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<tr>
<td><strong>Citation</strong></td>
<td>American Journal of Translational Research, 2011, v. 3 n. 5, p. 479-491</td>
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<tr>
<td><strong>Issued Date</strong></td>
<td>2011</td>
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The gold (III) porphyrin complex, gold-2a, suppresses \textit{WNT1} expression in breast cancer cells by enhancing the promoter association of YY1

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Received September 30, 2011; accepted October 12, 2011; Epub October 13, 2011; Published October 31, 2011

**Abstract:** The gold (III) porphyrin complex, gold-2a, elicits anti-tumor activity by targeting the Wnt/\(\beta\)-catenin signaling pathway [Chow KH et al, Cancer Research 2010;70(1):329-37]. Here, the molecular mechanisms underlying the inhibitory effects of this compound on \textit{WNT1} gene expression were elucidated further. A response element to gold-2a was identified located within the -1290 to -1112 nt region of the \textit{WNT1} promoter, containing a binding site for the transcription regulator Yin Yang 1 (YY1). Gold-2a promoted the association of YY1 and suppressor of zeste 12 (Suz12; a component of the polycomb repressor complex 2) with the \textit{WNT1} promoter. Under normal culture conditions, the intracellular translocalization of YY1 was synchronized with cell cycle progression and \textit{WNT1} expression. Gold-2a promoted the nuclear accumulation and abolished the nuclear exportation of YY1, resulting in a persistent inhibition of \textit{WNT1} expression and a cell cycle arrest at G1/S phase. A dimorphic role of YY1 in regulating cell proliferation and division was revealed. Thus, the present study extends the understanding of the anti-tumor mechanism of gold-2a to the epigenetic level, which involves the modulation of the dynamic interactions between YY1 and a specific region of the \textit{WNT1} promoter.

**Keywords:** Gold(III) porphyrin complex, anti-cancer drug, \textit{WNT1}, YY1, breast cancer

**Introduction**

The therapeutic value of metal-based drug compounds has been established for almost a century [1-5]. Cisplatin is the typical example of metal compounds being widely used in patients as an anti-cancer agent. Gold(III) is isoelectronic with platinum (II) and four coordinate gold(III) complexes also adopt a square-planar geometry as cisplatin [6, 7]. In fact, the potent tumor-suppressive effects of gold(III) complexes have been demonstrated in a wide range of cancer cells and animal models [8-16].

Gold-2a [5-hydroxyphenyl-10,15,20-triphenylpor-phyrinato gold(III) chloride], a gold(III) porphyrin analogue, suppresses proliferation in a panel of human breast cancer cells and exhibits potent anti-tumor activity in nude mice implanted orthotopically with human breast cancer MDA-MB-231 cells [12]. The cytotoxicity of gold-2a is ~3,000-fold higher than cisplatin. Moreover, these two drugs exert their anti-tumor activities through completely different mechanisms. Gold-2a acts as a histone deacetylase inhibitor (HDACi) and selectively blocks Wnt/\(\beta\)-catenin signaling at the transcriptional level [12]. The present study was designed to further investigate the molecular mechanisms underlying gold-2a-mediated inhibition of \textit{WNT1} gene expression. The transcription factor YY1 was shown to interact with a gold-2a response element of the \textit{WNT1} promoter and to recruit a repressor complex for suppressing \textit{WNT1} gene expression. Gold-2a treatment blocked YY1 shuttling to the cytosol and promoted its nuclear accumulation, which in turn arrested cell cycle in the G1/S phase. In addition, gold-2a selectively eliminated HDAC3 from the YY1-containing protein complex and promoted its cytosol translocation.
Materials and methods

