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Supplemental Information

Control of Platelet CLEC-2-Mediated Activation by Receptor Clustering

and Tyrosine Kinase Signaling

Alexey A. Martyanov, Fedor A. Balabin, Joanne L. Dunster, Mikhail A. Panteleev, Jonathan M. Gibbins, and Anastasia N. Sveshnikova

1. Supporting results

1.1. Quiescent state reactions incorporated in our model of CLEC-2-induced platelet activation.

The quiescent state of platelet's tyrosine kinase network is supported by a set of phosphatases, among which CD148 (also known as DEP-1 or PTPRJ) has a dominant role (1–3). Here we assume that SFK can exist in four different states which differ in the degree of activation: non-active SFK (Y527 phosphorylated), a third (1/3) active SFK (Y527 dephosphorylated), two thirds (2/3) active (Y416 phosphorylated) and fully active SFK (Y416 phosphorylated and bound to a phosphorylated tyrosine by its SH-2 domain) (4). Non-active SFK is transferred to the 1/3 active state by active CD148 phosphatases (2, 4). On the contrary, 1/3 active SFK can be deactivated by active Csk kinases, which phosphorylate SFK at Y527 (2, 5). 1/3 active SFK turn to a 2/3 active state via autophosphorylation on Y416 (2). This transition is negatively regulated by the active CD148 (1, 2, 4, 6). We assume that fully active SFK are not produced in the quiescent state due to the absence of the phosphorylated receptor molecules. All types of active SFK mediate phosphorylation of CD148 at Y1311 (6), which results in CD148 activation. On the other side, all types of active SFK also mediate Csk activation (7, 8). It is noteworthy that Csk activation in platelets is not regulated directly by SFK. Namely, SFK phosphorylates a protein called paxillin adapter, which binds Csk and this results in Csk activation (7). Active SFK phosphorylates Syk at Y346, which results in Syk initial activation (9).

It is noteworthy that in *in vivo* experiments with SFK-/- mice CLEC-2 phosphorylation was present upon stimulation by rhodocytin, while further signal propagation was significantly weakened (10). Furthermore, Hughes *et al.* 2015 demonstrated that for CLEC-2 signalling SFK acts mostly as a positive mediator of Syk basal activation (9).

1.2. A detailed description of the model construction in a modular fashion

The "CLEC-2 clustering" module (Fig. 2A) consists of variables for concentrations of CLEC-2 in free, ligand-bound and cluster forms (3 variables, all located in the plasma membrane), fucoidan (1 variable, located in the extracellular space) and 7 parameters, among which 4 concern receptor clustering.

In order to describe cluster formation, we initially used an "N-equation" model (Fig. S1A), which could capture the behavior of the receptor clusters of all sizes (where N is the size of the largest cluster). "N-equation" model of clustering contains 4 parameters: single receptor association and dissociation with clusters rates (k_1 , k_1 , respectively) and two clusters association and dissociation rates (k_2 , k_2 , respectively) (11). Formation of clusters of all sizes was described using mass-action kinetics. For example, behaviouor of cluster of size three was described by the following equation:

$$
\frac{d[3R]}{dt} = k_1([2R] \times [R] - [3R] \times [R]) + k_{-1}([4R] - [3R]) + k_2([2R] \times [R] - [3R] \times [2R]) + k_{-2}([5R] - [3R]).
$$

Average cluster size $(\sum_{i=1}^nc_i i/\sum_{i=1}^nc_i)$ where c_i – The concentration of the cluster of size i), predicted by the model, was fitted to the data from (12). Calculated distribution of cluster sizes at 300s (Fig. S1C) show that the dimerised receptor concentration is prevailing, while a small fraction of receptors remains in a non-dimerized state.

Although the "N-equation" model could capture the literature data, it was poorly applicable to stochastic calculations. Thus, in order to describe receptor clustering, we utilised a "2-equation model" (13) to describe results obtained by the "N-equation" model.

2-equation model contains 5 parameters, which were determined in the process of fitting the 2-equation model to "N-equation" model, which, in turn, was fitted to experimental data from (12) (for equations and parameter values see Tables S2-S4). Average cluster size was calculated as $s = \frac{C_0^* - C^*}{2}$ $\sqrt{\mathcal{L}}$ *Clust*, where C_0^* - initial concentration of non-clustered CLEC-2 species, C_0^* - transient concentration of the non-clustered CLEC-2 and C^{Clust} – transient CLEC-2 cluster concentration.

