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Cyclin-D1 Modulation of Vitamin D-Induced Gene Expression in Oral Keratinocytes

A thesis submitted in partial satisfaction
of the requirements for the degree Master of Science
in Oral Biology by

Michael Connely Woods

2013

Abstract of Thesis

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by

Michael Connely Woods

Masters of Science in Oral Biology

University of California, Los Angeles 2013

Professor Dr. Sanjay Mallya, Chair

Background: Oral cancer is the sixth most frequent cancer worldwide, with approximately 400,000 new cases diagnosed per year. More than 90% of oral cancers are characterized as squamous cell carcinomas (SCC), which develops in the cells of the oral epithelium, is a highly aggressive and destructive cancer with a propensity for invasion of surrounding tissues and recurrence. More than 50% of oral SCCs harbor amplification or overexpression of the cyclin D1 oncogene, a key regulator of the G1-S phase of the cell cycle. However, there is emerging evidence that cyclin D1 may have additional roles in transcriptional control. We recently discovered that cyclin D1 binds to the vitamin D receptor (VDR), a nuclear hormone receptor that mediates the actions of vitamin D.

Objectives: The objective of our research is to investigate the effect of cyclin D1 on vitamin D signaling. We will examine the effects of cyclin D1 on vitamin D-induced gene expression. We will also examine the effects of cyclin D1 overexpression on cellular localization of key components in both the vitamin D signaling pathway.

Methods: An oral keratinocyte cell line, engineered to overexpress cyclin D1 (OKF6-D1) will be used to examine the relationship between the VDR and Cyclin D1 pathways. To analyze global gene expression, we will use microarray analyses. Immuno-staining of key pathway components will be used to localize these components to nuclear or cytoplasmic compartments that can be visualized by immunofluorescence (IF) .

Results: Microarray analyses identified 599 known genes that were modulated by $1,25(\text{OH})_2\text{D}_3$ in normal oral keratinocytes. These genes have known functions in keratinocyte differentiation, cell metabolism and immune modulation. Interestingly, cyclin D1 overexpression partially inhibited expression of several vitamin D-induced genes. The most significant effects were observed for keratinocyte differentiation genes. Vitamin D induced increase in VDR protein levels from 2 to 6 hours. VDR protein levels peaked at 6 hours for both OKF6 and OKF6-D1 keratinocytes. However, VDR protein levels were lower in OKF6-D1 keratinocytes at 12 and 24 hours of $1,25(\text{OH})_2\text{D}_3$ treatment. Cyclin D1 did not alter $1,25(\text{OH})_2\text{D}_3$ - induced nuclear VDR translocation. Confocal immunofluorescence did not demonstrate any significant difference in the localization of VDR following $1,25(\text{OH})_2\text{D}_3$ treatment. Interestingly, RXR α staining in $1,25(\text{OH})_2\text{D}_3$ treated OKF6-D1 keratinocytes showed a small but noticeable reduction in peri-nuclear staining compared to OKF6 keratinocytes. Cyclin D1 overexpression markedly attenuated $1,25(\text{OH})_2\text{D}_3$ -induced VDR-RXR heterodimerization.

Conclusions: Cyclin D1 modulates $1,25(\text{OH})_2\text{D}_3$ -induced gene expression in oral keratinocytes, especially, genes involved in keratinocyte differentiation. Cyclin D1's effect on modulation of vitamin D signaling may be in part due to its inhibition of VDR-RXR heterodimerization.

The thesis of Michael Connely Woods is approved.

Shen Hu

Sotirios Tetradis

Sanjay Mallya, Committee Chair

University of California, Los Angeles

2013

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Introduction

Oral cancer represents the sixth most frequent cancer, with nearly 400,000 new diagnoses each year [1]. The majority of oral cancers are classified as squamous cell carcinomas (SCC), which are characteristically aggressive, and locally destructive, often invading underlying bone and connective tissue. Thus, treatment demands aggressive resection to increase the likelihood of remission. Unfortunately, oral-pharyngeal cancer survivors have one of the highest susceptibilities to recurrence. Despite advancements in surgical techniques and medicine, survival rates have marginally improved over the past decades[2]. Consequently, there is an increasing need to identify preventative therapies for treating oral cancer survivors. Developing a strategy for prevention demands a comprehensive appreciation for the architecture that constitutes development of a healthy oral epithelium.

Oral Epithelium and Keratinocyte Development

The oral mucosa lining the intraoral compartment is divided into two major categories. First, the *masticatory mucosa* is comprised of a para-keratinized stratified squamous epithelium, which lines the dorsum of the tongue, hard palate, and the attached gingiva. Second, the lining mucosa is comprised of non-keratinized stratified squamous epithelium, which lines the remaining structures in the mouth. The epitheliums found in both mucosae constitute a stratified (layered) arrangement of keratinocytes. Within the epithelium keratinocytes are chronologically polarized, with immature cells localized at the base (Stratum basale) and differentiated cells at the surface as shown in **Figure 1**. Proliferating cells at the base of the epithelium provide a source of immature cells which gradually differentiate as they migrate away (towards the surface) to form a permeability barrier at the surface. Diverse cell to cell contacts, formed by proteins within the cellular membrane of these keratinocytes, help to create a barrier and serve as markers for keratinocyte differentiation (involucrin, transglutaminase, etc). Calcium and vitamin D_{1,25}(OH)₂D₃ are pivotal in regulating this process.

In vivo studies of the epithelium reveal a calcium gradient that increases from the base (stratum basale) to the surface, which supports in vitro findings. The gradient is responsible for providing a signal to migrating cells for differentiation. In addition to calcium, keratinocytes at the stratum basale are encouraged to differentiate by the

bioactive form of vitamin D ($1,25(\text{OH})_2\text{D}_3$) via the nuclear vitamin D receptor (VDR). Interestingly, keratinocytes at the stratum basale possess the metabolic machinery needed for synthesis of the nuclear hormone $1,25(\text{OH})_2\text{D}_3$ (via the vitamin D-25 hydroxylase & 25 OHD-1OHase) from vitamin D₃ in the same manner as liver and kidney enzymes[3-6].

Vitamin D: Vitamin D is a century old nutrient, initially used to prevent a devastating skeletal disease characterized by softening of the bone (Rickets). Today, we know a great deal more about the broad group of secosteroid's that constitute the vitamin and their involvement in mineral metabolism, skeletal integrity, and modulation of cell growth and differentiation in a variety of tissues. Since mammals possess a unique capacity to manufacture the nutrient when exposed to ultraviolet sun rays, vitamin D is not a true vitamin in the sense of the word $1,25(\text{OH})_2\text{D}_3$, the bioactive form of the vitamin also known as calcitriol, is produced internally by sequential hydroxylation of the secosteroid precursor's obtained from the diet (ergocalciferol, D₂) or sun exposed skin (cholecalciferol, D₃)[7, 8]. The first hydroxylation is catalyzed by 25-hydroxylase in the liver to produce 25-hydroxy vitamin D, the major circulating form. The final hydroxylation follows in the kidney's where 1-alpha-hydroxylase (1- α OHase) catalyzes the formation of $1,25(\text{OH})_2\text{D}_3$. A tightly controlled feedback system is directly exerted by the bioactive form of vitamin D at genes involved in the ligands production and degradation [9]. $1,25(\text{OH})_2\text{D}_3$ suppresses renal expression of the 1- α OHase responsible for its synthesis, and induces expression of the 24-OHase responsible for its degradation to calcitroic acid[9, 10]. In addition $1,25(\text{OH})_2\text{D}_3$ auto-regulates the expression of its own receptor, VDR[11, 12] (**Figure 2**). Similarly, a classic endocrine system monitors serum levels of calcium, phosphorus, and PTH to maintain serum levels $1,25(\text{OH})_2\text{D}_3$ [7, 8].

The biologic effects of $1,25(\text{OH})_2\text{D}_3$ are orchestrated by the nuclear hormone vitamin D receptor (VDR). The interaction of $1,25(\text{OH})_2\text{D}_3$ with VDR promotes its heterodimerization with the retinoid-x-receptor, a common partner of class II nuclear receptors[13]. The ligand activated heterodimer functions as a transcription factor for select target genes in the vitamin D pathway [14-16].

Vitamin D Receptor: Discovered in 1974, the vitamin D receptor (VDR) is a nuclear hormone receptor that facilitates differentiation by altering gene expression [17, 18]. Structurally VDR is composed of 3 distinct regions (FIGURE); N-terminal DNA binding domain, C-terminal ligand binding domain, and a linking region connecting the two domains [19, 20]. The binding domain contains a zinc finger typical of most steroid receptors[13, 21]. The ligand binding domain facilitates the formation of two independent surfaces for heterodimeric partner and co-regulatory complex interactions[22]. The role of ligand activated VDR is to direct cellular transcription by recruiting the appropriate machinery to specific genomic sites.

