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Synergistic Effect of *Curcuma longa* Extract in Combination with *Phyllanthus niruri* Extract in Regulating Annexin A2, Epidermal Growth Factor Receptor, Matrix Metalloproteinases, and Pyruvate Kinase M1/2 Signaling Pathway on Breast Cancer Stem Cell

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Abstract

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AIM: This study aimed to investigate the synergistic effects of the combination between *Curcuma longa* extract (CL) and *Phyllanthus niruri* extract (PN) in inhibiting optimally the MDA-MB-231 breast cancer stem cells (BCSCs) growth and metastatic by exploring the target and molecular mechanism using integrative bioinformatics approaches and *in vitro*.

METHODS: CL and PN extracts were prepared by maceration method using ethanol 70%. The antiproliferative effect of CL and PN single and combination treatment was examined by 3-[4,5-dimethyl-2-thiazolyl]-2,5-diphenyl-2H-tetrazolium bromide assay. The bioinformatic approach was performed to identify molecular targets, key proteins, and molecular mechanism of curcumin and phyllanthin as CL and PN secondary metabolite, respectively, targeted at stemness and migration pathway of BCSCs.

RESULTS: The *in vitro* study showed that CL and PN possess cytotoxic activity in time- and dose-dependent manner. The combination of CL and PN has a synergistic effect by modulating the sensitivity of cells. Using a bioinformatics approach, the annexin A2 (ANXA2), epidermal growth factor receptor (EGFR), matrix metalloproteinases (MMPs), and pyruvate kinase M1/2 (PKM) as potential targets of curcumin and phyllanthin correlated with metastatic inhibition of BC. In addition, molecular docking showed that curcumin and phyllanthin performed similar or better interaction to stemness differentiation regulator pathway particularly histone deacetylase 1, EGFR, Heat Shock Protein 90 Alpha Family Class B Member 1, Hypoxia Inducible Factor 1 Subunit Alpha, and MMP9.

CONCLUSION: Combination of CL and PN has potential for the treatment of metastatic BCSCs by targeting ANXA2, EGFR, MMPs, and PKM to resolve stemness and inhibit of BCSCs.

Background

Breast cancer (BC) is the most common cancer among women, presenting a major public issue around the world [1]. BC stem cells (BCSCs), a subpopulation of cancer cells that have tumor-initiating properties play a critical role in cancer recurrence, stemness, and metastasis [2], [3]. The highest mortality rate of BC is caused by a cancer recurrence and metastatic complication [4]. The previous study reported that the activation of the epidermal growth factor receptor (EGFR) signaling induces epithelial-mesenchymal transition (EMT) correlated with aggressive metastatic features [5]. Recent studies provided evidences that annexin A2 (ANXA2) is involved in EGFR signaling.

The ANXA2 expression also may promotes the TGF-β upregulation leading to activation of matrix metalloproteinases (MMPs). This phenomenon correlated to metastatic enhancement and stemness phenotype of BCSCs [6]. Therefore, blocking ANXA2 function lead to the inhibition of the EGFR and TGF-β downstream pathway associated with the reduce of BCSCs stemness ability in cell progression, migration, and metastatic reduction [7]. On the other hand, the pyruvate kinase M1/2 (PKM2) overexpression, promotes metastasis of cancer cells that correlated with ANXA2 expression in vivo [8]. In recent years, increased attention has focused on ANXA2 and its role in regulating BC development [9], [10].

In well-established medical treatment, the use of chemotherapy to control metastatic BC

has been developed as a therapeutic protocol of cancer, irrespective of surgical treatments [11], [12]. Unfortunately, the chemotherapy effectiveness is limited by acquired chemoresistance. The previous study reported that overexpression of ANXA2 associated with chemoresistance evidence [13]. Therefore, developing natural chemotherapeutic agents to eliminate cancer cells without emerging drug resistances remain still a challenging project. The benefit used of plant extracts with natural multi-targeting capability in killing cancer cells and relatively safer to normal tissues is the one predominance reason to utilize the medical plant extracts including *Curcuma longa* (CL) and *Phyllanthus niruri* (PN) [14], [15], [16].

CL and PN are the common medicinal plants used in Indonesia with many biological effects including anticancer activity on various cancer cells [17], [18], [19], [20], [21]. Recent studies have shown that CL extracts might suppress cancer cell proliferation by inducing the G0/G1 cell cycle arrest and trigger cell apoptosis [22], [23], [24]. Furthermore, curcumin as one of the secondary metabolite compound of CL extracts has specific-binding with ANXA2 proteins to reduce the growth and size of tumor mass [18], [25], [26]. On the other hand, several studies reported that PN extracts also possess cytotoxic effects on various cancer cells such as promyelocytic leukemia HL-60 cell lines, human oral cancer HSC and BC [20], [27]. The phytochemical studies of the PN have shown that those extracts contain a variety of components, particularly phyllanthin inhibited metastatic of lung cancer through decrease MMP9 expression [28].

Recently, the combination of two or more natural chemotherapeutic agent might achieve efficacy with lower doses and in the absence of toxicity. Therefore, using the combination CL and PN was supposed to have synergistic effects in optimally inhibiting the cancer cells growth and possibly fewer side effects. In this study, we use MDA-MB-231 cells, a highly metastatic BC cell line with a high population of BCSCs. This study aimed to investigate the synergistic effects of the combination between CL and PN in inhibiting optimally the MDA-MB-231 BC cells growth and metastatic by exploring the target and molecular mechanism using integrative bioinformatics approaches.

Materials and Methods

Plant material

CL and PN were collected in November 2019 and February 2020, respectively, in Tawangmangu, Karanganyar Central Java, Indonesia (Latitude 7°40'39.3"S; Longitude 111°08'09.4"E). The plant identification was verified by the biologist from the

center for research and development of medicinal plants and traditional medicine (B2P2TOOT), Indonesia. For biological determination, the herbs of PN and rhizome of CL were dried with circulated at 40°C and renewal of air oven until completely dehydrated.

Extraction procedure

CL and PN were cleaned and air-dried to constant weight at room temperature for 3 days before being ground powder in a blender. The powder of PN (500 g) and CL (500 g) was extracted individually by maceration method using ethanol for 72 h (three cycles) based on Tanvir et al. [29] with slight modification. Then, the solutions were filtered through Whatman no.1 filter paper and the solvent was evaporated under reduced pressure (100 psi) in a rotary vacuum evaporator (IKA HB 10 basic) at 400C to result in the crude extracts. The extracts were collected and preserved at 40C for subsequent analysis.

Cell culture

MDA-MB-231 (ECACC #92020424) was maintained in Dulbecco's Modified Eagle's Mediumhigh glucose (Gibco, USA) supplemented with 10% fetal bovine serum (Gibco, USA), 12.5 μ g/ml Amphotericin B (Gibco, USA), 150 μ g/ml Streptomycin, and 150 IU/ml Penicillin (Gibco, USA). Cells were cultivated at 37°C under 5% CO₂. Culture media were renewed every 2 to 3 days, and cells were subculture when confluent of 80–90%. For assays, only cells with >90% viability, passage number <10, and in the log growth phase were used according to Amalina *et al.* [30].

Cytotoxic assay

The cytotoxic assay was based on a 3-[4,5-dimethyl-2-thiazolyl]-2,5-diphenyl-2Htetrazolium bromide (MTT) assay according to Mosmann [31] with slight modification. Briefly, the density of 5 × 10³ cells/well was seeded into 96 wellplate and incubated at 37°C under 5% CO₂ for 24 h. Subsequently, cells were treated in a triple with CL rhizome (5-200 µg/ml) and PN herbs (5-200 μg/ml) and exposed for 24 h. Untreated cells were regarded as negative controls. After treatment, cells were treated with 0.5 mg/mL of MTT (Biovision) and incubated further for 4 h. MTT formazan was soluble using 100 μ l DMSO and incubate for 15 min. After incubation, the absorbance was measured by ELISA reader (BioRad iMark $^{\text{TM}}$ Microplate Reader) at λ 595 nm. The absorbance was transformed into a percentage of cell viability by comparing the treated group with the untreated group at a particular time course. To calculated IC_{50} value, linear regression between concentration [x] and % cell viability [y], giving the equation y= Bx+A. Using the linear equation of this

graph for y=50 value x point becomes IC_{50} value, that is the concentration that prevents the cell proliferation of 50%. The data of this study were carried out with three replication experiments [32].