Antibodies and reagents

Antibodies against Suz12 and beta-actin were obtained from Cell Signaling (Beverly, MA, USA). Antibodies against HDAC1, HDAC3, HDAC8 and YY1 were obtained from Santa Cruz Biotechnology Inc. (Santa Cruz, CA, USA). SYBR® Green-ER™ qPCR Supermix, Lipofectamine™ transfection reagent, TRIzol®, pcDNA3.1+ vector, DAB substrate kit and ProLong® Gold antifade reagent with DAPI were from Invitrogen (Carlsbad, CA, USA). QIAquick gel extraction kit and T4 DNA ligase were from Qiagen (Hilden, Germany). The human breast carcinoma MDA-MB-231 cell lines were obtained from American Type Culture Collection on December 2004. The identities of these cells were confirmed by STR-profiling using the Cell ID System from Promega (last tested on 18/01/10). The synthesis of the gold (III) porphyrin complex (gold-2a) and the elemental analyses were conducted as described [12]. Gold-2a was dissolved in dimethyl sulfoxide (DMSO) and further diluted with phosphate buffered saline (PBS). A concentration of 0.1 μM gold-2a was used for all experiments of the present study.

Quantitative reverse transcription-PCR and chromatin immunoprecipitation-PCR

Quantitative reverse transcription-PCR (QPCR) was performed as described [12]. All reactions were analyzed using the melting curve to ensure the specificity of the real-time PCR reaction. The QPCR primers for human WNT1 (NM_005430.2) were forward 5’-GCA GCG ACA ACA TGG ACT TC-3’ and reverse 5’-GTG GCA CCT GCA CTC CTG-3’. The procedure of chromatin immunoprecipitation (ChIP)-PCR has been described [12]. PCR amplifications were performed using 10% of the chromatin samples, and the resulting products were quantified by both densitometry (Multianalyst Software, Bio-Rad) and QPCR analysis. For determination of gene expression, values obtained were normalized to those of the internal control 18S RNA. For promoter analysis by ChIP-PCR, values obtained were normalized against those of the corresponding input samples before immunoprecipitation. The primers used are listed in Supplementary Table S1.

Construction of reporter vectors for promoter activity analysis

The human WNT1 promoter sequences were amplified using the genomic DNA template derived from MDA-MB-231 cells. Primers used for different promoter regions are listed in Supplementary Table S2. The PCR products (digested with restriction enzymes Xhol and HindIII) were cloned into the pGL3-basic vector. The inserts were confirmed by DNA sequencing. To analyze the transcription activities of WNT1 promoter, the reporter vectors were transfected transiently into MDA-MB-231 cells and the luciferase activity was measured using cell lysates as described [17]. All values were normalized to the control Renilla luciferase signals. The cloning primers are listed in Supplementary Table S2.

Construction of YY1 mammalian expression vector

RNA was extracted from MDA-MB-231 cells using TRIzol® reagent according to the manufacturer’s instructions. One microgram of total RNA was used for the synthesis of first strand cDNA using the ImProm-II™ Reverse Transcription System. The primers for cloning human YY1 gene were 5’-CTG CGG ATC CAT GGA CTA CAA GGA TGA TGA CAA GAG CCA TGG CCT CGG GCG A-3’ (forward) and 5’-CTG CCT CGA GCT ACT GGT TGT TTT TGG CCT TAG GTG-3’ (reverse). The restriction enzymes (BamHI and Xhol)-digested PCR fragments were cloned into a pcDNA3.1+ vector to generate the mammalian expression vector pcDNA-YY1, which encoded an NH2-terminus FLAG-tagged human YY1.

siRNA knocking down of YY1 expressions

Three sets of YY1 siRNAs were obtained from Fulengen Co. (Guangzhou, China) for suppressing YY1 expression in MDA-MB-231 cells. The siRNA sequences are listed in Supplementary Table S3. Ten microliters of 20 μM siRNA mixture or scramble siRNA control were introduced into the cells using Lipofectamine™ 2000 transfection reagent. The down-regulations of YY1 were confirmed by Western blotting and QPCR.
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**Cell proliferation and [³H] thymidine incorporation assays**

Cells were seeded at a density of 2 x 10⁴ cells / well in 24-well plates. Transient transfection was performed for overexpression or downregulation of YY1. After fasting for 24 hours, 10% FBS was added into the culture. Radio-labeling was performed by adding 1 µCi/ml of [³H-methyl]-thymidine into the culture for the last six hours. At the end of the experimental period, the number of viable cells was counted manually by mixing with trypan blue dye. The protein amounts were quantified with a BCA protein assay (Pierce). For radiolabeled cells, after washing and trichloroacetic acid precipitation, DNA was solubilized with 0.2 M NaOH, neutralised with 0.2 M HCl and the radioactivity was quantified with a liquid scintillation counter.

