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Author	Geumyoung Sok ¹ , Zhijie Deng ² , Dong-Hwan Kim ¹ , Kichoon Lee ²
Affiliation	1 Department of Animal Science, College of Natural Resources & Life Science, Pusan National University, Miryang 50463, South Korea 2 Department of Animal Sciences, The Ohio State University, Columbus, OH 43210, USA
ORCID (for more information, please visit https://orcid.org)	Geumyoung Sok (https://orcid.org/0009-0004-0501-1857) Zhijie Deng (https://orcid.org/0009-0007-6628-8712) Dong-Hwan Kim (https://orcid.org/0000-0002-3993-4025) Kichoon Lee (https://orcid.org/0000-0001-6169-7516)
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CORRESPONDING AUTHOR CONTACT INFORMATION

For the corresponding author (responsible for correspondence, proofreading, and reprints)	Fill in information in each box below
First name, middle initial, last name	Kichoon Lee
Email address – this is where your proofs will be sent	lee.2626@osu.edu
Secondary Email address	donghwank@pusan.ac.kr
Address	Department of Animal Sciences, The Ohio State University, Columbus, OH 43210, USA
Cell phone number	
Office phone number	+1-614-688-7963
Fax number	

Vitamin A signaling in Adipocyte Differentiation: From Molecular Mechanisms to Livestock Production

Geumyoung Sok¹, Zhijie Deng², Dong-Hwan Kim^{1,*}, Kichoon Lee^{2,*}

¹ Department of Animal Science, College of Natural Resources & Life Science, Pusan National University, Miryang 50463, South Korea

² Department of Animal Sciences, The Ohio State University, Columbus, OH 43210, USA

* Corresponding author: Dong-Hwan Kim (donghwank@pusan.ac.kr), Kichoon Lee (lee.2626@osu.edu)

Abstract

Adipogenesis, the differentiation of fibroblast-like precursor cells into mature adipocytes, is a complex process governed by transcriptional networks and nutrient signaling. Among micronutrients, vitamin A and its active metabolites, all-trans retinoic acid (atRA), have emerged as potent regulators of adipocyte development, linking nutritional status to metabolic and physiological outcomes. atRA is generated from retinol through sequential oxidation by retinol and aldehyde dehydrogenases and exerts transcriptional control primarily via retinoic acid receptors (RARs) and retinoid X receptors (RXRs). It functions in dynamic crosstalk with Wnt/b-catenin and other signaling pathways to influence the expression of key adipogenic transcription factors, including PPAR γ and C/EBP α . In vitro evidence from 3T3-L1 and other mammalian cell models demonstrates that low concentrations of atRA (0.01 to 100 nM) promote adipogenic commitment and lipid accumulation, whereas higher concentrations (over 1 μ M) inhibit differentiation and stimulate apoptosis through mitochondrial pathways. Comparative in vitro studies across livestock species reveal that atRA exerts species-specific effects which suppresses adipogenesis in porcine and bovine cells, while promoting PPAR γ -mediated transdifferentiation of avian myoblasts into adipocytes. In vivo, atRA modulates adipose tissue development in a developmental stage-dependent manner, enhancing intramuscular fat deposition during fetal and neonatal stages but suppressing white adipose tissue expansion in adults. Collectively, these findings highlight atRA as a critical integrator of micronutrient signaling, gene regulation, and adipose tissue plasticity. Understanding the mechanisms of atRA-mediated adipogenesis provides key insights into the prevention of metabolic disorders and offers practical strategies to improve meat quality and feed efficiency in animal production system.

Keywords: Vitamin A; all-trans retinoic acid; Adipocyte; Adiposity; Livestock

INTRODUCTION

Adipogenesis, the biological process in which fibroblast-like precursor cells differentiate into fully developed adipocytes, is a tightly controlled process primarily by transcription factors such as peroxisome proliferator-activated receptor gamma (PPAR- γ) and the CCAAT/enhancer-binding protein (C/EBP) family members [1]. Beyond energy storage, adipocytes act as endocrine organs, regulating systemic metabolism and inflammatory responses. Changes in adipose tissue mass occur through hypertrophy [2] or hyperplasia [3], both closely linked with conditions such as obesity, cardiovascular diseases, and diabetes [4]. Therefore, understanding adipogenesis is fundamental for elucidating metabolic disorders and therapeutic strategies. Its regulation is also crucial for livestock production, directly affecting meat quality, flavor, and feed efficiency [5,6]. Ultimately, clarifying adipogenesis mechanisms benefits both human health and advancements in animal agriculture.

Vitamin A (also known as retinol) of which active form is all-trans retinoic acid (atRA) is an essential fat-soluble nutrient [7]. It plays essential roles in maintaining visual function [8], immune regulation [9], reproduction, and epithelial tissue homeostasis [10,11]. Vitamin A is acquired through dietary sources, either as preformed vitamin A from animal products or as provitamin A carotenoids derived from plant foods, which are converted into active forms within the body [12]. Maintaining an optimal balance of vitamin A is crucial; deficiency leads to severe health problems, such as night blindness [13,14], impaired immune function [11], and growth retardation [15,16], while hypervitaminosis A can result in toxicity, characterized by symptoms such as liver damage and teratogenicity [17,18]. In addition to its systemic effects, the regulation of adipocyte differentiation by vitamin A metabolism highlights its broad significance, impacting not only the prevention and management of metabolic diseases but also various aspects of animal agriculture.