Combination activity

The first set of combination experiment, we evaluate the effectiveness of a particular concentration of CL rhizome, PN herbs, and its combination on MDA-MB-231 cells, was determined using MTT assay as described previously. MDA-MB-231 cells (5×10^3) were seeded in 96-well microplate and incubated at 37°C in 5% CO $_2$ for 24 h. The cells were treated with one-half IC $_{50}$, one-fourth IC $_{50}$, one-eighth IC $_{50}$, and one-sixteenth IC $_{50}$ of CL, PN, and its combination for 24 h. After 24 h of treatment, the percentage of viable cells was determined using the *in vitro* cytotoxicity assay method described above.

Analysis of combination activity

The combination of CL and PN was determined using isobologram analysis and represented with the combination index value. CI value <1 indicated the synergism effect and CI value >1 indicated antagonism. The combination index analysis was based on the principle of the median effect and calculated using the following formula. Combination index = $D_{1}/[Dx]_{1} + D_{2}/[Dx]_{2}$ [Dx], where D, and [Dx], are concentrations of CL Rhizome and PN herbs, respectively, which inhibit cell growth to 50% of control when used alone, and D, and [Dx], are concentrations of CL rhizome and PN herbs, respectively, which have the same effect when used in combination [33]. Combination index values based on the Chou-Talalay method, calculated using CompuSyn software, indicate the effects of drug combinations [34], [35].

Data collection and processing

Cytotoxicity and mRNA arrays data were collected from NCI 60 direct target proteins (DTP) website. The analysis of COMPARE from the NCI 60 cell line panel was employed using public library procedures to collect drugs compounds that have similarities with Curcumin and Phyllantin. The similarity of the pattern is expressed as a Pearson coefficient of correlation. The list of compounds and genes in this study was limited to the Pearson correlation <-0.5 and >0.5.

Analysis of functional and pathway enrichment

Analysis of Gene Ontology (GO) and Kyoto encyclopedia of Genes and Genomes (KEGG) pathway enrichment were performed by the Database

for Annotation Visualization and Integrated Discovery, the cutoff value was selected with p < 0.05. In addition, pathway enrichment was also performed using Overrepresentation Enrichment Analysis (ORA) from WEB-based GEne SeT Analysis Toolkit (WebGenestalt) with FDR <0.05 as the cutoff value.

Construction of protein-protein interaction (PPI) network

STRING-DB v11.0 was used to construct the PPI network. Confidence scores >0.4 were considered to be significant. Cytoscape software was used to visualize the PPI network. 10 Genes with the highest degree of the score were evaluated using Cytohubba and selected as hub genes.

Molecular docking

Simulation of docking was conducted to predict the binding interaction of curcumin and phyllanthin on histone deacetylase 1 (HDAC1), EGFR, Heat Shock Protein 90 Alpha Family Class B Member 1 (HSP90AB1), Hypoxia Inducible Factor 1 Subunit Alpha (HIF1A), and MMP9. The protein structure was obtained from the protein data bank (PDB). Chemical structure of CL and PN was preparation using ChemDraw. The energy-minimized structure of ligand and protein interaction was simulated using AutoDock Vina 1.1.2. The interaction energy between the ligand and the receptor was calculated for the entire binding site and expressed as affinity (kcal/mol). The Pymol program self-generated schematic 2D representations of the interfaces of protein-ligand complexes from standard pdb file input.

Data analysis

Molecular docking results were validated by determining the RMSD value of conformation bearing the lowest docking score. The validity of the molecular docking method was represented as RMSD value <2. Cytotoxic potencies against several cell lines were statistically analyzed basing from the IC $_{50}$ values through linear regression with p > 0.05. Values were presented as the mean \pm SD.

Results

Cytotoxic effect of single doses of CL and PN in inhibiting MDA-MB-231 cells proliferation

The cytotoxic activities of CL and PN individually and in combination against MDA-MB-231 BC cells were determine used MTT assay in various concentration.

MDA-MB-231 incubates in the presence of 10-200 µg/ ml CL and PN individually for 24 h. In this study, we found that CL and PN in single treatment significantly decreased the cell viability with degree depletion in a dose-dependent manner. A single treatment of CL showed the cytotoxic effect on MDA-MB-231 with IC₅₀ value of 126 μg/ml for 24 h (Figure 1a). In addition, the CL also caused morphological changes under inverted microscope observation (Figure 1b). Low concentration of CL has not shown significant morphological changes, but there is clearly a reduction in cell density compared to untreated. Interestingly, in the middle and high concentration of CL induced cell shrinkage, pyknosis, and fragmentation. Cell shrinkage and pyknosis are visible through inverted microscopy during the early process of apoptosis [36]. With cell shrinkage, the size of the cells is smaller, the cytoplasm denser, and the organelles tighter. Pyknosis is the result of the condensation of chromatin and the most characteristic feature of apoptosis [37], [38]. These findings clearly indicated that CL has a potential to reduce cell viability against MDA-MB-231 BC cells may be through apoptosis induction.

The same phenomenon also occurs in the presence of PN. The IC $_{50}$ value of PN with respect to MDA-MB-231 was found to be 359 $\mu g/ml$ for 24 h (Figure 2a). Under the inverted microscope, only in a high concentration of PN shows that the morphology of detached round cells that floated medium with the bubbled membrane, wrinkled nucleolus, was obliviously observed in the MDA-MB-231 cells. Such morphological characteristics are a sign of cell death and have not been seen in the untreated cells (Figure 2b). In this regard, CL had a strong inhibitory effect more than PN. For further exploration we observed the effects of combination CL-PN on MDA-MB-231 cell growth to increase efficacy.

Synergistic effect of combination CL and PN to inhibit MDA-MB-231 cells proliferation

Cells were treated for 24 h with several concentrations of CL and PN for to investigated the combination effect of CL and PN on the viability of triple negative BC (TNBC) with high population of BCSCs MDA-MB-231 cells. In CL-PN combination, the IC $_{50}$ value obtained after single treatment of CL and PN was used to determine their concentration. The concentration used wa calculated as one-half (65 $\mu g/ml$; 180 $\mu g/ml$), one-fourths (32.5 $\mu g/ml$; 90 $\mu g/ml$), and one-eight (16.25 $\mu g/ml$; 45 $\mu g/ml$) or one-sixteenth (8.125 $\mu g/ml$; 22.5 $\mu g/ml$) of CL and PN, respectively. The results indicated that all concentration of either CL (Figure 1a) or PN (Figure 2a) in single treatment inhibited cell growth by <50%.

In contrast to the single treatment of CL and PN, their combination at the four concentrations above showed significantly reduced cell viability

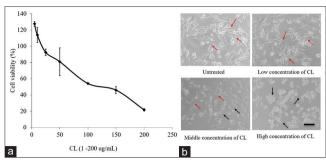


Figure 1: (a) Inhibitory effect of Curcuma longa (CL) on MDAMB-231 cells proliferation. MDAMB-231 cells viability was measured after 24 h of CL. Cell viability profile expressed mean \pm SD of three experiments. IC $_{50}$ obtained from a linear regression calculation of log concentration versus cell viability with p < 0.05. (b) The effect of CL on cell morphology. Visible morphological changes and population of cells in treatment of untreated, low concentration of CL (5 μ g/ml), middle concentration of CL (100 μ g/ml), and high concentration of CL (200 μ g/ml). Red arrows indicated normal living cells, while black arrow indicate the morphological changes of cells. Observations of cell morphology performed using an inverted microscope with a magnification of ×100. Scale bar: 100 μ m

(Figure 3a). At all concentrations the percentage of viable cells between 50.71% and 5.93%. The smallest number of viable cells was observed with maximum combination concentration of CL and PN (65 μg/ml and 180 μg/ml), respectively. In addition, combination suppressed doses-dependent manner of MDA-MB-231 cells proliferation. The combination index value of CL-PN was calculated using CompuSyn, these data showed synergistic to very strong synergistic effect with CI value between 0.09 and 0.36 (Table 1). Curve of concentrationeffect of CL, PN, and its combination (Figure 4a). The combination index plot showed that all of combination of treatment exhibited a synergism effect, caused the isoboles of combination CL-PN were located to the below of the curve, which indicated that CL-PN