Upon ligand binding, the vitamin D receptor binds to specific DNA sequences known as VDRE's (vitamin D responsive elements). The VDRE's contain two hexameric nucleotide half sites, separated by 3 base pairs [14, 23]. The two half sites accommodate binding of a heterodimer comprised of the VDR/ RXR receptors[13]. Changes in gene expression are indirectly facilitated by VDRs recruitment of diverse co-regulatory complexes to these specific DNA sequences[24]. Co-regulatory complexes, include nucleosomal remodeling ATPases, enzymes with selective chromatin histone modifying capabilities, and RNA polymerase recruitment molecules.

Roles for Vitamin D in Prevention

Vitamin D's use in therapeutic interventions: A considerable amount of preclinical data suggest anti-cancer activities for vitamin metabolites ranging from anti-proliferation, anti-angiogenesis, pro-apoptosis, and pro-differentiation[25-27]. Clinical studies using vitamin D metabolites alone or in combination with chemotherapy have been conducted for various cancers, but mostly prostate cancer patients[28-38]. Single agent use of bioactive vitamin D (calcitriol) in preventive therapy produced limited success, with hypercalcemia representing a major drawback.

Interestingly, pre-clinical combination therapies suggest a synergistic or additive anti-cancer effect when calcitriol and cytotoxic agents are combined in chemotherapeutics[39-43]. Pre-clinical success with combination therapy has prompted the development of combination therapy trials. However, clinical trials have been underwhelming, largely due to confounded issues with dosing[44]. The first clinical studies for calcitriol were conducted in myelodysplastic syndrome (MDS) and acute leukemia (AML) patients[45-48]. The combination of cytarabine (chemotherapeutic agent) and calcitriol were successful in lowering remission of both disease in elderly patients, however the daily regimen was associated with hypercalcemia in 10-30% of patients. Critics of these experiments point to lack of dose optimization specific to anti-cancer properties, and emphasize the need to develop a maximum tolerated dose (MTD) or optimal biologic dose (OBD) (Vit D Cancer Review). Failed attempts at translating experimental findings into clinical success led to the development of vitamin D analogs in the hope of eliminating hyper-calcemia and enhancing anti-cancer properties[49, 50]. Although promising, the reduction in hypercalcemia afforded by vitamin D analogs has been plagued by reduced anti-cancer properties[25].

Risk Factors for Oral Cancer: Excessive environmental insults to the epidermis can be extremely detrimental over time. The rapidly proliferating cells at the base of the oral epithelium are of particular concern, since DNA damage caused by prolonged abuse provides an expedient pathway towards the unregulated growth characteristic of cancer.

Although numerous, the major risk factors for cancer of the oral cavity are known to be alcohol and tobacco consumption[51]. Other risk factors include poor oral hygiene; poor diet (low in fruits and vegetables) and low socioeconomic status[52, 53]. In addition to local carcinogen exposure, strong epidemiological and molecular evidence suggest a causal relationship between high risk human papilloma virus infection (HPV16/18) and oral SCC (8,9). More recently, two epidemiological studies have identified an association between vitamin D deficiency and oral squamous cell carcinoma[54, 55].

The Biology of Oral Cancer

Oncogenes/ anti-oncogenes (tumor suppressor genes): Cancer results from a multi-step process of gene activation or inactivation. The discovery of consistently amplified genes (cellular oncogenes) in specific cancers provided an inclination of their role in the pathogenesis of cancer[56-59]. Oncogenes, represent normal genes with the potential to cause cancer when highly expressed. Activated oncogenes allow cells to bypass cell death (apoptosis) in favor of proliferation and survival. There are several mechanisms responsible for their overexpression including; gene mutation [60], chromosomal duplication[61], and chromosomal translocation[62, 63]. Certain neoplasms frequently amplify such genes (N myc in neuroblastoma[64-66], L myc in small cell lung cancer [61, 67, 68]) of particular interest in our research is cyclin D1 in oral cancer, which has been shown to be amplified in more than 50% of OSCCs[69, 70].

Cell cycle regulator: cyclin D1: Cyclin D1 is a key regulator of the G1-S phase, which precedes cell cycle entry and proliferation. It binds to and activates cyclin-dependent kinases (CDK4 and CDK6), which encourage cell cycle progression by inactivating the retinoblastoma protein, a well-known tumor suppressor (**Figure 3**). This pathway is generally accepted as the central source of cyclin D1's oncogenic function. Thus, cyclin D1's amplification represents a likely driver of unregulated proliferation. Not surprisingly, the amplification of cyclin D1 is common in oral SCC [69-73]. Unclear, is whether cyclin D1's role in pathogenesis is dependent on its kinase partners.

Link between VDR and Cell Cycle Regulator

Previous research in our laboratory investigating the impact of over-expressing CDK4/6, revealed an inability to sufficiently disrupt keratinocyte differentiation in a manner that simulated keratinocytes in oral OSCC [74]). These findings suggest that cyclin D1's role in oncogenesis may be mediated through some other means. The precise mechanism by which cyclin D1 exerts its oncogenic effect remains unclear. In previous studies, we have used a transgenic animal model to demonstrate that cyclin D1 overexpression enhances susceptibility to carcinogen-induced oro-esophageal neoplasia [75]. Emerging evidence

suggests that in addition to its regulation of the cell cycle, cyclin D1 may play a part in transcription. Studies from numerous cell types have revealed that cyclin D1 binds transcriptional regulators including the estrogen receptor, androgen receptor, thyroid receptor, and STAT3[76, 77]. These studies helped shape our hypothesis, that cyclin D1 has a role in transcriptional control, and that this novel interaction contributes to its oncogenic function[76]. In support of this hypothesis, previous work in our lab demonstrates that cyclin D1 associates with the receptor responsible for directly mediating vitamin D's signaling effects (VDR). We have recently found that cyclin D1 modulates the transcriptional activity VDR, thereby altering the sensitivity of oral keratinocytes to vitamin D.

In this study we aim to investigate the impact of cyclin D1 over-expression on vitamin D signaling. Affymetrix was used to investigate the functional significance of the cyclin D1-VDR association on vitamin D induced gene expression. Microarray findings were validated with RT-PCR analysis. Secondly, we aim to investigate the impact of cyclin D1 over-expression on the localization and interaction of Cyclin D1 and components critical to vitamin D signaling (VDR & RXR). Both immunofluorescence and co-immunoprecipitation assays (data not shown) were used to investigate changes in the localization of vitamin D signaling components and VDR-RXR heterodimerization respectively.

Materials & Methods

Cells & culture conditions

OKF6-TERT1 cells (obtained from Dr. James Rheinwald, Brigham and Women's Hospital, Boston, MA) are immortalized, but non-transformed oral keratinocyte cell lines that stably express hTERT—the catalytic subunit of telomerase [78]. Cells were grown in keratinocyte serum-free medium (Invitrogen corporation, Carlsbad, CA) supplemented with bovine pituitary extract (25 µg/ml), epidermal growth factor (0.2 ng/ml), penicillin (100 IU/ml) and streptomycin (100µg/ml). The calcium concentration of the media was adjusted to 0.03mM. To induce keratinocyte differentiation, cells were grown either in the presence of 1,25(OH)₂D₃ (10⁻⁷M). OKF6-D1 cells were derived from OKF6-TERT1 cells by stable transduction with lentiviral constructs expressing the human cyclin D1 cDNA as previously described [74].

RNA isolation

For RNA isolation, total RNA was extracted using Trizol reagent (Invitrogen, Carlsbad, CA) and partially purified using the RNEasy Micro kit[79]. The aqueous phase from Trizol lysis was used as the starting material in the column based purification. DNase was used following on column purification to eliminate any remaining trace elements of DNA. The RNA concentration was determined using by spectrophotometry. The microarray was performed on the Affymetrix U-133 +2.0 platform.

Quantitative real-time PCR

For quantitative PCR analyses, total RNA was extracted using Trizol reagent (Invitrogen, Carlsbad, CA) and reverse transcribed using random hexamers. The cDNA templates were amplified using gene-specific primers to amplify S100A7, S100A9, SPRR1A, SPRR1B, SerpinB3 and the TATA-binding protein (TBP, as endogenous control). Sequences of the primers are as follows: S100A7 (Forward: 5'-TCTTGTCATCACGTCTGGTGT-3', Reverse: 5'-CTACTCGTGACGCTTCCCA-3'), S100A9 (Forward: 5'-TCAGCTGCTTGTCTGCATTT-3', Reverse: 5'-GGAATTCAAAGAGCTGGTGC-3'), SPRR1A (Forward: 5'-

TCACCTGCTGCTGCTGAG-3', Reverse: 5'-AGCCCATTCTGCTCCGTAT-3');
SPRR1B (Forward: 5'-AGGGCTGCTTCTGCTGC-3', Reverse: 5'-
GCAGTTCTAAGGGACCATACAGA-3'); SerpinB3 (Forward: 5'-
AGAGCTTGTTGGCGATCTTC-3'; Reverse: 5'-AACACCACAGGAAAAGCTGC-3');
Cyclin D1 (Forward: 5'-CAGAGGCGGAGGAGAACAAA-3', Reverse: 5'-
ATGGAGGGCGGATTGGAA-3'); TBP (Forward: 5'-CACGAACCACGGCACTGATT-
3', Reverse: 5'-TTTTCTTGCTGCCAGTCTGGAC-3'). Real time PCR reactions were
done in triplicate on an ABI 7900HT real-time PCR unit using the SYBR green
detection and analyzed using the delta-delta CT method.