In this review, we discuss previously reported studies focusing on the functions of vitamin A in adipogenesis both *in vitro* and *in vivo*. In particular, we delve into the molecular mechanisms underlying regulatory effects of vitamin A on adipocyte differentiation, encompassing both its pro-adipogenic and anti-adipogenic actions, and their implications for metabolic health and animal agriculture.

BIOSYNTHESIS, METABOLISM, AND MECHANISM OF ACTION

atRA Biosynthesis and Metabolic Pathways

atRA is a major bioactive form of retinol. It serves as a critical signaling molecule involved in various cellular activities such as cell growth, lineage commitment [19], apoptosis [20], and metabolic regulation [21]. The biosynthesis of atRA is tightly regulated within cells through a two-step oxidative process (Fig. 1a). In the first step, retinol is reversibly oxidized to retinaldehyde by retinol dehydrogenases (RDHs), is

68 considered the rate-limiting step in the pathway, and its efficiency is influenced by the availability of
69 cofactors and binding proteins [22]. In the second, irreversible step, retinaldehyde is further oxidized to
70 atRA by aldehyde dehydrogenases (ALDHs), particularly those expressed selectively depending on the type
71 of tissue. This step represents a crucial regulatory point to produce active atRA biologically [22,23]. Unlike
72 other retinoic acid derivatives, atRA binds with high affinity to retinoic acid receptors (RARs), through
73 which it directly regulates the transcription of specific target genes via retinoic acid response elements
74 (RAREs) [19].

75 In the storage pathway, lecithin: retinol acyltransferase (LRAT) facilitates the conversion of retinol to
76 retinyl esters through esterification, which are subsequently stored in lipid droplets [24]. This process
77 indirectly limits the availability of retinol for atRA synthesis. The activity of LRAT itself is tightly regulated,
78 being rapidly and markedly upregulated by atRA [25]. When the intracellular concentration of atRA
79 increases excessively, cytochrome P450 family 26 enzymes (CYP26) are upregulated and become actively
80 involved in the breakdown of atRA into hydroxylated inactive metabolites [26,27]. This serves as a key
81 negative feedback mechanism to regulate RA signaling tightly (Fig. 1b). Dysregulation of this feedback
82 may lead to retinoid toxicity or impaired differentiation processes, especially in tissues with high retinoid
83 turnover.

84 The regulation of the retinoid metabolic network is further refined by cellular retinol-binding proteins
85 (CRBPs) and cellular retinoic acid-binding proteins (CRABPs), which play essential roles in transporting
86 retinoids within the cell, facilitating their storage, transport, and targeted delivery to specific enzymes or
87 nuclear receptors. CRBPs primarily bind retinol, directing it either toward storage via esterification or
88 toward oxidation for atRA biosynthesis, depending on the cell's physiological needs. CRABPs, which are
89 structurally and immunologically distinct from CRBPs, bind retinoic acid [28] and determine its fate by
90 mediating its interaction with nuclear receptors like RARs [29] or targeting it for catabolism via CYP26
91 enzymes [30–32]. The distribution and levels of CRBPs and CRABPs vary across tissues and are subject
92 to independent regulation. The precise balance of retinoids, maintained by these binding proteins, is crucial.
93 If these binding proteins do not work properly, the balance of retinoids in the cell can be disturbed, which
94 may affect how cells grow, develop, and respond to the immune system. Together, these pathways and
95 binding proteins help control atRA levels in specific tissues [33,34] and keep retinoid balance stable,
96 making sure that RA signals are precisely regulated in different biological processes and stages of
97 development.

98 Recent multi-omics studies have revealed complex molecular signaling networks through which atRA
99 regulates adipocyte differentiation in livestock species. An integrated analysis of transcriptome and
100 metabolome in bovine preadipocytes identified 5,257 differentially expressed genes (DEGs) and 328
101 differentially expressed metabolites (DEMs) during adipogenic differentiation, highlighting key lipid
102 metabolic regulators such as FADS2, ACOT7, and ACOT2, while revealing that distinct FADS2 isoforms
103 differentially influence unsaturated fatty acid biosynthesis and adipogenic regulation [35]. Meanwhile, in

bovine skeletal muscle-derived cells, atRA treatment exhibited a development-phase specific effect on adipogenic and myogenic gene expression, such as up-regulation of ZFP423 and PPAR γ in the proliferative phase, but suppression of adipogenic markers during differentiation [36]. These results illustrate that retinoid signaling in livestock is not simply a linear regulation of RAR/RXR to target gene but rather integrates with broader lipid and energy metabolic pathways, and its impact depends on the developmental stage and cellular context. Moreover, such omics-driven insights pave the way identifying novel biomarkers and species-specific retinoid-responsive modules that could optimize intramuscular fat deposition or adipose tissue composition in production animals.

Nuclear Receptors and Signaling Pathways

atRA functions as an important signaling molecule involved in diverse cellular activities. Within the cell, atRA binds with high affinity to RAR α , β , and γ , as well as retinoid X receptors (RXR) α , β , and γ . These nuclear receptors form heterodimers that directly bind to RAREs, enabling precise regulation of gene expression. These complexes orchestrate diverse transcriptional programs tailored to the physiological functions of specific tissues, including liver [37,38], adipose tissue [39], skin [40], and immune cells [41]. Moreover, their transcriptional activities are finely tuned through dynamic interactions with a variety of coactivators, such as the NCoA family (SRC-1, TIF2/GRIP1, AIB1) and histone acetyltransferases like CBP/p300, which promote chromatin remodeling and gene activation [42]. Conversely, in the absence of ligand binding, RAR/RXR complexes recruit corepressors like NCoR and SMRT to induce chromatin condensation and repress target gene expression [43]. These regulatory mechanisms enable context-dependent and precise control of gene expression by retinoic acid signaling across different tissues and cell types.