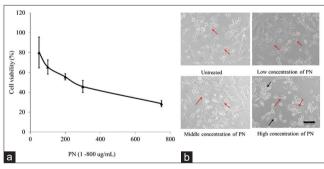


Figure 2: (a) Inhibitory effect of PN on MDAMB-231 cells proliferation. MDAMB-231 cells viability was measured after 24 h of PN. Cell viability profile expressed mean \pm SD of three experiments. IC_{50} obtained from a linear regression calculation of log concentration versus cell viability with p < 0.05. (b) The effect of PN on cell morphology. Visible morphological changes and population of cells in treatment of untreated, low concentration of Phyllanthus niruri (PN) (5 $\mu g/ml)$, middle concentration of PN (100 $\mu g/ml)$, and high concentration of PN (200 $\mu g/ml)$). Red arrows indicated normal living cells, while black arrow indicate the morphological changes of cells. Observations of Cell morphology performed using an inverted microscope with a magnification of ×100. Scale bar: 100 μm

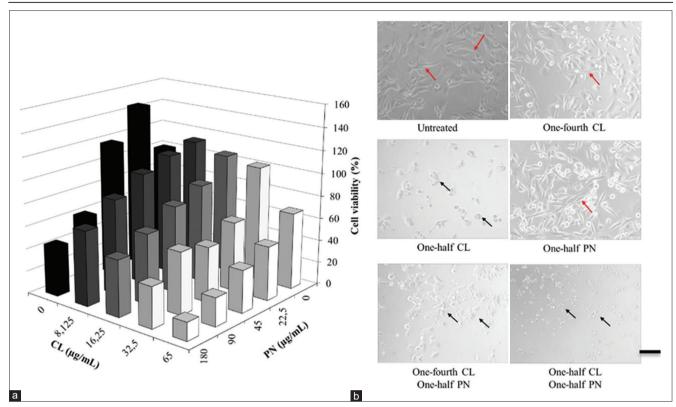


Figure 3: Combination effect of Curcuma longa-Phyllanthus niruri (CL-PN) on MDA-MB-231 cells. (a) Cells 5×10³ were seeded for 24 h in 96-well plate, then treated with CL, PN in single treatment and its combination for 24 h. Cell viability profile expressed mean ± SD of three experiments. (b) The effect of combination CL-PN on cell morphology. Red arrows indicated normal living cells, while black arrow indicate the morphological changes of cells. Observations of Cell morphology performed using an inverted microscope with a magnification of ×100. Scale bar: 100 μm

has synergism effect (Figure 4b). The viability cells decreased dramatically in the two observed concentration combination (one-half PN-one-fourth CL and one-half PN-one-half CL), marked by unique morphological changes including improvement in the integrity of the membrane, formation of apoptotic bodies, cytoplasmic condensation, and fragmentation of DNA (Figure 3b). It was supported by previous study reported that curcumin a major compound from CL decreased the IC₅₀ of MDA-MB-231 alone and in combination with paclitaxel, cisplatin, or doxorubicin. In addition, curcumin could increase by 15- and 5-fold drug sensitivity of MDA-MB-231 and MCF-7, respectively. BCSCs of MDA-MB-231 proliferate only to the fourth generation under combined treatment of Mitomycin C and curcumin [39]. This is an interesting phenomenon that should be explored further especially a molecular mechanism that involved in this activity, so we carried out the

Table 1: Combination index value of CL-PN calculated using CompuSyn

Concentration	CL (µg/ml)						
	8.125	16.25	32.5	65			
PN (μg/ml)							
22.5	0.29**	0.21**	0.09*	0.09*			
45	0.11**	0.13**	0.10**	0.13**			
90	0.29**	0.35#	0.18**	0.24**			
180	0.22**	0.27**	0.36#	0.18**			

^{*}Combination index value <0.1 indicate very strong synergism, **Combination index value 0.1–0.3 indicate strong synergism, #Combination index value 0.3–0.7 indicated synergism. CL-PN: Curcuma longa-Phyllanthus niruri.

molecular mechanism exploration using integrative bioinformatics approaches.

COMPARE analysis reveals the target list of mRNA and the standard agent

The molecular mechanism of CL and PN in BCSCs was explored using a bioinformatics approach. Curcumin and phyllanthin are the major compounds of CL and PN was used for subject analysis in this approach. The microarray level of mRNA expression analyzed by COMPARE revealed that 147 gene (93 gene with a positive Pearson correlation and 54 gene with a negative Pearson correlation) (Supplementary Table 1) and 200 gene (151 gene with a positive Pearson correlation and 49 gene with a negative Pearson correlation) (Supplementary Table 2) expression in the NCI-60 cell line panel that was affected by treatment with curcumin and phyllanthin, respectively. In addition, MANEAL, HNRNPR, and RPL11 the gene regulated by curcumin and TBL3, PAG1, and ADAM22, the gene regulated by phyllanthin showed the highest Pearson correlation coefficient. A positive correlation coefficient indicates a direct correlation and implies that a higher mRNA expression enhances stemness capability of BCSCs and vice versa. Furthermore, the PubMed search using the keyword "BCSCs" resulted in 1478 gene associated with BCSCs (Supplementary Table 3).

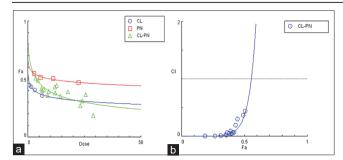


Figure 4: (a) Dose-effect curves of Curcuma longa, Phyllanthus niruri, and its combination. Dose-effect curves were generated from the CompuSyn calculation, and the value are the mean of three experiment. (b) Combination index plot among 16 combination, all off data point on the synergy side (CI <1)

Further, a Venny 2.1 diagram analysis (Figure 5a) of microarray data and PubMed gene list generated 1 gene that was regulated by curcumin, phyllanthin and related to BCSCs, 11 and 9 genes that were related to BCSCs and regulated by curcumin and phyllanthin individually, respectively (Supplementary Table 4). ANXA2 is a gene that was regulated by curcumin and phyllanthin. ANXA2 has the -0.52 Pearson correlation coefficient, it indicated the higher ANXA2 expression, the higher BCSCs formation. We also obtained 10 DTP of curcumin under chemical association network (STITCH) analysis, including CASP3, PTGS2, PPARG, HMOX1, AKT1, TP53, MMP9, STAT3, CCND1, and EGFR (Figure 5b). However, no one of DTP was affected by phyllanthin.

GO analysis and KEGG pathway enrichment of potential curcumin and phyllanthin target genes

GO analysis was categorized as cellular component, biological process, and molecular function. 22 gene regulated by curcumin, phyllanthin and related to BCSCs participated in the biological process of protein kinase activity, cadherin binding involved in cell-cell adhesion, cell-cell adherent junction, cell-cell adhesion, and positive regulation of protein phosphorylation. The 22 gene are located in the cell surface, membrane, plasma membrane, nucleus, and nucleoplasm. They also exert a molecular function in ATP binding, DNA binding, and transcriptional factor binding activity (Supplementary Table 4). KEGG pathway enrichment based on FDR of <0.05 demonstrated various pathways regulated by curcumin and phyllanthin such as cell-cell adhesion, stem cell differentiation, I-kappaB kinase/NF-kappaB signaling, metastatic, and response to oxidative stress. Pathway enrichment analyzed by WebGestalt showed stem cell differentiation regulated by curcumin and phyllanthin (Figure 6). The stem cell differentiation indicated that BCSCs loses of stemness properties and transforms into mature cells [40], [41], [42]. In addition, cell-cell adhesion significantly contributes to cancer metastatic and progression [43]. ANXA2

is involved in adhesion and also regulates the remodeling of ECM [44].

PPI analysis of gene regulated by curcumin, phyllanthin and related to BCSCs

The biological role of differential expression genes was examined using STRING data based. PPI networks were constructed of 22 genes consist of 22 nodes, 88 edges, eight average node degree, 0.0697 average local clustering coefficient, and <4.23 e-05 PPI enrichment p-value (Figure 7a). The top ten genes with the highest score have been identified as HDAC1, EGFR, HSP90AB1, HIF1A, MMP9, PKM, TBK1, TNFAIP3, CHD4, and TCF3 (Figure 7b and c). These proteins correlated with stem cell differentiation and cell proliferation [45], [46].

