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Nuclear Role of WASp in Gene Transcription Is Uncoupled from Its ARP2/3-Dependent Cytoplasmic Role in Actin Polymerization

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Defects in Wiskott–Aldrich Syndrome protein (WASp) underlie development of WAS, an X-linked immunodeficiency and autoimmunity disorder of childhood. Nucleation-promoting factors (NPFs) of the WASp family generate F-actin in the cytosol via the VCA (verprolin-homology, cofillin-homology, and acidic) domain and support RNA polymerase II–dependent transcription in the nucleus. Whether nuclear-WASp requires the integration of its actin-related protein (ARP)2/3-dependent cytoplasmic function to reprogram gene transcription, however, remains unresolved. Using the model of human T H1 cell differentiation, we find that WASp has a functional nuclear localizing and nuclear exit sequences, and accordingly, its effects on transcription are controlled mainly at the level of its nuclear entry and exit via the nuclear pore. Human WASp does not use its VCA-dependent, ARP2/3-driven, cytoplasmic effector mechanisms to support histone H3K4 methyltransferase activity in the nucleus of T H1-skewed cells. Accordingly, an isolated deficiency of nuclear-WASp is sufficient to impair the transcriptional reprogramming of T B21 and IFNG promoters in T H1-skewed cells, whereas an isolated deficiency of cytosolic-WASp does not impair this process. In contrast, nuclear presence of WASp in T H2-skewed cells is small, and its loss does not impair transcriptional reprogramming of GATA3 and IL4 promoters. Our study unveils an ARP2/3–VCA-independent function of nuclear-WASp in T H1 gene activation that is uncoupled from its cytoplasmic role in actin polymerization. The Journal of Immunology, 2014, 193: 150–160.
4–9, as well as actin-binding proteins such as N-WASP, WAVE, JMY, and WASP, have all been shown to locate and function in the nucleus, mostly in gene transcription (24–30). We showed that a portion of WASP translocates to the T\(_h\)1 cell nucleus, where it participates in the transcription of TBX21 gene, at the chromatin level (28). Furthermore, we demonstrated that human WASP associates with histone H3K4 trimethylase activity in vitro, and therefore, its loss resulted in diminished enrichment of histone H3K4me3 mark at the TBX21 promoter in vivo (28). This study (28) was the first to unveil a transcriptional role for a bona fide actin-polymerizing cytoplasmic protein WASP. Reciprocally, a bona fide nuclear protein EZH2, a histone H3K27 methylease has been shown to have a critical cytoplasmic function of modifying F-actin cytoskeleton in T cells (31).

The dual location of the cytoplasmic NPFs and nuclear EZH2, however, present a major outstanding question, that is, which of its two compartment-delimited functions is essential in transcriptional reprogramming? To wit, we asked whether the nucleus-located WASP integrates its cytoplasmic F-actin polymerizing role to epigenetically activate the genomic loci with which it interacts in the T\(_h\)1 cells? Or does the dual locations of WASP form the basis of completely separate physiological functions in the two subcellular compartments? To this end, using the binary developmental paradigms of T\(_h\)1 and T\(_h\)2 differentiation, we tested the hypothesis that changes in nuclear WASP transport and/or defects in the nucleus-resident functions of WASP alone result in impaired gene activation that contributes to immune dysregulation in WAS.

In this study, we identified transport proteins and WASP domains involved in its nuclear import and export. Using this information, we devised a strategy of stably reconstituting WASP in either the cytosol or nucleus of patient-derived WAS\(_{null}\) T\(_h\)1 cells and then testing for restoration of gene activation defects linked to WAS (32, 33). We chose the human IFNG and TBX21 (T\(_h\)1 genes) or IL4 and GATA3 (T\(_h\)2 genes) as a model system to investigate chromatin-signaling events, because their proximal promoters are well characterized. We provide multiple levels of evidence that demonstrate an uncoupling of nuclear role of WASP from its ARP2/3-dependent F-actin role in gene activation. Our findings demonstrating that the disparate functions of dual compartment-resident WASP do not rest on the same effector activity (i.e., of actin polymerization), potentially establish a new paradigm for the noncytoplasmic functions of other NPFs in their regulation of nuclear functions during development or cell-fate choices.

**Materials and Methods**

**Cells**

Human primary CD\(_4^+\) T\(_h\) cells, Jurkat T cells, WAS\(_{null}\) CD\(_4^+\) T\(_h\) cell line, WAS\(_{null}\) T\(_h\)1 cell line expressing the various domain-deleted mutants, normal CD\(_4^+\) T\(_h\) cell line, and HeLa cells were cultured under T\(_h\)1-skewing (recombinant human [rh]IL-12, anti–IL-4 Ab, and rhIL-2) or T\(_h\)2-skewing (rhIL-4, anti–IL-12 Ab, anti–IFN-\(\gamma\) Ab, and rhIL-2) or nonskipping T\(_h\)0 (only rhIL-2) conditions for 6 d and further activated with CD3/CD28-coated beads for another 1 d to induce TCR activation. WAS\(_{null}\) T\(_h\)1 cell line was generated from a WAS patient carrying the WASnull T cells by Amaxa Cell Line Nucleofector Kit V (Lonza) and into HeLa by Lipofectamine 2000 Transfection Reagent (Invitrogen). Successful transfection and stable expression of different constructs were verified by immunoblotting and flow cytometry using BD CytoFix/CytoPerm Kit (BD Biosciences). See Supplemental Table I for primer sequences.

