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## Structure-function of platelet glycoprotein Ib-IX

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## Abstract

The glycoprotein (GP)Ib-IX receptor complex plays a critical role in platelet physiology and pathology. Its interaction with von Willebrand factor (VWF) on the subendothelial matrix instigates platelet arrest at the site of vascular injury, and is vital to primary hemostasis. Its reception to other ligands and counter-receptors in the blood stream also contribute to various processes of platelet biology that are still being discovered. While its basic composition and its link to congenital bleeding disorders were well documented and firmly established more than 25 years ago, recent years have witnessed critical advances in the organization, dynamics, activation, regulation and functions of the GPIb-IX complex. This review summarizes important findings and identifies questions that remain about this unique platelet mechanoreceptor complex.

#### Keywords

Platelet; Thrombosis; Thrombocytopenia; Mechanoreceptor; Glycoprotein Ib

## Introduction

Platelets play an invaluable role in hemostasis. After vessel injury, platelets arrest, activate, and form a platelet plug essential for sealing the site of insult and preventing excessive blood loss. However, insufficient or excessive platelet activation can both lead to pathologies. Therefore, platelet activity is tightly regulated. Platelets express a wide variety of receptors that enable their response to diverse physiological and pathological stimulants. The glycoprotein (GP)Ib-IX complex is the second most abundant platelet surface receptor [1, 2]. GPIb-IX is a major platelet mechanoreceptor and participates in several diverse functions including adhesion, activation, clearance, and thrombopoiesis. This review covers GPIb-IX's structure and function, with an emphasis on advances made in the last decade.

#### Structure and organization of GPIb-IX

GPIb-IX is a highly integrated hetero-tetrameric receptor complex containing three unique subunits: GPIba, GPIbβ, and GPIX, arranged in a 1:2:1 stoichiometry[3]. Each subunit is an

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independently expressed transmembrane protein with a short cytoplasmic tail, a single transmembrane domain, and a glycosylated extracellular domain[4]. Efficient expression of the GPIb-IX complex on the platelet membrane depends on co-expression of all subunits[5, 6]. GPIb-IX also associates with GPV, likely at a 1:1 stoichiometry, but the association is relatively weak and can be disrupted by nonionic detergents[7].

GPIba is the "business end" of the complex, by far the largest subunit, and responsible for binding to almost all known ligands of the complex. At its extracellular N-terminus, GPIba begins with a ~45-kDa domain containing 7 leucine-rich repeats (LRR), also known as the ligand-binding domain (LBD) (Fig. 1). The C-terminal portion of the LBD contains a small "thumb" region crucial for effective binding to the A1 domain of von Willebrand factor (VWF)[8]. Following the LBD is a short anionic stretch involved in thrombin binding and a flexible stalk known as the macroglycopeptide or sialomucin region, spanning 30-40 nm[4]. The sialomucin region is characterized by a variable number of tandem repeats and its excessive O-glycosylation which, by some estimates, accounts for as much as 70% of the entire sialic acid content on the platelet surface[9]. It helps raise the LBD high above the platelet membrane and facilitates its interaction with various ligands and counter-receptors in circulation. The stretch closest to the platelet membrane contains the quasi-stable mechanosensory domain (MSD), the structure of which remains to be determined[10, 11]. The MSD contains the shedding cleavage site by ADAM17, the physiological sheddase of GPIba[12–14]. The extracellular domains of GPIbß and GPIX are smaller than that of GPIba; each of them contains one LRR sequence[15].

The transmembrane (TM) domains of GPIb-IX's constituent subunits are highly conserved and contribute to the structural organization of the complex. The organization and assembly of GPIb-IX have been reviewed extensively elsewhere[16]. Briefly, the TM domains of GPIba, GPIb $\beta$ , and GPIX associate to form a four-helical bundle, stabilizing the complex and facilitating formation of disulfide linkages between GPIba and each GPIb $\beta$  subunit[3, 17]. GPIX and GPIb $\beta$  are also associated through noncovalent interactions between their extracellular domains[15]. Aside from stability granted by this interaction, disruption of the specific interfaces between GPIX and GPIb $\beta$  significantly decreases surface expression of the complex[15, 18]. The GPIb $\beta$  and GPIX extracellular domains are directly adjacent to the MSD of GPIba (Fig. 1). Their association in the complex was recently proposed to be of significant functional consequence[19], although direct evidence for such an association is still missing. A summary of the structural features and binding partners for GPIb-IX is included in Figure 1.

#### GPIb-IX mutations in congenital diseases

The earliest recognition of GPIb-IX's importance in hemostasis dates back to 1948 and the first description of the rare but severe bleeding condition, Bernard-Soulier syndrome (BSS), a congenital disorder presenting as bleeding and macrothrombocytopenia[20]. However, it was not until the 1970s that deficiency or dysfunction of GPIb-IX platelet was identified as the causative factor in BSS[21]. The etiological link between GPIb-IX deficiency and BSS was further cemented when BSS-like phenotypes were observed in knockout mice missing either GPIba or GPIb $\beta$ [22–24]. BSS platelets are characterized by impaired ristocetin- and

thrombin-induced aggregation. Genetic sequencing of BSS patients has identified mutations in genes encoding all three GPIb-IX subunits. Overall, the symptoms in BSS patients and the phenotypes of knockout mice are consistent with the requirement of expression of all subunits for efficient expression of GPIb-IX in the plasma membrane of transfected mammalian cells[5].