Microarray Analysis

Human U133plus2.0 array hybridizations were performed by UCLA Clinical
Microarray Core following standard Affymetrix GeneChip Expression Analysis
protocol. The acquisition of array image was undertaken by using Affymetrix
GeneChip Command Console 1.1 (AGCC). Subsequent raw data were analyzed using
Partek genomics Suite 6.4. We used RMA algorithms for data
normalization. Thresholds for selecting significant genes were set at ≥ 2 -fold
and $p < 0.05$. Genes met both criteria simultaneously were considered as significant
changes. Global functional analyses, network analyses and canonical pathway
analyses were performed using Ingenuity Pathway Analysis (Ingenuity® Systems,
www.ingenuity.com).

Co-immunoprecipitation & Western blot analyses

Cells were treated with $1,25(\text{OH})_2\text{D}_3$ 6 hours prior to lysis in all experiments except
VDR time course. Vitamin D treatment in VDR time course varied from 0,2,6, and
12 hours. Following incubation with VDR cells were lysed in preparation for
immunostaining.

Cells were lysed in radioimmunoprecipitation assay (RIPA) buffer for 1 hour on ice.
Cell debris was removed by centrifugation at 10,000xg for 10 minutes at 4° C. For
immunoblotting, equal amounts of protein were layered onto reducing SDS-PAGE
gels and electroblotted onto PVDF membranes. For immunoprecipitation, pre-
cleared whole cell lysates, containing approximately 0.8 to 1 mg of total protein,
were incubated with anti-VDR (Clone 9A7, Affinity Bioreagents, Golden, CO, or

clone D-6, Santa Cruz Biotechnology, Santa Cruz, CA) or anti-cyclin D1 (Clone DCS-6, Santa Cruz Biotechnologies, Santa Cruz, CA) antibodies for 12-16 hours. Pre-equilibrated protein G-agarose beads (Santa Cruz Biotechnology, Santa Cruz, CA) were added and collected by centrifugation after 2 h of incubation and then gently washed three times with the lysis buffer. Bound proteins were eluted by heating in lamelli buffer, resolved on an SDS-PAGE gel and transferred onto PVDF membranes.

The following primary antibodies were used for immunoblotting: mouse monoclonal anti-human cyclin D1 (clone DCS-6), rat monoclonal anti-chicken VDR (Clone 9A7), mouse monoclonal anti-human VDR (Clone D-6), mouse monoclonal anti-human involucrin (clone SY-5, Sigma-Aldrich, St. Louis, MO), rabbit polyclonal anti-human RXR (Δ N197 and D-20, Santacruz Biotechnology) and mouse monoclonal antibody against human GAPDH, as loading control (Abcam Inc, Cambridge, MA). Binding of the primary antibody was detected using the appropriate horseradish peroxidase-conjugated IgG and Luminol reagent (Santa Cruz Biotechnology, Santa Cruz, CA).

Immunofluorescence

Cells were allowed to attach overnight to chambered glass coverslips. The calcium concentration was unchanged for OKF6 keratinocytes or replaced with 1,25 vitamin D (10^{-7} M) and the cells were incubated for 6 hours. Cells were fixed with 4% formaldehyde for 10 minutes and washed in PBS. To detect vitamin D signaling components (VDR, RXR α) or cyclin D1, cells were blocked with 5% goat serum and incubated with the primary antibody (mouse monoclonal anti-human VDR (D6), rabbit polyclonal anti-human RXR α (D20), and mouse monoclonal anti-human Cyclin D1 (DCS6) from Santa Cruz Biotechnology, Santa Cruz, CA) for 2 hours at room temperature. Bound primary antibody was detected using an Alexa Fluor 568-conjugated goat anti-mouse IgG or goat anti-rabbit IgG (Invitrogen Corporation, Carlsbad, CA) and the nuclei were counterstained with DAPI (Invitrogen Corporation, Carlsbad, CA). Sections were examined by confocal microscopy.

Results

Microarray Data

Microarray analysis was used to investigate the global impact of cyclin D1 over-expression on vitamin D signaling. We used a stringent threshold for differential gene expression (\pm 3-fold change over untreated, baseline expression). Only the highest differentially expressed genes were selected for further investigation. We identified 599 known genes that were modulated by 1,25(OH)₂D₃ in normal oral keratinocytes these genes have known functions in keratinocyte differentiation, cell metabolism and immune modulation (**Figure 4**)

Heat Mapping: Microarray expression profiling demonstrates differences in gene expression for both 1,25(OH)₂D₃ treatment and cyclin D1 over-expression. A gene was accepted as differentially expressed if there was a three-fold or greater difference in its expression between study groups. This segregated 770 differentially expressed genes. The heat map revealed a distinctive pattern in the keratinocytes treated with 1,25(OH)₂D₃, and a less distinctive pattern for keratinocytes over-expressing cyclin D1. Genes that showed increased expression are shown in red and genes showing decreased expression in blue. Clearly, 1,25(OH)₂D₃ treatment had a significant impact on the expression profiles of both OKF6 and OKF6-D1 over-expressing keratinocytes. (**Figure 4A**).

PCA Mapping: To better visualize the large data sets obtained from the DNA expression microarray studies, principle component analysis (PCA) was performed. PCA uses a three-dimensional scatter plot, derived from the gene list used to generate the heat map. This analysis uses distance between samples to illustrate their unique differences. The y-axis indicates that 27% of the variability between groups was attributed to the over-expression of cyclin D1. The x-axis indicates that 48% of the variability between groups could be attributed to 1,25(OH)₂D₃ treatment. Thus, 1,25(OH)₂D₃ treatment is responsible for the majority of variability in gene expression. The impact of 1,25(OH)₂D₃ treatment on the expression profile can be visualized by observing horizontal distance between proliferating keratinocytes (OKF6/ OKF6-D1) and keratinocytes induced to differentiate (OKF6 + vit D/ OKF6-

D1 + vit D respectively) with $1,25(\text{OH})_2\text{D}_3$. The horizontal shift between these respective groups suggests that the expression profile of differentiating keratinocytes differs considerably from proliferating keratinocytes irrespective of the over-expression of cyclin D1. Interestingly, the PCA map clearly indicates that the difference in gene expression profiles between OKF6 and OKF6-D1 over-expressing keratinocytes (indicated by the vertical distance between E & D1 on PCA map), becomes smaller following $1,25(\text{OH})_2\text{D}_3$ treatment (indicated by vertical difference between E+vit D & D1+vit D) (**Figure 4B**). This finding suggests that vitamin D treatment brings the expression profile of OKF6-D1 keratinocytes closer to that of OKF6 keratinocytes (and vice versa), thus reducing the extent of variability introduced by cyclin D1 over-expression.

RT-PCR Analyses

A group of genes with functions related to cornified envelope development (S100A7, S100A9, SPRR1A, SPRR1B, and SerpinB3) were among those found to be highly differentially expressed. RT-PCR was used to validate the differential expression of these candidate genes in OKF6 and OKF6-D1 over-expressing KCs treated with vitamin D. In each experiment the expression level in OKF6 cells were used as a baseline for comparison. Vitamin D treatment in OKF6 and OKF6-D1 cells induced increased expression of the majority of these genes. However, the scale of induction was reduced in keratinocytes over-expressing cyclin D1 (**Figure 5**). These findings suggest that cyclin D1 over-expression is associated with a deregulation of vitamin D signaling. We hypothesized that mechanism for such deregulation is either directly attributed to cyclin D1's interaction with VDR or indirectly related to cyclin D1 induced changes in the localization of vitamin D signaling components. To investigate our hypotheses further we implemented co-immuno-precipitation assays and immunofluorescence respectively.