Molecular docking

Induction of stem cell differentiation can be used as a strategic method to overcome stemness of BC cells. And also, this method could better contribute to curing patients [47]. In this study, we conducted a molecular docking simulation to predict the potential inhibitory activity of curcumin and phyllanthin in metastatic and stem cells differentiation pathway. Protein-ligand binding was visualized using Pymol (Figure 8). The ANXA2, HDAC1, EGFR, HSP90AB1, HIF1A, and MMP9 as protein target were picked from the top ten genes with the highest degree score based on their drug target uniqueness. Curcumin showed no binding interaction with HDAC1, it indicated that HDAC1 does not bind nor reacts preferentially with curcumin. However, HDAC1 slightly bind to phyllanthin with docking score value -10.4140. The lowest docking score of curcumin and phyllanthin was found on HSP90AB1 and the highest docking score of curcumin and phyllanthin was found on MMP9 and HDAC1, respectively (Supplementary Table 5). The lower docking score suggested that highest potential of ligand binding affinity.

Discussion

BCSCs as play important role of cancer progression, cancer relapse, metastatic, and drug resistance due to of their ability to self-renew and differentiate into heterogeneous lineages of cancer cells [48]. Cancer relapse and metastatic appear to be the biggest problem for cancer patient management cause the chemotherapy only target the bulk of cancer and are unable to target BCSCs [49]. This is due to the high resistance of BCSCs, which contributes to metastasis and recurrence of cancer.

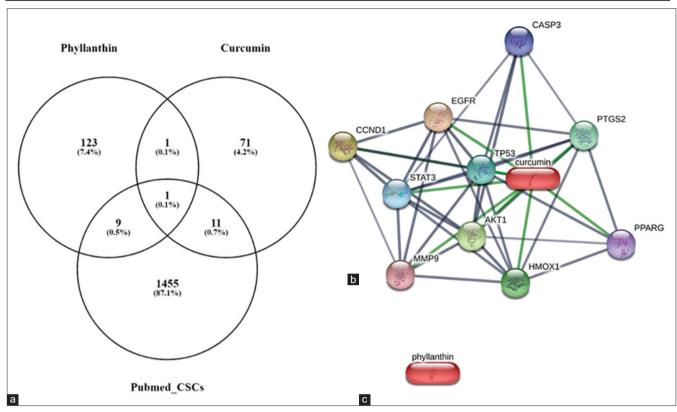


Figure 5: (a) a venn diagram of curcumin and phyllanthin potential targets against BBCSCs. (b) Curcumin interaction and is direct target proteins (DTP). (c) Phyllanthin interaction and its DTP

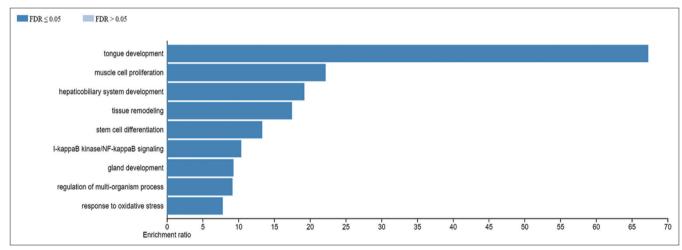


Figure 6: Kyoto encyclopedia of Genes and Genomes pathway enrichment analysis using the Overrepresentation Enrichment Analysis, WebGestalt

Until now chemotherapy remains one of the key therapeutic modalities. However, chemoresistance is limited in effectiveness. Thus, potential therapy to prevent resistance is needed such as using natural chemotherapy. The concepts of natural chemotherapy are intended to enhance efficacy and reduce the side effects of a chemical chemotherapeutic agent [50]. CL and PN are medicinal plants commonly used to treat cancer. CL possess cytotoxic effect on several cancer cells [19], [51], [52]. PN has also been reported to exert many biological effects such as anticancer on various cancer cells [20], [27]. CL and PN have been shown to affect many pathways and factors associated with

tumorigenesis and induced cancer cells death in large targets selectively [53]. However, in recent years the used of herbal medicine is limited as co-chemotherapy. The combination of two herbal medicines is still limited, even though natural compound that is abundant in nature is very potential to be developed further.

The present study resulted in an important finding relevant to the potential of combination natural chemotherapeutic agent, especially in triple negative BC cells (TNBC) with high population of BCSCs. The cytotoxic assay resulted in this study showed that CL and PN are a very strong cytotoxic agent against

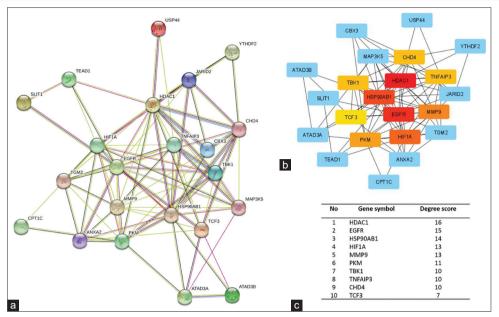


Figure 7: (a) Protein-protein interaction networks of 22 genes analyzed using STRING-DB, (b) Hub genes network analyzed using Cytohubba (red, orange and yellow box indicated the highest degree score of hub genes) and (c) Top ten hub genes based on degree score

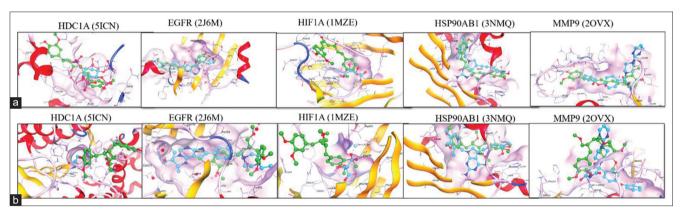


Figure 8: Molecular docking binding conformations (visualized by PyMol software) of top ten hub genes with (a) Curcumin and (b) Phyllanthin

MDA-MB-231 cells. CL and PN normally exhibited in vitro anticancer activities through a variety of mechanism in many cancer cells types, including cell cycle arrest and apoptosis induction [54]. CL also leads to an imbalance in the form of the Bcl/Bax associated apoptosis complex, which eventually causes BCSCs to lose their proliferation ability [55]. In addition, the apoptosis induction due to herbal administration through decreased expression of anti-apoptotic protein including surviving [56]. In comparison, PN was reported to be able to inhibited of MMP expression can affect the cell migration and metastasis process [57]. Based on the different mechanism of action of CL and PN, it can be predicted that these activities will be increased in combination therapy. In addition, combination therapies derived from herbal medicine significantly reduce the side effect of drug toxicity and drug resistance. Resistance condition after treatment with chemotherapy prompted the development of new compound called co-chemotherapy, which combined with chemotherapeutic agents. Co-chemotherapy usually consists of one natural compound and chemical

chemotherapy, but in this study, we will combine the two potential herbal compounds without chemotherapy to get a better effect and reduce side effect.

Furthermore, the study was continued to use the combination of CL-PN to investigated combination ability to increase cytotoxic effect. The effect of combination treatment with CL and PN on proliferation depends on their single concentration, suggesting a synergistic effect. Synergy is concluded when the use of drug combinations at different doses results in greater efficacy relative to the amount of the anticancer effects produced by using the individual drugs at the same dose. Combination index values calculated using CompuSyn support this finding, in which the combination index values represent a strong or very strong synergy (combination index 0.09–0.36). Interestingly, the combination of CL-PN showed decreased dramatically of cell viability up to 20.5%. These findings supported by the previous study that curcumin from CL in combination with Mitocymin C inhibits BCSCs proliferation [39]. Thus, combination of CL and PN could improve the therapeutic effect and

reduce side effect by sensitizing BC cells with high population of BCSCs and may provide a novel approach for cancer therapy. In this study, we also analysis using bioinformatics approaches to explored underlying target and molecular mechanism of the combination CL and PN in BCSCs.