Pulse labeling studies indicate that GPIb-IX assembles initially in the endoplasmic reticulum (ER), with additional glycosylation modification including sialylation occurring in the Golgi compartment[25, 26]. Unassembled subunits, particularly GPIba, are targeted for rapid degradation in the lysosome[25]. Recent studies have begun to identify the cellular machinery involved in folding and assembly of GPIb-IX, or degradation of misassembled GPIb-IX. For instance, mice with an inducible knockout of heat shock protein gp96/grp94, a molecular chaperone in the ER and a critical component of the unfolded protein response (UPR), present a phenotype indistinguishable from that of BSS[27]. Most mice missing core 1  $\beta$ 1,3-galactosyltransferase in their hematopoietic system and therefore extended or branched O-glycans on their platelets die perinatally from hemorrhage[28, 29], but the few survivors exhibit BSS-like phenotypes including bleeding, macrothrombocytopenia and markedly reduced expression of GPIba on platelets[28]. The importance of O-glycans to GPIb-IX expression in platelets can be attributed to the stabilization of the MSD in GPIba by sialic acids on these O-glycans, as removal of sialic acids by neuraminidase results in unfolding of the MSD and increased ectodomain shedding of GPIba[30, 31].

Rapid degradation of newly synthesized GPIba in the absence of other subunits suggests that unassembled GPIba contains a region that can be recognized by the cellular machinery but is masked by the associated GPIb $\beta$  and GPIX. Recent studies suggest that such region is located in the MSD, since removal or replacement of the MSD, but not any other domains, resulted in significant increase of GPIba expression in transfected mammalian cells without GPIb $\beta$  and GPIX[6, 19]. As the MSD is quasi-stable, it is conceivable that, in the absence of adjoining GPIb $\beta$  and GPIX extracellular domains, the isolated MSD could readily unfold and thus induce the unfolded protein response (UPR) in the ER[19].

Investigations of GPIb-IX mutations in BSS patient platelets and transfected cells suggest three general types of mutations that reduce the expression and/or function of GPIb-IX. Type 1 mutations disrupt the interaction between GPIb-IX subunits and include all frameshift or nonsense mutations in extracellular (including signal sequence) or TM domains of GPIb-IX. These mutations abolish the interaction between the TM domains and prevent stable assembly of the native complex[16]. Type 2 mutations include missense mutations in the LBD of GPIba that impair ligand-binding activity. Many of these mutations interfere with the folding or stability of the LBD, which presumably induces UPR and markedly reduces GPIba expression[32]. Type 3 mutations do not impact GPIb-IX expression and assembly, but instead abolish signaling. To-date, the sole example of this type is a homozygous nonsense mutation at residue Gln545 in the GPIba cytoplasmic domain[33]. Platelets from the BSS patient bearing this mutation exhibit normal levels of GPIb-IX, consistent with earlier findings that the cytoplasmic domain of GPIba does not participate in complex assembly or expression. Like other BSS patients, this patient responds poorly to ristocetin or thrombin stimulation. In this case, poor response is likely due to defects in GPIb-IX signal

transduction, as the truncation at Gln545 eliminates the binding site for Filamin A (FlnA) (Fig. 1b) and possibly other signaling molecules[33].

In most cases BSS is inherited as an autosomal recessive disorder, presumably because 50% of the normal gene dose is enough to sustain platelet genesis and function. However, for several missense mutations in the LBD of GPIbα and a number of Type 1 mutations in GPIbβ, BSS is transmitted in an autosomal dominant manner[34, 35]. Many of these patients present mild macrothrombocytopenia and markedly reduced but detectable expression level of GPIb-IX. On the other hand, patients with 22q11 deletion syndrome (22q11DS) lack 0.7–3 million base pairs in their eponymous chromosome, which encompasses the GP1BB gene that encodes GPIbβ. Typically being hemizygotes for GP1BB, these patients have larger platelets, lower platelet counts, and bleed more excessively after reparative cardiac surgery[36]. However, a recent analysis found no correlation of the GP1BB copy number with either macrothrombocytopenia or bleeding[37].

Mutations in GPIba can also lead to alterations in its binding to VWF. Under normal physiological conditions, plasma VWF is auto-inhibited and does not spontaneously bind to GPIba and platelets. However, in platelet-type von Willebrand disease (PT-VWD), mutations in GPIba cause spontaneous association with plasma VWF, somehow overcoming VWF autoinhibition. Four reported PT-VWD mutations are localized to the thumb region of GPIba's LBD[38]. Mouse models expressing these mutations largely recapitulate major symptoms observed in human patients[39, 40]. While these mutations likely cause structural or conformational alteration in the LBD[41], a fifth mutation, a 27-bp deletion at the junction of the sialomucin region and MSD of GPIba, was also reported in one patient diagnosed with PT-VWD[42]. However, no follow-up studies have been reported, and the structural basis for this mutation's effect on VWF binding remains to be seen. For comparison, a large deletion of the sialomucin region including the region in question does not alter ristocetin-mediated VWF binding under static conditions[43].