At higher concentrations ($\geq 1 \mu\text{M}$), atRA activates the Wnt/ β -catenin signaling pathway, which is closely associated with the inhibition of adipocyte differentiation [44]. Binding of Wnt ligands to their receptors inhibits phosphorylation of β -catenin by CK1 and GSK3 β , leading to its stabilization and nuclear accumulation of β -catenin [45–47]. In the nucleus, β -catenin interacts with LEF/TCF transcription factors to induce the expression of Wnt target genes, such as Axin2 [48]. In this context, atRA, acting through RAR γ , enhances Axin2 expression [49]. Axin2 suppresses the transcription of key adipogenic regulators, including C/EBP α and PPAR γ , thereby reinforcing the anti-adipogenic effects [50]. Additionally, atRA inhibits the expression of PPAR γ and C/EBP α , delaying or blocking adipocyte differentiation [51,52]. This functional crosstalk between atRA and Wnt signaling represents a critical regulatory mechanism in adipocyte differentiation (Fig. 1a).

The functional interaction between atRA and Wnt signaling is mediated by the RAR/ β -catenin/Axin2 axis, which plays a key role in cell fate determination. Wnt signaling is known to inhibit adipogenesis [53], while atRA can antagonize or modulate this inhibitory effect. This regulatory interplay is closely connected to the physiological development of adipocytes [54,55]. atRA also directly influences adipocyte fate by

regulating the expression of crucial adipogenic transcription factors such as PPAR γ and C/EBP α through the nuclear RAR/RXR heterodimer. The transcriptional effects of atRA depend on its concentration and timing of exposure [44,56,57], which affects adipocyte maturation and function. Therefore, understanding the crosstalk between atRA and Wnt signaling is fundamental to revealing the complex mechanisms governing adipocyte differentiation.

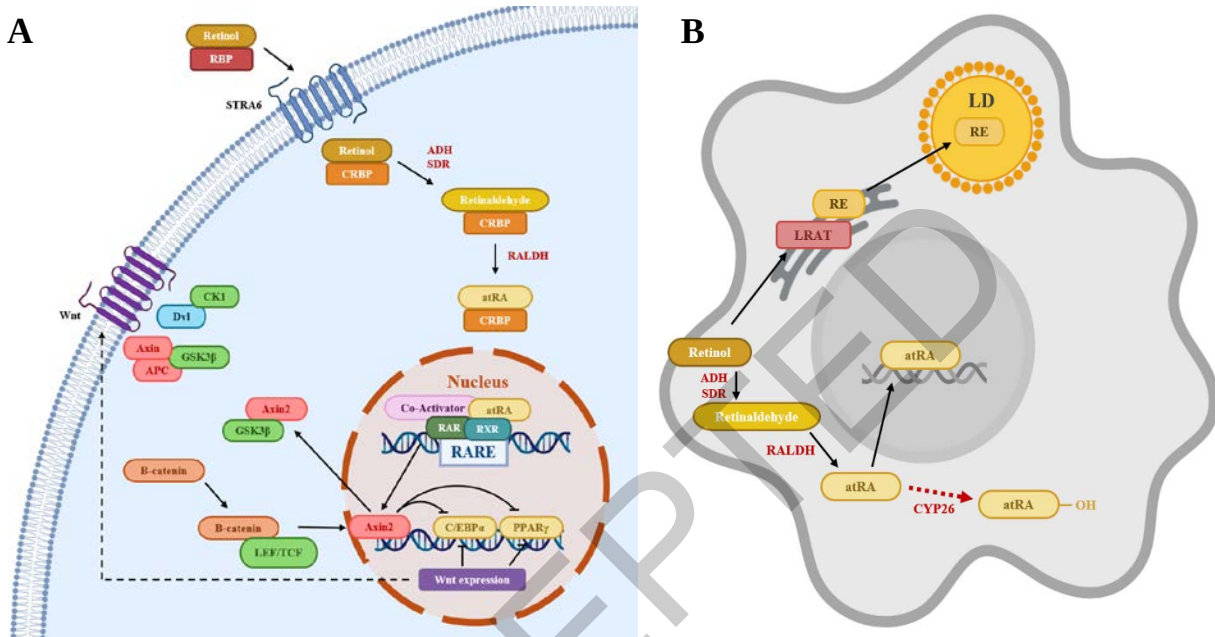


Fig. 1 An Illustrative Overview of atRA Biosynthesis and Metabolic Regulation. **A.** atRA Action and Crosstalk with Wnt Signaling. Retinol is enzymatically converted to atRA, which binds to RARs and regulates gene transcription by interacting with DNA response elements. atRA inhibits the expression of key adipogenic factors such as C/EBP α and PPAR γ , while activating Wnt signaling pathways, thereby playing a crucial role in controlling cell differentiation. **B.** atRA Biosynthesis and Metabolism. Retinol can be stored as retinyl esters (RE) in lipid droplets (LD) via the enzyme LRAT. A crucial negative feedback loop is shown, where excessive atRA is inactivated by CYP26 enzymes to maintain retinoid homeostasis.