Both the full model and 2-equation model were capable of accurately simulating available literature data (Fig. S1D). Furthermore, the number of single receptor molecules, predicted by "2-equation" model, corresponded to the value, predicted by "N-equation" model. Based on these results, we considered "2-equation" model applicable for the description of receptor clustering. Thus, "2-equation" model was used in all further calculations.

The "Quiescent state" module (Fig. 2B) of the model consists of variables for concentrations of CD148 phosphatase in active and passive states (2 variables); Csk in active and passive states (2 variables); SFK in a set of gradually active states: non-active, 1/3 active and 2/3 active (3 variables); Syk kinases in active and passive states (2 variables); TULA-2 in active and passive states (2 variables). "Quiescent state" module contains 19 parameters, common with "Tyrosine kinase" module. The initial concentrations of the species (Table S5) were at steady-state values for the module. The "Quiescent state" module was tuned in order to obtain 5% active Syk kinases required for CLEC-2 phosphorylation (9, 10) and 10% of SFKs (Kr^{CD148} , Kr^{Syk} , Kr^{Syk} parameters were estimated). The parameters of the reactions are given in Table S6.

The "Tyrosine kinase" module (Fig. 2C) of the model consists of variables for concentrations of active and inactive Syk kinases(2 variables); SFK in gradually active states: non active, one-third, two-thirds and fully active (4 variables); clustered non phosphorylated and clustered phosphorylated CLEC-2 receptors (2 variables); active and non-active TULA-2 (2 variables).

The unknown parameters of the module (Kr^{CLEC2} , k_{S1}^{S12} , Kr_{TULA2}^{Syk} , Kf_{Syk}^{TULA2} , $Kr_{Syk}^{TULA2})$ were estimated by fitting number of active Syk to data from (14), and the number of Y416 phosphorylated SFK to data from (15) (Fig. 2E and S3, correspondingly).

The "LAT-PLCγ2" module (Fig. 2D) consists of variables for concentrations of active Syk (1 variable); phosphorylated and non-phosphorylated LAT (2 variables); LAT-PLCγ2 complexes (1 variable); LAT-PLCγ2-PI3K complexes (1 variable); phosphoinositides (IP₃, PIP₂ and PIP₃, 3 variables); active and non-active Btk (2 variables). The "LAT-PLCy2" module contains 16 parameters. Unknown parameters (Kr^{LAT} , Kr^{PLC} , k_1^{Btk} , Kr^{PIP_3}) were estimated by fitting numbers of phosphorylated LAT and active PLCγ2 to data from (14) (Fig. 2F and 2G, correspondingly). Initial concentrations of the species in the model and parameter values with equations of the model can be found in tables S7 and S8, correspondingly. The model of Ca^{2+} release (Fig. 2D, "Calcium" module) is described in our previous work (16, 17). It is noteworthy that IP₃ concentration in the model of CLEC-2 signalling is a sole link to calcium module and no other positive or negative feedbacks exist in the model. Thus, being the sole generator of IP₃, active PLC γ 2 was selected as the main output of the model.

2. Supporting Tables.

Table S1. Geometric region details.

Name	Reaction		Equation	Parameters	Ref.
CLEC-2	$M_{\rm i}$	$\leftrightarrows R^*$ R	$\int S_{PM} \times V_{EC} \times Kf^{Lig} \times Liq \times R$	$Kf^{Lig} = 1 s^{-1} \times \mu mol^{-1}$	this
ligation		$+$ Lig	$-S_{PM} \times Kr^{Lig} \times R^*$ κ .	$Kr^{Lig} = 0.0302 s^{-1}$	work

Table S4. "CLEC-2 clustering" module: receptor clustering description (rapid-receptor dimerisation).

Table S5. "Tyrosine kinase" and "Quiescent state" module: initial conditions.

Table S6. "Tyrosine kinase" and "Quiescent state" module: equations and parameters.

Table S7. "LAT-PLCγ2" module: initial conditions.

Table S8. "LAT-PLCγ2" module: equations and parameters.

Detailed calcium module description is given in (19).

Table S9. Models in COPASI Software.

