeat donors of the same blood establishment.

### 11. Residual risks

The approach to residual risk estimation proposed by these Guidelines requires less detailed data on individual donors when compared to other models published in the scientific literature. A recent comparison of seven different models for estimating HIV incidence was performed by simulating donor populations with different donation frequencies combined with different incidence rates (44). The approach proposed by these Guidelines was retrospectively included in the same simulation scenarios. In summary, this exercise revealed a slight overestimation of incidence (by up to 20%) in the scenarios with low donation frequency. This finding confirms the validity of the approach proposed in these Guidelines and is in line with the worst-case scenarios chosen for the different parameters, for example: (a) the proposed lengths of the vDWP (Table A4.1);
(b) the assumption of one virus particle in 20 mL plasma being infectious; or (c) the use of the maximal viral concentration for all vDWP donations for the calculation of potential plasma pool contamination (Table A4.2).

11.1 Infection of recipients of non-pathogen-inactivated blood components

The actual infection risk in recipients of non-pathogen-inactivated blood components is dependent on factors such as the amount of intact viruses transmitted, the presence of potentially neutralizing antibodies in the donation or recipient, virus properties and recipient immunological factors (30). Using worst-case scenarios, the probability of viraemic donations escaping screening can be estimated using Formula 2 in section 10.2 above. For whole blood donations, different blood components (red cells, platelets and plasma) may be obtained from the same donation and transfused to recipients, each contributing to the residual risk. The amount of plasma in the blood component, the probability of non-detection by the screening assay(s) and the infectivity of the virus after storage of the blood component are all important factors influencing the infection risk but are beyond the scope of these Guidelines (24, 30).

11.2 Contamination of plasma pools

Plasma prepared from whole blood donations (recovered plasma) or obtained by plasmapheresis may be used as source material for plasma-derived products manufactured from plasma pools (such as immunoglobulins, albumin and clotting factors). These pools may be contaminated with HIV, HBV or HCV as a result of the inclusion of plasma units originating from window-period donations not detected by the screening assays. The extent of potential plasma-pool contamination depends upon a number of factors:

- the expected probability of obtaining donations during the vDWP of the screening assay used;
- the (maximal) amount of virus contamination in vDWP plasma units;
- the volume of contaminated plasma unit(s) relative to pool size.

The proportion of viraemic plasma units is estimated by the residual risk calculation. The (maximal) level of virus contamination in respective plasma units can be calculated from the individual plasma volume and its virus concentration. For these calculations, the maximal viral load of window-period donations (shown above in Table A4.2 for the different assay categories) should be taken as the worst-case scenario, even though only a minority of window-period plasma units will reach the maximal viral load.
Authors and acknowledgements

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Between September 2015 and May 2016 the draft document was presented and extensively discussed at a range of international workshops and other forums. The resulting revised draft document was then published on the WHO Biologicals website during a round of public consultation (11 July–26 September 2016). During this phase further comments were received from the following organizations, institutions and individuals: European Blood Alliance (EBA); International Plasma Fractionation Association (IPFA); International Society of Blood Transfusion (ISBT); Permanent United Nations Representation of France; Plasma Protein Therapeutics Association (PPTA); Dr P. Akolkar and Dr I. Hewlett, United States Food and Drug Administration, the USA; Dr D. Brambilla, Dr S. Kleinman, Dr M. Busch, Dr R. Dodd, and S. Glynn for the Recipient Epidemiology and Donor Evaluation Study (REDS)-III; Dr N. Lelie, Consultant, Amsterdam, the Netherlands; Dr F. Moftah, Egyptian Society for Blood Services, and Arab Transfusion Medicine Forum, Egypt; Dr M-L. Hecquet, European Directorate for the Quality of Medicines & HealthCare, France; Dr E. Lindberg, Medical Products Agency, Sweden; Dr M. Jannssen, University Medical Center Utrecht, the Netherlands; Dr G. Praefcke, Paul-Ehrlich-Institut, Germany; A. Sands, World Health Organization, Switzerland; M. Vermeulen, South African National Blood Service, South Africa;

In October 2016, following review and incorporation of all comments received, the final draft document WHO/BS/2016.2283 was prepared.

