Introduction

Immunization against human platelet alloantigens (HPAs) can induce several alloimmune thrombocytopenic syndromes with the clinical risk of severe bleeding. The serologic diagnosis of these syndromes is based on HPA typing and characterization of the corresponding platelet-specific alloantibodies (alloabs).

Heterogeneity of Platelet Alloantigens and Alloantibodies: New Insights into Structure and Function

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Key Words
Alloantigens, human platelet: structure, function · Thrombocytopenia, alloimmune

Summary
Human platelet alloantigens (HPAs) and their corresponding alloantibodies (alloabs) play an essential role in fetal and neonatal alloimmune thrombocytopenia, posttransfusion purpura and platelet transfusion refractoriness. Emerging genotyping methods (e.g., microarray technology) will allow an automated throughput for HPA typing of large donor cohorts in the near future. For the clinical diagnosis of alloimmune thrombocytopenia, however, the proof of pathogenic alloabs still remains a prerequisite. Nowadays, monoclonal antibody-based antigen capture assays are the state of the art in many laboratories. This technique seems to come up against limiting factors. In a certain number of cases that are highly suspicious for alloimmune thrombocytopenia, platelet-specific alloabs are not detectable. Current observations indicate that these alloabs are heterogeneous in terms of their alloantigenic determinants as well as the consequences on platelet function. This heterogeneity may correlate to the severe bleeding complications sometimes seen in patients with alloimmune thrombocytopenia. New insights on the role of pathogenic alloabs will help us to improve diagnostic and therapeutic approaches for the adequate treatment of affected patients.

Zusammenfassung
During the last years, several molecular biological methods were developed for HPA typing, which allow reliable and fast determination of platelet allotypes [1, 2]. In contrast, the detection of alloabs is technically still challenging. Nowadays, monoclonal antibody (mab)-based antigen capture assays (MAIPA) represent the standard technique for platelet alloabs testing [3, 4]. However, in a certain number of cases that are highly suspicious for alloimmune thrombocytopenia, platelet-specific alloabs are not detectable [5–7]. Another interesting aspect is the heterogeneity of the clinical presentation of alloimmune thrombocytopenic syndromes varying from mild thrombocytopenia to severe, sometimes life-threatening bleeding [7]. Until now, the reasons for this heterogeneous clinical picture are not well understood. Over the last years, evidence has accumulated that platelet-specific alloabs are heterogeneous in several ways. The binding region of HPA-1a alloabs on \( \alpha_{IIb}\beta_3 \) integrin differs from one individual to another [8], and platelet function impairment due to alloabs has been observed. The epitope heterogeneity may influence platelet antibody testing and may also cause platelet function deficits that are responsible for pronounced bleeding. The purpose of this review is to highlight recent data about heterogeneity of platelet-specific alloabs.

### Human Platelet Alloantigens

The currently known HPAs are listed in table 1 [9]. So far, 6 diallelic alloantigen systems (HPA-1, -2, -3, -4, -5 and -15) and 10 low-frequency HPAs have been discovered. They are located on the platelet membrane glycoproteins (GPs) GPIIa/IIa (\( \alpha_{IIb}\beta_1 \) integrin), GPIb/IIa (\( \alpha_{IIb}\beta_3 \) integrin), GPIb/IX and CD109. Most all HPAs are formed by single missense mutations of the respective gene. Only HPA-14w is formed by a single amino acid deletion of the \( \beta_3 \) integrin subunit [10].