VDR Expression Time Course

To investigate Cyclin D1's role in deregulation of vitamin D signaling, we monitored changes in VDR expression following ligand treatment. Western blot analysis of lysates from OKF6 and OKF6-D1 over-expressing keratinocytes treated with $1,25(\text{OH})_2\text{D}_3$ for 2, 6, 12, and 24 hours were used to examine changes in VDR induction. Expression of the VDR protein is modulated by $1,25(\text{OH})_2\text{D}_3$ -treatment. In OKF6 keratinocytes VDR expression by increased by 2 hours and was maximal after 6 hours of treatment, after which a decrease in the amount of VDR protein was detected (**Figure 6**). A similar pattern was also observed in cyclin D1 cells. However, VDR protein levels following 12 and 24 hours of $1,25(\text{OH})_2\text{D}_3$ -treatment, was considerably lower in cyclin D1 over-expressing cells compared to OKF6 cells (**Figure 6**). These findings suggest that cyclin D1 may modulate vitamin D signaling by modulating ligand-induced VDR expression.

Co-Immunoprecipitation Assays

VDR's transcriptional activity is regulated by heterodimerization with RXR. To further examine the functional significance of VDR-cyclin D1 association, we examined whether cyclin D1 overexpression modulated VDR-RXR association, as determined by co-immunoprecipitation assays. In the first set of experiments we used an anti-RXR antibody (ΔN197) that recognizes all three isoforms of RXR. Using this antibody, RXR-VDR association was detected in untreated OKF6 and cyclin D1 overexpressing cells. However, there was a marked attenuation of RXR-VDR association in $1,25(\text{OH})_2\text{D}_3$ -treated cyclin D1 overexpressing cells (**Figure 7A**). In the second set of experiments we used an antibody that specifically detects the RXR α isoform. There was no detectable RXR-VDR association in either OKF6 or OKF6-D1 overexpressing cells. In OKF6 cells, RXR α -VDR association was induced by $1,25(\text{OH})_2\text{D}_3$ -treatment. In contrast, there was almost complete attenuation of RXR α -VDR association in $1,25(\text{OH})_2\text{D}_3$ -treated cyclin D1-overexpressing cells (**Figure 7B**). Overall, these data demonstrate that cyclin D1 may interfere with VDR-RXR heterodimerization, specifically the RXR α -isoform.

Immunofluorescence

To investigate whether an abrogation of VDR–RXR heterodimerization was due to a direct inhibition of the binding of the two proteins, or due to cyclin D1-induced cellular sequestration of the two proteins, we used immunofluorescence to examine cellular localization of VDR and RXR. OKF6 and OKF6-D1 cells were treated with 1,25(OH)₂D₃ for 6 hours. Cellular localization of VDR, RXR and cyclin D1 was examined by immunofluorescence. Cells were stained with DAPI to counterstain the nucleus. (**Figure 8**).

Cyclin D1: Immunofluorescence (IF) demonstrated predominantly nuclear localization of cyclin D1 in untreated OKF6 cells. 1,25(OH)₂D₃ treatment of OKF6 cells did not alter the pattern of localization. In contrast, untreated OKF6-D1 cells displayed robust cytoplasmic and nuclear staining. Similar to OKF6 cells, vitamin D treatment had a minimal effect on cyclin D1's localization. (**Figure 8A**).

VDR: Immunofluorescence demonstrated VDR localization in both cytoplasmic and nuclear, with predominant nuclear accumulation in untreated OKF6 cells. Upon 1,25(OH)₂D₃-treatment, VDR localization was predominantly nuclear. This pattern of localization was similar in OKF6-D1 cells. Interestingly, the intensity of VDR staining was lower in OKF6-D1 keratinocytes compared with OKF6 cells (**Figure 8B**).

RXRalpha: In untreated OKF6 cells RXRalpha was detected in both the nucleus and the cytoplasm, although the pattern of staining was diffuse in both compartments. Upon 1,25(OH)₂D₃-treatment, RXR localization was changed to a strong peri-nuclear accumulation. A similar pattern of RXR localization was detected in OKF6-D1 cells. However, 1,25(OH)₂D₃-treated OKF6-D1 cells showed a more diffuse perinuclear accumulation compared with OKF6 cells (**Figure 8C**).

Discussion

Cyclin D1 amplification is a frequent aberration that contributes to OSCC pathogenesis. However the mechanism of its pathogenicity is not fully understood. Cyclin D1 is frequently amplified in cancer, leading to unregulated proliferation and a diminished ability to terminally differentiate. Cyclin D1's oncogenic capacity is attributed to alterations in its role as "gate keeper" to cell cycle entry. The mitogenic effects of cyclin D1 are generally attributed to its two cyclin dependent kinase (CDK) partners, CDK4 and CDK6. This pathway has been thought to be the primary mechanism for cyclin D1's oncogenic functions.

Interestingly however, our discovery of an interaction between cyclin D1 and the nuclear hormone, VDR, raises questions about additional pathways for cyclin D1s pathogenesis. Although new to oral keratinocytes, the link between cyclin D1 and transcriptional machinery (specifically nuclear hormone receptors) is not uncommon. Previous studies have demonstrated from other cells types has shown that cyclin D1 interacts with other transcriptional regulators—the estrogen receptor in mammary epithelial cells, and the androgen receptor in prostate cells ([80, 81]). The intersection of the vitamin D and cyclin D1 pathway is intriguing because it links two essential hallmarks of cancer: deregulation of proliferation and differentiation. Vitamin D's less commonly known role in cell cycle inhibition and the promotion differentiation, consists of a cascade of intracellular interactions that lead to the modulation of gene expression, whereas cyclin D1 promotes cell proliferation.

Our microarray results clearly indicate a difference in $1,25(\text{OH})_2\text{D}_3$ -induced gene expression between cyclin D1-overexpressing and control oral keratinocytes. In particular, is cyclin D1's effect on modulation of $1,25(\text{OH})_2\text{D}_3$ -induced expression of keratinocyte differentiation genes. Our data strongly support a role for cyclin D1 in modulating vitamin D signaling in oral keratinocytes. Interestingly, we previously showed that cells over-expressing either cyclin D1 or CDK4/6 retain the ability to respond to calcium-induced differentiation ([74]). Thus, our current finding of cyclin D1' effect on deregulated vitamin D-signaling suggest that these effects are specific to the vitamin D-signaling pathway and are not non-specific effects related to an increased proliferative state induced by cyclin D1 overexpression.

In considering the mechanism for cyclin D1's effects on vitamin D signaling, we speculated that cyclin D1 overexpression may alter cellular localization of VDR and/or its partner RXR. Our data did not indicate any major alteration in cellular trafficking of these two proteins in cyclin D1-overexpressing cells. However, we detected that cyclin D1 markedly inhibited RXR α –VDR association (**Figure 7**). Furthermore, VDR protein levels were considerably lower in cyclin D1 over-expressing keratinocytes (**Figure 6**). The loss of this interaction has direct implications for the transcription of vitamin D genes. Interestingly, ligand induced changes in the VDR protein revealed diminished protein levels after 6 hours of treatment in D1 over-expressing cells; however VDR protein levels remained elevated in OKF6 cells 24 hours after exposure to vitamin D (**Figure 6**). Reduced levels of VDR would directly impact the vitamin D pathways ability to stimulate the expression of genes in the vitamin D pathway. The mechanism of deregulated vitamin D signaling could be explained in a number of ways, including changes in the localization of key signaling components or key signaling interactions. We conducted immunofluorescence to rule out changes in the localization of key components as a potential mechanism for disruption. The lack of change in the localization of key vitamin D signaling components (RXR & VDR) and cyclin D1 as seen in immunofluorescence ruled this out as a potential explanation. Although no major changes in localization were observed in vitamin D treated keratinocytes overexpressing cyclin D1, notable minor changes were observed. Peri-nuclear localization of RXR α was observed in both ligand treated OKF6 and OKF6-D1 keratinocytes, suggesting that the VDR-RXR α interaction occurs somewhere along the nuclear membrane (**Figure 5C**). This finding is consistent with the notion that RXR and VDR form a complex that targets the nucleus for modulation of gene expression. We did observe reduced peri-nuclear staining and a shift towards a more diffuse cytoplasmic staining in ligand treated D1 cells. This finding was consistent with our co-immunoprecipitation results, which show inhibition of the RXR α –VDR interaction in ligand treated D1 cells. Disruption of this complex will inhibit VDRs ability to modulate gene expression. The nuclear accumulation of VDR following ligand treatment was observed in both OKF6 and OKF6-D1 cells. This finding ruled out nuclear exclusion of VDR as a plausible means of deregulating vitamin D signaling.

In summary, our results highlight the importance of the interaction between the cyclin D1 oncogene and the vitamin D pathway. We have shown that the overexpression of cyclin D1

is associated with disruption of the normal physiology attributed to vitamin D signaling and inhibition of early signaling interactions. The early interaction of VDR and RXR are required for modulation of gene expression. The vitamin D signaling pathway is important for normal keratinocyte physiology (pro-differentiation and anti-proliferation), especially since it has been shown too important in other types of cancer. This is the first study linking vitamin D signaling to the specific oncogenic interactions of cyclin D1. In the future we hope to further explore the implications of cyclin D1-VDR interaction by examining the impact on VDRs ability to bind DNA using chromatin immunoprecipitation (ChIP) assays to quantify changes in VDR's ability to bind DNA.