**Immunoprecipitation and immunoblotting**

Coimmunoprecipitations (co-IP) were performed with the Universal Magnetic Coimmunoprecipitation kit (Active Motif), as per the manufacturer’s specifications using the commercial reagents, kits, and Abs listed in Supplemental Table II. The same blots were sequentially reprobed with four subcellular fractions was monitored by Abs listed in Supplemental Table II. The same blot was sequentially reprobed with multiple Abs for consistency. For each experiment, IP with the corresponding isotype Ig Ab served as a negative control. Ten percent of the total input was loaded and resolved with immunoblotting.

**Deconvolution immunofluorescence microscopy**

Deconvolution imaging of differentially transplanted paraformaldehyde-fixed T\(_h\)1-skewed and TCR-activated cells was performed with Zeiss inverted digital microscopy workstation integrated with SlideBook software, as described previously (35). Approximately 20–30 z-stack images were acquired at the step size of 0.2 \(\mu\)m at \(\times63\) oil immersion magnification. Approximately 20–30 single T\(_h\)1 cells chosen randomly from multiple experiments were analyzed for each Ab combination.

**Flow cytometry**

The LIVE/DEAD Fixable Dead Cell Stain Kit (Invitrogen) was used for gating on viable T\(_h\)1 cells, which were cultured under T\(_h\)1- or T\(_h\)2-skewing or nonskewing T\(_h\)0 conditions. For intracellular protein staining, the cells were further activated by plate-bound anti-human CD3 and CD28 Abs in the presence of 1 \(\mu\)L BD GolgiPlug and 0.6 \(\mu\)L BD GolgiStop (BD Biosciences) added to \(\sim10^5\) cells/ml of T\(_h\) cell culture for 4–6 h. After fixation and permeabilization using CytoFix/CytoPerm solutions, T\(_h\) cells were stained for intracellular cytokines/or transcription factors using fluorochrome-conjugated Abs. For surface receptor staining, nonpermeabilized fixed cells were labeled with anti-human fluorochrome-conjugated Abs for 30–45 min as per the manufacturers’ recommendations. Corresponding isotype Ig Ab controls were always included to rule out background fluorescence or autofluorescence. Cells were analyzed on a BD Biosciences LSR II using FACSDiva software. The data were generated by cytofluorometric analysis of 10,000 events. Percentage of each positive population and mean fluorescence intensity (geometric mean) were determined by using either quadrant statistics or histograms.

**Quantitative real-time PCR**

Total RNA prepared from \(\sim5000\) nonskewed T\(_h\)0 and T\(_h\)1- or T\(_h\)2-skewed cells using the Quick-RNA MiniPrep Kit (Zymo Research) was used to synthesize cDNA using the High Capacity cDNA Reverse Transcription Kit (Applied Biosystems), and the samples used as templates for quanti-
tative PCR (qPCR) analysis were performed on the 7500HT Real-Time PCR System (Applied Biosystems) using Perfecta qPCR SuperMix, carboxy-X-rhodamine (ROX) (Quanta Bioscience) and TaqMan Gene Expression Assay primers/probes, detailed in Supplemental Table I. The derived C<sub>_i</sub> values were converted to absolute copy numbers with a cloned DNA plasmid standard dilution curve, as previously described by our group (28).

ELISA
The supernatant was harvested from untransfected and WASp-mutant–transfected T<sub>0</sub> (nonskewed) or T<sub>1</sub>- or T<sub>2</sub>-skewed cells, as well as from normal human T<sub>_i</sub> cells in culture, and the expression of GM-CSF, IFNG, and IL-4 cytokines was quantitated by the Solid Phase Sandwich ELISA assay (R&D Systems) in three independent experiments.

Pharmacological inhibition assay
To inhibit CRM1 (Exportin 1)-dependent nuclear export pathway, T cells were incubated in culture with 20 ng/ml leptomycin B (Sigma-Aldrich) or DMSO for 4, 6, 8, and 24 h. Nuclear and cytosolic fractions were isolated from the treated cells and used for downstream assays. To inhibit MT İşte dyneskeleton, T cells were incubated in culture with 5 μM nocodazole for 15 h or with 100 μM orthovanadate for 4 and 24 h or with their DMSO control.

Histone methylation assay
A Western blot–based assay was used to test the in vitro H3 lysine methyltransferase activity of immunoprecipitated (IP) WASp and its various mutants on 5 μg human recombinant unmodified H3 histone octamer subunits (NEB) in the presence or absence of 20 μM nonradioactive S-adenosyl methionine (Sigma-Aldrich) as described previously (28).