In the bioinformatics study, we used curcumin and phyllanthin as a major compound of CL and PN, to predict tumor responsiveness to a natural product. COMPARE analysis identified 145 and 200 gene regulated by curcumin and phyllanthin, respectively. Curcumin regulated gene of RASAL2, CLIP4, and RFC3 and phyllanthin regulated gene FLJ41649, RND3, and SPATS2L with highest negative Pearson correlation coefficient. A PubMed gene data based found 1478 gene related with BCSCs. Further, a Venn diagram of COMPARE microarray data PubMed gene list produced 22 genes that were regulated by curcumin, phyllanthin and related to BCSCs. ANXA2 is only one gene that was regulated by curcumin and phyllanthin. ANXA2 involve in the cell proliferation, CSC formation and initiated EMT [58]. Indirect downregulated ANXA2 suppress protein levels of stemness-related transcription factors (Nanog, Oct4, and Sox2) through the inhibiting Akt pathway. ANXA2 also promoted the invasion and metastasis [58]. On the other hand, curcumin also exhibit a mechanism of action on several genes individually, MMP9 and EGFR are BCSCs-associated genes and can be directly affected by curcumin. The previous research reported that EGFR pathway play a critical role in regulating BCSCs [45]. Hence, curcumin and phyllanthin are multi-target and have a synergistic effect.

Analysis of KEGG pathway enrichment revealed that stem cell differentiation and NF-kß are regulated by curcumin and phyllanthin. The previous study demonstrated that induced of cancer stem cell differentiation could be better therapy that kills cancer cells. The control of the stem cell differentiation and proliferation signaling pathway play an essential role in killing cancer cells [47]. Moreover, the PPI network reported that 12 genes had a degree score more than 10. HDAC1, EGFR, HSP90AB1, HIF1A, and MMP9 are the five genes with highest degree scores. HIF1A is a master transcriptional regulator of hypoxia condition, which induces EMT and BCSCs niche formation and also chemo and radio resistance of BCSCs. Under hypoxia, HIF1A regulate resistance and metastatic potential to BCSCs. It indicates that HIF1A is critically for survival, self-renewal, and BCSCs growth [59]. Further, the interaction of curcumin and phyllanthin on HIF1A genes in BCSCs may present breakthrough therapy for induced BCSCs differentiation to mature cells. Thus, mature cancer cells could make them easy to kill. In the other hand, activation of EGFR a member of EGFR/ErbB tyrosine kinases family also could increase tumorsphere formation, a characteristic ability of BCSCs [45]. Interestingly, curcumin and phyllanthin

showed high binding affinity with EGFR based on molecular docking simulation. It indicated that the interaction between curcumin and phyllanthin to EGFR could inhibit EGFR activation pathway which impact on inhibited metastasis. The results support the previous findings that treatment with EGFR inhibitor, results in loss of tumorsphere-forming ability [60]. In addition, inhibiting EGFR components of signaling pathway resulting in the reduced survival and higher motility of BCSCs. Curcumin and phyllanthin also showed effect on direct interaction with MMP9. Previously has been reported that downregulation of MMP9 inhibited the cancer invasion. In addition, the previous study also confirms that curcumin induced downregulation of MMP9 through inhibition of $I\kappa B-\alpha$ degradation [61]. Hence, inhibition a cancer BCSCs one of marker stem cells differentiation can be used a strategic method to overcome the stemness. Another mechanism of CL-PN is influence on HSB90AB1 gene. The lowest docking score of curcumin and phyllanthin embedded into HSB90AB1 showed that CL-PN influence on cancer stem cells differentiation pathway and cell migration, invasion and metastasis. A recent study established a crucial role of HSP90AB1 in the stemness development in immunerefractory tumors: The NANOG-driven HSP90A/TCL1A/ Akt pathway is responsible for the emergence of CSClike tumor cells exhibiting an insusceptibility to immune attack, aggressiveness, and multi-modal resistance. Using selective inhibitors of HSP90AB1 such as curcumin and phyllanthin can be conductive EMT in carcinoma of different localization. Hence, inhibition of intracellular HSP90AB1 was reported to inhibit EMT via activation of HIF1A and NF-kß [62].

Conclusion

In this study, CL and PN suggested strong synergistic effect to inhibited BC cells proliferation. Moreover, CL and PN in combination showed that induced sensitivity on BC cell line with a high population of BCSCs. More important, using a bioinformatics approach curcumin and phyllanthin a major compound of CL and PN, respectively demonstrated that regulated on stem cell differentiation and metastatic pathway in overcoming stemness in BC. Molecular docking study showed the possible target of curcumin and phyllanthin against stem cell differentiation regulator pathway. Overall, combination of CL and PN has potential for the treatment of BCSCs and the finding of this study could be beneficial for research on accelerating and directing the screening of possible targets and identifying the molecular mechanism of curcumin and phyllanthin to resolve stemness of BCSCs.

Authors' Contributions

AG and DH contributed to the conception of the work. AG, DH, DM, AL, and NDA contributed to the acquisition of the work. DH and NDA contributed to the analysis and interpretation of data. AG and NDA contributed to drafting the work. AG, DNA, and DH contributed to revising the work critically. DM contributed to the revising of the manuscript. AG is responsible for giving the final approval of the manuscript.