Conclusion

In conclusion, we demonstrated that the over-expression of cyclin D1 in OKF6 cells leads to the deregulation of vitamin D induced gene expression. The loss of vitamin D signaling is evidence by partial inhibition of vitamin D induced genes, reduction in VDR protein levels, and disruption of VDR-RXR interactions.

Figures

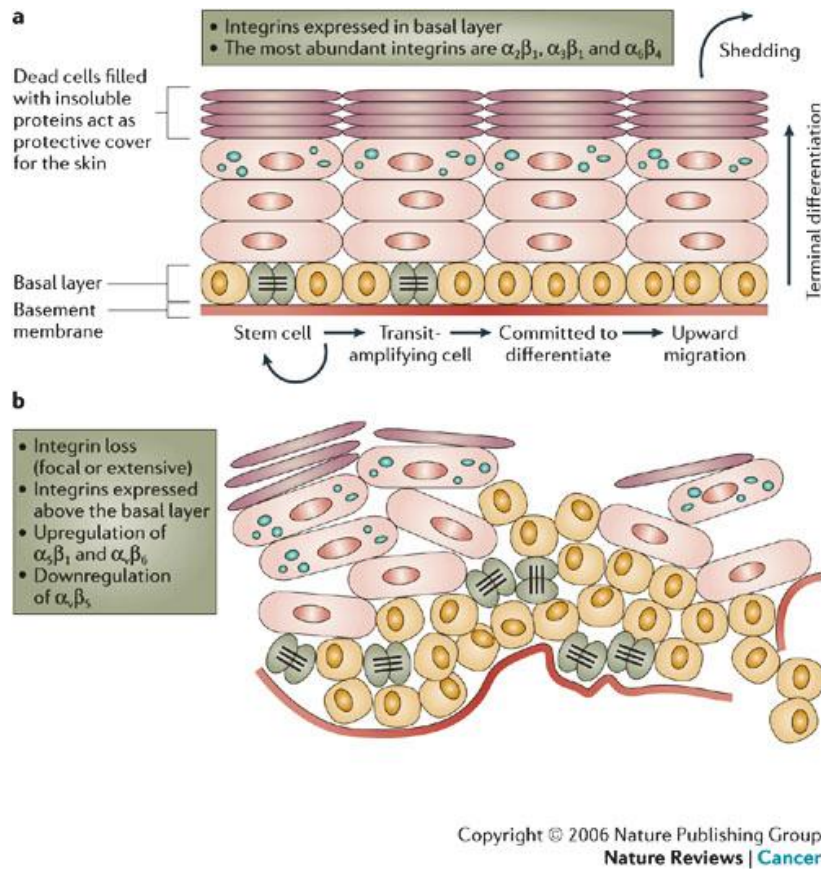


Figure 1. Cellular organization in normal epidermis and squamous-cell carcinoma. (a) In the human epidermis and oral epithelium immature proliferating keratinocytes are derived from stem cells at the basement membrane. Keratinocytes that destined for terminal differentiation, lose their ability to divide and detach from the basement membrane. The migration of these cells from the basal layer correlates the formation of tight intercellular interactions as these cells become specialized to form the protective outer covering of the skin. (b) Squamous cell carcinomas are characterized by focal or extensive loss of the basement membrane, increased proliferating cells, and reduced number of cells undergoing terminal differentiation. The spatial organization of the epithelium is disrupted, such that cells no longer maintain discrete arrangement of layers that constitutes the protective network of cells found in normal epithelium. Reference: Sam M. Janes and Fiona M. Watt. (2006). New roles for integrins in squamous-cell carcinoma. *Nature Reviews Cancer*. doi:10.1038/nrc1817

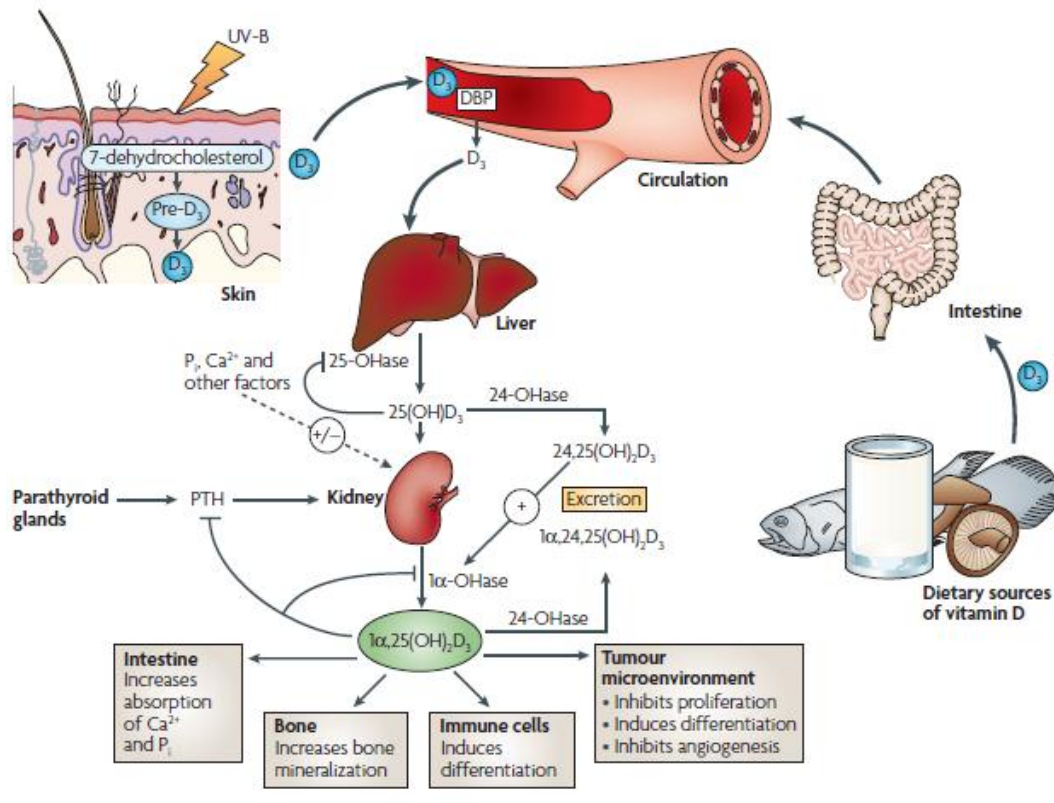


Figure 2. Vitamin D metabolism. Vitamin D is a broad term used to describe a number of derivatives. The primary sources of vitamin D are sun exposed skin and the diet. In the skin, cholesterol (7-dehydrocholesterol) is converted to pre-vitamin D-3 in response to ultraviolet B rays from the sun. Pre-vitamin D₃ absorbed from the diet or synthesized in the skin binds to vitamin D-binding protein (DBP) in the bloodstream for transport to the liver. In the liver D₃ is hydroxylated by 25-hydroxylases to the major circulating form 25-hydroxy D₃. Stimulated by parathyroid hormone and suppressed by Ca²⁺, P_i and 1α,25(OH)₂D₃ itself, the kidney converts this secosteroid (25 OHD₃) into the bioactive hormone 1α,25(OH)₂D₃ (calcitriol) from 25(OH)D₃. This hormone has numerous effects on various target tissue (highlighted above). Deeb, K.K., D.L. Trump, and C.S. Johnson, *Vitamin D signalling pathways in cancer: potential for anticancer therapeutics*. Nat Rev Cancer, 2007. 7(9): p. 684-700.

