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

Sanjoy Sadhukhan,*1 Koustav Sarkar,‡*,†1 Matthew Taylor,* Fabio Candotti,‡ and Yatin M. Vyas*†‡

Defects in Wiskott–Aldrich Syndrome protein (WASp) underlie development of WAS, an X-linked immunodeficiency and autoimmunity disorder of childhood. Nuclear-activating factors (NPFs) of the WASp family generate F-actin in the cytosol via the VCA (verprolin-homology, cofilin-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)/23-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, ARP23-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 TBX21 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 ARP23/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.

Wiskott–Aldrich syndrome (WAS) is an X-linked genetic disorder manifesting in thrombocytopenia, primary immune deficiency, autoimmunity, and lymphoid malignancy (1, 2). A panoply of mutations in the WAS gene, which encodes WAS protein (WASp), is causative of this life-threatening disease of childhood. WASp is expressed exclusively in the cells of the hematopoietic lineage, and accordingly, its loss results in a variety of defects in the lymphocytes, dendritic cells, myeloid cells, and megakaryocytes/platelets (3). Functionally, WASp is a member of the type I nucleation promoting factors (NPFs), which are known mainly for their cytoplasmic role in generating F-actin via the actin-nucleating and actinverifying domains. The online version of this article contains supplemental material.

Abbreviations used in this article: ARP, actin-related protein; ChIP, chromatin immunoprecipitation; CM, purified cellular membrane; CF, cytoplasm depleted of total cellular membrane; CRMI, chromosomal region maintenance 1; ER, endoplasmic reticulum; FL, full length; IP, immunoprecipitated; KAP, karyopherin; LMB, leptomycin B; MS, mass spectrometry; MT, microtubular; NES, nuclear export signal; NLS, nuclear localization signal; NM, purified nuclear membrane; NP, nucleoplasm depleted of total cellular membrane; NPF, nucleation promoting factor; NUP, nucleoporin; qPCR, quantitative PCR; rh, recombinant human; VCA, verprolin-homology, cofilin-homology, and acidic; WAS, Wiskott–Aldrich syndrome; WASp, WAS protein.

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K.S. and S.S. performed the majority of the experiments; M.T. assisted in imaging studies; F.C. provided WAS patient cell lines; and Y.M.V. conceived the study, designed the experiments, analyzed the data, and wrote the paper.

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4–9, as well as actin-binding proteins such as N-WASP, WAVE1, 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 T41 cell nucleus, where it participates in the transcription of TBX27 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 TBX27 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 methylase 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 T41 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 T41 and T42 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 WASnull T41 cells and then testing for restoration of gene activation defects linked to WAS (32, 33). We chose the human IFNG and TBX27 (T41 genes) or IL4 and GATA3 (T42 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 CD4+ T41 cells, Jurkat T cells, WASnull CD4+ T41 cell line, WASnull T41 cell line expressing the various domain-deleted mutants, normal CD4+ T42 cell line, and HeLa cells were cultured under T41-skewing (recombinant human [rh]IL-12, anti–IL-4 Ab, and rhIL-2) or T42-skewing (rhIL-4, anti-IL-12 Ab, anti-IFN-γ Ab, and rhIL-2) or nonskewing T40 (only rhIL-2) conditions for 6 d and further activated with CD3/CD28-coated beads for another 1 d to induce TCR activation. WASnull T41 cell line was generated from a WAS patient carrying the mutation 236LeG (G801X44), which resulted in complete loss of WASp expression in lymphocytes and manifesting in the highest clinical severity score of 5. This WAS T41 cell line (WASnull) was used in the reconstitution studies of domain-deleted WASp mutants.