Quantitative chromatin IP–qPCR assay
All chromatin IP (ChIP) assays were performed with MNase-digested chromatin isolated from ~5000 cells after fixing protein–DNA interactions with 1% formaldehyde as previously described (36) and modified by our group (28). Briefly, ChIP-grade Abs and their isotype Ig control Abs listed in Supplemental Table II were used to pull down DNA:protein complexes. ChIP samples were used as templates for the RT-qPCR analysis and the derived Ct values converted to absolute copy numbers with a cloned DNA plasmid standard dilution curve. Nonspecific signals obtained with control IgG ChIP were subtracted from those obtained in the test samples.

Results
WASp contains nuclear localization signal–like and nuclear export signal–like motifs that are evolutionary conserved from Drosophila to humans
Because the ~65 kDa WASp is beyond the exclusion limit of nuclear pores (nuclear pore complex) for simple diffusion, we sought to identify a mechanism for its nuclear transport. WASp contains nuclear localization signal (NLS)–like motif `25XPADKKRSGKKKSKIC255` in the basic domain encoded by exon 7 (Fig. 1A). The hydro-pathicity and PONDR plots predict this NLS region to be polar (hydrophobic index ~ +2.0) and intrinsically disordered (PONDR score ~ 1.0), respectively (Fig. 1B), properties that render NLS region accessible to engage in inter- or intramolecular interactions. It also contains two hydrophobic leucine-rich motifs: nuclear export signal (NES) `1L3FLEMLGRKRKLITM14` and NES2 `43IRYGLQAGRLLWEQELYSSLQ17` in the Pleckstrin-homology/WASp-homology domain–1–domain encoded by exons 1 and 2. In NES1, the five hydrophobic residues (φ) follow the conventional φ–(x2)–φ–(x2)–φ–(x2)–φ–(x2)–φ spacing, whereas in NES2, the φ–x–φ–x–φ–x–φ–x–φ–x–φ spacing is unconventional. Yet, both motifs satisfy the minimum in silico requirements for CRM1 binding (37). Notably, the NLS/NES sequences demonstrate the highest conservation between human and mice, although the general consensus is conserved down to Drosophila, suggesting a nucleocytoplasmic shuttling property for WASp in both higher and lower eukaryotes.

Identification of WASp-associated nuclear transport proteins
Because NLS- and NES-bearing cargoes typically bind karyopherins (KAPs) and certain nucleoporins (NUPs), we predicted that WASp would also bind these transport factors, in vivo. To identify WASp-transport proteins, we performed multiple rounds of liquid chromatography-tandem mass spectrometric analyses of proteins that co-IP with endogenous WASp in human primary CD4+ T<sub>0</sub> cells and exogenous FL WASp (FLAG:MyC doubly-tagged) expressed in Jurkat T cells, both TCR activated and T<sub>1</sub>-skewed. Because WASp is located in both cytosol and nucleus (28), we IP‘ed WASp-containing complexes from the cellular fractions enriched for: 1) cytoplasm depleted of total cellular membranes (CP), 2) cellular membranes (CM), 3) nucleoplasm depleted of total cellular membranes (NP), and 4) nuclear membranes (NM). For investigating the composition of nuclear-WASp complexes, the T<sub>1</sub> cell nuclei were additionally treated with micrococcocal nuclease (MNase) to optimize recovery of chromatin-bound complexes. The purity of the four subcellular fractions was monitored by Western blotting for compartment-specific markers (Fig. 1C). This showed, lysosomal-associated membrane protein 1 (lysosomal/endosomal marker) and ZAP-70 (cytoplasmic signaling protein in T cells) enriched in CP, ankyrin G (plasma membrane marker) in CM, nucleophosmin B23 (nucleolus marker) in NP, and lamin B1 (inner nuclear membrane marker) in NM. Ryanodine receptor RyR1, a known endoplasmic reticulum (ER) protein, was absent from the NP fraction, implying that our NP fractions were free of cortical-ER that is contiguous with outer NM. Samples submitted for MS analyses were confirmed for the presence of WASp (or Flag/Myc) in all fractions, by Western blot (Fig. 2C).

The subcellular fractions were incubated with anti-WASp or anti-FLAG:MyC (two-step purification) Ab or their control Ig Abs, and bound polypeptides were detected by Coomassie blue (Fig. 1D). WASp-IPs (both endogenous and transfected WASp) gave more bands, ranging from <200 to >200 kDa, than control Ig-IPs. Both visible (in WASp-IP) and corresponding size non-visible (in Ig-IP) bands were included for MS. We excluded from analyses proteins that met our filtering criteria: 1) more or equal number of peptides captured also in the control Ig sample, 2) only one peptide captured in only one MS sample, 3) peptides scoring low on two Sequent parameters (XCorr value < 1.5 and ΔCn < 0.1), 4) common MS contaminants such as keratin, albumin, trypsin, and heat shock proteins 5) known components of mitochondria, Golgi, ER, lysosomes, and ribosomes, since these were not directly relevant to the study question. In multiple independent MS experiments, while a number of proteins were identified as WASp-interacting partners, we focused only on those that might be involved in nucleocytoplasmic transport.