#### Table 1. Molecular genetics of human platelet alloantigens

<table>
<thead>
<tr>
<th>Antigen</th>
<th>Synonym</th>
<th>Glycoprotein</th>
<th>HGNC</th>
<th>Nucleotide substitution</th>
<th>Amino acid substitution</th>
</tr>
</thead>
<tbody>
<tr>
<td>HPA-1a</td>
<td>Zw(^a), PlA(^{A1})</td>
<td>GPIIa</td>
<td>ITGB3</td>
<td>T176</td>
<td>Leu33</td>
</tr>
<tr>
<td>HPA-1b</td>
<td>Zw(^b), PlA(^{A2})</td>
<td>GPIIa</td>
<td>ITGB3</td>
<td>C176</td>
<td>Pro33</td>
</tr>
<tr>
<td>HPA-2a</td>
<td>Ko(^b)</td>
<td>GPIIa</td>
<td>GP1BA</td>
<td>C482</td>
<td>Thr145</td>
</tr>
<tr>
<td>HPA-2b</td>
<td>Ko(^a), Sib(^b)</td>
<td>GPIIb</td>
<td>GP1BA</td>
<td>T482</td>
<td>Met145</td>
</tr>
<tr>
<td>HPA-3a</td>
<td>Bak(^b), Lek(^a)</td>
<td>GPIIb</td>
<td>ITGA2B</td>
<td>T2621</td>
<td>Ile843</td>
</tr>
<tr>
<td>HPA-3b</td>
<td>Bakb</td>
<td>GPIIb</td>
<td>ITGA2B</td>
<td>G2621</td>
<td>Ser843</td>
</tr>
<tr>
<td>HPA-4a</td>
<td>Yuk(^b), Pen(^a)</td>
<td>GPIIa</td>
<td>ITGB3</td>
<td>G506</td>
<td>ArgL43</td>
</tr>
<tr>
<td>HPA-4b</td>
<td>Yuk(^a), Pen(^b)</td>
<td>GPIIa</td>
<td>ITGB3</td>
<td>A506</td>
<td>GlyG43</td>
</tr>
<tr>
<td>HPA-5a</td>
<td>Br(^a), Zav(^b)</td>
<td>GPIa</td>
<td>ITGA2</td>
<td>G1600</td>
<td>Glu505</td>
</tr>
<tr>
<td>HPA-5b</td>
<td>Br(^b), Zav(^a), Hc(^a)</td>
<td>GPIa</td>
<td>ITGA2</td>
<td>A1600</td>
<td>Lys505</td>
</tr>
<tr>
<td>HPA-6w</td>
<td>Ca(^a), Tu(^b)</td>
<td>GPIIa</td>
<td>ITGB3</td>
<td>1544C &gt; A</td>
<td>ArgG489Gln</td>
</tr>
<tr>
<td>HPA-7w</td>
<td>Mo(^a)</td>
<td>GPIIa</td>
<td>ITGB3</td>
<td>1297C &gt; G</td>
<td>Pro80TAla</td>
</tr>
<tr>
<td>HPA-8w</td>
<td>Sr(^a)</td>
<td>GPIIa</td>
<td>ITGB3</td>
<td>1984C &gt; T</td>
<td>ArgG636Gys</td>
</tr>
<tr>
<td>HPA-9w</td>
<td>Max(^a)</td>
<td>GPIIa</td>
<td>ITGB3</td>
<td>2602G &gt; A</td>
<td>ArgG636Cys</td>
</tr>
<tr>
<td>HPA-10w</td>
<td>La(^a)</td>
<td>GPIIa</td>
<td>ITGB3</td>
<td>263G &gt; A</td>
<td>ArgG62Gls</td>
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<tr>
<td>HPA-11w</td>
<td>Gro(^a)</td>
<td>GPIIa</td>
<td>ITGB3</td>
<td>1976G &gt; A</td>
<td>ArgG636His</td>
</tr>
<tr>
<td>HPA-12w</td>
<td>Iy(^a)</td>
<td>GPIbb</td>
<td>GPIBB</td>
<td>119G &gt; A</td>
<td>ArgG636Gys</td>
</tr>
<tr>
<td>HPA-13w</td>
<td>Sit(^a)</td>
<td>GPIa</td>
<td>ITGA2</td>
<td>2483C &gt; T</td>
<td>Thr879Met</td>
</tr>
<tr>
<td>HPA-14w</td>
<td>Oe(^a)</td>
<td>GPIIa</td>
<td>ITGB3</td>
<td>1909, 1911delAAAG</td>
<td>Lys611del</td>
</tr>
<tr>
<td>HPA-15a</td>
<td>Gov(^b)</td>
<td>CD109</td>
<td>CD109</td>
<td>C2108</td>
<td>Ser682</td>
</tr>
<tr>
<td>HPA-15b</td>
<td>Gov(^a)</td>
<td>CD109</td>
<td>CD109</td>
<td>A2108</td>
<td>Tyr682</td>
</tr>
<tr>
<td>HPA-16w</td>
<td>Duv(^a)</td>
<td>GPIIa</td>
<td>ITGB3</td>
<td>497C &gt; T</td>
<td>Thr140Ile</td>
</tr>
</tbody>
</table>