**Cell cycle analysis**

Cells fixed with 70% ethanol were resuspended in staining buffer [100 mM Tris, pH 7.4, 150 mM NaCl, 1 mM CaCl₂, 0.5 mM MgCl₂, 0.1% NP-40 and 2 mg/ml propidium iodide] and incubated in the dark for 20 minutes on ice. The analysis was carried out with an EPICS® Elite ESP Flow Cytometer and EXPO software (Beckman Coulter, Miami, FL, USA). Data was acquired from 1 x 10⁵ cells per sample and gating of G1/S, S, and G2/M populations was subsequently performed manually using WinList software (Purdue University Cytometry Laboratories, West Lafayette, IN, USA).

**Subcellular fractionation and Western blotting**

Cells were resuspended in a hypotonic buffer (10 mM Tris-HCl, pH 7.5, 25 mM KCl, 2 mM Mg acetate, 1 mM DTT, 0.5 mM PMSF and protease inhibitor cocktails). After incubating on ice for ten minutes, cell membranes were disrupted by passing through a 23-gauge needle and nuclear isolation was monitored under a light microscope. After centrifugation for five minutes at 1000 x g, the supernatant was saved as “cytoplasmic fraction”. The nuclear pellet was washed once with the hypotonic buffer and lysed with hypertonic buffer (hypotonic buffer plus 400 mM KCl and 20% glycerol). The lysates were then centrifuged at 12,000 x g for five minutes, and the supernatant was collected as “nuclear fraction”. Protein concentrations were determined by the BCA method. Total cell lysates, cytoplasmic or nuclear fractions were separated by SDS-PAGE, transferred to PVDF membranes and then probed with various primary antibodies. The antibody-antigen complexes were detected using an enhanced chemiluminescence kit from GE Healthcare (Uppsala, Sweden).

**Co-immunoprecipitation**

Total cell lysates were prepared by homogenization in RIPA buffer [50 mM Tris-HCl, pH 7.4; 1 mM EDTA; 150 mM NaCl; 1 % Nonidel P40; 1 % Triton X-100; 0.5 % deoxycholic acid sodium salt; 1 mM NaF; 1 mM sodium orthovanadate; and a complete protease inhibitor cocktail] on ice and centrifuged for ten minutes at 12,000 x g to remove any large debris. The protein concentration of the supernatant was determined with a BCA Protein Reagent Kit. Five hundred micrograms of the total cell lysates were incubated with non-immune rabbit IgG and pre-cleared with 50 μl of protein G-Sepharose beads, and then incubated with two micrograms of antibody overnight at 4°C. Fifty microliter of protein G-Sepharose beads were added and the incubation was prolonged for another two hours. The beads-bound immune complexes were collected by centrifugation, washed twice, and eluted into a buffer containing 0.2 M Glycine-HCl, pH 2.5. After neutralization, the eluants were subjected to SDS-PAGE and Western blotting analysis.

**Immunocytochemical staining**

Transient transfection was performed in MDA-MB-231 cells seeded on cover slips. After methanol fixation, cells were blocked with 5% FBS in TBS-T buffer (0.1 % Triton X-100, 0.15 M NaCl, 0.05 M Tris-HCl, pH7.4) for one hour and incubated overnight with different antibodies at 4 °C. The cells were subsequently washed with TBST and incubated with anti-mouse Alexafluor (Invitrogen) for one hour at room temperature in the dark. ProLong® Gold antifade reagent was used as the mounting medium. Signals were detected and images were captured using a fluorescent microscope (Leica Microsystems, Bensheim, Germany).