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AQ1

Supplementary Tables

AQ2

suplementary Table 1 ???						suplementary Table I: (Continued)					
Rank	Correlation	Seed vector	Target Vector idebt	Target vector	Rank	Correlation	Seed vector	Target Vector idebt	Target vect		
7	0.50	description for	For display	Display for		0.5	description for	For display	Display for		
	0.52	CURCUMIN	GC382441	CHD4	55	-0.5	CURCUMIN	GC274893	CRIM1		
	0.52 0.52	CURCUMIN	GC382639	KHDRBS1	56 57	-0.5 -0.5	CURCUMIN	GC402719	AHNAK2		
		CURCUMIN	GC415957	U2AF1			CURCUMIN	GC384111	THBD		
	0.52	CURCUMIN	GC397232	SMARCC1	58	-0.5	CURCUMIN	GC269658	TMEM245		
	0.52 0.52	CURCUMIN CURCUMIN	GC16214 GC32693	CPT1C TAF12	59 60	-0.5 -0.5	CURCUMIN CURCUMIN	GC267119 GC101811	CLIP4		
	0.52	CURCUMIN	GC410576	RPF2	61	-0.5 -0.5	CURCUMIN	GC269693	null TMEM245		
	0.52	CURCUMIN	GC397403	HDAC1	62	-0.5	CURCUMIN	GC249354	TNFAIP2		
	0.52	CURCUMIN	GC257044	RBBP4	63	-0.5	CURCUMIN	GC177839	null		
	0.52	CURCUMIN	GC397651	KHDRBS1	64	-0.5	CURCUMIN	GC28815	TGM2		
	0.52	CURCUMIN	GC255719	TCF3	65	-0.5	CURCUMIN	GC392961	TMEM245		
)	0.52	CURCUMIN	GC16168	PPP1R8	66	-0.5	CURCUMIN	GC269694	TMEM245		
2	0.51	CURCUMIN	GC56403	CHEK2	67	-0.5	CURCUMIN	GC268109	ANKRD2		
3	0.51	CURCUMIN	GC184242	RABEPK	1	0.72	CURCUMIN	GC16324	MANEAL		
	0.51	CURCUMIN	GC382464	SRRM1	2	0.64	CURCUMIN	GC386657	HNRNPR		
i	0.51	CURCUMIN	GC282748	C22orf34	3	0.63	CURCUMIN	GC397562	RPL11		
	0.51	CURCUMIN	GC382380	TRA2B	5	0.62	CURCUMIN	GC386658	HNRNPR		
)	0.51	CURCUMIN	GC171597	HNRNPR	6	0.6	CURCUMIN	GC170494	ATAD3B		
)	0.51	CURCUMIN	GC187777	ATAD3A	7	0.6	CURCUMIN	GC397563	RPL11		
2	0.51	CURCUMIN	GC384395	CCNF	8	0.59	CURCUMIN	GC15534	PMPCB		
3	0.51	CURCUMIN	GC384141	ZBTB40	9	0.59	CURCUMIN	GC385739	PPP1R8		
	0.51	CURCUMIN	GC264147	RBBP4	10	0.59	CURCUMIN	GC391502	ATAD3A		
i	0.51	CURCUMIN	GC393435	S100PBP	11	0.59	CURCUMIN	GC393846	ATAD3A		
6	0.51	CURCUMIN	GC257220	ODF2	13	0.57	CURCUMIN	GC388725	SRSF10		
7	0.51	CURCUMIN	GC35203	NFATC2IP	14	0.57	CURCUMIN	GC33307	RBBP4		
3	0.51	CURCUMIN	GC37811	SLC25A36	16	0.57	CURCUMIN	GC390415	PNRC2		
)	0.51	CURCUMIN	GC85211	ATAD3B	17	0.57	CURCUMIN	GC392815	ATAD3B		
1	0.51	CURCUMIN	GC421500	C1orf174	18	0.57	CURCUMIN	GC11583	MMP9		
2	0.51	CURCUMIN	GC396851	SRSF4	19	0.56	CURCUMIN	GC30216	HNRNPR		
5	0.51	CURCUMIN	GC383951	PCNT	20	0.56	CURCUMIN	GC164030	ATAD3A		
3	0.51	CURCUMIN	GC384561	ZZEF1	22	0.55	CURCUMIN	GC265230	TMEM39B		
,	0.5	CURCUMIN	GC386207	SLC19A1	23	0.55	CURCUMIN	GC386665	TCP1		
9	0.5	CURCUMIN	GC270113	ZNRD1	24	0.55	CURCUMIN	GC385792	SRSF10		
00	0.5	CURCUMIN	GC31073	BTAF1	25	0.55	CURCUMIN	GC393018	YTHDF2		
)2	0.5	CURCUMIN	GC15330	PNRC2	26	0.55	CURCUMIN	GC396451	STAG1		
5	0.5	CURCUMIN	GC171761	ATAD3B	28	0.55	CURCUMIN	GC392055	COQ3		
06	0.5	CURCUMIN	GC257194	GRK4	29	0.55	CURCUMIN	GC382442	CHD4		
)7	0.5	CURCUMIN	GC102206	HNRNPA2B1	30	0.55	CURCUMIN	GC37945	DFFB		
80	0.5	CURCUMIN	GC391447	CCNL1	32	0.55	CURCUMIN	GC397652	KHDRBS1		
)9	0.5	CURCUMIN	GC98228	DCP1A	33	0.55	CURCUMIN	GC13127	HNRNPR		
10	0.5	CURCUMIN	GC397043	SDHB	34	0.54	CURCUMIN	GC383648	MDC1		
12	0.5	CURCUMIN	GC382062	DDX39B	35	0.54	CURCUMIN	GC14383	SPI1		
14	0.5	CURCUMIN	GC391207	PDSS1	37	0.54	CURCUMIN	GC27389	SRSF4		
15	0.5	CURCUMIN	GC408960	RCC2	38	0.54	CURCUMIN	GC247512	RPL11		
16	0.5	CURCUMIN	GC392212	MRTO4	39	0.54	CURCUMIN	GC396479	HSP90AB1		
17	0.5	CURCUMIN	GC96349	SLC19A1	40	0.54	CURCUMIN	GC413387	SNHG12		
	-0.63	CURCUMIN	GC265288	RASAL2	41	0.54	CURCUMIN	GC48107	DCP1A		
	-0.59	CURCUMIN	GC281649	RASAL2	42	0.54	CURCUMIN	GC382534	SMARCC1		
	-0.59	CURCUMIN	GC405831	CLIP4	43	0.54	CURCUMIN	GC384140	ZBTB40		
	-0.58	CURCUMIN	GC409778	CLIP4	45	0.53	CURCUMIN	GC30500	MTHFD2		
	-0.57	CURCUMIN	GC14289	RFC3	46	0.53	CURCUMIN	GC31808	SNRNP40		
	-0.57	CURCUMIN	GC9827	TMCO1	47	0.53	CURCUMIN	GC413381	SNHG12		
	-0.55	CURCUMIN	GC10417	GIGYF2	48	0.53	CURCUMIN	GC386272	SLC19A1		
)	-0.55	CURCUMIN	GC98923	RASAL2	49	0.53	CURCUMIN	GC421454	YARS		
	-0.55	CURCUMIN	GC392962	TMEM245	50	0.53	CURCUMIN	GC265256	DAZAP1		
2	-0.54	CURCUMIN	GC92198	RASAL2	51	0.53	CURCUMIN	GC31222	AK2		
3	-0.54	CURCUMIN	GC175647	RASAL2	52	0.53	CURCUMIN	GC394915	ATAD3B		
5	-0.54	CURCUMIN	GC189569	CLIP4	53	0.53	CURCUMIN	GC382463	SRRM1		
,	-0.54	CURCUMIN	GC160964	AHNAK2	55	0.53	CURCUMIN	GC383649	MDC1		
	-0.54	CURCUMIN	GC388269	EGFR	56	0.53	CURCUMIN	GC255478	HNRNPR		
3	-0.53	CURCUMIN	GC54614	WWC1							
	-0.53	CURCUMIN	GC387675	EGFR							
	-0.53	CURCUMIN	GC67614	RASAL2							
2	-0.53	CURCUMIN	GC395520	LOC100288911							
3	-0.53	CURCUMIN	GC73287	CLIP4							
	-0.53	CURCUMIN	GC283235	LOC100288911							
; ,	-0.53	CURCUMIN	GC272846	CLIP4							
,	-0.53	CURCUMIN	GC269551	RASAL2							
3	-0.52	CURCUMIN	GC78555	C15orf52							
	-0.52	CURCUMIN	GC151105	WWC1							
	-0.52	CURCUMIN	GC412092	FAM200B							
	-0.52	CURCUMIN	GC249495	CRIM1							
	-0.52	CURCUMIN	GC162374	RASAL2							
	-0.52	CURCUMIN	GC279709	ARHGEF28							
	-0.52	CURCUMIN	GC383037	EGFR							
i	-0.52	CURCUMIN	GC246094	ANXA2							
)	-0.51	CURCUMIN	GC85752	ANXA2							
	-0.51	CURCUMIN	GC255693	ANXA2P2							
	-0.51	CURCUMIN	GC283236	LOC100288911							
	-0.51	CURCUMIN	GC15805	HIF1A							
5	-0.51	CURCUMIN	GC382912	EGFR							
	-0.51	CURCUMIN	GC183517	RASAL2							
7	-0.51	CURCUMIN	GC419198	LOC100288911							
)	-0.51	CURCUMIN	GC179764	RASAL2							
)	-0.51	CURCUMIN	GC269692	TMEM245							
2	-0.51	CURCUMIN	GC271961	HIBADH							
1	-0.5	CURCUMIN	GC397070	HIF1A							

AQ2 suplementary Table 2 ???