HGNC = Human Gene Nomenclature Committee.

#### Table 2. Antibody specificities in serologically verified cases of FNAIT (Gießen, 1987–2002, n = 569)

<table>
<thead>
<tr>
<th>HPA-</th>
<th>Cases, n (%)</th>
</tr>
</thead>
<tbody>
<tr>
<td>1a</td>
<td>428 (75.1)</td>
</tr>
<tr>
<td>5b</td>
<td>101 (17.7)</td>
</tr>
<tr>
<td>1a+5b</td>
<td>13 (2.3)</td>
</tr>
<tr>
<td>3a</td>
<td>10 (1.8)</td>
</tr>
<tr>
<td>1b</td>
<td>3</td>
</tr>
<tr>
<td>2b</td>
<td>3</td>
</tr>
<tr>
<td>4b</td>
<td>1</td>
</tr>
<tr>
<td>5a</td>
<td>2</td>
</tr>
<tr>
<td>8w</td>
<td>1 + 1*</td>
</tr>
<tr>
<td>11w</td>
<td>1</td>
</tr>
<tr>
<td>12w</td>
<td>1</td>
</tr>
<tr>
<td>13w</td>
<td>2</td>
</tr>
<tr>
<td>14w</td>
<td>1</td>
</tr>
<tr>
<td>15b</td>
<td>2</td>
</tr>
</tbody>
</table>

*1 additional case of anti-HPA-8w without FNAIT was observed.
Alloimmune Thrombocytopenic Syndromes

HPAs are involved in 3 major clinical syndromes: fetal and neonatal alloimmune thrombocytopenia (FNAIT), posttransfusion purpura (PTP) and platelet transfusion refractoriness (PTR). FNAIT results from feto-maternal HPA incompatibility. Maternal IgG antibodies cross the placenta and mediate the destruction of fetal platelets. In the white population, alloimmunization against HPA-1a is the major cause of FNAIT accounting for 75% of all serologically verified cases [11]. Anti-HPA-1a may lead to intracranial hemorrhage in 10–20% of cases, half of which occur already in utero [7]. No predictors for severe bleeding complications have been identified except for the history of older siblings, indicating that the individual nature of the antibody is crucial for the clinical expression of FNAIT [12]. The second most frequent antigen involved in FNAIT is HPA-5b. Interestingly, FNAIT due to HPA-5b alloabs is usually milder than FNAIT due to anti-HPA-1a [13]. This observation indicates that epitope and/or antigen specificity of alloabs is closely related to clinical presentation, which was one of the first points that triggered our interest in antibody heterogeneity associated with alloimmune thrombocytopenia. Anti-HPA-3a, which is involved in at least 1–2% of cases, usually causes severe FNAIT [14]. In contrast, the clinical relevance of anti-HPA-15 alloabs for FNAIT is not yet clear [15]. The frequency of all other HPA alloabs is too low to estimate a clear relationship between specificity and clinical consequence. Recent reports suggest that HPA-9w may be more important for FNAIT than previously suspected [16, 17]. It will be interesting to study how the clinical presentation of HPA-9w and HPA-3 alloabs compare, since the underlying polymorphisms are located closely to each other. Table 2 summarizes the specificities of HPA alloabs in serologically verified cases of FNAIT which we diagnosed over a 16-year period [11]. Future studies and registries will focus on the development of predictors of clinical severity in immunizations against low-frequency HPAs. Recently, a novel murine model of FNAIT using β3 integrin-deficient (β3−/−) mice was established [18]. In this model, platelet antibodies against β3 integrin produced the clinically relevant bleeding disorder as exhibited in human cases of FNAIT. One can hope that such models will help to obtain further insights into the pathogenic relevance of heterogeneous alloabs.