Table S10. Sensitivity scores of the most influential parameters for the number of active Syk kinases at the point of maximal activation.

	reverse rate of Syk	Kr^{Syk}	$10 s^{-1}$	$5 - 25$	0.775836
	activation by SFK kinases				
	Syk deactivation by	Kr_{TULA2}^{Syk}	7.5 $s^{-1} \times \mu M^{-1}$	$2 - 20$	0.734043
	TULA-2 rate				
	the forward rate of	Kf_{SVk}^{TULA2}	$0.1 \mu M^{-1} \times s^{-1}$	$0.05 - 0.5$	0.559938
	TULA-2 activation				
	by Syk				
	reverse rate of	Kr_{Syk}^{TULA2}	$0.007 s^{-1}$	$0.01 - 0.1$	0.21001
	TULA-2 activation				
	by Syk				
	the turnover rate	k_{cat}^{Src}	$2.1 s^{-1}$	$0.5 - 5$	0.17258
	of SFK kinases				
	Michaelis constant	Km^{CD148}	$9.1 \, mM$	4550 - 18200	0.010652
	of CD148				
	reverse rate of	$\overline{Kr^{CD148}}$	$90.8 s^{-1}$	$40 - 200$	0.010623
	CD148 activation				
	the turnover rate	k_{cat}^{CD148}	$9.7 s^{-1}$	$4 - 20$	0.010536
	of CD148				
	Syk initial number	S	5000	2500 - 10000	1.46352
	TULA-2 initial	T	8000	3750 - 15000	0.680195
	number				
	SFK initial number	F_p	36800	$10000 -$	0.010381
				40000	
Comp.	platelet cytosol	V_{Cyt}	4.5 fl	$2.25 - 9$	$\mathbf{1}$
Sizes	volume				
	plasma membrane	S_{PM}	$45 \mu m^2$	$25 - 90$	0.152712
	area				

Table S11. Sensitivity scores of the most influential parameters for the number of phosphorylated LAT at the point of maximal activation.

Table S12. Sensitivity scores of the most influential parameters for the number of active PLCγ2 at point of maximal activation.

Table S13. Sensitivity scores of the most influential parameters for the IP₃ concentration at the point of maximal activation.

	PI3K kD from	kD_{LP}	$0.22 \mu M$	$0.11 - 0.44$	0.015487
	phosphorylated				
	LAT				
	LAT initial number		4900	2500 - 10000	1.3449
	Btk initial number	B	11100	5000 - 25000	1.17598
	$PLCy2$ initial	\boldsymbol{p}	2000	1000 - 4000	0.225426
	number				
	PI3K initial number	P	1900	$950 - 3800$	0.016803
Comp.	plasma membrane	S_{PM}	$45 \mu m^2$	$25 - 90$	2.70157
Sizes	area				

Table S14. Sensitivity scores of the most influential parameters for the calcium concentration at the point of

		k_1 ; $s^{-1} \times \mu$ mol ⁻¹ k_{-2} ; $s^{-1} \times \mu$ mol ⁻¹	k_3 ; s^{-1}
37° C	13924.4	348.26	2.7×10^{-6}
25° C.	2249	251.16	1.8×10^{-6}
25°C, 1mM mβCD	164	208.07	1×10^{-6}

Table S15. "CLEC-2 clustering" module parameters, corresponding to different activatory conditions.

System of differential equations corresponding to the biochemical reactions incorporated in the stochastic model:

$$
\frac{dT^*}{dt} \times V_{Cyl} = K_6
$$
\n
$$
\frac{dS}{dt} \times V_{Cyl} = -K_8
$$
\n
$$
\frac{dS}{dt} \times V_{Cyl} = K_9
$$
\n
$$
\frac{dL^*}{dt} \times S_{PM} = PL_1
$$
\n
$$
\frac{dL}{dt} \times S_{PM} = PL_1
$$
\n
$$
\frac{dL}{dt} \times S_{PM} = PL_2
$$
\n
$$
\frac{dL}{dt} \times V_{CN} = -PL_2
$$
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\frac{dL}{dt} \times V_{CN} = -PL_2
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\frac{dL}{dt} \times V_{CN} = -PL_2
$$
\n
$$
\frac{dL}{dt} \times V_{CN} = -PL_3
$$
\n
$$
\frac{dL}{dt} \times S_{PM} = PL_4
$$
\n
$$
\frac{dL}{dt} \times S_{PM} = PL_4
$$
\n
$$
\frac{dL}{dt} \times V_{CN} = -PL_5
$$
\n
$$
\frac{dL}{dt} \times V_{CN} = PL_5
$$
\n
$$
\frac{dL^*}{dt} \times S_{PM} = PL_5
$$
\n
$$
\frac{dL^*}{dt} \times S_{PM} = PL_6
$$
\n
$$
\frac{dL}{dt} \times V_{CN} = PL_7
$$
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\frac{dL}{dt} \times V_{CN} = PL_7
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$$
\frac{dL}{dt} \times V_{CN} = PL_7
$$
\n
$$
\frac{dL}{dt} \times V_{CN} = 2L_7
$$
\n
$$
\frac{dL}{dt} \times V_{CN} = -2L_7
$$
\n<math display="</math>