IN VITRO STUDIES OF atRA

Effects on Cell Proliferation, Differentiation, and Apoptosis

Most in vitro studies investigating atRA's role in adipogenesis have been conducted using mammalian models [58–61], particularly a mouse-derived preadipocyte cell line, 3T3-L1 cells [44,62–64]. These studies have revealed that atRA exerts opposing effects on adipocyte differentiation depending on the treatment concentration and timing, promoting differentiation within certain concentration ranges while inhibiting it at others [44,64] (Fig. 2). In 3T3-L1 adipocytes, atRA exerts cell type-specific effects through a sequential process ranging from the uptake of extracellular retinol to the activation of nuclear receptors.

High concentrations of atRA ($\geq 1 \mu\text{M}$) suppress the expression of the key adipogenic transcription factors PPAR γ and C/EBP α [44] and activate the Wnt/ β -catenin signaling pathway [65,66], thereby inhibiting the differentiation of preadipocytes. High concentrations of atRA inhibit adipocyte differentiation during the early stages by selectively activating RAR γ [67,68]. Activation of RAR γ promotes the maintenance of a stem-like state [69,70]. Low concentrations of atRA (0.01-100 nM) promote lipid accumulation and increase the expression of mature adipocyte marker genes such as FABP4 [44], adiponectin [71], and LPL [72] (Fig. 2a).

The process of adipocyte differentiation can be broadly divided into three stages: the early transcriptional phase, the mitotic clonal expansion (MCE) phase, and the late terminal differentiation phase [73]. Among these, the MCE phase is characterized by cells re-entering the cell cycle and proliferating after the activation of early transcription factors [73], thereby increasing cell number to establish a sufficient cellular pool necessary for subsequent adipocyte differentiation. Multiple studies have demonstrated that MCE is an essential prerequisite for adipogenesis, emphasizing that precise regulation of cell cycle entry and exit critically influences differentiation efficiency [74–76]. Notably, atRA has been reported to exert a significant regulatory effect on the MCE phase in the 3T3-L1 cell model [44]. Treatment with a low concentration of atRA (1 nM) resulted in the highest proliferation rate and simultaneous G0/G1 cell cycle arrest observed at day 2, suggesting a dual mechanism by which atRA coordinates cell division and growth inhibition to secure an adequate cell number during MCE and activate the differentiation program. Furthermore, atRA concentrations ranging from 0.01 to 100 nM progressively increased the expression of S/G2 phase-related proteins such as Cdk1 and Cdk2, which are likely to promote DNA synthesis and entry into cell division, thereby maximizing proliferative capacity in the early MCE stage. Conversely, high concentrations of atRA (1 to 10 μM) led to dominant expression of G0/G1 phase marker proteins, including Cdk4, a key regulator of the G1/S transition through its interaction with Cyclin D, when overexpressed, can cause prolonged retention of cells in the G1 phase before S phase entry. Combined with changes in Cdk1 expression, this results in cells being arrested in G1 rather than progressing through S/G2/M phases, ultimately inhibiting DNA synthesis and cell division and delaying or blocking the adipogenic differentiation program (Fig. 2b).

Although direct reports on atRA-induced apoptosis in mature adipocytes are limited [77], studies on adipose-derived stem cells (ADSCs) have shown that atRA treatment notably increases the expression of pro-apoptotic proteins, such as BAX and BAK, and promotes caspase-3 expression. It also alters the expression of anti-apoptotic proteins, such as BCL-2, and increases mitochondrial membrane permeability, indicating apoptosis via the intrinsic mitochondrial pathway [78]. This trend is like mechanisms reported in acute promyelocytic leukemia (APL) cells [78–80] and other cancer cell models [20,81,82], where atRA induces upregulation of BAX, suppression of BCL-2 expression, triggers activation of the caspase signaling cascade, and facilitates the release of cytochrome c. These findings suggest that atRA triggers apoptosis

primarily through mitochondrial functional alterations and regulation of BCL-2 family proteins. These findings suggest that atRA influences adipose tissue by regulating adipocyte numbers and remodeling metabolism, yet the specific stages of adipogenesis and the signaling pathways involved remain to be fully understood.