**Data analysis and statistics**

All experiments were performed with three to six samples per group, and results were derived.
Results

Gold-2a inhibited WNT1 promoter activity in MDA-MB-231 cells

Previous study revealed that treatment with gold-2a blocked the gene expression of WNT1 in MDA-MB-231 cells [12]. To further delineate the underlying mechanisms, luciferase reporters of WNT1 promoter were constructed by inserting fragments of various lengths within the 1.5 kb region upstream of the ATG initiation codon into a pGL3-Basic vector (Figure 1A). Transient transfection was performed in MDA-MB-231 cells to test the activity of these WNT1 promoter reporters. In cells cultured under both serum free and serum containing conditions, the promoter activities of pGL3-WNT1(-1290 to -1) and pGL3-WNT1(-1415 to -1) were consistently lower than those of pGL3-WNT1(-1503 to -1) and pGL3-WNT1(-1112 to -1). Compared to serum free cultures, incubation with 10 % FBS significantly elevated the luciferase signal in cells transfected with pGL3-WNT1(-1290 to -1) and pGL3-WNT1(-1415 to -1) (Figure 1B). By contrast, serum had no stimulatory effects on the promoter activity of pGL3-WNT1(-1112 to -1) and pGL3-WNT1(-1503 to -1). In cells exposed to gold-2a, as early as two hours after adding the compound, the activities of WNT1 promoters covering the regions of -1290 to -1 nt and -1415 to -1 nt were significantly reduced by approximately 50 to 70% compared to vehicle controls, in both serum free and serum containing conditions (Figure 1C). In addition, gold-2a attenuated the activity of pGL3-WNT1(-1503 to -1) by approximately 20 to 40%. These results suggest that the region between -1290 to -1112 nt of the WNT1 promoter contains regulatory elements responsible for both serum-mediated activation and gold-2a-induced inhibition of WNT1 expression.

Gold-2a facilitated the associations of YY1 and Suz12 with the WNT1 promoter

In mouse embryonal cells, the 1.5 kb Wnt1 promoter upstream of the ATG site is the target of Suz12, a major component of the Polycomb Repressive Complex 2 (PRC2) [18]. Similar association of Suz12 has been demonstrated to
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occur at the same region of the WNT1 promoter in SW480 human colon cancer cells [19]. YY1 is a transcription regulator physically interacting with Suz12 and acting as a mediator to recruit the polycomb group proteins to participate in the gene silencing process [20].

In silico prediction (MatInspector v2.2 program [21], JASPAR [22], and TFSEARCH [23]) suggested that there were in total six YY1 binding sites (CCAT) within the human WNT1 promoter (Figure 2A). Four of them resided within the region between -1503 to -1112 nt upstream of ATG site. Among these, the “CCAT” located between -1290 and -1112 nt (-1265/-1262) was conserved in both mouse and human WNT1 gene promoters (Figure 2B).

Next, the potential ability of gold-2a to modulate the binding of Suz12 and YY1 to WNT1 promoter was examined. Four sets of primers covering different regions of the 1.5kb fragment were designed and used for ChIP-PCR experiments (Figure 3A and Supplementary Table S2). Gold-2a significantly elevated the amount of these two transcriptional regulators bound to the WNT1 promoter (by approximately 18 and 30 folds, for Suz12 and YY1, respectively), mainly at the region covered by primer 3 (Figure 3B). The promoter associations of the three class I HDACs were also evaluated. Gold-2a treatment decreased the amounts of HDAC3 at all four tested regions of the WNT1 pro-

Figure 2. In silico analysis of YY1 binding motifs of the WNT1 promoter. A, A schematic illustration of the locations of potential YY1 binding sites within the 1.5 kb upstream of the WNT1 promoter and the promoter reporters. B, Homology comparison of human and murine WNT1 promoters.
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The highest inhibition was detected by ChIP-PCR using primer 3 (-1356 to -1113 nt).

The protein-protein interaction between YY1 and Suz12 was evaluated by co-immunoprecipitation in cells treated with or without the drug compound. Gold-2a significantly increased the amount of Suz12 bound to YY1. By contrast, a significant reduction of HDAC3 in the immunocomplex was observed in cells treated with gold-2a (Figure 3C), whereas the interactions of HDAC1 and HDAC8 with YY1 were not significantly affected.