The combined MS data (~5 experiments) showed several peptides of WASp and its known cytoplasmic partners actin and ARP2/3, which authenticated our MS approach (Fig. 1E). The nucleocytoplasmic transporters that copurified with WASp included KAPs (KPN1-A4 [also known as importin-a isoforms], KPN1 [also known as importin β1], XPO1 [exportin1], XPO2 [exportin 2], NUPs [NUP358 [also known as RANBP2], NUP98], and RAN proteins (RANGAP1, RAN). WASp associates with many of these transport proteins in both cytosol and nucleus, which is consistent with their role in nucleocytoplasmic transport across nuclear pore complex. Note, the MS profile of IgG-IP captured peptides of actin, ARP2/3, and some KAPs, but the absolute peptide numbers were dramatically lower in IgG-IP compared with that in WASp-IP or Flag/Myc-IP. Nevertheless, the association of WASp with these KAPs/NUPs was verified by co-IP, which not only validated our MS results but also revealed that...
the occasional peptide association with IgG was nonspecific (Fig. 1F). Taken together, our findings propose a KAP/NUP-mediated, nucleocytoplasmic transport pathway for WASp.

**Nuclear import of WASp requires its NLS motif**

To test the functionality of NLS in WASp nuclear import, we generated three WASp-mutants that: 1) lack NLS (ΔNLS) (aa 222–235), 2) lack exons 7 and 8 (Δexon7/8) (aa 187–259), which encodes NLS-containing WASp domain, and 3) lack exon 7 but retain NLS motif (Δexon7/8+NLS) (aa 187–221 and 236–259) (Supplemental Fig. 1A). FL WASp and empty (mock) vector served as positive and negative controls, respectively. These proteins fused to Flag/Myc tags were stably expressed both in Jurkat T cells and in a WAS patient CD4+ T<sub>H</sub> line (genotype: 23delG; G8QfsX44) lacking endogenous WASp expression (Supplemental Fig. 2B–D). Phenotypically, both WAS and normal T<sub>H</sub> lines express surface markers classically present in naive T<sub>H</sub> cells (CD4+, CD45RA<sup>+</sup>, CD45RO<sup>2</sup>) (Supplemental Fig. 2A) (38, 39), making them suitable for the proposed studies.
The above T cells were transfected with different mutants, achieving >90% stable expression on day 8 of transfection determined by flow cytometry after staining with anti-Myc Ab (Supplemental Fig. 2D). Transfected Tcells were activated with plate-bound CD3/28 under Th1-skewing conditions, and TCR activation monitored with antiphosphorylated CD3ζ (Tyr142) and nuclear translocation of NF-κB (p65) (a surrogate marker of calcium flux downstream of productive TCR activation), which were both prominent in Th1-skewed cells compared with nonskewed Th0 cells (Fig. 2A). Notably, the expression of WASp-mutants did not change the total cellular F-actin content determined by phalloidin-FITC staining and Western blot analysis (Fig. 2A, Supplemental Fig. 2E), implying that loss of these transport motifs do not dramatically perturb F-actin generating mechanisms in the cytosol or nucleus (Fig. 2A).

Significantly, unlike FL-WASp, ΔNLS- and Δexon7/8 mutants both fail to accumulate in the nucleus in Th1-skewed cells, whereas their cytosolic presence is comparable to that of FL-WASp, by Western blot (Fig. 2A, 2B) and imaging (Fig. 2C). MT/dynein inhibition assays. Serial Western blotting with the indicated Abs of the nuclear (nu) and cytoplasmic (cyt) fractions derived from primary human Th1-skewed cells after treating with the indicated pharmacological agents or their controls. (F) Serial Western blotting with the indicated Abs of the nuclear (nu) and cytoplasmic (cyt) fractions of human primary Th1-skewed cells treated with leptomycin B (LMB) or control (ctrl)/DMSO for indicated durations. The data are representative of two experiments. (G) Western blot: the description is similar to that for (B).
WASP nuclear import is MT-assisted. Primary TH cells, TH1-skewed and treated concomitantly with nocodazole (inhibitor of MT assembly) or Vanadate (inhibitor of dynein ATPase activity), showed a reduction in the nuclear localization of WASp (Fig. 2E). Nuclear localization of CREB, known to be MT-independent, and that of p53, known to be MT-dependent, served as our specificity controls. This data suggests that the dynein/MT pathway, which is known to transport cargoes toward the nuclear periphery, is a facilitator of nuclear WASp transport.

**Nuclear export of WASp require its NES2 but not NES1 motif**

Because WASp contains two NES-like motifs and binds XPO1 (CRM1), we postulated that the nuclear location of WASp might be regulated also at the level of its export. Normal TH cells skewed under TH1-biasing conditions were concomitantly treated with leptomycin B (LMB, a CRM1 inhibitor) or DMSO (control) for 2, 4, 8, and 24 h and their cytosolic and nuclear fractions tested for the presence of WASp by Western blotting. In the LMB-treated cells, the amount of endogenous WASp in the cytosolic and nuclear fractions was both reduced at ~8 h, although cytosolic WASp more than nuclear WASp. However, at ~24 h, WASp level in the cytosol was completely depleted whereas that in the nucleus was restored (Fig. 2F). The LMB treatment, however, did not decrease the export of β-actin in the same cells, which reconfirms the previously reported finding of CRM1-independent actin export pathway (41). The LMB data suggest that functional NES(s) exit in WASp that uses CRM1.