$$
\frac{dI_3}{dt} \times V_{\mathit{Cyt}} = PL_7 \tag{29}
$$

3. Supporting Figures

Figure S1. CLEC-2 receptor clustering models. In order to describe platelet CLEC-2 receptor clustering two approaches were used: N-equation model of receptor clustering, which describes behavior of the clusters of the receptors of each size explicitly (A – scheme, C- average cluster size) – (11) and 2-equation model, that describes behavior of the receptor clusters in general $(B) - (13)$. Both models were capable of describing experimental data showing the clustering of CLEC-2, calculated from absolute fluorescent intensity data (12) under the assumption that only CLEC-2 monomers and dimers are present on the surface of resting platelets (29) (D). More simplistic approach – 2-equation model – was used for the construction of the complete model of CLEC-2 signalling, because it both allowed to describe experimental data and to reduce computational complexity.

Figure S2. Network diagram of the platelet CLEC-2 signalling model. Black lines represent transitions between the different state of the incorporated species. Red lines represent catalysis. Green lines represent calcium ions transitions from DTS to the cytosol. Unknown parameter values are highlighted in red. All parameter values can be found in Supplementary Tables S4,5,7,9.

Figure S3. Model validation. Comparison of the numbers of Y416 phosphorylated amount of SFK predicted by the model to experimental data available from the literature (15).

Figure S4. Explicit variation of the parameters of the "CLEC-2 clusteri ng module". (A-C) Impact of the "CLEC-2 clustering" parameters on maximal CLEC-2 cluster size (S_{Max}) in "Ligand mediated receptor dimerisation" mode: CLEC-2 initial number (A), CLEC-2 clustering k_1 (B), CLEC-2 clustering k_1 (C), CLEC-2 clustering k_2 (D), CLEC-2 clustering k_2 (E), CLEC-2 clustering k_3 (F). (G-L) Impact of the "CLEC-2 clustering" parameters on maximal CLEC-2 cluster size (S_{Max}) in "Ligand mediated receptor dimerisation" mode: CLEC-2 initial number (G), CLEC-2 clustering k_1 (H), CLEC-2 clustering k_1 (I), CLEC-2 clustering k_2 (J), CLEC-2 clustering k_2 (K), CLEC-2 clustering k_3 (L).

Figure S5. Local sensitivity analysis. Sensitivity score of the most influential parameters from each of the module and the most influential initial concentration, concerning: number of active Syk kinases (A), number of phosphorylated LAT (B), IP³ concentration (C), cytosolic calcium concentration (D). Red colour highlights "CLEC-2 clustering" module, blue – "Tyrosine kinase" module, green – "LAT-PLCγ2" module, purple – initial volumes of the model compartments.

Figure S6. Explicit variation of the parameters with the sensitivity score above 0.01 for effect on maximal amount of active PLCγ2 and time to maximum (from CLEC-2 clustering k¹ to TULA-2 initial concentration). CLEC-2 clustering k¹ (A), reverse rate of Syk activation by SFK kinases (B), reverse rate of CLEC-2 phosphorylation (C), Syk deactivation by TULA-2 rate (D), forward rate of TULA-2 activation by Syk (E), turnover rate of SFK kinases (F), reverse rate of TULA-2 activation by Syk (G), Syk SH-2 domains kD from phosphorylated tyrosine residues in hemITAM sequences (H), TULA-2 initial number (I). Red colour highlights "CLEC-2 clustering" module, blue – "Tyrosine kinase" module.

Figure S7. Explicit variation of the parameters with the sensitivity score above 0.01 for effect on maximal amount of active PLCγ2 and time to maximum (from PI3K turnover rate to plasma membrane area). PI3K turnover rate (A), reverse rate of PIP₃ production by PI3K (B), reverse rate of PLCγ2 activation (C), PLCγ2 kD from phosphorylated LAT (D), Michaelis constant of PI3K (E), forward rate of Btk activation upon PIP³ binding (F), PI3K kD from phosphorylated LAT (G), Btk initial number (H), PLCy2 initial number (I), PI3K initial number (J), plasma membrane area (K). Green – "LAT-PLCγ2" module, purple – initial volumes of the model compartments.