#### Platelet mechanosensation via GPlb-IX

When the endothelium suffers damage, the wound must be quickly sealed. In order to prevent significant blood loss, platelets must recognize endothelial damage, arrest, and remain in place long enough to begin forming a platelet plug under significant shear from blood flow. Although platelets activate readily at the site of injury, it is also critical that they remain inert in circulation. In mammalian platelets, GPIb-IX facilitates binding to damaged endothelia and mediates a force-dependent response. Although several receptors on platelets stabilize the adhesion of platelets to subendothelial matrix, these receptors cannot initiate thrombus formation without an initial interaction between GPIb-IX and collagen-tethered VWF, especially in high-shear regions of the vasculature[44, 45].

Although the GPIb-IX/VWF interaction has been recognized as the key event in sensing and responding to shear stress for over 25 years[1], a unified mechanism for GPIb-IX activation by ligand binding under shear has remained elusive until recently. In the early 2000s, a "clustering model" of GPIb-IX activation was proposed[46]. This model explained the observation that monoclonal antibodies (MAbs) targeting the LBD of GPIba can activate GPIb-IX, provided they are bivalent (not monomeric Fab fragments)[47, 48]. Under this

model, MAbs binding to two copies of GPIba (one with each Fab) induces lateral dimerization or "clustering" of GPIb-IX and subsequent clearance[49]. However, the clustering model falls short of unifying all available evidence regarding GPIb-IX mechanosensation and activation. It offers no explanation for why MAbs targeting other regions of GPIb-IX don't induce receptor activation[50], does not account for the well-established requirement of shear in VWF-mediated GPIb-IX signaling[1], and does not address numerous observations that the extracellular domains of GPIbβ participate in GPIb-IX signaling[14, 24, 51]. Thus, evidence for clustering of GPIb-IX in the membrane alone may not be sufficient to demonstrate activation of the receptor complex.

Recent studies using single-molecule optical tweezers to "pull" on the LBD of GPIba have identified a force-sensitive domain in GPIba's extracellular domain that unfolds when pulling force is applied to anchored GPIb-IX from the LBD. Unfolding was localized to the juxtamembrane mechanosensory domain (MSD) between the sialomucin region and the TM domain[10]. The MSD unfolds under a continuous pulling force of ~15 pN[11, 14, 52]. Although the precise boundary of the MSD is not settled, estimates based on mutagenesis and fitting of single-molecule data estimate that the MSD spans about 60 residues. Recent studies indicate that this domain is structured and quasi-stable, and its stability is altered by O-glycosylation therein[10, 30].

The trigger model of GPIb-IX activation—In the mid-1990s, Kroll et al. described the mechanism of platelet shear-sensitivity as follows, "The initial shear-induced triggering event has so far been elusive...one hypothesis proposed to explain the mechanism of shearinduced platelet activation states that platelet GPIba, following shear-induced binding of *vWF*, undergoes a conformational change that...triggers signals for cellular activation."In their 2016 study, Deng et al. proposed the trigger model of GPIb-IX activation. Applying physiological shear stress to platelet-rich plasma, they demonstrate that VWF binding to the LBD leads to shear-dependent MSD unfolding and platelet signaling including elevation of intracellular calcium, P-selectin exposure, and surface desialylation[14]. Within the MSD, which is poorly conserved between species, a short 12-residue segment immediately preceding the TM domain exhibits remarkable sequence conservation in mammals (Fig 2). Exposure of this region, dubbed the "trigger sequence", following MSD unfolding appears to be the crucial step in GPIb-IX activation. Deletion of the MSD leaving only the trigger sequence leads to constitutive ligand-free activation of GPIb-IX in CHO cells expressing this mutant[14]. IL4R-IbaTg mice express a chimeric GPIba in which most of the extracellular domain has been replaced by that of the  $\alpha$ -subunit of the interleukin-4 receptor (IL4R) leaving only the trigger sequence. These mice have a significantly lower platelet count and their platelets have a higher base level of activation [14, 53]. Utilizing a biomembrane force probe instrument to measure force and cell signaling at the single-cell and single-molecule level, the Zhu group characterized pulling force regimens for recombinant A1 domain or anti-GPIba antibodies binding to an immobilized platelet. An extension event consistent with unfolding of the MSD for a certain time period, and sometimes in conjunction with unfolding of the LBD, was required to induce intracellular calcium flux in the platelet, thus providing additional evidence linking MSD unfolding to GPIb-IX signaling[52]. Together, these data support a trigger model of GPIb-IX signaling, wherein a pulling force exerted on

GPIba through the LBD leads to unfolding of the MSD, exposure of the trigger sequence, activation of the receptor, and subsequent platelet signaling and/or clearance (Fig. 3). Under this model, collagen-anchored VWF binds to the LBD and shear from blood flow may provide the force required to unfold the MSD, thereby activating GPIb-IX.