WASp domain-deleted mutants

Full-length (FL) WASp cDNA was subcloned into mammalian expression vector pCMV6-Entry containing Flag (also known as DDK) and Myc dual-tags at the C-terminal end (Origene). This TrueClone plasmid vector allows stable integration and expression over a longer time course. All domain deletions in WASp cDNA were performed using the QuickChange II PCR-Based Site-Directed Mutagenesis Kit (Stratagene), and the mutant sequences periodically reconfirmed by DNA sequencing before transcription. FL WASp and its mutants were transfected into Jurkat or WASnull T cells by Amaxa Cell Line Nucleofector Kit V (Lonza) and into HeLa by Lipofectamine 2000 Transfection Reagent (Invitrogen). Successful transcription 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.

Mass spectrometry

Total nuclear and cytosolic fractions were isolated using combination of techniques including sucrose-density gradient centrifugation and the NE-PER Nuclear and Cytoplasmic Extraction Kit (Pierce). Further purification to isolate nuclear and cytosolic membranes was achieved by using the Mem-PER Eukaryotic Membrane Protein Extraction Kit (Pierce), and the purity of four subcellular fractions was monitored by Abs listed in Supplemental Table II. For the mass spectrometry (MS) assays, nuclear lysates from micrococcal nuclease (MNase)-treated nuclei of human primary T41-skewed cells or Jurkat T41-skewed cells expressing Flag/Myc dual-tagged WASp were incubated with anti-WASP or –Flag–Myc (for two-step sequential immunofluoarity purification) or their corresponding isotype Ig Ab as described previously (34). Bound proteins were eluted, separated on 4–15% Tris-glycine SD-SAGE gel, and stained with Coomassie blue. Between 8 and 12 visible bands were excised from the test sample lane and the corresponding size bands from the control lane, even if none were visible in the latter. All bands were individually analyzed for the recovered polypeptides by nano liquid chromatography-tandem MS on a Thermo Fisher LTQ Orbitrap Velos mass spectrometer. Data were processed with Thermo Fisher Discoverer Daemon 1.3 for database searching with SEQUEST using a target/decoy approach against the Uniprot complete human database. A multiconfusius report for the polypeptides of the WASp proteome recovered from each subcellular fraction was generated and used for the displayed data.

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 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 transfected paraformaldehyde-fixed T41-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 μm at ×63 oil immersion magnification. Approximately 20–30 single T41 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 T41 cells, which were cultured under T41- or T42-skewing or nonskewing T40 conditions. For intracellular protein staining, the cells were further activated by plate-bound anti-human CD3 and CD28 Abs in the presence of 1 μg of CD GolgiPlug and 0.6 μg of CD GolgiStop (BD Biosciences) added to ~107 cells/ml T cell culture for 4–6 h. After fixation and permeabilization using CytoFix/CytoPerm solutions, T 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 ~5000 nonskewed T40 and T41- or T42-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 qRT-PCR.
Identification of WASp-associated nuclear transport proteins

Because NLS- and NES-bearing cargos 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 cells and exogenous FL WASp (FLAG:Myc doubly-tagged) expressed in Jurkat T cells, both TCR activated and T41 skived. 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 T41 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/endoosomal marker) and ZAP-70 (cytoplasmic signaling protein in T cells) enriched in CP, ankyrin G (plasma membrane marker) in CM, nucleophosmin B23 (nucleolar 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 <20 to >200 kDa, than control Ig-IPs. Both visible (in WASp-IP) and corresponding size nonvisible (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, al- bumin, 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 (n = 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-α 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 cell line (genotype: 23delG; G8QfsX44) lacking endogenous WASp expression (Supplemental Fig. 2B–D). Phenotypically, both WAS and normal T cell lines express surface markers classically present in naive T cells (CD4+, CD45RA+) and neither spontaneously expresses CXCR3 or CCR6, chemokine receptors typically expressed in already differentiated T(H)1 (CXCR3+; CCR6+) or T(H)2 (CXCR3+), or T(H)17 (CXCR3–; CCR6+) cells (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 T H cells were activated with plate-bound CD3/28 under T H1-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 T H1-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 T H1-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 T H1-skewed cells after treating with the indicated pharmacological agents or their controls. (G) Western blot: the description is similar to that for (B).