Figure S8. Explicit variation of the parameters with the sensitivity score above 0.01 for effect on maximal amount of active Syk kinases and time to maximum (from CLEC-2 clustering k-2 to turnover rate of SFK). CLEC-2 clustering k-2 (A), CLEC-2 clustering k-1 (B), CLEC-2 clustering k₁ (C), forward rate of Syk activation upon SH-2 domain binding to dually phosphorylated hemITAMs (D), reverse rate of CLEC-2 phosphorylation (E), turnover rate of Syk kinases (F), Michaelis constant of Syk kinases (G), reverse rate of Syk activation by SFK kinases (H), Syk deactivation by TULA-2 rate (I), forward rate of TULA-2 activation by Syk (J), reverse rate of TULA-2 activation by Syk (K), turnover rate of SFK kinases (L). Red colour highlights "CLEC-2 clustering" module, blue – "Tyrosine kinase" module.

Figure S9. Explicit variation of the parameters with the sensitivity score above 0.01 for effect on maximal amount of active Syk kinases and time to maximum (from Michaelis constant of CD148 to platelet cytosol volume). Michaelis constant of CD148 (A), reverse rate of CD148 activation (B), turnover rate of CD148 (C), Syk initial number (D), TULA-2 initial number (E), SFK initial number (F), plasma membrane area (I), platelet cytosol volume (J). Blue – "Tyrosine kinase" module, purple – initial volumes of the model compartments.

Figure S10. Explicit variation of the parameters with the sensitivity score above 0.01 for effect on maximal amount of phosphorylated LAT and time to maximum (from CLEC-2 clustering k-2 to turnover rate of SFK). CLEC-2 clustering k₋₂ (A), CLEC-2 clustering k₋₁ (B), CLEC-2 clustering k₁ (C), CLEC-2 initial number (D), turnover rate of Syk kinases (E), Michaelis constant of Syk kinases (F), forward rate of Syk activation upon SH-2 domain binding to dually phosphorylated hemITAMs (G), reverse rate of Syk activation by SFK kinases (H), reverse rate of CLEC-2 phosphorylation (I), Syk deactivation by TULA-2 rate (J), forward rate of TULA-2 activation by Syk (K), turnover rate of SFK kinases (L). Red colour highlights "CLEC-2 clustering" module, blue – "Tyrosine kinase" module.

Figure S11. Explicit variation of the parameters with the sensitivity score above 0.01 for effect on maximal amount of phosphorylated LAT and time to maximum (from the reverse rate of TULA-2 activation by Syk to plasma membrane area). Reverse rate of TULA-2 activation by Syk (A), Syk SH-2 domains kD from phosphorylated tyrosine residues in hemITAM sequences (B), Syk initial number (C), TULA-2 initial number (D), reverse rate of LAT phosphorylation (F), LAT initial number (G), plasma membrane area (I). Blue – "Tyrosine kinase" module, green – "LAT-PLCγ2" module, purple – initial volumes of the model compartments.

Figure S12. Explicit variation of the parameters with the sensitivity score above 0.01 for effect on the maximal concentration of IP³ and time to maximum (from CLEC-2 clustering k-2 to forward rate of TULA-2 activation by Syk). Inflexion point on the graph corresponds to the initiation of calcium oscillations. CLEC-2 clustering k₋₂ (A), CLEC-2 clustering k₋₁ (B), CLEC-2 clustering k₁ (C), CLEC-2 clustering k₃ (D), CLEC-2 initial number (E), turnover rate of Syk kinases (F), Michaelis constant of Syk kinases (G), forward rate of Syk activation upon SH-2 domain binding to dually phosphorylated hemITAMs (H), reverse rate of Syk activation by SFK kinases (I), reverse rate of CLEC-2 phosphorylation (J), Syk deactivation by TULA-2 rate (K), forward rate of TULA-2 activation by Syk (L). Red colour highlights "CLEC-2 clustering" module, blue - "Tyrosine kinase" module.

Figure S13. Explicit variation of the parameters with the sensitivity score above 0.01 for effect on the maximal concentration of IP³ and time to maximum (turnover rate of SFK to turnover rate of Btk). Inflexion point on the graph corresponds to the initiation of calcium oscillations. Turnover rate of SFK (A), reverse rate of TULA-2 activation by Syk (B), Syk SH-2 domains kD from phosphorylated tyrosine residues in hemITAM sequences (C), reverse rate of CD148 activation (D), turnover rate of CD148 (E), Michaelis constant of CD148 (F), Syk initial number (G), TULA-2 initial number (H), SFK initial number (I), reverse rate of LAT phosphorylation (J), reverse rate of IP₃ production (K), turnover rate of Btk (L). Blue – "Tyrosine kinase" module, green – "LAT-PLCγ2" module.