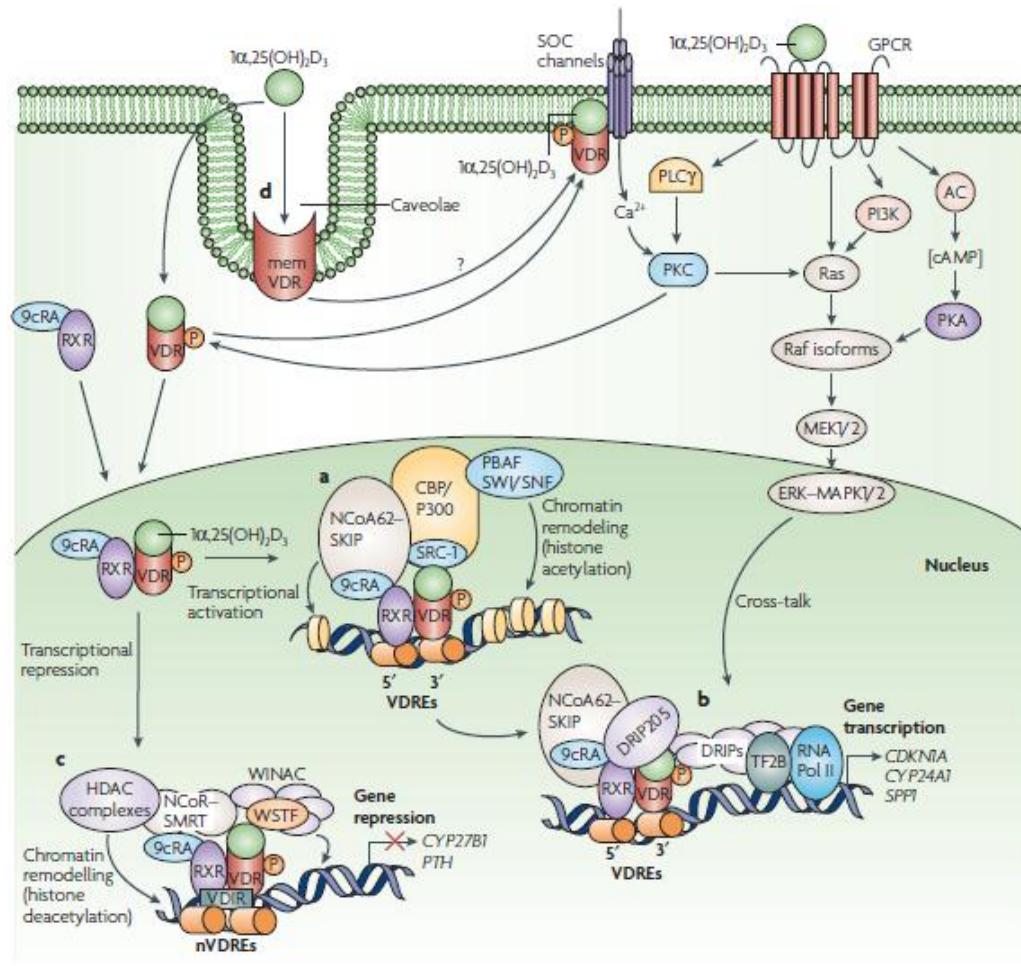


Figure 3. $1\alpha,25(\text{OH})_2\text{D}_3$ -mediated transcriptional regulation. The classical actions of bioactive vitamin D3 are mediated by the vitamin D receptor (VDR), and 9-cis-retinoic acid receptor (RXR) which complex to form an active transcription factor. Ligand activated VDR forms a complex with VDR capable of modulating transcription at specific regions of called vitamin D response elements (VDREs). (a) Transcriptional activation is mediated by a number of coactivators and mediators, which function to initiate (b) or repress (c) the recruitment of transcriptional machinery. (d) Non-genomic, rapid actions of $1\alpha,25(\text{OH})_2\text{D}_3$ are hypothesized to involve binding a cytosolic and membrane VDR. Deeb, K.K., D.L. Trump, and C.S. Johnson, *Vitamin D signalling pathways in cancer: potential for anticancer therapeutics*. *Nat Rev Cancer*, 2007. **7**(9): p. 684-700.

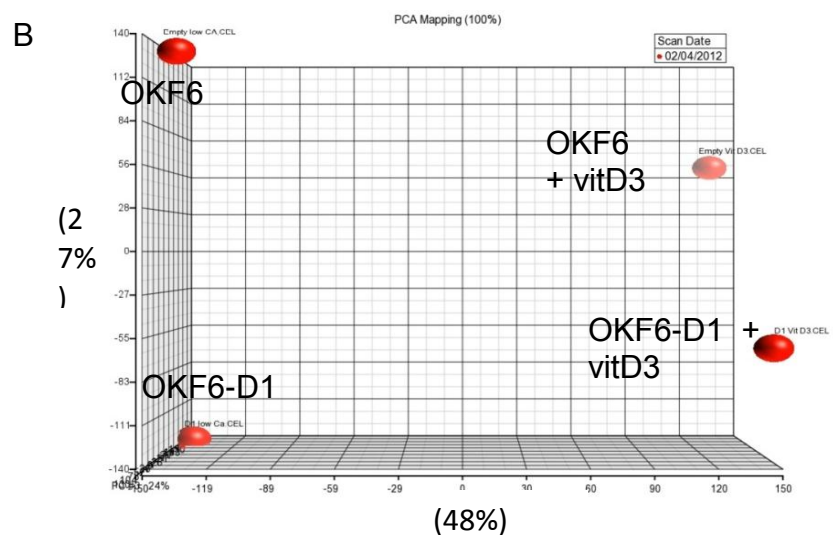
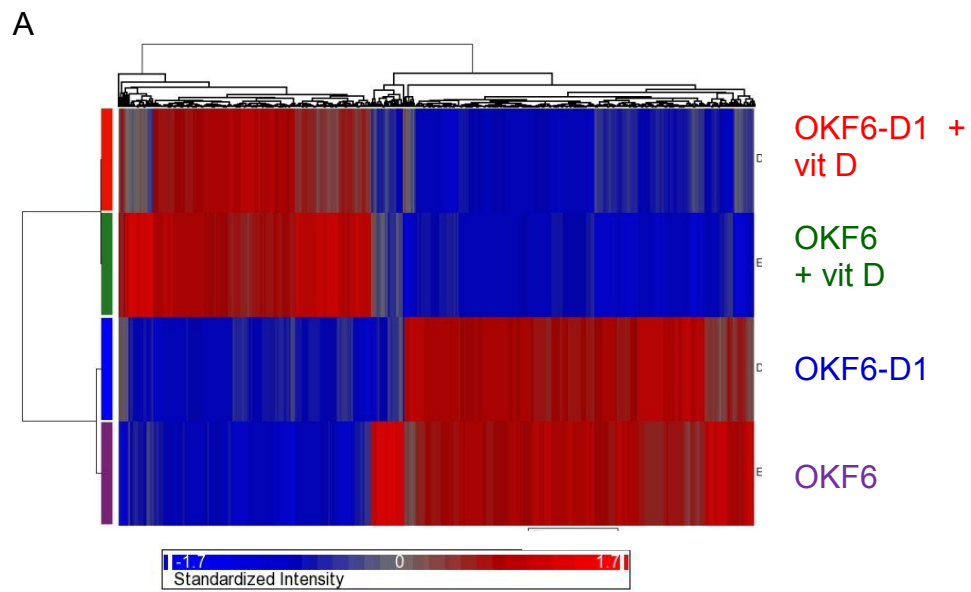


Figure 4. Microarray analysis of vitamin D induced gene expression. (a) Hierarchical clustering of OKF6 and OKF6-D1 keratinocytes treated with vitamin D. Each row represents each sample tested and each column represents a single gene probe. Relative gene expression is color represented: red indicates higher gene expression, blue is lower, and grey is no change. The heat-map displays 770 differentially expressed with greater than or equal to a 3 fold change in gene expression (inclusion criteria). (b) Principal Component Analysis (PCA) of vitamin D induced gene expression in keratinocytes overexpressing cyclin D1 vs normal keratinocytes. PCA is a 3D scatter plot used to visual display the differences in global expression profiles with and following vitamin D treatment. Analysis of 4 samples resulted in 4 relatively distinct components of gene expression.