Microtubular/dynein cytoskeleton facilitates nuclear import of WASp

Because microtubular (MT)-cytoskeleton facilitates KAP-dependent nuclear import of NLS-bearing cargoes (40), we tested whether...
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 reaffirms 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 lines (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 location, whereas its control FL-WASP was distributed in both compartments (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 TH1 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 WAS were restored. TH1-skewed cells reconstituted with FL-WASP (WASmut) 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, WASANNES2 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, WASmut, or WASANNES2 T cells (Fig. 4B). However, in WASmut and WASANLS TH cells, CSF2 mRNA level is increased in the face of IFNG deficiency (~4-fold decrease in the nuclear/ cytosolic (nu/cyt) fractions of HeLa cells stably transfected with FL-WASP or the indicated WASp-mutants. HeLa core histones and material IP with anti-RBBP5 Ab are the positive controls, whereas Flag-IP in the mock transfected cells and IgG-IP are the negative controls. Reaction mixtures were immunoblotted with the indicated series of Abs. The data are representative of at least two independent assays from two separate transfection events.
Characterizing the effect of WASp domain-deleted mutants on TH1 and TH2 activation. (A) Sequential Western blotting with the indicated Abs of the nuclear (nu) and cytosolic (cyt) fractions of human primary CD4+ TH cells, TH1-skewed, TH2-skewed, or nonskewed TH0 (all three CD3/28-activated). (B) RT-qPCR quantitation of candidate TH1- or TH2 genes in WASnull T cells reconstituted with FL-WASp or its indicated mutants after CD3/28 activation under TH1- or TH2-skewing or TH0-nonskewing conditions. Normal T cell line is the control. The mRNA copy numbers derived from the control TH0 cells are not shown but were subtracted from the displayed final mRNA values of the TH1- or TH2-skewed cells. Absolute copy numbers adjusted to GAPDH are displayed as fold change (up or down) in TH1 or TH2 cells compared with their TH0 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-
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 TH10 > 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 promoters of the TH1 genes, the chromatin landscape of which is consistent with “active” gene transcription (Fig. 5). Accordingly, enrichment of the markers of transcription elongation (phospho-RNA polymerase II [CTD Ser2] 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 (pCD3\(^\gamma\)y142) and calcium signaling (NF-kB-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 VCA-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 VCA 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 WASp\(^{VCA}\) 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 WASp\(^{FL}\) 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?
This was an important question not just for clarifying the immunopathology 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 TH 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 TH0-nonskewed cells that are differentiated down the TH1 lineage is sufficient to impair the epigenetic and transcriptional activation of “core” TH1 network genes, which in turn disallows acquisition of TH1 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 TH1 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 TH cell to pattern a compartment-specific functional outcome than was suspected previously.