Further changes were subsequently made to document WHO/BS/2016.2283 by the WHO Expert Committee on Biological Standardization.
References


Appendix 1

Evaluation of new blood-screening assays

Depending on the legal structure in a country, a regulatory body or the national blood system itself may be responsible for decisions on the acceptability of new blood-screening assays. It is recommended that previous assessments of quality features of the assay performed by experienced regulatory authorities (for example, United States FDA approval, European CE certification, and Australian Therapeutic Goods Administration (TGA) or Health Canada marketing authorizations) or by the WHO Prequalification Programme for IVDs should be taken into account. Previous assessments by such stringent regulatory bodies will have included the review of analytical and clinical performance data submitted by the manufacturer, and of the manufacturer’s quality management system and batch-to-batch consistency – and in the case of WHO prequalification, an independent performance evaluation.

As a result, a country’s assessment of manufacturer documentation, with a focus on the specific regional situation and needs, may be sufficient for assays already approved elsewhere under stringent regulation.

If local regulation requires a performance evaluation of new assays (for example, by a national reference laboratory) prior to their implementation, it is recommended that the evaluation focuses on essential assay features through a targeted performance evaluation.

Assessment of documents

Documents provided by the IVD manufacturer may be assessed, with a special focus placed on the specific regional situation and needs. Such a focus may include assessing whether or not the stability studies performed by the manufacturer cover the regional environmental conditions (for example, with regard to temperature and humidity) or whether the Instructions for Use are appropriate for the target users.

In addition, performance evaluation studies documented by the IVD manufacturer may be reviewed to evaluate the extent of representation of specimens reflecting the regional situation (for example, with regard to viral genotypes or variants) or to assess potential interference with the test result by other regionally more prevalent infections.
Targeted performance evaluation of new assays used for blood screening

If laboratory testing of a new IVD is a component of the national or regional evaluation and approval scheme, it is advisable not to repeat evaluation elements already performed by other bodies, but to focus instead on regionally important quality aspects. This would involve, for example, a focused assessment of performance data with respect to viral variants or genotypes prevalent in the region.

Well-characterized specimen panels representing the regional epidemiological situation with regard to viral variants/genotypes of HIV, HBV or HCV may be helpful for comparative independent evaluation of new assays. A comparative database obtained using a number of assays may then be the scientific basis for the definition of acceptance criteria for new assays and for the identification of less suitable assays.

The preconditions for the suitability of such panels are the inclusion of specimens differentiating between different assays (for example, low-positive specimens or positive specimens previously tested discrepantly by different assays) and the availability of sufficient volumes to allow a number of evaluations to obtain comparative data. The recommended size of such a panel strongly depends on its composition, with more critical panel members (for example, low-positive or early infection specimens) able to differentiate between assays being more important than a high number of strong positive specimens. Panels used for this type of exercise typically comprise 20–50 members collected from different phases of the infection. A strategy for the replacement of panel members should be in place.

Furthermore, WHO offers through its IVD standardization programme a range of biological reference preparations that may be useful in the confirmation of basic assay features. WHO International Standards (expressed in IU) are available for the confirmation of analytical sensitivity, while WHO Reference Panels representing the major viral genotypes could be used to check genotype-detection efficiency.

These WHO reference preparations are usually lyophilized to facilitate worldwide shipping and are listed in the WHO online catalogue (http://www.who.int/bloodproducts/catalogue/en/). They can be obtained from the WHO Collaborating Centres which act as WHO custodians in this field – namely, the National Institute for Biological Standards and Control (NIBSC), England, or the Paul-Ehrlich-Institut (PEI), Germany.
Table A4A1.1 summarizes the most important WHO reference preparations currently available in the field of blood screening.

Table A4A1.1
**WHO reference preparations in the field of blood screening**

<table>
<thead>
<tr>
<th>Marker</th>
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<th>Details</th>
<th>Custodian</th>
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<tr>
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<td>HIV-1 subtypes A, B, C, CRF01_AE; group O; HIV-2</td>
<td>NIBSC</td>
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<td></td>
<td>Lyophilized</td>
<td>No unitage</td>
<td></td>
</tr>
<tr>
<td>HIV-1 p24</td>
<td>1st International Reference Reagent</td>
<td>–</td>
<td>NIBSC</td>
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<td></td>
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<td>1000 IU/ampoule</td>
<td></td>
</tr>
<tr>
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<td>3rd International Standard</td>
<td>–</td>
<td>NIBSC</td>
</tr>
<tr>
<td></td>
<td>Lyophilized</td>
<td>185 000 IU/mL</td>
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</tr>
<tr>
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<td>HIV-1 CRFs 11GJ, 02AG, 01AE, 01AGJU,BG24; subtypes J, G, C; group O</td>
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<td></td>
<td>circulating recombinant forms (CRFs)</td>
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<td></td>
<td>Lyophilized</td>
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<td></td>
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<td></td>
<td>Lyophilized</td>
<td>No unitage</td>
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</tr>
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<td>NIBSC</td>
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<td>Details</td>
<td>Custodian</td>
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<tr>
<td>------------------------</td>
<td>--------------------------------------</td>
<td>---------</td>
<td>-----------</td>
</tr>
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<td>HCV RNA</td>
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<td>–</td>
<td>NIBSC</td>
</tr>
</tbody>
</table>
Appendix 2