Figure S14. Explicit variation of the parameters with the sensitivity score above 0.01 for effect on the maximal concentration of IP³ and time to maximum (from Michaelis constant of Btk to plasma membrane area). Inflexion point on the graph corresponds to the initiation of calcium oscillations. Michaelis constant of Btk (A), turnover rate of PI3K (B), reverse rate of PIP₃ production by PI3K (C), PLCγ2 kD from phosphorylated LAT (D), Michaelis constant of PI3K (E), forward rate of Btk activation upon PIP₃ binding (F), PI3K kD from phosphorylated LAT (G), reverse rate of PLCγ2 activation (H), LAT initial number (I), Btk initial number (J), PLCγ2 initial number (K), PI3K initial number (L), plasma membrane area (M). Green – "LAT-PLCγ2" module, purple – initial volumes of the model compartments.

Figure S15. Explicit variation of the parameters with the sensitivity score above 0.01 for effect on the maximal concentration of cytosolic calcium and time to maximum (from CLEC-2 clustering k-2 to turnover rate of SFK). Inflexion point on the graph corresponds to the initiation of calcium oscillations. CLEC-2 clustering k₋₂ (A), CLEC-2 clustering k₋₁ (B), CLEC-2 clustering k₁ (C), CLEC-2 initial number (D), turnover rate of Syk kinases (E), Michaelis constant of Syk kinases (F), forward rate of Syk activation upon SH-2 domain binding to dually phosphorylated hemITAMs (G), reverse rate of Syk activation by SFK kinases (H), reverse rate of CLEC-2 phosphorylation (I), Syk deactivation by TULA-2 rate (J), forward rate of TULA-2 activation by Syk (K), turnover rate of SFK (L). Red colour highlights "CLEC-2 clustering" module, blue - "Tyrosine kinase" module.

Figure S16. Explicit variation of the parameters with the sensitivity score above 0.01 for effect on the maximal concentration of cytosolic calcium and time to maximum (turnover rate of SFK to turnover rate of Btk). Inflexion point on the graph corresponds to the initiation of calcium oscillations. Reverse rate of TULA-2 activation by Syk (A), Syk initial number (B), TULA-2 initial number (C), reverse rate of LAT phosphorylation (D), reverse rate of IP₃ production (E), turnover rate of Btk (F), Michaelis constant of Btk (G), turnover rate of PI3K (H), reverse rate of PIP₃ production by PI3K (I), PLCγ2 kD from phosphorylated LAT (D) (J), Michaelis constant of PI3K (K), reverse rate of PLCγ2 activation (L), LAT initial number (M), Btk initial number (N), PLCγ2 initial number (O), plasma membrane area (P).

Figure S17. Activation of platelets by 2µM ADP was independent of temperature conditions.

Figure S18. CLEC-2 induced calcium response in platelets, averaged over 100 stochastic runs at different CLEC-2 cluster formation rates.

Figure S19. Immunefluorescence of platelets activated by 100 µg/ml Fucoidan at 37°C, fixed at different time**points and stained for phosphorylated LAT.** (A) Resting platelets; (B) 30 second incubation with the activator; (C) 60 second incubation with the activator; (D) 300 second incubation with the activator.

Figure S20. Immunefluorescence of platelets activated by 100 µg/ml Fucoidan at 25°C, fixed at different time**points and stained for phosphorylated LAT.** (A) Resting platelets; (B) 30 second incubation with the activator; (C) 60 second incubation with the activator; (D) 300 second incubation with the activator.

Figure S21. Immunefluorescence of cholesterol depleted platelets activated by 100 µg/ml Fucoidan at 25^oC, fixed at different time-points and stained for phosphorylated LAT. (A) Resting platelets; (B) 30 second incubation with the activator; (C) 60 second incubation with the activator; (D) 300 second incubation with the activator.

Figure S22. Immunefluorescence of platelets activated either by 5 µg/ml CRP or incubated with MQ, fixed at different time-points and stained for phosphorylated LAT. (A) Resting platelets; (B) 300 second incubation with the activator; (C) resting platelets; (D) 300 second incubation with MQ.