Taken in conjunction, these findings suggested that gold-2a promoted the binding of a transcription repressor complex containing YY1 and Suz12 to a DNA element located within the region of -1356 to -1113 of the WNT1 promoter.

YY1 acted as a negative regulator of WNT1 expression in MDA-MB-231 cells

To confirm the role of YY1 in regulating WNT1 gene expression, a mammalian expression vector (pcDNA-YY1) encoding a NH2-terminal Flag-tagged YY1 was constructed. In addition, a specific siRNA was designed for downregulation of YY1 expression. Compared to thestarved MDA-MB-231 cells, serum treatment had no significant effect on the mRNA levels of YY1, but elevated those of WNT1 by approximately 13 folds (Figure 4A). Overexpression of YY1 by transient transfection of pcDNA-YY1 vector almost abolished the serum-stimulated WNT1 expression, at both gene and protein levels, whereas knocking down of YY1 (by approximately 70%) led to a 30 to 40 folds increase of WNT1 mRNA and protein expression levels (Figure 4B). To locate the exact region of WNT1 promoter regulated by YY1, MDA-MB-231 cells were transfected with either pcDNA-YY1 vector or YY1 siRNA, together with different pGL3-WNT1 reporters. Except for those driven by pGL3-WNT1(-1112 to -1), overexpression of YY1 significantly inhibited the other three WNT1 promoter fragments-mediated reporter activities (Figure 4C). Knocking down of YY1 elevated the reporter activities of both pGL3-WNT1(-1290 to -1) and pGL3-WNT1(-1415 to -1). Moreover, the association
of Suz12 with WNT1 promoter appeared to be regulated by YY1. ChIP-PCR analysis revealed that the most significant changes were observed at -1356 to -1113 nt of the WNT1 promoter (covered by primer 3), which contained only one YY1 binding motif (-1265/-1262). The amount of Suz12 bound to this region was significantly increased (over four fold) in cells overexpressing YY1 and reduced (by approximately 70%) in those transfected with YY1 siRNA (Figure 4D). In summary, these data indicated that YY1 was able to recruit the polycomb group protein Suz12 to a specific region of WNT1 promoter, resulting in transcriptional repression.

Serum-induced nucleocytoplasmic shuttling of YY1 was blocked by gold-2a treatment

It has been reported previously that YY1 shuttles between cytosol and the nucleus [24]. Here, in MDA-MB-231 cells, at as early as two hours after FBS-stimulated cell cycle release, YY1 was exported from the nucleus into the cytosol (Figure 5A). At 12 hours, when cells almost completed G2/M phase and prior to the start of another cycle, YY1 was shuttled back into the nuclei (Figure 5B). An oscillation of WNT1 gene and protein expression was observed to synchronize the translocation of YY1 between nucleus and cytosol (Figure 5C). HDAC3 was also actively shuttling between nucleus and cytosol during cell cycle progression, but in a manner opposite to that of YY1 (Figure 5A). Gold-2a blocked YY1 shuttling to the cytosol and promoted its nuclear accumulation (Figure 5A), which was accompanied by an arrested cell cycle progression at G1/S phase (Figure 5B). Compared to the vehicle control group, the average numbers of cells in G2/M phase were reduced by approximately two to six folds after 12

Figure 4. YY1 represses WNT1 promoter activity in MDA-MB-231 cells. Transient transfection was performed for up- or down-regulation of YY1 expression. Twenty four hours after transfection, the mRNA (A) and protein (B) levels of YY1 and WNT1 were quantified by QPCR and Western blotting, respectively. The promoter activity was evaluated as described in Methods by co-transfection with the four different WNT1 promoter reporters (C). The association of Suz12 with WNT1 promoter was evaluated by quantitative ChiP-PCR and the results expressed as fold changes against the pcDNA group of the same primer set (D). *, P < 0.05 versus pcDNA group; #, P < 0.05 versus scramble RNA group (n=5).
Gold-2a and YY1 elicited similar anti-proliferative effects by promoting cell cycle arrest at G1/S phase