To identify which of the two NES motifs (or both) is/are functional, we generated WASp mutants lacking NES1 motif (ΔNES1) or NES2 motif (ΔNES2) (Supplemental Fig. 1B) and stably expressed them in Jurkat or WASmut TH cells (Supplemental Fig. 2D). The NES1-mutant like FL-WASp locates both to the cytosol and nucleus (Fig. 2G), implying that despite the in silico prediction (37), the NES1 motif does not function to reimport WASp to the cytosol, in vivo. In contrast, ΔNES2-mutant accumulates predominantly in the nucleus, verified both by cell fractionation and imaging (Fig. 2A, 2C). Accordingly, ΔNES2-mutant does not bind CRM1 or its cofactor RanBP3 in the nucleus, where it accumulates (Fig. 2D). These results implicate NES2 motif in CRM1-dependent nuclear export of WASp in TCR-activated, TH1-skewed cells.

**Only nuclear, not cytosolic, WASp complexes catalyze histone H3K4 trimethylation**

Our ability to isolate WASp in the cytosol or nucleus of TH cells created an opportunity to test whether compositionally distinct cytosolic and nuclear WASp pools are also functionally distinct. Because we previously showed that cellular WASp associates with histone H3 HMTase activity, in vitro (28), we chose this readout to test the above hypothesis. Accordingly, we tested whether the ΔNLS-WASp mutant, which cannot locate to the nucleus, catalyzes H3K4 trimethylation, or not. After 48 h in culture, the ΔNLS mutant expressed in HeLa cells showed an exclusive cytosolic localization, whereas its control FL-WASp was distributed in both compartments (Supplemental Fig. 3). The HMTase assay revealed that the cytosol-trapped ΔNLS-WASp mutant does not catalyze trimethylation of H3K4, demonstrating that unlike EZH2 (31), WASp does not associate with any putative cytosolic H3 HMTase complexes. Whether WASp can catalyze methylation of other nonhistone cytosolic substrates remains to be determined. In contrast, nucleus-only–located ΔNES2-WASp mutant effectively catalyzes H3K4 trimethylation. Taken together, the data suggest that nuclear but not cytosolic WASp complexes associate with chromatin-modifying activity.

**Nuclear WASp is essential for TH1 but not TH2 gene induction**

Our identification of nuclear WASp in TH1 cells (28) raised the question whether WASp locates to the nucleus also in TH2 cells. Primary TH cells isolated from normal human donors were activated in vitro under TH1- or TH2-skewing or nonskewing TH0 condition. CD3/28 activation and IL-2 were common to three culture conditions. Presence of cytosolic phosphorylated ZAP70 (Tyr319) validated ongoing TCR activation (Fig. 4A). Similarly, augmented nuclear signals of phospho-STAT1 (Ser727) in TH1 but not TH0 or TH2 and of phospho-STAT6 (Tyr641) in TH2 but not TH1 or TH0 cells validated our in vitro TH1-skewing conditions. Reprobing the same gel with anti-WASp Ab demonstrates that the magnitude of nuclear WASp translocation (or retention) is higher in TH1 compared with TH2 or TH0 cells, finding that was reproducible in multiple experiments.

The physical presence of WASp in nucleus and cytosol of both TH1 and TH2 cells and our identification of the functional NLS and NES allowed us to investigate the functional interdependency of the two WASp pools on gene activation in TH1-skewed or TH2-skewed cells. We reconstituted human WASmut TH1 cells (WASUT) with ΔNES2 (nucleus “only” location) or ΔNLS (cytosol “only” location) and quantified the degree to which the gene activation defects of WASp were restored. TH1-skewed cells reconstituted with FL-WASp (WASFL) demonstrate a significant increase in the mRNA expression of two core TH1 genes (TBX21, IFNG), compared with uncorrected WASUT (p < 0.01) (Fig. 4B). In contrast, although WASANLS cells fail to upregulate these genes, WASANSES2 cells show near-normal TH1 gene upregulation. Taken together, these results demonstrate that the physical presence of WASp in the nucleus but not in cytosol is necessary for TH1 cytokine–driven gene activation.