**Triggering thrombocytopenic disorders**—In addition to GPIb-IX's role in normal hemostasis, the trigger model also explains several GPIb-IX-centric disease states. GPIb-IX is a common target for autoantibodies in patients with immune thrombocytopenia (ITP). The presence of antibodies against GPIb-IX is strongly associated with refractoriness to common first-line immunosuppressive treatments like intravenous immunoglobulin (IVIg) and corticosteroids[54]. Antibodies targeting the LBD of GPIba can activate the receptor and cause platelet desialylation[55, 56]. In the case of IVIg-resistant ITP, the dimeric structure of activating anti-LBD MAbs permits them to crosslink platelets via GPIb-IX (56]. Under physiological shear, this generates a pulling force on GPIba, activating GPIb-IX via MSD unfolding and inducing immune-independent clearance. Furthermore, if an antibody's unbinding force from the LBD is insufficient to sustain the force applied by physiological shear, it will not induce GPIb-IX-mediated clearance[56]. Thus, it appears that the defining characteristic of an activating ligand to GPIb-IX is the ability to bind to the LBD and sustain at least 15 pN of force, the amount required to unfold the MSD.

Association of VWF and GPIba underlies many thrombocytopenic and thrombotic disorders. In contexts where VWF binds spontaneously to GPIba in bloodstream, multimeric VWF may act as a crosslinking ligand capable of forming VWF-platelet complex and activating GPIb-IX therein. Ristocetin (used as an antibiotic) can induce the VWF-GPIba interaction in the absence of shear and was pulled from clinical use because it caused thrombocytopenia[57]. Injection of botrocetin, a snake venom that causes spontaneous VWF-GPIba interaction, induces acute thrombocytopenia in animals[58]. Patients with type 2B VWD exhibit spontaneous VWF-GPIba binding and, similar to the effects of anti-GPIb-IX antibodies in ITP patients, present with accelerated platelet clearance, reduced thrombopoiesis, and thrombocytopenia[59]. Transgenic mice expressing type 2B VWF or PT-VWD mutant GPIba exhibit thrombocytopenia partly due to clearance of large VWFplatelet complexes[40, 60]. The etiology of the bleeding disorder thrombotic thrombocytopenia purpura (TTP) follows a similar pattern. In individuals with TTP, a deficiency of functional ADAMTS13 prevents cleavage of ultra-long (UL)VWF, permitting spontaneous binding to GPIba and subsequent thrombocytopenia. Not unrelatedly, increased or altered hemodynamic shear produced by mechanic pumps in circulatory support devices such as ventricular assist devices and extracorporeal membrane oxygenation machine likely activate VWF, induce formation of VWF-platelet complexes, and result in undesired thrombocytopenic and thrombotic complications[61, 62]. Moreover, pathological binding of VWF to GPIba also appears to be a mechanism of thrombocytopenia during infection of malaria parasite or dengue virus [63, 64]. It should be nonetheless noted that, although desialylated VWF binds GPIba spontaneously, neuraminidase can induce platelet clearance in a VWF-independent manner by directly desialylate O-glycans in GPIba[30].

**Ligand- and shear-free mechanisms of GPIb-IX activation**—Recent studies suggest that GPIba ectodomain shedding mediated by ADAM17 and desialylation-dependent unfolding of the MSD are unique mechanisms of GPIb-IX activation which proceed in congruence with the trigger model of GPIb-IX activation, but without the requirement of shear.

In addition to the trigger sequence, the MSD of GPIba also contains the cleavage site for the metalloproteinase ADAM17 (Fig. 2), which continuously sheds the majority of the extracellular domain of GPIba (known as glycocalicin) from the platelet surface[12]. Although the shedding cleavage site is still accessible when the MSD is folded, consistent with constant shedding of glycocalicin from resting platelets, shear-induced MSD unfolding may further expose this sequence to ADAM17[14]. Since glycocalicin contains the LBD, ectodomain shedding of GPIba via ADAM17 reduces the association of VWF multimer with the platelet and is thought as a means to down-regulate formation of the VWF-platelet complex. On the other hand, as the shedding cleavage site is N-terminal to the trigger sequence, upon cleavage by ADAM17, the structure of the MSD may be disrupted, exposing the trigger sequence and inducing GPIb-IX signaling (Fig. 3B). Indeed, GPIba mutants disrupting the MSD's structure and exposing the trigger sequence lead to ligand-free signaling and platelet clearance[14]. Shedding of GPIba is an important event linked to platelet clearance, especially in the context of platelet storage[65]. The extent of GPIba shedding is tightly correlated to the platelet storage lesion and inhibition of shedding has been proposed as a potential strategy for improving the survival of stored platelets. Blocking GPIba shedding with metalloproteinase inhibitors or a GPIba-specific MAb 5G6 improves the survival of *in vitro* aged platelets[66, 67] (Fig. 3B).