4. Supporting references

- 1. Mori, J., Y.J. Wang, S. Ellison, S. Heising, B.G. Neel, M.L. Tremblay, S.P. Watson, and Y.A. Senis. 2012. Dominant role of the protein-tyrosine phosphatase CD148 in regulating platelet activation relative to protein-tyrosine phosphatase-1B. Arterioscler. Thromb. Vasc. Biol. 32: 2956–2965.
- 2. Senis, Y.A., A. Mazharian, and J. Mori. 2014. Src family kinases: at the forefront of platelet activation. Blood. 124: 2013–2024.
- 3. Coxon, C.H., M.J. Geer, and Y.A. Senis. 2017. ITIM receptors: More than just inhibitors of platelet activation. Blood. 129: 3407–3418.
- 4. Bradshaw, J.M. 2010. The Src, Syk, and Tec family kinases: Distinct types of molecular switches. Cell. Signal. 22: 1175–1184.
- 5. Tiganis, T., and A.M. Bennett. 2007. Protein tyrosine phosphatase function: the substrate perspective. Biochem. J. 402: 1 LP – 15.
- 6. Spring, K., C. Chabot, S. Langlois, L. Lapointe, N.T.N. Trinh, C. Caron, J.K. Hebda, J. Gavard, M. Elchebly, and I. Royal. 2012. Tyrosine phosphorylation of DEP-1/CD148 as a mechanism controlling Src kinase activation, endothelial cell permeability, invasion, and capillary formation. Blood. 120: 2745–2756.
- 7. Rathore, V.B., M. Okada, P.J. Newman, and D.K. Newman. 2007. Paxillin family members function as Cskbinding proteins that regulate Lyn activity in human and murine platelets. Biochem. J. 403: 275–281.
- 8. Lin, X., S. Lee, and G. Sun. 2003. Functions of the activation loop in Csk protein-tyrosine kinase. J. Biol. Chem. 278: 24072–24077.
- 9. Hughes, C.E., B.A. Finney, F. Koentgen, K.L. Lowe, and S.P. Watson. 2015. The N-terminal SH2 domain of Syk is required for (hem) ITAM , but not integrin , signaling in mouse platelets. Blood. 125: 144–155.
- 10. Severin, S., A.Y. Pollitt, L. Navarro-Nunez, C.A. Nash, D. Mour??o-S??, J.A. Eble, Y.A. Senis, and S.P. Watson. 2011. Syk-dependent phosphorylation of CLEC-2: A novel mechanism of hem-immunoreceptor tyrosinebased activation motif signaling. J. Biol. Chem. 286: 4107–4116.
- 11. Garzon Dasgupta, A.K., A.A. Martyanov, A.A. Filkova, M.A. Panteleev, and A.N. Sveshnikova. 2020. Development of a simple kinetic mathematical model of aggregation of proteins or clustering of receptors. Submiss. .
- 12. Pollitt, A.Y., N.S. Poulter, E. Gitz, L. Navarro-Nuñez, Y.J. Wang, C.E. Hughes, S.G. Thomas, B. Nieswandt, M.R. Douglas, D.M. Owen, D.G. Jackson, M.L. Dustin, and S.P. Watson. 2014. Syk and src family kinases regulate c-type lectin receptor 2 (clec-2)-mediated clustering of podoplanin and platelet adhesion to lymphatic endothelial cells. J. Biol. Chem. 289: 35695–35710.
- 13. Filkova, A.A., A.A. Martyanov, A.K. Garzon Dasgupta, M.A. Panteleev, and A.N. Sveshnikova. 2019. Quantitative dynamics of reversible platelet aggregation: mathematical modelling and experiments. Sci. Rep. 9: 6217.
- 14. Manne, B.K., T.M. Getz, C.E. Hughes, O. Alshehri, C. Dangelmaier, U.P. Naik, S.P. Watson, and S.P. Kunapuli. 2013. Fucoidan is a novel platelet agonist for the C-type lectin-like receptor 2 (CLEC-2). J. Biol. Chem. 288: 7717–7726.
- 15. Musumeci, L., M.J. Kuijpers, K. Gilio, A. Hego, E. Th????tre, L. Maurissen, M. Vandereyken, C. V. Diogo, C. Lecut, W. Guilmain, E. V. Bobkova, J.A. Eble, R. Dahl, P. Drion, J. Rascon, Y. Mostofi, H. Yuan, E. Sergienko, T.D.Y. Chung, M. Thiry, Y. Senis, M. Moutschen, T. Mustelin, P. Lancellotti, J.W.M. Heemskerk, L. Tautz, C. Oury, and S. Rahmouni. 2015. Dual-specificity phosphatase 3 deficiency or inhibition limits platelet activation and arterial thrombosis. Circulation. 131: 656–668.
- 16. Sveshnikova, A.N., A. V. Balatskiy, A.S. Demianova, T.O. Shepelyuk, S.S. Shakhidzhanov, M.N. Balatskaya, A. V. Pichugin, F.I. Ataullakhanov, and M.A. Panteleev. 2016. Systems biology insights into the meaning of the platelet's dual-receptor thrombin signaling. J. Thromb. Haemost. 14: 2045–2057.
- 17. Balabin, F.A., and A.N. Sveshnikova. 2016. Computational biology analysis of platelet signaling reveals roles of feedbacks through phospholipase C and inositol 1,4,5-trisphosphate 3-kinase in controlling amplitude and duration of calcium oscillations. Math. Biosci. 276: 67–74.
- 18. Dunster, J.L., F. Mazet, M.J. Fry, J.M. Gibbins, and M.J. Tindall. 2015. Regulation of Early Steps of GPVI Signal Transduction by Phosphatases: A Systems Biology Approach. PLoS Comput. Biol. 11: 1–26.
- 19. Sveshnikova, A.N., F.I. Ataullakhanov, and M.A. Panteleev. 2015. Compartmentalized calcium signaling triggers subpopulation formation upon platelet activation through PAR1. Mol. BioSyst. 11: 1052–1060.
- 20. Eckly, A., J.Y. Rinckel, F. Proamer, N. Ulas, S. Joshi, S.W. Whiteheart, and C. Gachet. 2016. Respective contributions of single and compound granule fusion to secretion by activated platelets. Blood. 128: 2538– 2549.
- 21. Gitz, E., A.Y. Pollitt, J.J. Gitz-Francois, O. Alshehri, J. Mori, S. Montague, G.B. Nash, M.R. Douglas, E.E. Gardiner, R.K. Andrews, C.D. Buckley, P. Harrison, and S.P. Watson. 2014. CLEC-2 expression is maintained on activated platelets and on platelet microparticles. Blood. 124: 2262–2270.
- 22. Burkhart, J.M., M. Vaudel, S. Gambaryan, S. Radau, U. Walter, L. Martens, J. Geiger, A. Sickmann, and R.P. Zahedi. 2012. The first comprehensive and quantitative analysis of human platelet protein composition allows the comparative analysis of structural and functional pathways. Blood. 120.
- 23. Kemble, D.J., Y.H. Wang, and G. Sun. 2006. Bacterial expression and characterization of catalytic loop mutants of Src protein tyrosine kinase. Biochemistry. 45: 14749–14754.
- 24. Ren, L., X. Chen, R. Luechapanichkul, N.G. Selner, T.M. Meyer, A.-S. Wavreille, R. Chan, C. Iorio, X. Zhou, B.G. Neel, and D. Pei. 2011. Substrate Specificity of Protein Tyrosine Phosphatases 1B, RPTPα, SHP-1, and SHP-2.