**FIGURE 5.** Chromatin-remodeling effects of WASp on its target gene loci. MNase-ChIP-qPCR. Chromatin enrichment profiles of the indicated proteins, at 5′-untranslated region or 3′-exon ends of the indicated genes in TH1- or TH2-skewed cells, normal or WASnull TH cells, untransfected (UT) or stably transfected with the indicated WASp mutants. The efficiency of MNase digested chromatin is displayed in Supplemental Fig. 2F. The displayed ChIP values (percentage of total input), shown as stacked columns, were derived after subtracting the background values obtained with isotype IgG Ab control ChIPs, the latter not shown. Data are expressed as percent immunoprecipitation relative to nuclear input chromatin (mean ± SEM) and represent an average of at least five independent experiments performed in duplicates from at least three separate transfection events. Intergenic region between COL8A2 and TRAPPC3 genes on Chr.1, which does not contain known protein-coding genes, served as a negative control. The genomic location of PCR primer/probes is indicated by red asterisk. For TBX21, the 5′-untranslated region primers were designed within the genomic region that also contains a GAS (γ-activated sequence) site (5′-TTCAGGCAA-3′ at about −770 bp from first coding ATG). For IFNG, the primers are located between −200 and −250 bp from first coding ATG, a region known to contain functional promoter elements (51). DNase I HS profile for the primary human peripheral TH1 cells (in gray) available from the ENCODE-University of Washington was aligned alongside our custom tracks to give context to the location of our ChIP-PCR primer/probes. (A) WASp and transcription factors; (B) histone methylases and modifications, and (C) RNA polymerase II and SPT5. The data displayed in (A) and (B) are for 5′-located promoter regions of the indicated genes. In (C), 3′ denotes ChIP enrichment at the 3′-ends (last coding exon); 5′ denotes ChIP enrichment between 5′-untranslated region and first coding exon.
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<sub>4</sub> lymphocytes will be typical of its actions throughout biology where WASp or WASp-like proteins are expressed. Indeed, in addition to T<sub>4</sub> 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 <i>Drosophila</i>, 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 ARP2/3 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<sub>1</sub>1 versus T<sub>1</sub>2 cell fate choice**

We found that loss of nuclear WASp did not impair the chromatin and transcriptional signaling events of T<sub>1</sub>2 cell fate choice. Such a result is not entirely surprising because in WAS patients the T<sub>1</sub>1 activation defect is not associated with a concomitant T<sub>1</sub>2 activation defect (32). In fact, high T<sub>1</sub><sub>2</sub> cytokine-driven colitis is observed in a murine model of WAS (33). Mechanistically, we show that WASp enrichment at promoters of T<sub>1</sub>2 genes and IFNg genes under T<sub>1</sub>1-skewed conditions is significantly higher than that seen at the promoters of GATA3 or ILC<sub>4</sub> genes under T<sub>1</sub>2-skewed conditions. Why this might occur is not clear. One possible reason could be that the magnitude of nuclear translocation of WASp is much lower in T<sub>1</sub>2- compared with T<sub>1</sub>1-skewed cells. Pending experimental validation, such findings imply that both TCR signaling, which was common to both activation conditions, the differential (T<sub>1</sub>1 versus T<sub>1</sub>2) cytokine signaling intermediates (STATs, NFATs, NF-κB isoforms, Notch, and so on) might contribute toward calibrating WASp presence in the nucleus.

**ARP2/3:VCA domain–independent functions of WASp**

Because WASp is mainly known for its VCA-domain–dependent functions in the immune system, an unexpected finding of these investigations is that elimination of the VCA domain, known for WASp’s ARP2/3-dependent actin polymerizing function in the cytosol, results in a mutant protein that is still capable of interactions with chromatin and transcriptional signaling networks involved in T<sub>1</sub>1 cell fate choice. The observation that nuclear protein complexes IP’ed by WASp<sup>VCA</sup> mutant do not contain ARP2/3, and yet the T<sub>1</sub>1 cells expressing this mutant achieve T<sub>1</sub>1 functions at the same relative efficiency as that achieved by ARP2/3-containing WASp<sup>ΔV</sup> informs us that ARP2/3/WASp complexation is unnecessary for T<sub>1</sub>1 gene activation. Indeed, for the H3-HMTase effector activity of nuclear WASp, ARP2/3-dependent function is dispensable. Accordingly, our study demonstrates that WASp does not integrate ARP2/3 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 ARP2/3 binding and/or its activation (46). The collective evidence, therefore, establishes biologically important ARP2/3-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.rcai.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<sup>477</sup>, Ile<sup>481</sup>, and Asp<sup>485</sup>) 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<sup>477</sup> 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<sup>476</sup> was shown to support ARP2/3-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 spots” W AS3 missense mutations involve residues Thr<sup>15</sup> (n = 13 patients) Val<sup>73</sup> (n = 22), Arg<sup>86</sup> (n = 31), and Asp<sup>224</sup> (n = 547, 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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