Supplemental Materials

Lyn- and PLC-β3-dependent regulation of SHP-1 phosphorylation controls Stat5 activity and myelomonocytic leukemia-like disease

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List of Supplemental Items

- 1. Supplemental Methods
- 2. Supplemental Tables S1-S3
- 3. Supplemental Figures S1-S8

Histology and immunofluorescence

Tissues were fixed in 10% formalin, embedded in paraffin, sectioned at 6 mm, and stained with hematoxylin and eosin (H&E). Blood smears were stained in Wright-Giemsa. For immunofluorescence, tissues were fixed in 4% paraformaldehyde, embedded in O.C.T. Compound (Sakura Finetek). Frozen sections were permeabilized by ice-cold methanol, stained with rat anti-F4/80 (Abcam) and rabbit anti-Ym-1 (StemCell Technologies) antibodies, followed by anti-Rat (Texas red) (Southern Biotech) and anti-rabbit (Alexa Fluor 488) (Invitrogen) as second antibodies. Coverslips were mounted with ProLong Gold antifade reagent with DAPI (Invitrogen). Fluorescence was observed using a Marianas microscope system (Intelligent Imaging Innovations).

Identification, purification, and proliferation of HSC and progenitors

Cell sorting was performed by immunomagnetic-based pre-enrichment followed by flow cytometric sorting. Briefly, lineage (Lin)⁺ cells were depleted from BM cells using a lineage depletion Kit (StemCell Techologies), which contained biotin-conjugated antibodies for B220, Gr-1, CD11b, CD8, CD4, and Ter119. Lin^{-/lo} cells were incubated with PerCP-Cy5.5-conjugated streptavidin (eBioscience) and subsequently stained with rat anti-mouse Sca-1 (FITC), rat antimouse c-Kit (APC), and rat anti-mouse IL-7R (PE) (from PharMingen or eBioscience). Cells were also stained with 7-aminoactinomycin D to exclude dead cells. To detect LT-HSC, Lin-^{//o} cells were stained with rat anti-mouse CD34 (PE), rat anti-mouse Sca-1 (FITC), and rat antimouse c-Kit (APC). To identify the CMP, GMP, and MEP, the same Lin staining was performed together with rat anti-mouse c-Kit (APC), rat anti-mouse CD34 (FITC), and rat anti-mouse FcyR (PE) (PharMingen), and anti-Sca-1-biotin and anti-IL-7R α -biotin antibodies (visualized by streptavidin-TriColor). The phenotype of LT-HSC and ST-HSC was defined as Lin-IL-7Ra-Sca-1^{hi}c-Kit^{hi}CD34⁻ and Lin⁻IL-7Rα⁻Sca-1^{hi}c-Kit^{hi}CD34⁺, respectively; CMP as Lin⁻IL-7R⁻Sca-1⁻ CD34⁺FcyR^{lo}; GMP as Lin⁻IL-7R⁻Sca-1⁻CD34⁺FcyR^{hi}; MEP as Lin⁻IL-7R⁻Sca-1⁻CD34⁻FcyR^{lo}. SLAM markers were also used to identify HSCs by staining BM cells with biotin-conjugated Lineage cocktails revealed by PerCP-Cy5.5 conjugated strepavidin, anti-mouse c-Kit (APC), antimouse CD150 (PE, clone mShad150, eBioscience) and anti-mouse CD48 (FITC, clone HM48-1, eBioscience). Lin⁻c-Kit⁺CD150⁺CD48⁻ population was enriched for HSCs. All cell populations were sorted or analyzed using a FACSVantage Diva or FACS Aria (Becton Dickinson). The purity of all sorted HSC/progenitor populations was >98%. For proliferation assays, CD34⁻ KSL cells were sorted into a 96-well round bottom plate (50 cells per well) in 200 μ l of IMDM containing 5% FBS, 50 μ M 2-mercaptoethanol, and IL-3 (100 ng/ml) and SCF (100 ng/ml), and incubated at 37°C for the indicated periods.

Cell cycle analysis

For propidium iodide staining analysis, sorted KSL cells were incubated for 24 h in IMDM supplemented (or not) with IL-3 (100 ng/ml). Then cells were centrifuged and resuspended in a hypotonic buffer (0.1% sodium citrate, 0.1% Triton X-100) containing RNase and propidium iodide. Samples were analyzed within 1 h. For G_0/G_1 analysis, sorted KSL cells were incubated for 1 h at 37°C in Hank's balanced salt solution with 20 mM HEPES, 1 g/l glucose, 10% FCS, and 1.7 μ M Hoechst 33342 (Invitrogen). After washing, the cells were incubated in the same buffer containing Pyronin Y (1 μ g/ml; Sigma-Aldrich) for another hour at 37°C. Finally, cells were analyzed using an LSRII (Becton Dickinson) and a FlowJo software.