Biochemistry. 50: 2339–2356.

- 25. Park, M.J., R. Sheng, A. Silkov, D.J. Jung, Z.G. Wang, Y. Xin, H. Kim, P. Thiagarajan-Rosenkranz, S. Song, Y. Yoon, W. Nam, I. Kim, E. Kim, D.G. Lee, Y. Chen, I. Singaram, L. Wang, M.H. Jang, C.S. Hwang, B. Honig, S. Ryu, J. Lorieau, Y.M. Kim, and W. Cho. 2016. SH2 Domains Serve as Lipid-Binding Modules for pTyr-Signaling Proteins. Mol. Cell. 62: 7–20.
- 26. Tsang, E., A.M. Giannetti, D. Shaw, M. Dinh, J.K.Y. Tse, S. Gandhi, A. Ho, S. Wang, E. Papp, and J.M. Bradshaw. 2008. Molecular mechanism of the Syk activation switch. J. Biol. Chem. 283: 32650–32659.
- 27. Hughes, C.E., U. Sinha, A. Pandey, J.A. Eble, C.A. O'Callaghan, and S.P. Watson. 2013. Critical role for an acidic amino acid region in platelet signaling by the HemITAM (hemi-immunoreceptor tyrosine-based activation motif) containing receptor CLEC-2 (C-type lectin receptor-2). J. Biol. Chem. 288: 5127–5135.
- 28. Dinh, M., D. Grunberger, H. Ho, S.Y. Tsing, D. Shaw, S. Lee, J. Barnett, R.J. Hill, D.C. Swinney, and J.M. Bradshaw. 2007. Activation Mechanism and Steady State Kinetics of Bruton's Tyrosine Kinase. J. Biol. Chem. 282: 8768–8776.
- 29. Hughes, C.E., A.Y. Pollitt, J. Mori, J.A. Eble, M.G. Tomlinson, J.H. Hartwig, C.A. O'Callaghan, K. Fütterer, and S.P. Watson. 2010. CLEC-2 activates Syk through dimerization. Blood. 115: 2947–2955.