suplementary Table 2: Continued

76 -0.5 PHYLLANTHIN GC71505 SETD6 151 0.62 PHYLLANTHIN GC177885 ITK 59 -0.51 PHYLLANTHIN GC57513 ACER2 131 0.62 PHYLLANTHIN GC420450 LRRC70 63 -0.51 PHYLLANTHIN GC382090 CANX 138 0.62 PHYLLANTHIN GC261095 MTMR4 70 -0.51 PHYLLANTHIN GC382090 CANX 138 0.62 PHYLLANTHIN GC261095 MTMR4 70 -0.51 PHYLLANTHIN GC382633 CLTCL1 155 0.62 PHYLLANTHIN GC32017 PPP18:16B 69 -0.51 PHYLLANTHIN GC269143 GNG3 147 0.62 PHYLLANTHIN GC420450 RBM33 66 -0.51 PHYLLANTHIN GC12560 HOXB5 146 0.62 PHYLLANTHIN GC2029281 SEPT6 64 -0.51 PHYLLANTHIN GC12560 HOXB5 146 0.62 PHYLLANTHIN GC33384	Deal	Correlati	an Cood vester	Torgot \/aata= islah	Torget veeter		nlı	Correl	ation Cood ::==t==	Torget \/aata=:-!-!	nt Torget vector
98	Rank	Correlatio				Ка	nĸ	Correla			
74	9/	0.64	<u> </u>			144	n	0.62			. ,
73											
76 - 95											DTX2P1-UPK3BP1-PMS2P11
50 0.51 PHILLATTEN 052300											
10 15 Phyllathin G282098 CANK 136 625 Phyllathin G221078 MTMPR G25178 CAN G25178 C	59	-0.51	PHYLLANTHIN	GC57513	ACER2	13 ⁻	1	0.62	PHYLLANTHIN	GC420450	LRRC70
Total											
62 0-51											
69 0.51 PHYLLATHIN C0258945 CNGS 147 0.52 PHYLLATHIN C021087 EBMSS ESTE C021091											
66											
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60											
First									PHYLLANTHIN		
50	57	-0.51	PHYLLANTHIN						PHYLLANTHIN		CCDC69
55											
50											
50.52 PIPULANTHIN CC74837 MED12L											
46 -0.52											
53 -0.52 PHYLLANTHIN GC19988 RAPSING 124 0.63 PHYLLANTHIN GC29518 PAUL											
54 -0.52 PHYLLANTHIN CG19228 RHO 125 0.63 PHYLLANTHIN CG20221 PAXIPI											
51 - 0.52 PHYLLATHIN GC12826 SLC25A22 120 0.63 PHYLLATHIN GC26319 RAD51C C C C C C C C C C C C C C C C C C C											
92 - 0.53 PHYLLATHIN GC19270 GCA 114 0.63 PHYLLATHIN GC49935 USPA4 10-0.53 PHYLLATHIN GC395780 VMEIL1 1 0.63 PHYLLATHIN GC49935 VMEIL1 1 0.64 PHYLLATHIN GC19280 VMEIL1 1 0.64 PHYLLATHIN GC19280 VMEIL1 1 0.64 PHYLLATHIN GC4935 VMEIL1 1 0.64 PHYLLATHIN GC395780 VMEIL1 1 0.64 PHYLLATHIN GC4935 VMEIL1 1 0.64 PHYLLATHIN GC4935 CECR6 GMA13 1 0.55 PHYLLATHIN GC4935 VMEIL1 1 0.64 PHYLLAT	51	-0.52	PHYLLANTHIN		SLC25A22	120	0	0.63	PHYLLANTHIN		
39			PHYLLANTHIN	GC54897	DOPEY1	119	9				ST8SIA4
40											
14											
43 - 0,53 PHYLLANTHIN GC42721 SERPINH											
34 0.54 PHYLLANTHIN GC4221 CPNE8 89 0.64 PHYLLANTHIN GC58757 GRM5 110 0.64 PHYLLANTHIN GC58757 GRM5 111 0.64 PHYLLANTHIN GC58758 GRM5 GRM5 111 0.64 PHYLLANTHIN GC169896 GNA13 GRM7 GM7											
10											
19.54 PHYLLANTHIN GC69808 KIAA2013 105 0.64 PHYLLANTHIN GC18819 JARIDI JA											
37 - 0.54 PHYLLANTHIN GC9809 MYOIE 111 0.64 PHYLLANTHIN GC138319 JARIUZ C. 2. 0.50 PHYLLANTHIN GC14218 PPPIPITAGE 82 0.64 PHYLLANTHIN GC138317 NUDT16 107 0.64 PHYLLANTHIN GC363673 NUDT16 82 0.64 PHYLLANTHIN GC363673 NUDT16 82 0.64 PHYLLANTHIN GC363673 NEU3 PHYLLANTHIN GC16213 FAM1298 109 0.64 PHYLLANTHIN GC363673 NEU3 PAG1 1 PAG1											
32 - 0.54 PHYLLANTHIN GC14283 NUDT16 107 0.64 PHYLLANTHIN GC25941 MTMR4 S19 PP1F114C 82 0.64 PHYLLANTHIN GC25941 MTMR4 S19 PP1F114C 82 0.64 PHYLLANTHIN GC25941 NUSUS PHYLLANTHIN GC16013 TEAD1 84 0.65 PHYLLANTHIN GC16013 TEAD1 84 0.64 PHYLLANTHIN GC388787 NEUS PAG1 9.55 PHYLLANTHIN GC16013 FAM129B 108 0.64 PHYLLANTHIN GC279411 PAG1 9.65 PHYLLANTHIN GC36014 KIAA1432 98 0.64 PHYLLANTHIN GC25710 PAG1 9.65 PHYLLANTHIN GC36014 KIAA1432 98 0.64 PHYLLANTHIN GC25710 PAG1 9.65 PHYLLANTHIN GC36014 KIAA1432 98 0.64 PHYLLANTHIN GC25710 PAG1 9.65 PHYLLANTHIN GC36014 CAPN12 92 0.64 PHYLLANTHIN GC25710 PAG1 9.65 PHYLLANTHIN GC36014 CAPN12 92 0.64 PHYLLANTHIN GC36014 CAPN12 92 0.64 PHYLLANTHIN GC36014 CAPN12 92 0.65 PHYLLANTHIN GC16218 CAPN12 92 0.64 PHYLLANTHIN GC36014 CAPN12 92 0.65 PHYLLANTHIN GC16218 CAPN12 92 0.65 PHYLLANTHIN GC16218 FAM12 92 0.65 PHYLLANTHIN GC16201 PAG1 9.65 PHYLLANTHIN GC3601 PAG1 9.65 PHYLLANTHIN G											
15	32	-0.54			NUDT16	107	7	0.64			LOC100505555
24 -0.55 PHYLLANTHIN GC78604 KM1432 96 0.64 PHYLLANTHIN GC78614 KM1432 96 0.64 PHYLLANTHIN GC27811 PAG1 28 -0.55 PHYLLANTHIN GC397418 PKM 98 0.64 PHYLLANTHIN GC265705 PECAMI 21 -0.56 PHYLLANTHIN GC36188 BRAP 104 0.64 PHYLLANTHIN GC2628618 PLEKHO1 21 -0.56 PHYLLANTHIN GC18218 RAP 104 0.64 PHYLLANTHIN GC18268 PERFIG 20 -0.56 PHYLLANTHIN GC18273 PAG1 AC4 PHYLLANTHIN GC18288 SEPT6 15 -0.58 PHYLLANTHIN GC18273 PAG1 AC4 PHYLLANTHIN GC18283 STALIZ 15 -0.58 PHYLLANTHIN GC18297 IGFBP6 80 0.64 PHYLLANTHIN GC18263 STALIZ 15 -0.58 PHYLLANTHIN GC18257 TBK1 MO6	33	-0.54	PHYLLANTHIN	GC14218	PPP1R14C	82		0.64	PHYLLANTHIN	GC259441	MTMR4
26 -0.55 PHYLLANTHIN GC397614 PKM 98 0.64 PHYLLANTHIN GC257505 PECAMI 22 -0.56 PHYLLANTHIN GC397181 PKM 98 0.64 PHYLLANTHIN GC256755 PECAMI 21 -0.56 PHYLLANTHIN GC18216 CAPN12 92 0.46 PHYLLANTHIN GC252616 PPMIE 23 -0.56 PHYLLANTHIN GC18216 CAPN12 92 0.44 PHYLLANTHIN GC252616 PPMIE 23 -0.56 PHYLLANTHIN GC4018 STAR013-AS 99 0.64 PHYLLANTHIN GC26026 SLC841 16 -0.57 PHYLLANTHIN GC19273 SPECC1 91 0.64 PHYLLANTHIN GC18028 STAU2 15 -0.58 PHYLLANTHIN GC18227 IGF8P6 80 0.64 PHYLLANTHIN GC182383 STAU2 16 -0.58 PHYLLANTHIN GC18226 KPR1 MAC2424 PHYLANTHIN GC182383 TA <td></td>											
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23 0.56 PHYLLANTHIN GC16941 STARD13-AS 99 0.64 PHYLLANTHIN GC269026 SLGAM											
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13 -0.58 PHYLLANTHIN GC16157 TBH1 106 0.64 PHYLLANTHIN GC403774 YPEL1 12 -0.59 PHYLLANTHIN GC16157 TBH1 106 0.64 PHYLLANTHIN GC403774 YPEL1 12 -0.59 PHYLLANTHIN GC116157 KRT83 101 0.64 PHYLLANTHIN GC185652 YPEL1 105 0.6 PHYLLANTHIN GC185652 YPEL1 105 0.6 PHYLLANTHIN GC28803 CHRNA3 7 -0.64 PHYLLANTHIN GC16525 SKP1 107 0.6 PHYLLANTHIN GC309513 EVI 70 0.65 PHYLLANTHIN GC406751 ABHD17B 104 0.6 PHYLLANTHIN GC390513 EVI 70 0.65 PHYLLANTHIN GC406751 ABHD17B 104 0.6 PHYLLANTHIN GC387464 ITK 69 0.65 PHYLLANTHIN GC3954784 ADAM22 ADAM22 ADAM22 ADAM22 ADAM22 ADAM23 ADAM24 A	17	-0.57	PHYLLANTHIN	GC12073	SPECC1	91		0.64	PHYLLANTHIN	GC186043	STAU2
14 -0.58											
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196 0.6 PHYLLANTHIN GC389990 PMS2P1 68 0.65 PHYLLANTHIN GC388190 CHRNA3 185 0.61 PHYLLANTHIN GC260950 AZI1 67 0.65 PHYLLANTHIN GC388190 CHRNA3 185 0.61 PHYLLANTHIN GC408950 AZI1 67 0.65 PHYLLANTHIN GC388473 KIAA0195											
184											
186	184	0.61	PHYLLANTHIN		ATAD2	63		0.65			CHRNA3
176	185	0.61	PHYLLANTHIN	GC260950	AZI1	67		0.65	PHYLLANTHIN	GC186950	EVL
168											
175											
174											
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192											
178 0.61 PHYLLANTHIN GC288491 ESCO2 64 0.65 PHYLLANTHIN GC39325 ZNF85 173 0.61 PHYLLANTHIN GC273466 FYB 5 -0.65 PHYLLANTHIN GC402418 ADAM22 170 0.61 PHYLLANTHIN GC383807 JARID2 57 0.66 PHYLLANTHIN GC251191 ADRBK2 169 0.61 PHYLLANTHIN GC1577074 JARID2 57 0.66 PHYLLANTHIN GC391646 C170780 1991 0.61 PHYLLANTHIN GC154719 LOC728485 46 0.66 PHYLLANTHIN GC30396 CYTH1 160 0.61 PHYLLANTHIN GC406275 LPAR6 58 0.66 PHYLLANTHIN GC32544 PRKCH 179 0.61 PHYLLANTHIN GC406275 LPAR6 58 0.66 PHYLLANTHIN GC32554 PRKCH 179 0.61 PHYLLANTHIN GC406275 PMS2P1 50 0.66 PHYLLANTHIN GC32											
173 0.61 PHYLLANTHIN GC273466 FYB 5 -0.65 PHYLLANTHIN GC18789 RND3 162 0.61 PHYLLANTHIN GC881244 FYB 56 0.66 PHYLLANTHIN GC402418 ADAM22 169 0.61 PHYLLANTHIN GC383807 JARID2 57 0.66 PHYLLANTHIN GC251191 ADRBK2 169 0.61 PHYLLANTHIN GC177074 JARID2 51 0.66 PHYLLANTHIN GC391646 C17orf80 191 0.61 PHYLLANTHIN GC154719 LOC728485 46 0.66 PHYLLANTHIN GC90396 CYTH1 160 0.61 PHYLLANTHIN GC406275 LPAR6 58 0.66 PHYLLANTHIN GC148113 PMS222 179 0.61 PHYLLANTHIN GC406275 LPAR6 58 0.66 PHYLLANTHIN GC408295 ME2 49 0.66 PHYLLANTHIN GC403245 PRKCH 179 0.61 PHYLLANTHIN GC34575<											
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165 0.61 PHYLLANTHIN GC26995 ME2 49 0.66 PHYLLANTHIN GC33254 PRKCH 179 0.61 PHYLLANTHIN GC401644 PIKFYVE 50 0.66 PHYLLANTHIN GC391918 RAD51C 190 0.61 PHYLLANTHIN GC34575 PMS2P1 52 0.66 PHYLLANTHIN GC31918 RAD51C 190 0.61 PHYLLANTHIN GC152451 RASD1 59 0.66 PHYLLANTHIN GC47197 TFDP2 161 0.61 PHYLLANTHIN GC166154 SEPT6 48 0.66 PHYLLANTHIN GC249190 TNFAIP3 159 0.61 PHYLLANTHIN GC386647 SLIT1 60 0.66 PHYLLANTHIN GC409068 TNRC6C 187 0.61 PHYLLANTHIN GC398843 STAU2 41 0.67 PHYLLANTHIN GC49565 CCDC102B 182 0.61 PHYLLANTHIN GC38843 STAU2 41 0.67 PHYLLANTHIN GC49516 </td <td></td>											
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				GC188756						GC35292	
154 U.62 PHYLLANTHIN GC274494 ANXA2R 30 0.68 PHYLLANTHIN GC184532 PRKCH											
	154	0.62	PHYLLANTHIN	GC274494	ANXA2R	30		0.68	PHYLLANTHIN	GC184532	PRKCH