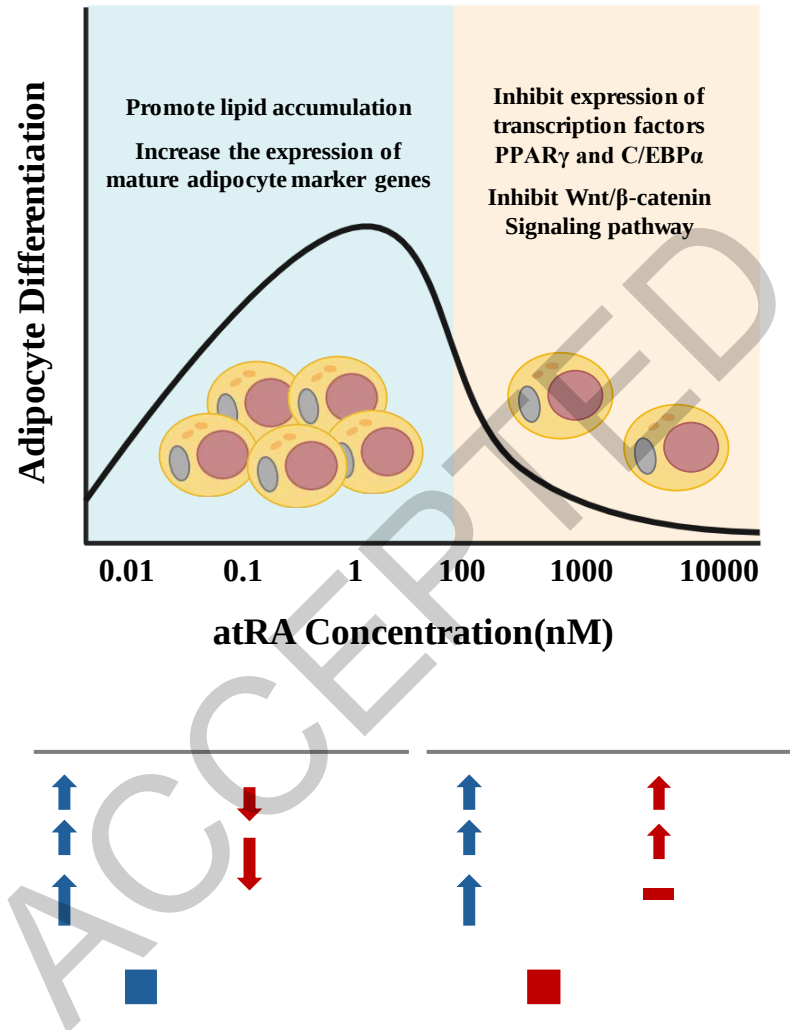


Fig. 2. Dual Regulation of Adipocyte Differentiation by atRA Concentration. **A.** At low atRA concentrations (approximately 0.01-100 nM), atRA promotes adipocyte differentiation by enhancing lipid accumulation and increasing the expression of mature adipocyte marker genes. Conversely, at high atRA concentrations (approximately >100 nM), atRA inhibits adipocyte differentiation by suppressing the expression of key transcription factors PPAR γ and C/EBP α , and by inhibiting the Wnt/ β -catenin signaling pathway. **B.** atRA modulates gene expression and cell cycle progression during adipocyte differentiation. During the Early transcriptional phase, low atRA (blue) upregulates C/EBP family transcription factors, while high atRA (red) suppresses. In the MCE phase, low atRA increases Cdk1 and Cdk2 expression,

facilitating G2/M phase entry. Conversely, high atRA reduces Cdk4 and Cdk1 levels, resulting in a pronounced G1 arrest.

Disease Modeling in Culture Systems

Using atRA in cell culture systems allows for precise explanation of molecular mechanisms related to metabolic diseases. In the 3T3-L1 adipocyte culture model, atRA exhibits dual effects depending on treatment concentration, timing, and the stage of cell differentiation. Low-dose or late-stage treatment promotes adipocyte differentiation by increasing the expression of mature adipocyte markers such as FABP4 and adiponectin, whereas high-dose treatment strongly inhibits lipid accumulation and differentiation by suppressing the expression of PPAR γ and C/EBP α [44]. In the hepatocyte cell model (HepG2 cells), atRA suppresses the expression of SREBP-1c and FASN genes involved in de novo lipogenesis [83,84], increases the transcription factor C/EBP α leading to inhibition of cell proliferation, and reduces PLA2 (involved in expansion and remodeling of adipose tissue) expression, thereby blocking pro-growth signals and decreasing hepatic lipid accumulation [85]. These results highlight the promise of atRA as a candidate treatment for non-alcoholic fatty liver disease (NAFLD). Additionally, in cardiovascular disease models, atRA inhibits excessive proliferation of vascular smooth muscle cells (VSMCs) and acts through activation of the AMPK signaling pathway to suppress mTOR signaling [86], demonstrating its influence on atherosclerosis and related cardiovascular conditions. atRA promotes myofiber formation and mitochondrial biogenesis in mouse myoblasts [87], and enhances insulin synthesis and secretion in the pancreatic beta-cell model, contributing to glucose homeostasis [88]. Furthermore, in inflammation-related disease models, atRA plays a key role in regulating macrophage M1/M2 polarization [89]. Studies in murine macrophage cells have shown that atRA suppresses the NF- κ B signaling pathway, leading to decreased expression of pro-inflammatory cytokines IL-6 and TNF- α , thereby alleviating metabolic inflammation [90]. Collectively, these results indicate that atRA exerts specific and context-dependent regulatory effects across diverse cell types and pathological environments, highlighting its value as a useful in vitro model for studying metabolic and inflammatory diseases as well as for potential therapeutic development.

To date, researches on disease modeling related to atRA have primarily focused on human and rodent cell lines; however, expanding studies to livestock species such as pigs, cattle, sheep, and chickens is critically important. Livestock play a vital role as food sources and provide more realistic models for studying metabolic and inflammatory diseases due to their distinct physiological characteristics and environmental exposures compared to humans. For example, atRA strongly inhibits differentiation of porcine preadipocytes by reducing the mRNA expression of PPAR γ , RXR α , SREBP-1c, and FABP4 through activation of retinoic acid receptors [61]. Additionally, atRA induces muscle fiber type switching in cultured bovine satellite cells (BSCs), increasing expression of oxidative metabolism-related MHC I and

decreasing MHC IIX via the PPAR δ pathway [91]. In ovine myoblasts, atRA suppresses cell proliferation while increasing expression of myogenin and myosin heavy chain proteins; this process involves elevated H3K4me3 and reduced H3K27me3, modulating transcriptional activation, and further activates GLUT4 expression and mTOR signaling pathways to influence muscle metabolism and growth [92].