PTP is a rare transfusion reaction characterized by a sudden onset of thrombocytopenia most probably as a consequence of an anamnestic immune response to HPA-mismatched platelets or their fragments [19–20]. The mechanism by which alloabs (mostly anti-HPA-1a) are able to destroy autologus platelets is not yet fully understood. The frequency has been estimated to be 1/50,000 transfusions [21] but is constantly declining since the introduction of general leukodepletion of blood components. PTP is almost invariably associated with severe bleeding.
Immunogenic PTR is mostly caused by HLA-class I alloabs. In approximately 10% of HLA-immunized patients, additional platelet-specific alloabs have been observed, most frequently against HPA-1b and HPA-5b [22]. However, cases of PTR induced by platelet-specific alloabs alone are rare [22] and have been reported due to anti-HPA-1a [23, 24] and anti-HPA-5b. Since many of the clinically most frequently involved HPAs are located on the αIIbβ3 integrin, we will focus in the following chapters on the structure-function relationship of HPAs residing on αIIb and β3.

**Integrin αIIbβ3 and HPAs**

Integrins are a large family of heterodimeric receptors which are involved in cell-matrix and cell-cell adhesion interactions. Each subunit (α and β) contains a large extracellular domain, a single-pass transmembrane domain and a short cytoplasmic tail [25]. Integrins are involved in numerous biological processes, such as development, angiogenesis, wound healing, neoplastic transformations and thrombosis [26–28].

The integrin αIIbβ3 is the major integrin on platelets. As adhesive for several ligands containing the RGD sequence (fibrinogen, fibronectin, vitronectin, collagen, von Willebrand factor), αIIbβ3 mediates platelet aggregation and platelet spreading on vascular matrices during hemostasis and arterial thrombosis. Recently, the crystal structure of αIIbβ3 was resolved [29–31] (fig. 1). The αIIb subunit comprises of 4 domains: an aminoterminal 7-bladed propeller, an immunoglobulin-like ‘thigh’ domain and 2 co-linear β-sandwich domains (calf-1 and calf-2). The β3 subunit has 8 domains: an aminoterminal PSI (plexins, semaphorins, integrins) domain, an immunoglobulin (Ig)-like hybrid domain that contains the ligand-binding αA-like domain (βA) inserted into the upper loops of the Ig-like hybrid domain. The hybrid domain is connected to 4 epidermal growth factor (EGF)-like domains and a novel β-tail domain (β-TD). A key structural feature of the PSI domain is a distinctively long interstrand AB loop formed by Cys13-Cys435. This feature leads to interface interaction between the PSI and EGF-2 domain, which is important for the integrin activation process.

Integrin αIIbβ3 primarily functions as a bidirectional conduit for inside-out and outside-in signaling processes across the plasma membrane [32]. Inside-out signaling modulates αIIbβ3 conformation and transforms integrin into a high-affinity form (ligand-binding state). In turn, ligand-binding induces structural rearrangements conveying distinct signals to the cell interior (outside-in signaling). In one model (‘switchblade’ model, [33]), it was proposed that physiologic ligand binding requires straightening of the genu region (highly flexible site, fig. 2), thereby αIIbβ3 snaps from the bent conformer (inactive state) to the extended conformer (active state). However, it is more likely that a less drastic change is required for the initial transformation of αIIbβ3 integrin from the low- to the
The identification of the domains in the integrin αIIbβ3 structure allows precise localization of HPAs (fig. 3). Whereas point mutations responsible for HPA-3 and HPA-9w located on αIIb subunit cluster on the calf-2 domain, no preferential domain for HPAs on the β3 subunit can be observed. Within the ligand-binding BA domain of β3 (RGD binding domain), HPA-4 and HPA-16w are located. Other rare HPAs are distributed on the hybrid domain (HPA-7w, HPA-10w), EGF domain (HPA-6w) and β-TD domain (HPA-8w, HPA-11w and HPA-14w). The PSI domain harbors the clinically important point mutation Pro33Leu responsible for the formation of HPA-1a and HPA-1b, respectively. In addition, a variant of HPA-1b (Leu40Arg) and a new variant of HPA-1a (Leu33Val) were found in this domain (fig. 1). The elucidation of the PSI domain confirmed previous observations that this domain plays an important role for integrin activity [31].