As previously mentioned, the MSD of GPIba contains several O-glycosylation sites. Neuraminidase, a glycolytic enzyme released by some bacterial infections and from platelets endogenously, hydrolyzes the glycosidic linkages to sialic acids in branched glycans and exposes the penultimate galactoses. Injection with exogenous neuraminidase leads to thrombocytopenia in animal models[68], and platelet neuraminidase appears to be critically involved in clearance[31, 55, 69]. Galactoses exposed by neuraminidase can mark platelets for clearance in the liver, in which the Ashwell-Morell receptor, macrophage galactose lectin, and other receptors have been implicated [29, 31, 70, 71]. Given the high percent of total platelet sialic acid that is bound to GPIba, it is conceivable that galactoses on desialylated GPIba may be important for recognition by clearance receptors. However, no direct evidence for the interaction of desialylated GPIba with a clearance receptor has been reported. It is noteworthy that while most of these clearance receptors are oligomeric and prefer to bind multiple galactoses on N-glycans with high affinity, murine GPIba does not contain the canonical N-glycosylation sites (i.e. NxS/T). A recent study has identified that neuraminidase-mediated desialylation of O-glycans on GPIba induces MSD unfolding and GPIb-IX signaling[30]. Here, GPIb-IX-mediated intracellular signaling includes further platelet desialylation, which could conceivably lead to desialylation of N-glycans of other glycoproteins on the platelet membrane, which can be recognized by clearance receptors.

#### Signaling of GPIb-IX

In addition to its adhesive functions, GPIb-IX activation and associated signaling are vital to the initiation of platelet activation during primary hemostasis. During this phase, VWF-dependent GPIb-IX activation leads to inside-out activation of the platelet integrin  $\alpha_{IIb}\beta_3$ [72, 73], formation of platelet microparticles[74, 75], TXA2 synthesis and release[76, 77], degranulation[77], desialylation via NEU1[55], and many other procoagulant phenomena. Many of these phenomena have also been observed when GPIb-IX is activated by anti-LBD MAbs[55, 56].

Several downstream signaling mediators of GPIb-IX have been identified including: Ca<sup>2+</sup>, Src family kinases, phospholipase C, PI<sub>3</sub>K; mitogen-activated protein kinase (MAPK) pathway; and LIM kinase pathway[78]. In particular, numerous studies have been published investigating the role of the regulatory protein 14-3-3 $\zeta$ , which binds to the cytoplasmic tails of both GPIba and GPIb $\beta$ [79, 80](Fig. 1b). Multiple binding sites for 14-3-3 $\zeta$  have been found in the GPIba cytoplasmic domain, and some of them may overlap or be in proximity to binding sites for PI3K and FlnA [78, 81]. Studies of transfected cells expressing GPIb-IX and  $\alpha_{IIb}\beta_3$  suggest that 14-3-3 $\zeta$ 's interaction with GPIba is necessary for VWF-induced activation of  $\alpha_{IIb}\beta_3$  binding to fibrinogen[72]. Consistently, addition of membranepermeable peptides that are derived from the GPIba intracellular tail and competitively inhibit 14-3-3 $\zeta$ 's interaction with GPIba to platelets inhibits ristocetin-induced platelet aggregation [82, 83]. It appears that 14-3-3 is involved in GPIb-IX-mediated platelet signaling, while another study suggests that sequestration of 14-3-3 $\zeta$  by GPIba may counteract  $\alpha_{IIb}\beta_3$  activation[84]. It has also been reported that GPIba-bound 14-3-3 $\zeta$ regulates adhesion to VWF [81-83, 85, 86] and platelet apoptosis[87, 88]. The distinctions between GPIb-IX signaling pathways leading to platelet clearance and platelet activation remain unclear.

#### Additional functions of GPIb-IX

The best-established and most extensively studied functions of GPIb-IX are in the context of hemostasis, where it mediates binding to vascular damage via VWF and initiates platelet signaling. However, GPIb-IX interacts with several other ligands and counter-receptors (Fig. 1), and ongoing work continues to reveal diverse roles for GPIb-IX in thrombosis, inflammation, and platelet genesis[74].

The leukocyte integrin  $\alpha_M\beta_2$  (Mac-1) interacts with GPIba, allowing leukocytes to adhere and migrate along sites where of vascular injury where platelets are accumulating[89]. Inhibition of this binding inhibits stable interactions between leukocytes and platelets, reducing leukocyte accumulation at the site of injury[90]. This implies that the  $\alpha_M\beta_2$ -GPIba interaction is vital to leukocyte adhesion and the inflammatory response to vascular injury. Alternatively, mice with mutant  $\alpha_M\beta_2$  deficient in GPIba binding or  $\alpha_M\beta_2$  knockout mice have delayed thrombosis, and it has been suggested that inhibition of the  $\alpha_M\beta_2$ -GPIba interaction has therapeutic potential as an anti-thrombotic[91].

GPIba is the high-affinity platelet receptor of thrombin[92]. GPIba binding to thrombin promotes thrombin's cleavage and activation of PAR1, its low-affinity platelet receptor, and

GPIb-IX-mediated signaling plays a role in cooperation with PAR1 signaling[93, 94]. Relatedly, recent animal studies suggest that the modest increase in acute coronary syndromes associated with the use of oral thrombin inhibitors involves the GPIba-thrombin interaction[95].