Studies on primary cultured preadipocytes from Holstein cattle showed that atRA inhibits proliferation and induces apoptosis in pre-confluent preadipocytes. In post-confluent preadipocytes, atRA suppressed differentiation by reducing PPAR γ and C/EBP α protein expression. In mature adipocytes, atRA (conc.: 0.2, 2, and 20 nM) stimulated basal lipolysis but did not affect epinephrine-stimulated lipolysis[59]. These results suggest that atRA regulates lipid accumulation and breakdown in bovine adipocytes, potentially playing a role in modulating lipid metabolism and preventing metabolic diseases in over-conditioned dry cows [59]. In avian myoblasts, atRA treatment increased intracellular lipid accumulation and adipogenic gene expression, notably by directly inducing PPAR γ expression[93]. The extent of transdifferentiation was dependent on PPAR γ activation, and treatment with PPAR γ agonists alone was insufficient to trigger adipocyte transdifferentiation in the absence of atRA[93]. These findings indicate that atRA-driven PPAR γ expression is critical for the conversion of myoblasts into adipocytes and highlight atRA as a potential novel regulator to improve marbling in poultry production [93].Collectively, these findings suggest that atRA exerts species-specific yet consist of regulatory functions on lipid metabolism and muscle development in livestock cells. For instance, atRA-mediated induction of PPAR γ is essential for transdifferentiation of myoblast into adipocyte in avian systems [93], while in porcine and bovine cells, atRA predominantly suppresses adipogenesis and modulates muscle fiber characteristics through nuclear receptor pathways [91]. Such comparative evidence highlights atRA as a central molecular determinant orchestrating the balance between myogenesis and adipogenesis across livestock species, linking its relevance not only to human metabolic disorders but also to meat quality traits in animal production.

Such livestock-based in vitro models are invaluable for specifically understanding the molecular mechanisms regulated by atRA in agriculturally important species. Research on atRA-related signaling and gene expression regulation in livestock cells contributes not only to improving animal health, productivity, meat quality, and resistance to metabolic diseases but also enhances comparative biological insights into atRA biology across mammals. Furthermore, these livestock models hold promise as platforms applicable to both human and animal studies for exploring nutritional or pharmacological interventions aimed at preventing or treating metabolic disorders.

THE EFFECT OF RETINOIC ACID ON ADIPOSE TISSUE OF ANIMAL

To extend cellular observations to physiological contexts, subsequent studies have investigated the effects of retinoic acid in animal models. In rodent studies, daily subcutaneous injection of atRA in adult

mice reduces adipocyte size and decreases white adipose tissue (WAT) mass in epididymal, inguinal, and retroperitoneal fat [94]. This morphological change is accompanied by upregulation of central regulators of fatty acid oxidation, including PGC-1 α , PPAR α , and CPT1, suggesting an enhanced capacity for lipid catabolism. Similarly, atRA treatment to adult obese mice promotes weight loss, reduces WAT mass, and alleviates hepatic lipid accumulation [95]. Moreover, atRA administration partially reverses the adiposity of mice induced by a vitamin A-deficient diet and downregulates PPAR γ 2 expression level in WAT, a key marker of lipogenesis and adipogenesis [96]. Collectively, these findings indicate that retinoic acid functions as an inhibitor of adipogenesis in mature mice.

In livestock, manipulating vitamin A status – through dietary supplementation, restriction, or intramuscular injection of retinoic acid – has emerged as a strategy to modulate intramuscular fat (marbling), a critical determinant of beef flavor and tenderness. In pregnant beef cattle, vitamin A supplementation from day 180 of gestation until parturition increases intramuscular fat deposition in the offspring throughout postnatal life, with elevated expression of the preadipocyte marker DLK1, and the adipogenic marker PPAR γ in neonatal skeletal muscle [97]. Likewise, intramuscular injection of vitamin A at birth and at 1 month of age in Black Angus steers enhances PDGFR α ⁺ adipose progenitors and improves marbling scores [98,99]. By contrast, in later life stages, vitamin A restriction is required to enhance marbling: mature steers fed low- or no-vitamin A diets exhibit greater intramuscular fat deposition largely through adipocyte hyperplasia [100–103]. Comparable effects have been reported in pigs and sheep. Lambs receiving vitamin A supplementation or intramuscular injections during early postnatal development show increased numbers of preadipocytes and intramuscular adipocytes, alongside upregulation of adipogenic markers such as CEBP α and CEBP β in the longissimus dorsi muscle [104,105]. In female pigs, restricting vitamin A intake during the grower and finisher phase enhances intramuscular fat levels in the longissimus muscle [106].