Notably, these effects of nuclear WASp are gene-specific, in that the expression of CSF2 mRNA (a non–TH1-specific growth factor, GM-CSF) in TH1-skewed cells is not significantly increased (~1.5- to 2-fold change; ns, p > 0.05) compared with that in nonskewed TH0, in normal, WASFL, or WASANSES2 T cells (Fig. 4B). However, in WASUT and WASANLS TH cells, CSF2 mRNA level is increased in the face of IFNG deficiency (~4-fold
FIGURE 4. Characterizing the effect of WASp domain-deleted mutants on T1 and T2 activation. (A) Sequential Western blotting with the indicated Abs of the nuclear (nu) and cytosolic (cyt) fractions of human primary CD4+ TH cells, T1-skewed, T2-skewed, or nonskewed T0 (all three CD3/28-activated). (B) RT-qPCR quantitation of candidate T1- or T2 genes in WASnull T cells reconstituted with FL-WASp or its indicated mutants after CD3/28 activation under T1- or T2-skewing or T0-nonskewing conditions. Normal T cell line is the control. The mRNA copy numbers derived from the control T0 cells are not shown but were subtracted from the displayed final mRNA values of the T1- or T2-skewed cells. Absolute copy numbers adjusted to GAPDH are displayed as fold change (up or down) in T1 or T2 cells compared with their T0 controls. Data represent the average of duplicates from at least five independent experiments from three separate transfections, with bars indicating SEM. Wilcoxon nonparametric test using the GraphPad InStat software determined the p values comparing the data between WASnull T cells (untransfected [UT]) and FL/or mutant- (Figure legend continues)
change). Such findings align with the previous report that showed an inverse correlation between TH1 cytokine expression and CSF2 activation (42). The above mRNA expression profiles mirrored their corresponding protein expression levels determined by ELISA and intracellular cytokine/transcription factor staining with flow cytometry (Fig. 4C, 4D).

In contrast to WASp effects on TH1 activation, loss of WASp (total or nuclear) did not impair the augmented mRNA or protein expression of the two core TH2 genes, IL4 and GATA3, under TH2-skewing conditions (Fig. 4B–D). Taken together, our findings demonstrate that the physical presence of WASp in the nucleus is necessary for TH1 gene activation, in vitro.

Loss of nuclear WASp impairs promoter activation of IFNG and TBX21 genes in TH1-skewed cells but not of IL4 or GATA3 in TH2-skewed cells

We sought to further characterize how nuclear WASp influences TH0 > TH1 transcriptional reprogramming of its target gene promoters, at the chromatin level. To this end, we performed MNase-ChiP-qPCR assays to examine the histone modifications and RNA polymerase II enrichment at gene promoters in the presence or absence of nuclear WASp (see Supplemental Fig. 2F for mononucleosomal chromatin shearing profile).

First, the chromatin enrichment of WASp-mutants was verified by both anti-FLAG and -WASp Abs, which gave comparable results (Fig. 5A). Although both FL and ΔNLS2 mutants were enriched at the 5′ promoter loci of TBX21 and IFNG, the ΔNLS mutant was not (Fig. 5A). Accordingly, the 5′ promoter locus of these genes displayed “repressive” or “poised” chromatin configuration (H3K4me3 and H3K27me3) in WASnull and WASΔNLS TH1 cells, whereas in WASFL and WASΔNLS2, the promoter chromatin displayed histone marks (H3K4me3 and absent/ or H3K27me3) that were conducive to active gene transcription (Fig. 5B).

Because we had previously shown that WASp impacts H3K4me3 modification at gene promoter by influencing the chromatin recruitment of RBBP5 (MLL complex protein involved in insulating the activating H3K4me3 mark) (28), we next examined the relative enrichment patterns of counterregulatory histone modifiers RBBP5 and EZH2 (Polycomb protein involved in repressive H3K27me3 mark). Consistent with the above histone configuration, we find decreased enrichment of RBBP5 in WASnull and WASΔNLS TH cells contemporaneously with increased enrichment of EZH2 at these TH1-gene promoters (Fig. 5B).

Surprisingly, in WASnull and WASΔNLS TH1-skewed cells, we find normal promoter enrichment of initiating phospho-RNA polymerase II (CTD Ser5) in TBX21 and IFNG, this despite low mRNA output of these genes (Fig. 5C). Such findings suggest that although WASp-lacking promoters may experience some transcriptional “activity,” the productive 5′→3′ “sense” transcription is still impaired. Indeed, a dramatically low enrichment of elongating phospho-RNA polymerase II (CTD Ser2) and SPT5 (transcription elongation factor) at the 3′-end of same genes supports this idea (Fig. 5C).

In contrast to WASp effects on IFNG and TBX21 promoter dynamics in TH1-skewed cells, histone configuration of the IL4 and GATA3 promoters in TH2-skewed cells was consistent with “active” gene transcription in all mutant-expressing cells (Fig. 5, right panels). Accordingly, enrichment of the markers of transcription elongation (phospho-RNA polymerase II [CTD Ser5] and SPT5) at the 3′ end of these TH2 genes suggested productive transcription. Taken together, our data demonstrate that a selective deficiency of nuclear WASp perturbs the chromatin events of gene activation during TH1 but not TH2 differentiation.

Loss of nuclear WASp impairs recruitment of STAT1 and T-BET to IFNG and TBX21 gene promoters in TH1-skewed cells

The dynamic recruitment of TH1 lineage specific transcription factors to gene promoters is critical for the actuation of TH1 versus TH2 gene activation program. To gain further insight into why loss of nuclear WASp selectively impairs TH1 but not TH2 differentiation, we examined the enrichment patterns of STAT1, T-BET (in TH1-skewed cells), STAT6, and GATA3 (in TH2-skewed cells). We show by ChiP-qPCR that the enrichment of TH1 transcription factors STAT1 and T-BET to IFNG and TBX21 promoters is diminished in TH1-differentiating cells lacking WASp, total or nuclear (Fig. 5A). In contrast, the enrichment of TH2 transcription factors STAT6 and GATA3 is unaffected by the absence of nuclear WASp. These data propose that the chromatin effect of WASp on TH1 target gene activation is mechanistically linked to STAT1 and T-BET.