Transplantation of retrovirally transduced HSCs

CD34⁻KSL cells were FACS-sorted into Retronectin-precoated wells (150 cells per well). These cells were infected with a concentrated high-titer virus (at the multiplicity of infection of 600) in the presence of IL-6 (100 ng/ml), FLT3L (20 ng/ml), and SCF (100 ng/ml). 3 days later, these cells (estimated 2000-5000 cells in total) were transplanted into lethally irradiated recipients together with 10⁷ Sca-1-depleted BM helper cells. The protocols for this and other experiments will be provided upon request.

	Wt	lyn ^{-/-}	PLC-β3 ^{-/-}	Dko	me ^v ‡
	(n=6)	(n=8)	(n=8)	(n=8)	(n=4)
Total WBC	11.23±2.75	6.22±1.76*	9.68±1.90	6.33±1.47*	5.85±0.63*
(x10 ³ /µl)					
Neutrophil	2.44 ± 0.71	2.62±1.03	2.85 ± 0.88	2.97 ± 0.66	3.43±0.86
Lymphocyte	7.82±1.85	3.15±0.54**	6.31±1.01	2.84±0.71**	1.84±0.21**
Monocyte	0.46 ± 0.15	0.41±0.16	0.47 ± 0.15	0.38±0.25	0.52 ± 0.11
Eosinophil	0.35 ± 0.34	0.04 ± 0.05	0.05 ± 0.03	0.09 ± 0.14	0.06 ± 0.03
basophil	0.16±0.19	0.01 ± 0.01	0.01 ± 0.01	0.04 ± 0.07	0.01 ± 0.01
Hemoglobulin	13.35±1.18	13.93±0.52	12.83±0.15	13.20±0.27	13.23±0.65
(g/dl)					
Platelet (x10 ³ /µl)	964±100	934±30.64	992±99.94	1009±192	928±200
Differential					
count (%)					
Neutrophil	21.71±3.38	41.04±4.68***	28.98±4.37*	47.38±6.59***	58.04±8.71***
Lymphocyte	69.86±3.42	51.86±5.88**	65.77±5.21	44.84±4.46**	31.82±6.77**
Monocyte	4.11±1.10	6.51±0.60	4.80±0.75	5.74±2.29	9.07±2.77*
Eosinophil	2.96 ± 2.57	0.51±0.63	0.43±0.23	1.40 ± 2.17	0.96 ± 0.41
basophil	1.36±1.49	0.09 ± 0.12	0.03 ± 0.02	0.63 ± 1.10	0.11±0.02

Table S1. Complete blood cell counts in 2 month-old mice

\$ 6 weeks old * p<0.05 vs wt, ** p<0.01 vs wt, *** p<0.001 vs wt

	Wt	lyn ^{-/-}	PLC-β3 ^{-/-}	Dko
	(n=6)	(n=8)	(n=8)	(n=8)
Total WBC	8.45±1.44	6.07±1.23	15.10±3.80**	9.28±2.8
(x10 ³ /µl)				
Neutrophil	1.88±0.25	2.41 ± 1.60	3.81±1.48*	4.72±2.05**
Lymphocyte	6.30±1.59	3.05±1.56*	10.74±2.07**	3.74±1.61
Monocyte	0.25 ± 0.11	0.40 ± 0.24	0.45±0.21	0.72±0.63*
Eosinophil	0.02 ± 0.02	0.15±0.21	0.09 ± 0.10	0.17 ± 0.18
basophil	0.01 ± 0.01	0.05 ± 0.09	0.01 ± 0.01	0.03±0.03
Hemoglobulin	12.85 ± 1.20	12.13±0.28	13.13±0.71	9.59±1.0***
(g/dl)				
Platelet (x10 ³ /µl)	1100±141	1078 ± 228	1334±190	549±139***
Differential count				
(%)				
Neutrophil	22.79±4.77	38.69±7.74	24.56±4.09	52.73±11.12***
Lymphocyte	73.92±6.28	52.25±9.32	72.02±4.78	38.07±12.83***
Monocyte	3.09±1.67	6.30±2.28	2.89 ± 0.65	7.40±2.77*
Eosinophil	0.16 ± 0.22	2.02 ± 2.55	0.50 ± 0.50	1.58±0.73**
basophil	0.04 ± 0.04	0.75 ± 1.03	0.03 ± 0.05	0.22±0.13*

 Table S2.
 Complete blood cell counts in 6 month-old mice

* p<0.05 vs wt, ** p<0.01 vs wt, *** p<0.001 vs wt

	Wt (n=6)	Dko (n=8)	
Total WBC	12.24±1.91	6.12±1.30**	
$(x10^{3}/\mu l)$			
Neutrophil	2.13±0.56	2.84±0.23*	
Lymphocyte	9.60±1.51	2.60±1.14***	
Monocyte	0.31±0.11	0.44±0.19	
Eosinophil	0.14 ± 0.09	0.17±0.11	
basophil	0.07 ± 0.06	0.07 ± 0.05	
Hemoglobulin	13.03±0.58	9.95±0.76*	
(g/dl)			
Platelet (x10 ³ / μ l)	786±150	469±184*	
Differential count			
(%)			
Neutrophil	17.41±3.71	42.20±3.67***	
Lymphocyte	78.54±4.15	46.01±5.69***	
Monocyte	2.46 ± 0.55	8.06±1.71***	
Eosinophil	1.09 ± 0.69	2.67±1.64	
basophil	0.51 ± 0.47	1.07 ± 0.95	