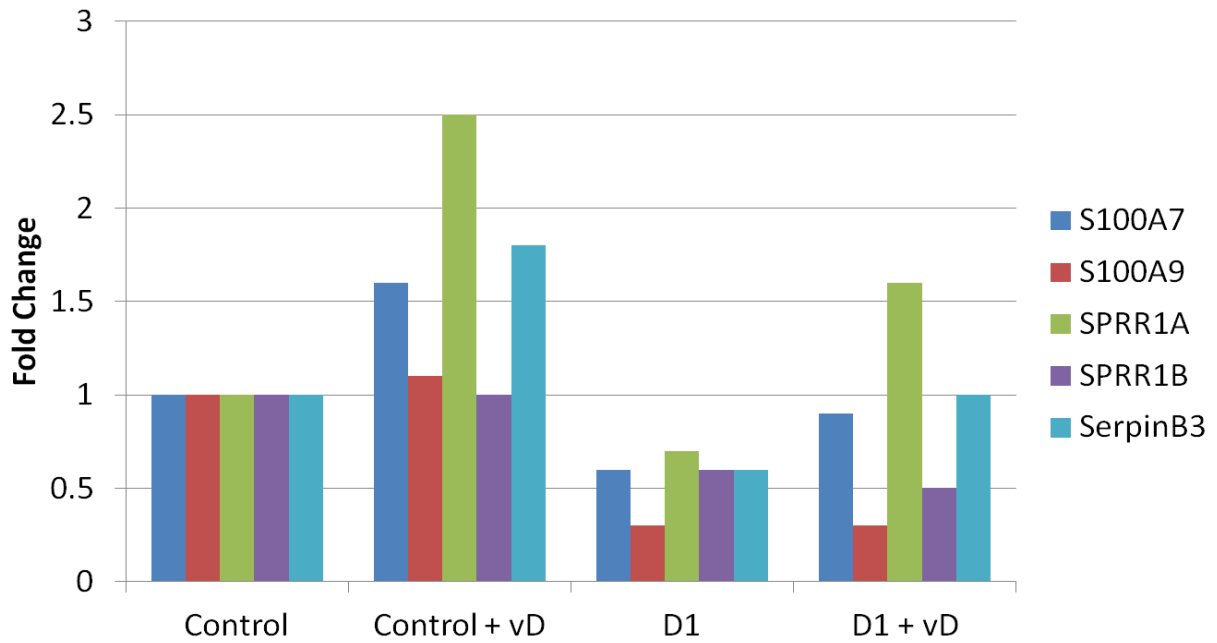


Figure 5. Cyclin D1 partially inhibits vitamin D's induction of cornified envelope proteins. RT-PCR analysis of OKF6 and OKF6-D1 over-expressing keratinocytes treated with vitamin D. Gene candidates in the pathway of differentiation were found to be highly differentially expressed by microarray analysis. These candidate genes were validated with RT-PCR, and the expression levels of OKF6 cells were used as a baseline for comparison.

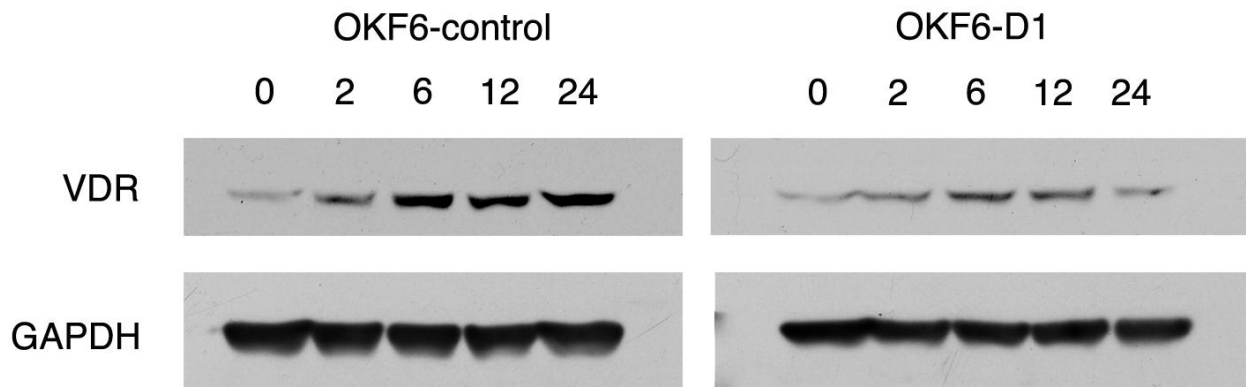


Figure 6. Vitamin D Induces VDR. Oral keratinocytes overexpressing cyclin D1 (D1) and OKF6keratinocytes show a vitamin D induced expression of VDR that gradual rises from 0 to 2 hours and peaks at 6 hours. VDR protein levels remain elevated at after 24 hours of treatment in OKF6cells, but declines in cyclin D1 over-expressing keratinocytes.

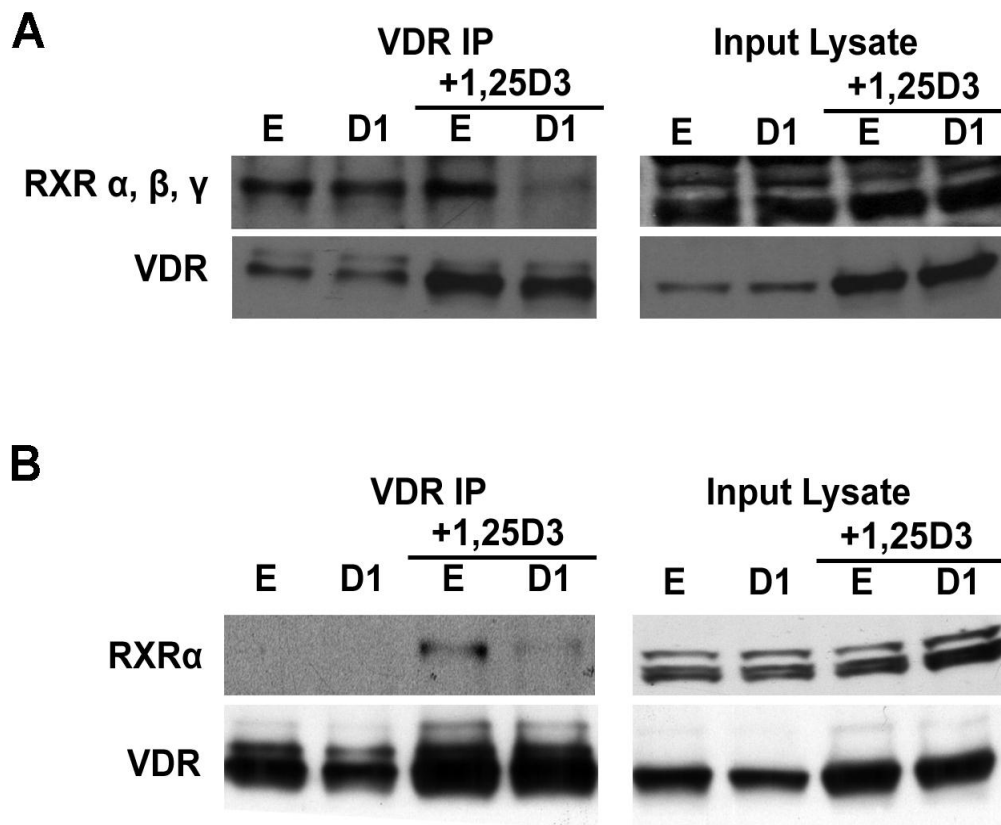
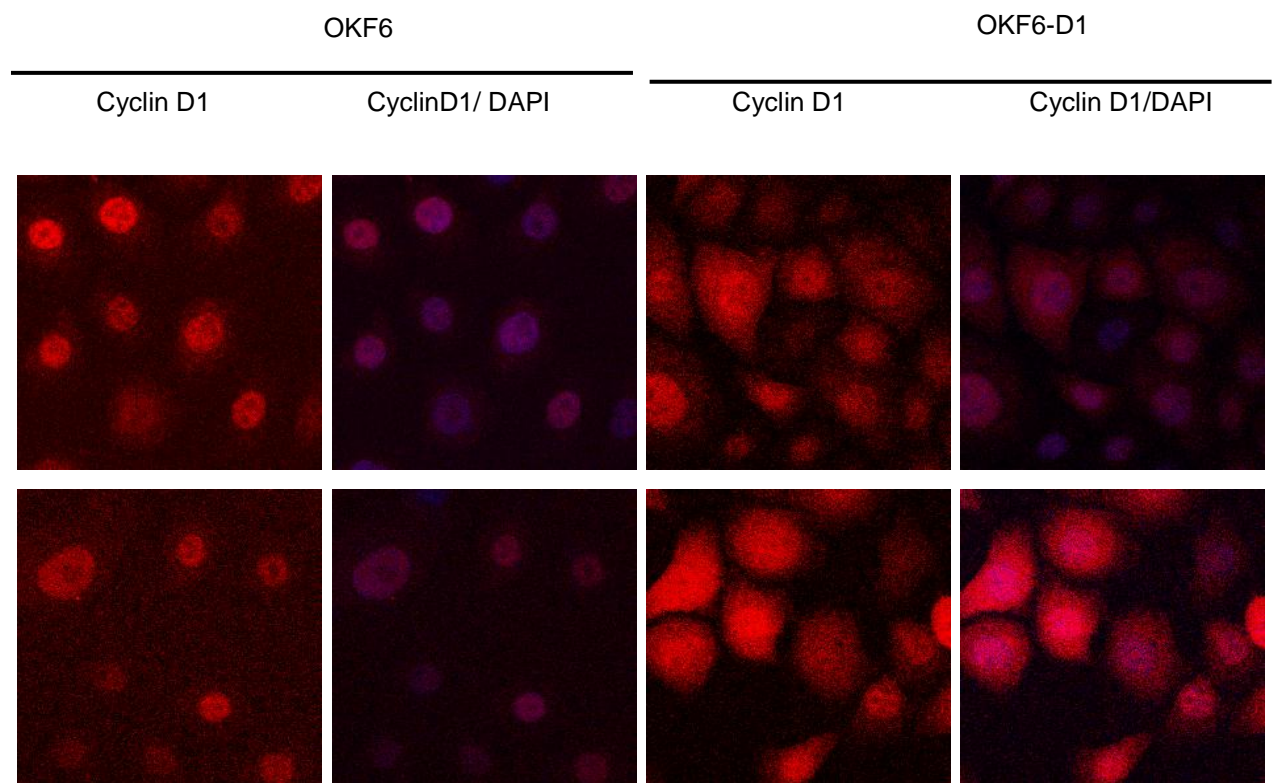
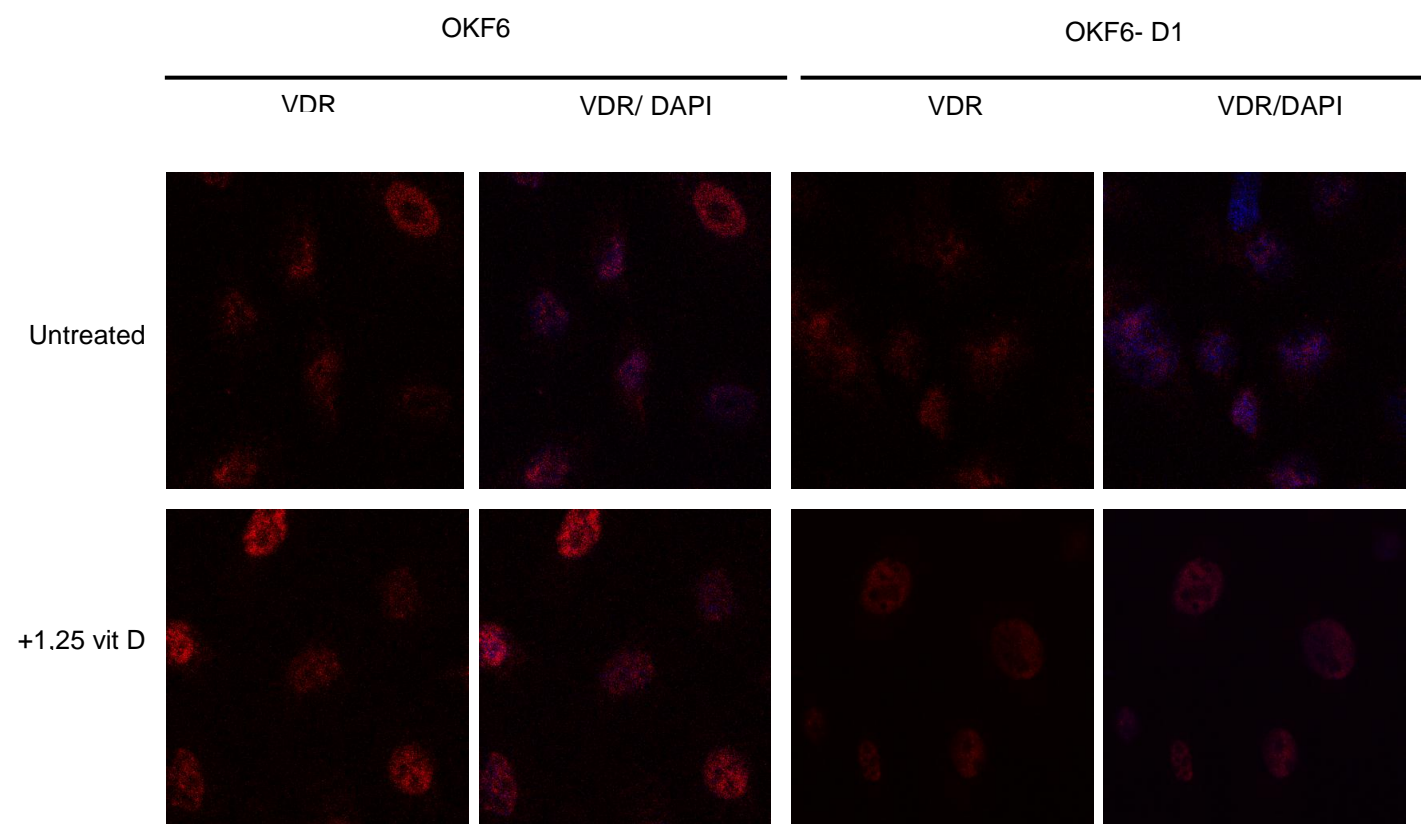