In avian species, vitamin A has long been implicated in adipogenesis, the direct effects of embryonic atRA exposure on adipose development have only recently been investigated. In quail embryos, in ovo administration of atRA at embryonic day (E) 7 led to increased inguinal fat mass and enlarged adipocytes by E14, accompanied by upregulation of pro-adipogenic genes (PPAR γ , Fabp4) and downregulation of the preadipocyte marker Dlk1 [56]. Similarly, in broiler chickens, in ovo injection of 500 nM atRA at E10 enhanced adipose tissue accumulation and adipocyte hypertrophy during embryogenesis, although these effects did not persist after hatching [107]. Beyond its roles in proliferation and apoptosis, atRA exerts distinct metabolic and transcriptional effects on white, beige, and brown adipocytes across both rodent and livestock species. In white adipocytes, high concentrations of atRA (≥ 1 μ M) generally suppress differentiation by downregulating PPAR γ and C/EBP α , thereby maintaining cells in a preadipocyte-like state [94]. Conversely, brown and beige adipocytes exhibit enhanced thermogenic activity in response to atRA exposure, characterized by the upregulation of UCP1, CIDEA and mitochondrial biogenesis genes [108]. Recent findings in bovine [109] and porcine [110] adipose tissues demonstrate that dietary vitamin A restriction or pharmacological modulation of retinoid signaling alters the mRNA expression levels of

UCP1, PGC-1 α , and ZFP423, suggesting that RA metabolism contributes to the recruitment of beige-like adipocytes even in livestock species [55,109]. Furthermore, chronic atRA treatment promotes oxidative metabolism, as evidenced by increased TCA cycle intermediates and glucose oxidation, coupled with the downregulation of glycolytic enzymes such as PFKP and G6PDH. This metabolic shift implies enhanced mitochondrial activation and fatty acid oxidation, particularly in metabolically active depots [55,111].

Retinoid signaling via RAR α and its metabolic enzyme RDH1 is essential for maintaining BAT atRA levels, mitochondrial integrity, and systemic glucose homeostasis [112]. Disruption of this regulatory axis, through RAR α inhibition or RDH1 deficiency[112,113], reduces UCP1 expression[108]. However, the mechanistic basis linking atRA to adipogenic fate determination (white vs. beige vs. brown) remains poorly defined in livestock. Species-specific differences in RAR/RXR sensitivity, local retinoid metabolism, and adipose depot-dependent signaling likely underlie the divergent adipogenic and metabolic outcomes observed among ruminants, pigs, and rodents. Thus, comparative in vitro and in vivo analyses are required to elucidate how atRA coordinates cellular differentiation, mitochondrial remodeling, and lipid metabolism across species knowledge that could ultimately inform nutritional or pharmacological strategies to modulate adipose plasticity in livestock.

In summary, these findings collectively indicate that the influence of retinoic acid on adipose development is both stage and species dependent. atRA promotes adipogenesis during early developmental stages particularly in embryos and neonates while in later life it generally suppresses adipogenesis. In avian embryos, however, their adipogenic effects appear largely restricted to the prenatal period.

Species	Age	Administration	VitA dose or concentration	Main effects	Overall adipogenic outcome	Reference
NMRI male mice	12-week-old	atRA s.c., once daily for 4 days	10, 50, 100 mg/kg	iWAT, eWAT, rWAT mass↓ WAT UCP1/2, PGC-1 α , PPAR α and CPT1 mRNA↑	Inhibit	[94]
C57BL/6Ntac mice	>16-week-old	subcutaneous implantation of RA pellet, 5 weeks	NA	eWAT and aWAT mass↓ Adipocyte size↓ Liver lipid accumulation↓	Inhibit	[95]
NMRI male mice	3-week-old	VitA-deficient diet for 10 weeks followed by atRA s.c. (once daily for 4 days)	VitA-deficient diet: <0.38 IU/kcal atRA s.c.: 100 mg/kg	VitA-deficient diet: iWAT and eWAT mass↑, adiposity index↑, eWAT PPAR γ 2, ADD1/SREBP1c and C/EBP α mRNA↑ atRA sc injection: body weight↓, eWAT mass↓, iWAT and eWAT PPAR γ 2 mRNA↓, eWAT ADD1/SREBP1c and C/EBP α mRNA↓	VitA-deficient diet: Promote atRA sc injection: Inhibit	[96]
Pregnant Angus-Simmental cross bred multiparous cows	Day 180 of gestation	Basal diet enriched with pure VitA until parturition	12200 IU VitA/kg in feed	Offspring calves: IMF%↑, skeletal muscle DLK1, PPAR γ ↑	Promote	[97]
Angus steer calves	Newborn	VitA i.m. at birth and 1-month-old	150000 IU	IMF%↑, marbling score↑, subcutaneous adipocyte diameter↓, <i>Biceps femoris</i> muscle PDGFR α , PPAR γ , and ZFP423 mRNA↑	Promote	[99]
Angus steer calves	Newborn	VitA i.m. at birth and 1-month-old	150000 or 300000 IU	IMF%↑, marbling score↑, <i>Biceps femoris</i> muscle PPAR γ and ZFP423 mRNA↑	Promote	[114]
Angus steers	12-month-old	Standard commercial feedlot ratios without VitA over 300 days	NA	IMF%↑	Promote	[115]

Holstein steers	NA	VitA-restricted diet for 131 or 243 days	~950 IU of VitA equivalents/kg of DM	VitA-restricted diet for 243 days: IMF%↑	Promote	[100]
Angus-cross steers	NA	No VitA supplementation in high-moisture or dry corn for 145 days	High-moisture corn: 1300 IU/kg VitA Dry corn: 1100 IU/kg VitA	Marbling score↑	Promote	[101]
Angus steers	12-month-old	Non VitA-supplemented diet for 10 months	NA	IMF%↑, marbling score↑, cell number per IMF fleck↑	Promote	[103]
Hu sheep lambs	Newborn	VitA or RA i.m. at 1, 7, 14, and 21 days of age	VitA i.m.: 7500 IU RA i.m.: 7500 IU	VitA i.m.: intramuscular SVF cells formed adipocytes↑, adipocyte numbers of LD and ST muscle↑, LD C/EBP α and C/EBP β mRNA↑	Promote	[104]
Rasa Aragonesa lambs	Newborn	VitA supplementation by capsule, twice a week until 58 days of age	500000 IU	IMF mass↑, the number of adipocytes in the perirenal depot↑	Promote	[105]
Crossbred (Large White $\times$ Landrace $\times$ Duroc) pigs	NA	Non VitA-supplemented diet during grower (68-124 days) and finisher (124-159 days) phase	NA	LD IMF%↑	Promote	[106]