 Table S3. Complete blood cell counts at 5 months after BM transplantation

* p<0.05 vs wt, ** p<0.01 vs wt, *** p<0.001 vs wt



Figure S1. H&E-stained organs of $lyn^{-/-}$; *PLC-* $\beta 3^{-/-}$ mice in comparison to wt, *PLC-* $\beta 3^{-/-}$, $lyn^{-/-}$ and me^{ν}/me^{ν} mice. Bars indicate 200 µm for X100 magnification images and 30 µm for X400 magnification images.



Figure S2. MDS/MPN in *lyn^{-/-};PLC-\beta3^{-/-}* **mice can be transferred with BM cells.** BM cells from the indicated mice (CD45.2⁺) were adoptively transferred to lethally irradiated CD45.1⁺ congenic B6 mice. (A) Four months after transplantation, peripheral blood leukocytes were analyzed by flow cytometry to measure CD11b⁺ cells among CD45.2⁺ cells. (B) Survival curves for mice that received BM cells of the indicated genotypes.



Figure S3. The MDS/MPN in $lyn^{-/-}$; *PLC*- $\beta 3^{-/-}$ mice originates from an LT-HSC population.

FACS-sorted cells were adoptively transferred to lethally irradiated CD45.1⁺ mice. Four months after transplantation, peripheral blood leukocytes were analyzed by flow cytometry to measure CD11b⁺ cells among CD45.2⁺ cells. LT, LT-HSCs represented by CD34⁺KSL cells; ST, ST-HSCs represented by CD34⁺KSL cells; MP, myeloid progenitors represented by Lin⁻c-Kit⁺Sca-1⁻ cells.



Figure S4. HSCs/progenitors have constitutive Stat5 phosphorylation in $lyn^{-/-}$;*PLC-* $\beta 3^{-/-}$ mice.

Stat5 phosphorylation at Tyr⁶⁹⁴ in non-stimulated or IL-3 stimulated KSL cells was analyzed by flow cytometry. Dashed line, wt; solid line, $lyn^{-/-}$; *PLC-* $\beta 3^{-/-}$





(A) BM cells were stimulated with GM-CSF, and phospho-Stat5 levels were analyzed by flow cytometry. Mean fluorescence intensity (MFI) of Stat5 phosphorylation in KSL cells is presented (n=6). (B) Sorted KSL cells were cultured in methylcellulose in the indicated concentrations of GM-CSF. 10 days later, the number of colonies (including CFU-G, CFU-M and CFU-GM) was counted.



Figure S6. Transduction with wt SHP-1 suppressed in vitro growth of CD34⁺KSL cells derived from wt, *PLC-\beta3^{-/-}* and *lyn^{-/-}* mice, but not *lyn^{-/-};PLC-\beta3^{-/-} mice.*

FACS sorted CD34-KSL cells were retrovirally transduced with wt SHP-1. The transduced cells were cultured in IL-3 and SCF.



Figure S7. Transduced wt SHP-1 is not phosphorylated at Tyr⁵³⁶ or Tyr⁵⁶⁴ in *lyn*^{-/-};*PLC*- β 3^{-/-} BMMCs.

 $Lyn^{-/-}$; *PLC-* $\beta3^{-/-}$ CD34-KSL cells were retrovirally transduced with the indicated SHP-1 constructs and cultured in IL-3 and SCF. The resulting BMMCs were analyzed by immunoblotting.



Figure S8. A model for SHP-1 activation and recognition of its substrate Stat5 based on accumulated studies (reviewed by Poole and Jones, Cell. Signalling 17:1323, 2005) and our current data. (A) SHP-1 is phosphorylated at Tyr⁵⁶⁴ predominantly by Lyn and at Tyr⁵³⁶ by Lyn and other kinase(s) including Jak2. Inactive SHP-1 (Top left) has a closed conformation with the catalytic site of the PTP domain capped by the N-SH2 domain (Yang, et al., J Biol. Chem. 278:6516, 2003). The Tyr⁵³⁶ phosphorylation site of SHP-1 interacts with Stat5 most probably via the SH2 domain of the latter molecule (Bottom) (this study). The Tyr⁵⁶⁴ phosphorylation site of SHP-1 interacts with N-SH2 to render the enzyme active. N-terminal ends of SHP-1 and Stat5 proteins are shown by 'N'. (B) SHP-1 and Lyn interact with the C-terminal domain of PLC-β3 (this study and Xiao et al., Cancer Cell 16:161, 2009). Tyr⁶⁹⁴ phosphorylated Stat5 is recruited to the PLC-β3-nucleated complex containing Lyn and SHP-1, and dephosphorylated by an active SHP-1 enzyme that is phosphorylated at Tyr⁵³⁶ and Tyr⁵⁶⁴. Stat5 dimer is depicted as a monomer for simplicity.