Thus, replacement of Leu33 with Pro33 may alter αIIbβ3 receptor activity in the binding of different ligands. In our current studies, we observed that a single amino acid substitution, Cys636, which directly forms HPA-8w, impaired cell adhesion to soluble fibrinogen (fig. 4). Since this mutation is located in the β-TD domain of β3 integrin, we speculate that activation via the ‘deadbolt’ mechanism during inside-out signaling is disturbed.

In the past years, increasing interest has focused on the impact of platelet polymorphisms on the development of acute coronary disease and cerebrovascular diseases [35, 36]. Since the first report [37], several studies have investigated whether the HPA-1b allele confers a risk for atherothrombosis. Clinical
epidemiology studies resulted in contradictory findings [38]. However, a recent meta-analysis comprising a large cohort of patients (n = 3,400) indicated that HPA-1b does confer a minor risk for coronary heart disease in comparison to controls (n = 3,500) [35]. Vijayan et al. [39] showed by using a model with transfected cells that HPA-1b bound significantly more to immobilized fibrinogen and exhibited a greater extent of cell spreading and clot retraction than HPA-1a cells. Recently, we established stable cell lines expressing Leu33 (HPA-1a), Pro33 (HPA-1b) and Val33 isoforms of the β3 integrin. In contrast to the previous finding, we found no significant difference between HPA-1a and HPA-1b cell adhesion onto fibrinogen. Interestingly, the neutral point mutation Leu33Val altered cell adhesion more strongly than the Leu33Pro mutation (fig. 5). These results indicate that a point mutation at position 33 is indeed critical for platelet receptor function (see below).

**Heterogeneity of Platelet-Specific Alloantigenic Determinants**

Although the mutations that are responsible for the formation of platelet-specific alloantigens are well defined, the actual antibody recognition sites have not been precisely identified. These binding sites seem to be critically dependent on the 3-dimensional structure of the GP and on the contribution of carbohydrate residues. Furthermore, they seem to be heterogeneous. In the last years, several laboratories have attempted to produce synthetic or recombinant peptides that mimic platelet alloantigenic determinants. All attempts to construct HPA-1a epitopes using short linear or cyclic peptides (13-mer) straddling the Leu33Pro dimorphism were unsuccessful [40, 41]. A small recombinant allelic β3 protein (66 residues) seems to mimic HPA-1a epitopes [42, 43], however, some HPA-1a alloabs failed to recognize this fragment. Further studies demonstrated that the long-range disulfide bond (Cys13-Cys435) is necessary for the structural integrity of the HPA-1a epitope [44–46]. Recently, Watkins et al. [47] showed that a naturally occurring Arg93Gln mutation in β3 integrin disrupted the binding of HPA-1a alloabs. This mutation is located in the A′B loop of the hybrid domain [31] which maintains the rigidity of the hybrid-PSI interface. The substitution of a positively charged arginine for glutamine at position 93 seems to alter this interface dramatically, leading to inaccessibility of HPA-1a alloabs. Other findings demonstrated that the actual binding site of HPA-1a alloabs might be heterogeneous. Some HPA-1a alloabs bind the amino-terminal domain of β3 integrin independently from the CYS13-CYS435 bond, and others recognize combinatorial epitopes which require this long-range disulfide bridge [8]. Furthermore, Liu et al. [48] observed the existence of a split in HPA-1a alloab reactivity. Inhibition studies with mab LK-4 against β3 integrin showed different HPA-1a alloab types: one that recognized the recombinant β3 fragment (66 residues) and was sensitive to LK-4 inhibition, and another that bound to epitopes on the 66-residue fragment as well as on other regions of platelet β3 integrin and was insensitive to LK-4 inhibition. Recently, we found the rare, naturally occurring point mutation Val33 on β3 integrin (Santoso et al., Transfusion 2006, in press). Serological studies with different HPA-1a alloabs indicated that Val33 defines a split in HPA-1a. When HPA-1a alloabs from FNAIT and PTP patients were tested, PTP sera recognized the β3-Val33 isoform, whereas most FNAIT sera did not. This difference in reactivity may be related to differences in the nature of these diseases. In contrast to HPA-1 epitopes [40], several studies have shown that carbohydrate residues contributed critically to the integrity of HPA-3a epitopes [49–51]. Djaffar et al. [52] demonstrated that presence of O-linked rather than N-linked carbohydrate moieties preserves HPA-3a alloantigenic determinants. This observation is in line with the finding of Calvete et al. [53] who localized the precise site of O-glycosylation to GPIIb (Ser847), which is only 4 amino acids away from the polymorphic residue 843.