339 s.c., subcutaneous injection; i.m., intramuscular injection; WAT, white adipose tissue; eWAT, epididymal WAT; iWAT, inguinal WAT; rWAT, retroperitoneal WAT;
 340 aWAT, abdominal WAT; RA, retinoic acid; atRA, *all-trans* retinoic acid; VitA, vitamin A; IMF, intramuscular fat; LD, Longissimus dorsi; ST, semitendinosus; SVF,
 341 stromal vascular fraction; NA, not available.
 342

CONCLUSION

Significant progress has been made in understanding the effects of atRA on adipogenesis, yet several critical knowledge gaps remain. Current knowledge is largely derived from murine cell lines, particularly 3T3-L1 preadipocytes, which cannot fully recapitulate the complexity of adipose biology across different species [44,63,116–119]. The different responses to atRA in rodents, ruminants, and poultry emphasize the importance of studying multiple species to identify which mechanisms are universal and which are specific to each species. Another major challenge lies in resolving the temporal and concentration-dependent effects of atRA. Evidence suggests that the stage of adipocyte differentiation and the local microenvironment strongly influence atRA signaling outcomes, yet systematic analyses across developmental stages and tissue contexts remain limited.

Moreover, while atRA has been shown to interact with nuclear receptors (RAR/RXR) [120,121] and signaling cascades such as Wnt/ β -catenin [122,123], MAPK [124], and PI3K/AKT [125], the context-dependent hierarchy and cross-regulation of these pathways are poorly understood. Advances in single-cell multi-omics, spatial transcriptomics, and metabolomics are likely to provide powerful tools to address these questions.

Understanding the regulatory role of atRA also holds important applied value. In livestock, targeted modulation of retinoid signaling can improve feed efficiency [6,56], meat quality [58], and metabolic regulation. In human medicine, selective manipulation of retinoid pathways may offer novel therapeutic strategies for obesity [21], diabetes [126], and nonalcoholic fatty liver disease [127]. Accordingly, the development of tissue-selective RAR/RXR agonists and antagonists, alongside nutritional interventions aimed at modulating endogenous retinoid metabolism, represents a promising frontier for future research.

However, practical applications of vitamin A modulation in livestock must carefully balance efficacy with safety. Excessive or prolonged supplementation can lead to hepatic toxicity, impaired growth, or reproductive disorders, while insufficient levels may compromise immune and metabolic function. For instance, in broiler breeders, dietary supplementation exceeding 45,000–135,000 IU vitamin A/kg feed induced liver dysfunction could reduce fertility and alter immune responses [128]. Excessive vitamin A intake in cattle has been associated with decreased feed intake, hepatic dysfunction, and abnormal bone growth, particularly when intake levels greatly exceed recommended dietary requirement [129]. These findings highlight the narrow physiological window required for optimal vitamin A status in livestock. Therefore, precise dose optimization, adherence to regulatory limits, and long-term safety evaluations are essential for translating retinoid signaling research into sustainable livestock production strategies.

Adipogenesis is a complex, tightly regulated process that integrates endocrine, nutritional, and molecular cues to maintain energy homeostasis and influence metabolic health. Among these regulatory factors, atRA emerges as a broadly acting and condition-dependent regulator. In vitro evidence suggests that low concentrations (approximately 0.01–100 nM) of atRA may facilitate early adipogenic commitment, whereas

higher concentrations (approximately $\geq 1 \mu\text{M}$) generally suppress differentiation through nuclear receptor-mediated transcriptional repression and activation of inhibitory signaling cascades [44]. atRA modulates fat accumulation in a stage- and timing-dependent manner in vivo, enhancing intramuscular fat and adipogenic marker expression (DLK1, PPAR γ , PDGFR α) during fetal and early postnatal stages [98,114], while reducing white adipose tissue and inhibiting adipogenesis in adults [94]. In avian, in ovo atRA treatment increases adipocyte hypertrophy and pro-adipogenic gene expression, though these effects do not persist after hatching [56,107].

Collectively, these findings position atRA as a critical link between micronutrient status, gene regulation, and adipose tissue biology. However, the complexity of its effects—depending on dose, timing, species, and developmental context—underscores the need for further mechanistic and translational studies. A comprehensive understanding of atRA-mediated adipogenesis will not only deepen our insight into fundamental adipose biology but also provide novel opportunities for improving livestock production and developing targeted interventions for metabolic disorders.

From an applied perspective, several strategies could advance the use of atRA in livestock production. Nutritional and developmental modulation involves optimizing dietary vitamin A or carotenoid intake and timing atRA or analog supplementation during key developmental stages to fine-tune fat deposition, enhance marbling, and improve feed efficiency. Selective RAR/RXR-targeted interventions use tissue-specific agonists or regulators of retinoid metabolism to differentially modulate adipogenesis in muscle versus subcutaneous depots. Integrating these approaches with genomic and metabolomic monitoring could enable precision control of adiposity, productivity, and meat quality in livestock.

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