GPIb-IX has been implicated in platelet generation and regulation of platelet size. The primary role for GPIb-IX in platelet genesis appears to be in thrombopoiesis, rather than megakaryopoiesis. Although BSS mice develop normal megakaryocytes (MKs), their proplatelet formation is impaired[96]. Shear flow is important for the development of proplatelets from MKs, especially in the context of *in vitro* platelet production. Interestingly, VWF binding to GPIba under shear has been implicated in this process, and inhibition of GPIba ectodomain shedding in MK cultures improves yields of functional platelets[97]. Thrombopoiesis is also altered in the context of type 2B VWD, wherein patients' MKs have disordered demarcation membrane systems, smaller proplatelets, and abnormal granule distribution[98]. In a mouse model of type 2B VWD, proplatelet formation is significantly reduced, likely as a result of upregulation of the LIM kinase pathway and actin disorganization[99]. Altogether these data suggest an important role for GPIb-IX, and specifically the VWF-GPIba interaction, in MK response to shear and regulation of proplatelet formation and fragmentation.

Recent studies have also utilized the IL4R-IbaTg mice to implicate GPIba in the process of platelet accumulation to the liver in the context of liver production of thrombopoietin or nonalcoholic fatty liver diseases[100, 101]. In these cases, GPIba appears to mediate association of platelets with cells in the liver, such as hepatocytes and Kupffer cells. Curiously, mice lacking P-selectin, VWF, or Mac-1, all of which are known ligands of GPIba, do not show delays in the onset of liver diseases[101]. This suggests on these cells the existence of a new counter-receptor for GPIba, the identity of which remains to be discovered.

Platelets have diverse roles in the progression of several cancers, interacting with tumor cells in many capacities. Studies in the 1980s and 1990s implicated GPIb-IX (specifically its interaction with VWF) in tumor cell-induced platelet aggregation (TCIPA), indicating that inhibition of the GPIba-VWF interaction interferes with TCIPA[102, 103]. Further, VWF<sup>-/-</sup> mice or IL4R-IbaTg mice show reduced metastasis[104, 105]. A comprehensive model of cancer cell expression of VWF, binding to platelets, and the mechanism by which these interactions promote metastasis is an ongoing area of research.

#### Modulation of GPIb-IX

Many adhesion receptor complexes mediate bidirectional signal transduction, as exemplified by the outside-in and inside-out activation of integrins. In this review, "GPIb-IX activation" refers to outside-in activation - the induction of GPIb-IX-mediated intracellular signaling as a result of its binding to ligands. Thus far, GPIba is the only subunit of GPIb-IX demonstrated to mediate receptor activation, containing both the MSD and the binding site for all known ligands. Unfolding of the MSD appears as a critical step in this process, converting the ligand-binding status under shear into a distinct conformational state that could be detected by and propagated through the rest of GPIb-IX. The extracellular domains of GPIX and GPIbβ are proximal to the MSD of GPIba (Fig. 3), and even assuming full

extension of the MSD, ~10 residues of the Trigger sequence could be in direct contact with them [15, 16]. However, the contributions of GPIb $\beta$  and GPIX to receptor activation and signaling remain ambiguous. Recent evidence suggests that GPIbb and GPIX extracellular domains are malleable and could undergo conformational changes[18]. Several studies indicate that RAM.1, a MAb targeting the extracellular domain of GPIb<sub>β</sub>, abolishes GPIb-IX signaling including intracellular Ca<sup>2+</sup> flux and changes in morphology without an effect on ligand binding[14, 24, 51] (Fig. 3A). Data from our lab indicate that another anti-GPIbß MAb, 3G6, can amplify or "potentiate" GPIb-IX activation by VWF and anti-LBD MAbs including degranulation, desialylation, and morphological changes (Quach et al. manuscript submitted). Although these findings clearly implicate GPIbB in the modulation of GPIb-IX signaling, the precise role of GPIb $\beta$  in GPIb-IX signal transduction, and the nature of the contacts between GPIb $\beta$  and the MSD remain elusive. Similarly, the role of GPV in GPIb-IX function is another area where our understanding is currently evolving. Genetic ablation of GPV accelerates GPIba/thrombin-dependent platelet activation, and GPV<sup>-/-</sup> mice exhibit faster occlusion times than wild-type[106, 107]. Thus, GPV may dampen GPIb-IX activation and signaling, but the underlying molecular mechanism remains elusive.

Is there inside-out modulation of GPIb-IX activity?—Inside-out activation of an adhesion receptor was first reported for integrin  $\alpha_{IIb}\beta_3$  when its binding affinity (not avidity) for ligands was substantially increased as a result of mutations in its cytoplasmic domains. This inside-out activation, in which conformational changes in the membrane-proximal portion of the integrin extend allosterically to its membrane-distal ligand-binding domain, is an important physiological step during platelet activation. It was reported in early 2000's that transfected cells expressing GPIb-IX with mutations in the cytoplasmic domains to perturb its interaction with 14-3-3 proteins exhibited altered binding to VWF in the presence of ristocetin or altered adhesion to VWF under flow conditions[82, 108, 109]. Based on these results, a toggle switch model in which switching of 14-3-3 c binding between GPIba and GPIb $\beta$  determines the binding affinity of GPIba, or its accessibility, to VWF by an inside-out mechanism was proposed in 2005 [78, 82]. However, as of the time of this publication, this model has not seen any follow-up in the literature, including details describing the changes in interactions between 14-3-3 $\zeta$  and its multiple binding sites in GPIba and GPIb $\beta$ . Unlike the case of  $\alpha_{IIb}\beta_3$  inside-out activation, it remains unclear how a change in the GPIba cytoplasmic domain induces a conformational change in the LBD or a change in its accessibility, particularly through the long sialomucin region. Thusfar, there have been no reports of the LBD exhibiting two distinct binding affinities to VWF or a specific shielding mechanism for the LBD.