**Functional Heterogeneity of Platelet Alloantibodies**

There have been some reports that platelet reactive antibodies could influence platelet functions either by activating or inhibitory effects. Inhibitory antibodies against the integrin
αIIbβ3 may result in a hemorrhagic disorder similar to the situation in patients with αIIbβ3 deficiency (acquired Glanzmann’s thrombasthenia) [54–57]. Other studies described platelet reactive antibodies that activate platelets by a Fc dependent mechanism, via the complement system or by direct occupation of platelet receptors [57]. Recently, Nardi et al. [58] described a novel mechanism of complement-independent platelet clearance in HIV-1-related immune thrombocytopenia. Binding of patient’s IgG antibodies against platelet β3 residues 49–66 caused platelet fragmentation by induction of reactive oxygen species in the absence of complement. Interestingly, antibodies directed neither against other regions of β3 integrin nor against GPIbα failed to induce platelet fragmentation. These findings indicated that only antibodies against specific regions of β3 integrin are able to activate a peroxide-generating pathway.

Two decades ago, van Leeuwen et al. [59] showed that non-complement fixing HPA-1a alloabs can inhibit fibrinogen binding and platelet aggregation in response to stimulation with agonists such as adenosine diphosphate and collagen. Since then, only limited data have been published [60, 61]. Studies are complicated by several factors that may influence processes of platelet activation. Many HPA-1a alloabs are accompanied by other platelet reactive antibodies, most frequently by HLA class I antibodies, which may also affect platelet function [62–64]. Since HPA-1a alloabs may recognize different functional epitopes, we sought to analyze the direct effect of different HPA-1a alloabs on αIIbβ3-mediated fibrinogen binding [65]. To prove the inhibitory effect of HPA-1a alloabs, transfected cells expressing HPA-1a or HPA-1b were incubated with sera from FNAIT and PTP patients and allowed to adhere to immobilized fibrinogen. Interestingly, 3 different patterns of reactivity were observed with alloabs showing i) no inhibition of cell adhesion, ii) allotype-specific inhibition (inhibition of HPA-1a cells only), and iii) non-allotype-specific inhibition (inhibition of both HPA-1a and HPA-1b cells). Blocking HPA-1a alloabs were found in sera of FNAIT (9.3%) and PTP (75%) patients. In some cases of PTP, the inhibition of fibrinogen binding was found to be associated with severe bleeding, suggesting that HPA-1a alloabs may contribute to pronounced bleeding in patients with alloimmune syndromes. Thus, some HPA-1a alloabs can occupy platelet fibrinogen receptors, leading to ‘thrombopathic thrombocytopenia’ as observed in patients with acquired Glanzmann’s thrombasthenia. However, further studies are necessary to explore the relevance of the different patterns in alloimmune-mediated thrombocytopenia.