VCA domain is nonessential for TH1 or TH2 gene activation

To test the role of VCA domain in WASp-dependent TH1 gene activation we generated VCA-lacking WASp mutant (Supplemental Fig. 1C), which we show is stably expressed (Supplemental Fig. 2D) and translocates to the nucleus of TH1-skewed cells (Fig. 2A, 2D). First, TCR activation (pCD3z and calcium signaling (NF-κB/p65 nuclear translocation) appear to be grossly intact in TH1-skewed cells expressing VCA-deleted WASp (Fig. 2A), as is the total cellular F-actin content (Fig. 2A, Supplemental Fig. 2E). Second, although this mutant does not bind ARP2/3, which is expected, it maintains association with transport KAPs/NUPs (Fig. 2E). Third, the nucleus-located ΔVCA-mutant catalyzes H3K4 HMTase activity at the level comparable to normal, full-length WASp (Fig. 3). These findings suggest that chromatin-based mechanism(s) used by nuclear-WASp to support TH1 gene activation, in vitro, does not integrate its VCA domain functions. Consequently, ChiP-qPCR assays show that the nuclear ΔVCA mutant is recruited to the 5′ promoters of the TH1 genes, the chromatin landscape of which is consistent with “active” gene transcription (Fig. 5). Accordingly, in WASΔVCA cells, the magnitude of TBX21 and IFNG (in TH1-skewed cells) and IL4 and GATA3 (in TH2-skewed cells) upregulation and the corresponding protein expression (by Western blot, FACS, and ELISA) appears to be comparable to that observed in WASFL or normal T cells (Fig. 4B–D).

Discussion

The recent discovery by our group of the nuclear location of WASp in T lymphocytes (28) raised a major outstanding question: does WASp integrate its cytosolic cortical remodeling function to modify chromatin of the genomic loci with which it interacts? expressing T cells (black asterisk, p < 0.01) or between FL and mutants (red asterisk, p < 0.01). In data where the differences did not reach statistical significance (i.e., p > 0.05), asterisk is not shown. (C) Flow cytometric histogram profiles showing expression of the indicated intracellular cytokines or transcription factors for TH0-nonskewed, TH1- and TH2-skewed, CD3/28-activated T cells transfected with the indicated WASp mutants. The bar graphs next to each histogram show the shift in mean fluorescence intensity (MFI) relative to their isotype controls and was quantified using the arithmetic average on a log scale (geometric mean). (D) Quantification of the secreted cytokines in the supernatants of cell cultures, whose mRNA profile is displayed in (C), was assessed by quantitative ELISA performed in triplicates from at least two independent assays. Bars indicate SEM. *p < 0.05.
This was an important question not just for clarifying the immuno-pathology of WAS, but had wider implications on how dual/multicompartment proteins function in a cell to mediate disparate cell biological outcomes. Using the example of WASp, our findings highlight that the protein functions limited to one location (i.e., nucleus) do not rest on the same activity (i.e., actin polymerization) as in the other (i.e., cytosol). Specifically, we show that the nuclear effects of WASp on reprogramming transcription are uncoupled from its cytoplasmic signaling and actin effects, thus demonstrating an ARP2/3-independent action of a type I NPF outside of cytoplasm. Significantly, this uncoupling of compartment-specific roles is immediately relevant to the development of T H cell–mediated immune dysfunction in WAS and imposes a shift in the thinking about WASp biology, in health and disease.

Uncoupling WASp’s nuclear from cytosolic functions during transcriptional reprogramming

Our most compelling finding is that only nuclear WASp can function as a gene-specific transcriptional cofactor, a role that cannot be substituted for by the actions of cytosol-constrained WASp. Consequently, creating nucleus-delimited deficiency of WASp by re-expressing ΔNLS mutant in the human WASnull T H0-nonskewed cells that are differentiated down the T H1 lineage is sufficient to impair the epigenetic and transcriptional activation of “core” T H1 network genes, which in turn disallows acquisition of T H1 functions. Strikingly, these chromatin defects occur despite preserved expression and functions of the ΔNLS mutant in the cytosol. Remarkably, in contrast, a cytosol-delimited deficiency of WASp created by ΔNES2 mutant expression still allows for chromatin signaling events sufficient for T H1 gene activation in culture conditions. Although beyond the scope of this study, pinpointing which of the many distinct compartments of the nucleus is/are the different sites of WASp nuclear activity will further refine our understanding of the full gamut of WASp nuclear functions in the immune system. At the minimum, our study reveals that there is considerably more complexity in how WASp signaling module is constructed in a T H cell to pattern a compartment-specific functional outcome than was suspected previously.
Whether a similar paradigm exits in other hematopoietic lineages is unknown, but we speculate that the compartment specificity of nuclear and cytosolic WASp functionality uncovered in the T_{H}1 lymphocytes will be typical of its actions throughout biology where WASp or WASp-like proteins are expressed. Indeed, in addition to T_{H}1 cells, nuclear WASp also has been found in human myelomonocytic cells (43), suggesting a putative nucleus-specific function of WASp in the innate immune system as well. Notably, in Drosophila, WASp is in the nucleus during the different stages of organogenesis (44). Similarly, Bacloviruses contain a WASp-like protein (p78/83) in its nucleocapsid, which translocates to the nucleus of the host cell, an event necessary for its replication and infectivity (45). In the wake of our study, it will be very interesting to know if the nuclear p78/83 drives specific forms of gene expression programs in the virally infected host cell. Notwithstanding, these and our studies highlight the evolutionary pressure to maintain the nuclear presence of WASp in widely divergent organisms, such as humans, flies, and viruses, implying that nuclear WASp supports an ancient, conserved role in fundamental nuclear processes. Besides human WASp, Xenopus Wave1, another ARPP/3 actin-binding protein also follows the paradigm unveiled by human WASp, wherein the “newfound” nuclear role of Wave1 in gene transcription is essential during oocyte development (29).