To extend the understanding of the role of YY1 on cell cycle progression, MDA-MB-231 cells with over- or reduced expression of YY1 were subjected to flow cytometry analysis (Figure 6). Upregulation of YY1 resulted in an increased number of cells in the G1/S phase, whereas downregulation of this protein elevated the mitotic cell populations in the G2/M phase and promoted cell cycle progression towards the post-G2/M phase [i.e. cells with a chromosome number of more than 4N]. Morphologically, a large portion of cells transfected with YY1 siRNA exhibited aneuploidy, as indicated by the presence of multiple nuclei. By contrast, cells overexpressing YY1 were enlarged with mononuclear (Figure 7A). Gold-2a elicited similar effects as YY1 in arresting the cell cycle at the G1/S phase (Figure 6). Cells treated with the drug showed a single enlarged nucleus and a spreading cytoplasm with YY1 mainly localized within the nucleus (Figure 7A). Cell proliferation analysis revealed that while both overexpression and downregulation of YY1 decreased the number of cells, their effects on DNA synthesis were opposite (Figure 7B). In general, knocking down of YY1 in MDA-MB-231 cells promoted DNA and protein synthesis. By contrast, gold-2a and YY1 upregulation reduced the total amount of DNA

Figure 5. Gold-2a treatment arrests cell cycle progression at G1/S phase and abolishes nucleocytoplasmic shuttling of YY1 and HDAC3. MDA-MB-231 cells were serum starved for 24 hours prior to serum (10% FBS) stimulation in the presence or absence of gold-2a. At different time points, cells were harvested for nuclear and cytosol fractionation and Western blotting (A), cell cycle analysis (B) and QPCR analysis of WNT1 gene expressions (C). Note that the cell cycle-dependent oscillation of WNT1 mRNA expression was abolished by gold-2a. The results were calculated as fold changes over the values at time zero.

hours of drug treatment. The oscillation of HDAC3 between cytosol and nucleus was also abolished in cells treated with gold-2a. In contrast to YY1, the nuclear HDAC3 contents were decreased, whereas the cytosol HDAC3 levels were elevated by gold-2a. Moreover, WNT1 expression, at both the mRNA and protein levels, could no longer be stimulated by serum and did not exhibit cell cycle-dependent oscillations (Figure 5, A and B). These results suggested that gold-2a elicited its anti-proliferative actions in part by blocking YY1 transportation from the nucleus to the cytoplasm, thus enhancing its nuclear accumulation, which in turn resulted in a constant inhibition of WNT1 gene expression and cell cycle progression.
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per cell. The suppressive effects of gold-2a on DNA synthesis and cell proliferation were more prominent than those of YY1. These results demonstrated that YY1 might play a dual role in both DNA synthesis and cytokinesis. Gold-2a exerted the cytotoxic activity at least in part by enhancing the action of YY1, which in turn blocked DNA synthesis and prevented subsequent mitosis.

Discussion

WNT signaling is essential for the normal development of multi-cellular organisms and perturbations in the canonical Wnt/β-catenin pathway play an important role in the genesis of various cancers, including breast, colon, liver, and lung tumors [25]. Since the discovery of INT1/Wnt1 in 1982 [26], limited information is available regarding the transcriptional regulation of human WNT1 gene expressions. Most studies have focused on murine Wnt1 gene expression [18, 27-35]. In undifferentiated mouse embryonic PC19 cells, Wnt1 expression can be triggered by retinoic acid [36]. A 128 bp (-370 to -347) of the 5′ upstream region of Wnt1 promoter is responsible for this retinoic acid-mediated transcription [34]. Paired box-3, a transcriptional factor that is essential for normal development of the somatic mesoderm, has been identified to interact with the -330 to -326 binding site and induce transcriptional activation of Wnt1 [29]. Several repressors of Wnt1 expression have been described [18, 30, 31]. Sine oculis-related homeobox-3 homolog (Six3) suppresses Wnt1 expression in mice embryos by binding to an unknown sequence at the 3′ end of its coding region as well as to the elements located within the 5′ promoter region (-1546 to -1518; and -1294 to -1266) [31]. Wnt1 is also a target gene for the polycomb group-2 complex (PRC2), composed of histone methyltransferase Enhancer of Zeste protein-2 (Ezh2), Extra Sex Combs protein (Eed) and Suppressor of Zeste-12 (Suz12). In F9 mouse embryonic teratocarcinoma cells, both Ezh2 and Suz12 bind to a region within the 1.5 kb upstream of the transcription starting site of the Wnt1 promoter to inactivate gene transcription [18]. An association of Suz12 within the -1000 to -2000 upstream region of WNT1 promoter has been demonstrated in SW480 human colon cancer cell, MCF-7 human mammary carcinoma cells, and Ntera2 human embryonic carcinoma cells [18, 19].