Figure 7. Cyclin D1 blocks VDR–RXR binding. OKF6-D1and OKF6keratinocytes were treated with 1,25(OH)₂D₃ for 6h. Lysates were immunoprecipitated with an anti-VDR antibody (clone 9A7) and immunoblotted with an antibody against all 3 isoforms (fig. 7A), RXR α alone (fig. 7B) or VDR (clone D-6).

A



B



C

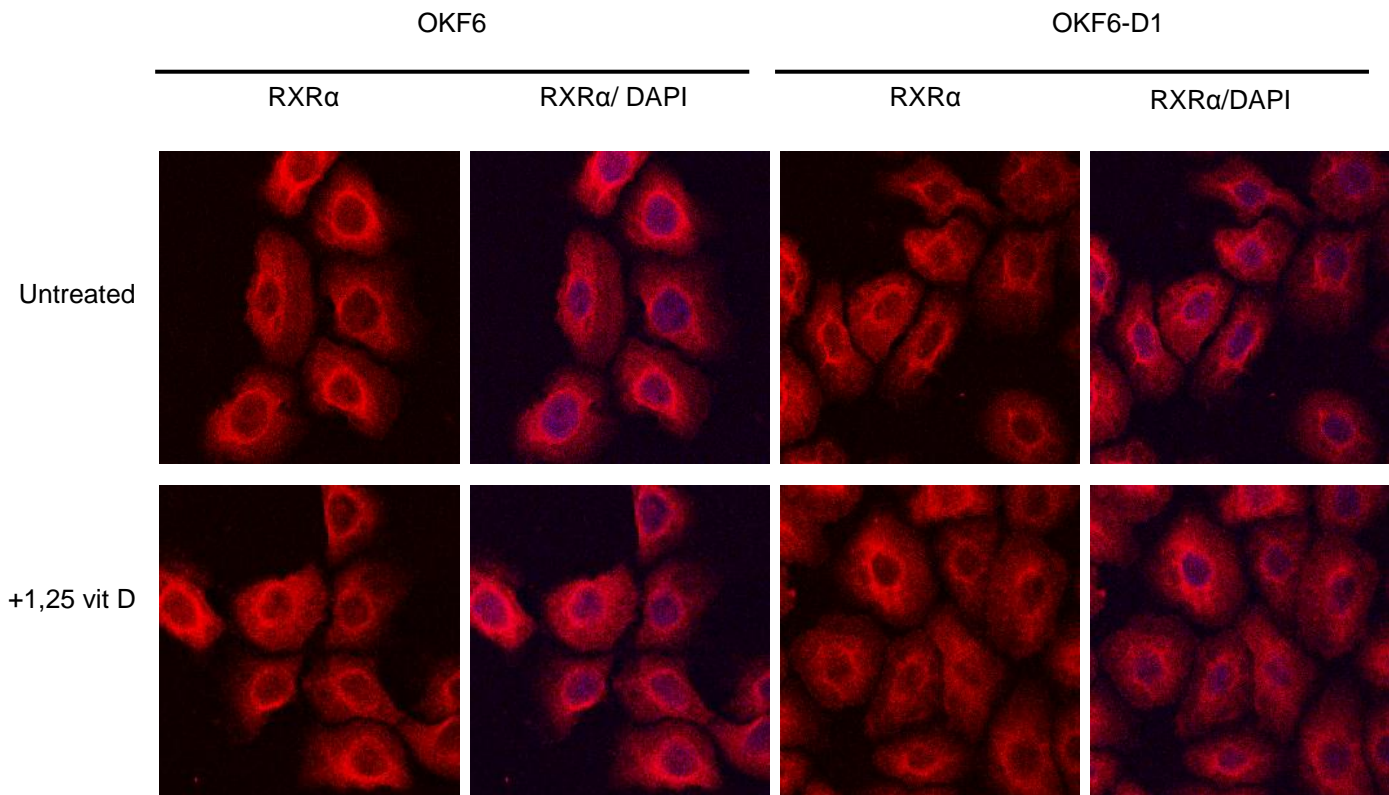


Figure 8. Cyclin D1 over-expression does not alter vitamin D induced changes in localization. Cells were treated with the 1,25(OH)₂D₃, 10⁻⁷M for 6h. VDR [A], RXR α [B] and cyclin D1 [C] were detected by immunofluorescence. Nuclei were counterstained with DAPI and visualized under a confocal microscope. Overlay images were generated to visualize and differentiate nuclear and cytoplasmic staining.

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