**Nuclear WASp in T_{H}1 versus T_{H}2 cell fate choice**

We found that loss of nuclear WASp did not impair the chromatin and transcriptional signaling events of T_{H}2 cell fate choice. Such a result is not entirely surprising because in WAS patients the T_{H}1 activation defect is not associated with a concomitant T_{H}2 activation defect (32). In fact, high T_{H}2 cytokine–driven colitis results in a mutant protein that is still capable of interacting with chromatin and transcriptional signaling networks involved in T_{H}1 cell fate choice. The observation that nuclear protein complexes IP'ed by WASp^{4VCA} mutant do not contain ARPP/3, and yet the T_{H}1 cells expressing this mutant achieve T_{H}1 functions at the same relative efficiency as that achieved by ARPP/3-containing WASp^{P4} informs us that ARPP/3/WASp complexation is unnecessary for T_{H}1 gene activation. Indeed, for the H3-HMTase effector activity of nuclear WASp, ARPP/3-dependent function is dispensable. Accordingly, our study demonstrates that WASp does not integrate ARPP/3 complex, which is otherwise important for its cytosolic functions, to modify the chromatin of its target genomic loci. Similar to human WASp, the transcriptional effects of Xenopus Wave1 are also independent of its VCA-like domain (VPH domain) (29). In yeast, the observed cellular dysmotility consequent to the mutational defects in type I NPFs is not related to the loss of ARPP/3 binding and/or its activation (46). The collective evidence, therefore, establishes biologically important ARPP/3-independent effects of WASp family proteins in both lower and higher organisms.

Moreover, the currently available genotype-phenotype data on human WAS does not convincingly link the VCA-domain missense mutations to the development of all clinical severity grades of human WAS. A case in point, of the 308 total (both unique and recurring) disease-causing mutations currently annotated in the WASp database (http://rapid.rci.riken.jp/RAPID, 238 (77%) are missense mutations, of which only 16 (~7%) are located in the VCA domain (aa 412–502). Furthermore, the majority of these VCA-domain missense mutations (e.g., Arg^{477}, Ile^{481}, and Asp^{485}) result in X-linked thrombocytopenia (mildest WAS phenotype) but not in classic/severe WAS (1, 47, 48). Importantly, no recurring “hot spot” missense mutations have yet been identified in the VCA domain that result in serious immune dysregulation, a complication that is emblematic of classic WAS phenotypes. From a cell biological perspective, a VCA-domain missense mutation involving Arg^{477} was shown to result in a significant actin-polymerizing defect, and yet this human mutation reportedly manifests clinically as stable, mild X-linked thrombocytopenia. In the same report, another VCA-domain mutation Lys^{476} was shown to support ARPP/3-dependent actin polymerization with a twice-normal efficiency (49), implying that F-actin defect does not occur with all VCA-domain mutations. In contrast, some of the common, disease-causing, “hot spot” WAS missense mutations involve residues Thr^{45} (n = 13 patients) Val^{75} (n = 22), Arg^{80} (n = 31), and Asp^{244} (n = 5) (47, 48, 50). But these variants occur within the nucleocytoplasmic transport domains (NLS and NESs) and not in the VCA domain. Accordingly, the reported WAS genotype/phenotype correlation place constraints on the F-actin-“centric” model as the sole basis for the development of all WAS clinical phenotypes, be it consequent to adaptive innate immune defects.

Future studies identifying disease-associated WAS missense mutations that differentially impact the cortical cytoskeletal and nuclear chromatin-modifying functions of WASp have the potential to enable better predictions of clinical outcomes for the affected patients. Clarifying the molecular details of how WASp orchestrates transcriptional reprogramming and what signals pattern gene-targeting specificity of WASp under varied cell differentiation programs could shed further light into the immunobiology of human WAS. Given the imperfect genotype-phenotype correlation in human WAS, such studies may provide deeper insights into how the loss of compartment-delimited WASp activities is linked to disease severity grades in WAS and whether the newer gene-editing strategies (e.g., CRISPR/Cas9) could reverse the disease phenotype that are consequent to single point mutations.

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**Disclosures**

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**References**