The present study demonstrates that overexpression of YY1 decreases, whereas knocking down of YY1 elevates WNT1 gene expression. YY1 is able to recruit a repressor complex containing Suz12 to the WNT1 promoter and suppress its gene expression. At the cellular level, as in previous findings [37], a dual role of YY1 in regulating cell cycle progression and cytokinesis has been observed. Downregulation of YY1 results in cytokinetic failure and genomic instability.
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YY1 plays a fundamental role in various biological processes [including embryogenesis, differentiation, development and tumorigenesis] by interacting with several other factors to initiate, activate or repress transcription [43, 44]. The majority of the clinical data show that YY1 is overexpressed in tumor tissues and may affect tumor behavior [45]. In human breast tumors, YY1 positively correlates with the expression of both ERBB2/HER2 and estrogen receptors [46, 47]. However, the prognostic value of these associations is not conclusive. Reduced YY1 expression may contribute to the invasive phenotype of breast cancer cells due to impaired epigenetic silencing [48]. Whether or not an actual association exists between YY1 and WNT1 expression in human breast tumors is unknown. Several lines of evidence support the role of YY1 in the occurrence of chemoresistance. Thus, YY1 inhibition sensitizes lymphoma B-NHL cells to Fas-induced apoptosis [49]. In prostate carcinoma PC-3 cells, downregulation of YY1 enhances TRAIL-mediated apoptosis [50]. In ovarian cancer patients, YY1 function is positively correlated with survival of patients treated with paclitaxel. Moreover, increased sensitivity to taxanes is found in NCI60 cancer cell lines with a high YY1 expression [51]. The effects of YY1 in modulating chemosensitivity of breast cancer cells have not been reported.

The gold (III) porphyrin complex, gold-2a, is a newly discovered cytotoxic drug compound showing potent anti-tumor activity against breast cancer [12]. It acts as a HDACi to modulate the gene expression in the canonical Wnt signaling pathway. The present study demonstrates that gold-2a inhibits WNT1 promoter activity at least in part by promoting the binding of the YY1 repressor complex to a specific region containing a conserved YY1 motif (“CCAT” located at -1265/-1262). Apparently, the regulatory elements responsible for serum-mediated activation of WNT1 gene expression are also
The authors declare no conflict of interest.

Acknowledgement

This work was supported by the grants from Seed Funding for Basic Research of the HKU (Y. Wang), Hong Kong Research Grant Council grants HKU 777908M (Y. Wang), and the Area of Excellent Scheme (AoE/P-10-01) established under University Grants Committee, HKSAR (C.-M. Che).

The authors declare no conflict of interest.

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References


In summary, the results of the present study suggest that YY1 is a transcriptional repressor and mediates the inhibitory effects of gold-2a on WNT1 gene expression. Gold-2a exerts its anti-proliferative and cell cycle arresting effects at least in part by blocking the intracellular translocation of YY1. Considering the potential role of YY1 in tumor cell resistance to chemotherapeutics, the present findings shed new lights on the potential development of gold-2a as an anti-cancer compound for clinical use.