Platelet Antibody Detection: New Approach

The specific and sensitive detection of platelet-specific alloabs is essential for adequate treatment of patients suffering from alloimmune thrombocytopenia. Several assays have been developed during the last 2 decades. Binding assays using whole platelets [66, 67] have limitations since they allow no discrimination between platelet-specific alloabs and HLA antibodies. This problem is encountered by the development of GP-specific assays (e.g. MAIPA) [3, 68]. Meanwhile, the MAIPA assay is the most widely used technique [4, 69, 70]. Recently, we established a panel of stable transfectants expressing low-frequency HPAs, which can be used for alloab identification if the corresponding platelets are lacking [11]. Recombinant HPAs for serology are supplemented by reference DNA from B-lymphoblastoid cell lines for clinical diagnosis [71]. In some cases that are clinically highly suspicious for FNAIT, platelet-specific alloabs are not detectable by MAIPA assay [7, 72].
One major disadvantage of the MAIPA assay is the necessity of selected mouse mabs. As mouse mabs may compete with the binding of patients alloabs, false-negative results could be obtained [73]. Furthermore, excessive washing procedure in the MAIPA assay may result in dissociation of alloabs (low-avidity).

Surface plasmon resonance (SPR) technology, known as biomolecular interaction analysis, allows a visualization of antigen-antibody binding in real time, without the use of labeling or washing processes [74–77]. Recently, SPR technology has been applied to measure IgG anti-A and anti-B levels in patient plasma [78]. In SPR, one of the interacting partners (e.g. antigen) is immobilized on a sensor chip, and the binding of the other partner (e.g. antibody) is delivered to the surface in a continuous buffer flow (fig. 6). The sensor chip consists of a glass surface which is coated with a dextran-modified gold layer creating the physical requirements for SPR. The SPR phenomenon arises from the total internal reflection of the polarized light into a prism that occurs when the light passes between 2 media of different refractive index. Association of antibodies to the antigen results in a reduction of the reflected light intensity, whereas dissociation leads to an increase in the reflected light intensity. This reflection of light occurs at a specific angle (the resonance angle) which is measurable in SPR technology.

In preliminary studies, we analyzed the binding characteristics of different mabs against HPA-1a using SPR technology. Integrin αIIbβ3 was purified by affinity chromatography from platelets derived from homozygous HPA-1a/a or HPA-1b/b donors and immobilized on a sensor chip. Mouse and human mabs against HPA-1a (SZ21, CamTran007) were injected into the reaction chamber. Real-time HPA-1a antibody binding characteristics were recorded. As shown in figure 7, mab SZ21, which is known to bind HPA-1a preferentially, dissociated more rapidly from HPA-1b than from HPA-1a. In contrast, human mab CamTran007, which was originally derived from a FNAIT mother, bound to HPA-1a but not to HPA-1b. Since SPR provides additional information on binding kinetics of HPA-1a antibodies in real-time, this technology may help to improve the diagnosis of platelet alloabs.

Conclusions and Perspectives

In the last years, several efforts have been made to optimize the genotyping method for HPAs. Now, the HPA microarray technology has become available which allows a reliable and fast genotyping procedure. In the near future, an automated throughput for complete typing of large donor cohorts can be obtained. For the diagnosis of alloimmune thrombocytopenia, however, the proof of pathogenic alloabs in patient sera is still indispensable. With the availability of well-defined mabs against platelet GPs, antigen-specific assays for alloab testing have become the state of the art. However, recent observations indicated a diversity of epitopes as well as structural and functional heterogeneity of alloabs. The introduction of functional assays (e.g. adhesion assay) and direct analysis of antigen-antibody interaction (e.g. by SPR technology) may help us to further characterize platelet-specific alloabs with respect to their clinical meaning. New insights into the pathogenesis will aid to develop diagnostic and therapeutic approaches for alloimmune thrombocytopenia. The identification of antibody-combining sites on platelet receptors might serve as a basis for future investigations.

Addendum

Some of the data presented in this review are part of the doctoral thesis of Ines Socher.


44 Beer J, Coller BS: Evidence that platelet glycoprotein IIIa has a large disulfide-bonded loop that is susceptible to proteolytic cleavage. J Biol Chem 1989;264:17564–17573.


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