It is noteworthy that 14-3-3 $\zeta$ 's association with GPIb-IX affects its binding to VWF multimers but not recombinant A1 domain of VWF [108]. In addition, RAM.1 significantly reduces adhesion of platelets or cells expressing wild-type GPIb-IX, but not cells expressing GPIb-IX with certain cytoplasmic mutations affecting 14-3-3 $\zeta$  association, to VWF under flow conditions[85]. Yet RAM.1 does not affect the binding affinity of purified GPIb-IX to VWF or recombinant A1-A2-A3 fragment[110]. Thus, it appears that 14-3-3 $\zeta$  modulates the binding avidity, rather than affinity, of GPIb-IX to VWF. As 14-3-3 $\zeta$  mediates GPIb-IX signaling, perturbing its association with GPIb-IX may alter the morphology of the host cell,

the spatial distribution of GPIb-IX therein, and subsequently cell association to VWF multimers or cell adhesion to VWF. In other words, 14-3-3 $\zeta$ 's effect on VWF binding/ adhesion may be due to GPIb-IX-mediated signaling rather than inside-out regulation of GPIb-IX.

#### Conclusion

The GPIb-IX complex on the platelet surface is critical to many aspects of platelet physiology, including platelet recruitment to vascular injuries, platelet activation, and platelet clearance. It is also implicated in thrombosis, inflammation, and many other associated pathologies. In particular, spontaneous or aberrant association of VWF with GPIba is a key feature in many pathological contexts, including type 2B VWD, TTP, and likely other thrombotic thrombocytopenic disorders. Recent elucidation of interactions between GPIba and the other subunits of GPIb-IX, particularly the identification and characterization of the MSD therein, has provided a new framework for future investigations of functions and regulations of GPIb-IX.

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#### Figure 1. Organization and structure of GPIb-IX.

Cartoon illustration of the GPIb-IX complex including GPIba (black), GPIb $\beta$  (green), GPIX (red). The N-terminal LBD of GPIba is labeled, the membrane-proximal MSD is highlighted in purple, and the trigger sequence therein is highlighted in blue. The complex is held together by strong associations among the transmembrane domains as well as weak associations between GPIb $\beta$  and GPIX extracellular domains and potentially the MSD of GPIba. Binding partners of the GPIba LBD are listed to the right, including thrombin and VWF-A1. Intracellularly, 14-3-3 $\zeta$  interacts with the intracellular tails of GPIb $\beta$  and GPIba. FinA binds to the tail of GPIba. Binding partners for which a specific binding site has not been identified are listed in gray.