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## Supporting Information

**Supplementary Table S1.** Primers used for ChIP-PCR.

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<th>Gene</th>
<th>Promoter region</th>
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| WNT1 (NC_000012.11) | -1567 → -1045 | (F): 5’-TGT GGT GGG AAC TAG AGC TT-3’  
(R): 5’-TGC GGA TGT CCA CTG TAT GT-3’ |
|      | -1418 → -1267  | (F): 5’-AGT GGA CAT CCG CAC CAT-3’  
(R): 5’- TGT CAC ACT GTG GTA TGT GTC AA-3’ |
|      | -1356 → -1163  | (F): 5’-AGG CTG GGT TCA CCT CAA TA-3’  
(R): 5’-CTG GAC TGT GTG TGG AGT GG-3’ |
|      | -839 → -627    | (F):5’-AGC AAA CTG CCT GTT GCT TT-3’  
(R): 5’-GAG TGT CGG AAG GAA AGC TG-3’ |
**Supplementary Table S2.** Sequences of primers used for constructing the WNT1 promoter reporters and the YY1 expression vector

<table>
<thead>
<tr>
<th>Vectors</th>
<th>Cloning primers</th>
</tr>
</thead>
<tbody>
<tr>
<td>pGL3-WNT1</td>
<td>(F): 5'-CTG CCT CGA GCA CAT GGA GGC ACA AGT TTC -3'</td>
</tr>
<tr>
<td>(-1503 to -1)</td>
<td>(R): 5'- CTG CAA GCT TGG CCT GCC TGG CTT TGC C-3’</td>
</tr>
<tr>
<td>pGL3-WNT1</td>
<td>(F): 5'-CTG CCT CGA GGA CAT CCG CAC CAT TTC CCA T -3'</td>
</tr>
<tr>
<td>(-1415 to -1)</td>
<td>(R): 5'- CTG CAA GCT TGG CCT GCC TGG CTT TGC C-3’</td>
</tr>
<tr>
<td>pGL3-WNT1</td>
<td>(F): 5'-CTG CCT CGA GCA CAT ACC ACA GTG TGA CAC GCC -3’</td>
</tr>
<tr>
<td>(-1290 to -1)</td>
<td>(R): 5'- CTG CAA GCT TGG CCT GCC TGG CTT TGC C-3’</td>
</tr>
<tr>
<td>pGL3-WNT1</td>
<td>(F): 5'-CTG CCT CGA GCC TCC TTC TCC TGA CAC TGC CC -3’</td>
</tr>
<tr>
<td>(-1112 to -1)</td>
<td>(R): 5'- CTG CAA GCT TGG CCT GCC TGG CTT TGC C-3’</td>
</tr>
<tr>
<td>pcDNA-YY1</td>
<td>(F): 5-CTG CGG ATC CAT GGA CTA CAA GGA TGA CTA CAA GAG CCA TGG CCT CGG GCG A-3’</td>
</tr>
<tr>
<td></td>
<td>(R): 5-CTG CCT CGA GCT ACT GGT TGT TTT TGG CCT TAG CAT GTG-3’</td>
</tr>
</tbody>
</table>
**Supplementary Table S3.** Sequences of RNA interference oligos

<table>
<thead>
<tr>
<th>Gene</th>
<th>Sequences</th>
</tr>
</thead>
<tbody>
<tr>
<td>YY1 (NM_003403)</td>
<td>(F): 5' CGACGACUACAUUGAACA dTdT 3'</td>
</tr>
<tr>
<td></td>
<td>(R): 3' dTdT GCUGCUGAUGUAACUGUU 5'</td>
</tr>
<tr>
<td></td>
<td>(F): 5' CAAAGAUGUUCAGGGAUAA dTdT 3'</td>
</tr>
<tr>
<td></td>
<td>(R): 3' dTdT GUUUCUACAAGUCCUAUU 5'</td>
</tr>
<tr>
<td></td>
<td>(F): 5' CCUGAAAUCUCACAUUU dTdT 3'</td>
</tr>
<tr>
<td></td>
<td>(R): 3' dTdT GGACUUUAGAGUGUAGAAU 5'</td>
</tr>
<tr>
<td>Scramble RNA control</td>
<td>(F): 5' GAUACACGAAGGAAUUCACUUCAA 3'</td>
</tr>
<tr>
<td></td>
<td>(R): 5' UUAGAAGUGAAUCCUCGUGUAUC 3'</td>
</tr>
</tbody>
</table>