Examples for estimation of residual risks

Example 1: HCV screening by anti-HCV EIA

Centre A; observation period 01.06.2011–31.05.2012
49 660 repeat donors; 100 313 donations; 45 anti-HCV pos (EIA)
11 452 first-time donors; 11 452 donations; 89 anti-HCV pos (EIA)

Table A4.1 (see section 6.2 main text) – anti-HCV EIA: vDWP = 60 days = 0.164 years
Table A4.2 (see section 7 main text) – anti-HCV EIA: maximal virus concentration: \(10^8\) IU HCV RNA/mL plasma of vDWP donation

A. Residual risk (RR) per blood donation from repeat donors

Incidence = \[
\frac{\text{number of repeat donors tested positive during one year}}{\text{total number of repeat donors in the year}} \times 100 000
\]
\[
= \frac{45}{49 660} \times 100 000
\]
\[
= 90.61 \text{ HCV infections per 100 000 donor years}
\]

RR per blood donation = vDWP \times incidence
\[
= 0.164 \times 0.000 906 1 = 0.000 148 600
\]
\[
= 148.60 \text{ per million donations}
\]

Number (N) of vDWP blood donations from repeat donors
\[
N = 100 313 \times \frac{148.60}{1 000 000} = 14.90
\]

B. Residual risk (RR) per blood donation from first-time donors

Positive screening test results for first-time donors represent mainly old (prevalent) infections. The rate of recent infections can be determined by specific investigations (for example, recency assays or NAT-only positive results).

In the absence of incidence data, the worst-case assumption is a three-fold incidence in first-time donors compared to the corresponding repeat donors.
RR = 0.000 148 61 × 3 = 0.000 445 = 445 per million donations

Number (N) of vDWP blood donations from first-time donors:

\[ N = \frac{11 452 \times 445}{1 000 000} = 5.10 \]

C. Expected number (N) and risk of window-phase donations for repeat and first-time donors combined (Centre A; observation period of 1 year)

\[ N = 14.90 + 5.10 = 20.00 \]

\[ RR = \frac{20}{100 313 + 11 452} = 0.000 179 = 179 \text{ per million donations} \]

Example 2: HBV screening by HBsAg RDT; HBV adjustment factor

Centre A; observation period 01.06.2011–31.05.2012

49 660 repeat donors; 100 313 donations; 184 HBsAg RDT pos
11 452 first-time donors; 11 452 donations; 291 HBsAg RDT pos

Table A4.1 (section 6.2 main text) – HBsAg RDT: vDWP = 55 days = 0.15 years
Table A4.3 (section 10.2.1 main text) – HBsAg RDTs: HBV marker detection period = 44 days

Average number of donations per repeat donor: 100 313/49 660 = 2.02

Interdonation interval (IDI)

\[ IDI = \frac{365 \text{ days}}{\text{average number of donations per repeat donor}} = 180.69 \text{ days} \]

A. Residual risk (RR) per blood donation from repeat donors (without adjustment for transient HBsAg)

Incidence = \[ \frac{\text{number of repeat donors tested positive during one year}}{\text{total number of repeat donors in the year}} \times 100 000 \]

\[ = \frac{184}{49 660} \times 100 000 \]

\[ = 370.52 \text{ HBV infections per 100 000 donor years} \]
vDWP = 55 days = 0.15 years

RR = vDWP \times \text{incidence}

= 0.15 \times 0.0037052 = 0.00055578

= 555.78 per million donations

B. HBV incidence adjustment factor

Probability (P) for HBsAg detection

\[
P = 70\% \times \frac{\text{HBV marker detection period}}{\text{IDI}} + 5\%
\]

\[
= 70\% \times \frac{44 \text{ days}}{180.69 \text{ days}} + 5\% = 70\% \times 0.24 + 5\% = 21.8\%
\]

HBV incidence adjustment factor =

\[
\frac{100\%}{P} = \frac{100\%}{21.8\%} = 4.58
\]

C. Residual risk (RR) per blood donation from repeat donors (with adjustment for transient HBsAg)

Adjusted RR = 4.58 \times 0.00055578 = 0.002545 = 2545 per million donations.