| A)              | MSD TM  |
|-----------------|---|
|                 | ADAM17 Trigger  |
| Human           | ATSPTILVSATSLITPKSTFLTTTKPVSLLESTKKTIPELDQPPKLRGVLQGHLESSRNDPFLHPDFCCLLF                |
| Chimpanzee      | ATSPTILVSATSLITPKSTFLTTTKPVSLLESTKKTIPELDQPPKLRGVLQGHLE <mark>SSRNDPFLHPD</mark> FCCLLF |
| Bonobo          | ATSPTILVSATSLITPKSTFLTTTKPVSLLESTKKTIPELDQPPKLRGVLQGHLESSRNDPFLHPDFCCLLF                |
| Gorilla         | ATSPTILVSATSLITPKSIIFLTTTKSVSLLESTKKTIPELDQPPKLRGVLQGHLESSRNDPFLHPDFCCLLF               |
| Orangutan       | ATSPTILESATSLITPKSIIFLTTTKPISLSESTKKTIPESDQPPKLHGVLQGRFQSSRNDPFLHPDFCCLLF               |
| Vervet          | ASSPTIPESATSLITPKSIIFLTTTKPVSLLESTKKTILEFDQQPKLRAVLQGHFESYRNDPFLHPDFCCLLF               |
| Macaque         | ATSPTIPESATSLITPKSIIFLTTTKPVSLLESTKKNIPEFDQQPKLRGVLQGHFESYRNDPFLHPDFCCLLF               |
| Mangabey        | ATSPTIPESATSLITPKSITFLTTTKPVSLLESTKNNIPEFDQQPKLRGVLQGHFESYRNDPFLHPDFCCLL                |
| Pig             | TTPTALEPRTTLKAPEPTIFLTSTGLPSALEFTVTTSSEYVNLSKSFGLAPENLDSSRNDPFLNLDSCCLSI                |
| Panda           | APTTPESTMSPILSELTTFFKMPELTSLSAILEYPAPTSPAHLPKAHEVVQGNLESSRNDPLLSPDFCCLL                 |
| Armadillo       | TTPEPTTTPTTPEPTIFSENTESISLPPIIGSTTVNIPETVNLPKVRGLAQGNLDSSRDDPFLNPDFCCLL                 |
| Tree Shrew      | TTPEPTTALTTPEPTTLFIKTEPTSTSATSESATVITTEFVDLPKVHGLAEGNWDSSRKDLFLNPDFCCLL                 |
| Yak             | TLEPTTPTTPEPISETLQPTIFLTSTESISLPTILESTITIISESDNPWKVQGLASSSNNPVLSSDSCCLF                 |
| Cat             | TTSPTPEPTIPPTTPTTSEITTFLTTPKATSFLTIWPRATTTLPEAQGVARENVRSPRNDPSLGGDTCCLL                 |
| Elephant        | ITFSEIPKLTKEHTTTAATPEMTTMPTSPEPTSLPTTFEPFNFLNIRGVAQGNVDTSRNDPFLHPDFCCLL                 |
| Ferret          | PPITPEPTTTLFLSELTTFFEIPKLTSLPTILGYPISPSSVHLPGAHEVVRGHPESSRNDPLFNPDFCCLL                 |
| Squirrel        | ALTSPEAIITLTMSVPLTSITAEPTTEYTSFPTNSGSLTISPESEMVLAAQGNFHSARNYPFLNPDICCFL                 |
| Rabbit          | TALKTPEPTTALTTSGPSSAPTTPEPTTVLMASLPTGLEFSAFPVVHEVSRGNFKSSRRDPFLNSDSCCLL                 |
| Mouse           | TTTLTTPESTPIETILEQFFTTELTLLPTLESTTTIIPEQNSFLNLPEVALVSSDTSESSPFLNSDFCCFL                 |
| Rat             | PVLTTTLAPPESIPKTVLEQFYTLEPTLPRTLESTIIIPEQNSLNSQAVPQASSDTPKSNPFLNSDFCCLL                 |
| Tasmanian Devil | TTMLQITSEFVTFPIIDSIVDPSMSVTPPSLFSTLILPKSNILPPNEAVTLGSLGDPSNSSSPISISCCLL:                |
| Chicken         | LVVPNTTLSIHTPTLSAPLDTTPFPHPSPPLRPPLLCPCSTPAQTPSVLHSQTGVKGLPWKHWVLNHCCLL                 |
| Aligator        | SLSSHVPPITFKPTPPSPLPHVPHHQPSPPPRAPPVCSCLTSPAKLPSMGYHLGGKGHSWGHWVLAHCCLL                 |
| Falcon          | LVSLALLVLTVLALAGWLAWMWLASRTPWHKPLQTQEVREPLLRWRGVTGSPAMHLSSFKSPLRRPTFCTI                 |
| Xenopus         | KLSTTIKTQTTLKLEMPDVQNTTWTKTVSPMVEEHSTPTIYLDTQVPVAPVGIGRLQSWLAEPITRYCCIL                 |
|                 |   |
| 3)              |   |
| Human           |   |
| Orangutan       |   |
| Vervet          |   |
| Macaque         |   |
| Mangabey        |   |
|                 |   |
| Rabbit          |   |
|                 | — Yak   |
|                 | Tasmanian_Devil   |
|                 | Chicken   |
|                 | Aligator  |
|                 | Xenopus Xenopus   |
|                 | Falcon  |
|                 | Rat   |
|                 | — Mouse   |
|                 | Cat   |
| Squirr          | rel   |
| Tree_Shree      | w   |
| Armadillo       |   |
| Ferret          |   |
| - Panda         |   |
| Elephant        |   |
| Chimpanzee      |   |

#### Figure 2. Multiple sequence alignment of the GPIba MSD.

0.8

1.0

0.4 0.6 branch length

Bonobo Gorilla

0.2

(A) MSD sequence of GPIba orthologs from various species. The MSD, transmembrane domain (TMD), and trigger sequence are demarcated. Residues with identity match to the human sequence are listed in red. The triangle denotes the ADAM17 shedding cleavage site in human GPIba. (B) Phylogenetic tree constructed from multiple sequence alignment of trigger sequences for each of the species in (a).

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#### Figure 3. Activation and regulation of GPIb-IX signaling.

(A) The Trigger model of GPIb-IX activation. Binding of VWF or anti-LBD antibodies to the LBD of GPIba under physiological shear induces MSD unfolding. Neuraminidase (Neu) treatment in the absence of shear also induces MSD unfolding. Unfolding of the MSD leads to exposure of the trigger sequence therein, likely inducing a conformational change in the adjoining GPIb $\beta$ /GPIX and subsequent GPIb-IX signaling into the cell. This activation is modulated by anti-GPIb $\beta$  MAbs 3G6 (which potentiates activation) and RAM.1 (which inhibits activation). MPaC competitively inhibits 14-3-3 $\zeta$  binding to the intracellular tail of GPIba, diminishes its downstream signaling, and reduces cell adhesion to VWF. The membrane-proximal MSD is highlighted in purple, and the trigger sequence therein is highlighted in blue (B) Ectodomain shedding of GPIb-IX induced by ADAM17 cleavage of a site within the MSD induces shear-independent activation. Shedding can be inhibited by the anti-MSD MAb 5G6 or metalloproteinase inhibitors such as GM6001. Note that unfolding of the MSD facilitates ADAM17-mediated shedding of GPIba.