(Contd) (Contd)

suplementary Table 2: Continued

Rank	Correlation	Seed vector	Target Vector idebt	Target vector
		description for	For display	Display for
32	0.68	PHYLLANTHIN	GC386035	YME1L1
18	0.69	PHYLLANTHIN	GC17987	CD1C
21	0.69	PHYLLANTHIN	GC16214	CPT1C
19	0.69	PHYLLANTHIN	GC383806	JARID2
23	0.69	PHYLLANTHIN	GC86218	KIAA0195
25	0.69	PHYLLANTHIN	GC164007	MTMR4
27	0.69	PHYLLANTHIN	GC426209	SLC8A1
2	-0.69	PHYLLANTHIN	GC10700	FLJ41649
14	0.7	PHYLLANTHIN	GC271745	GNA13
17	0.7	PHYLLANTHIN	GC163365	LINC00340
16	0.7	PHYLLANTHIN	GC387664	YME1L1
13	0.71	PHYLLANTHIN	GC399220	PRKCH
10	0.72	PHYLLANTHIN	GC290660	LOC100130476
8	0.73	PHYLLANTHIN	GC187551	C17orf80
7	0.73	PHYLLANTHIN	GC172216	ZNF577
5	0.74	PHYLLANTHIN	GC186260	KIAA0195
6	0.74	PHYLLANTHIN	GC151093	KIAA0825
4	0.75	PHYLLANTHIN	GC16782	TBL3
2	0.76	PHYLLANTHIN	GC254783	ADAM22
3	0.76	PHYLLANTHIN	GC411749	PAG1

Supplementary Table 4: A number of 22 mRNA that were related by curcumin and phyllanthin and were related to BBCSCs $\,$

S. No	Pearson correlation	Target	Gene	Gene name
	coefficient	vector ID	Symbol	
1	0.69	GC383806	JARID2	Jumonji And AT-Rich Interaction
				Domain Containing 2
2	0.65	GC271015	USP44	Ubiquitin Carbocyl-terminal
				hydrolase 44
3	0.64	GC249191	TNFAIP3	TNF alpha induced protein 3
4	0.61	GC28493	CBX3	Chromobox 3
5	0.61	GC386647	SLIT1	Slit Guidance Ligand 1
6	0.6	GC170494	ATAD3B	ATPase Family AAA Domain
				Containing 3B
7	0.59	GC393846	ATAD3A	ATPase Family AAA Domain
				Containing 3A
8	0.57	GC11583	MMP9	Matrix Metallopeptidase 9
9	0.55	GC382442	CHD4	Chromodomain Helicase DNA
				Binding Protein 4
10	0.55	GC393018	YTHDF2	YTH N6-Methyladenosine RNA
				Binding Protein 2
11	0.54	GC396479	HSP90AB1	Heat Shock Protein 90 Alpha
				Family Class B Member 1
12	0.52	GC397403	HDAC1	Histone Deacetylase 1
13	0.52	GC255719	TCF3	Transcription Factor 3
14	0.52	GC16214	CPT1C	Carnitine Palmitoyltransferase 1C
15	0.51	GC15805	HIF1A	Hypoxia Inducible Factor 1
				Subunit Alpha
16	-0.5	GC28815	TGM2	Transglutaminase 2
17	-0.52	GC246094	ANXA2	Annexin A2
18	-0.52	GC10662	MAP3K5	Mitogen-Activated Protein Kinase
				Kinase Kinase 5
19	-0.52	GC387675	EGFR	Epidermal Growth Factor Receptor
20	-0.54	GC14031	TEAD1	TEA Domain Transcription Factor 1
21	-0.55	GC397418	PKM	Pyruvate Kinase M1/2
22	-0.58	GC16157	TBK1	TANK Binding Kinase 1

Supplementary Table 5: Gene ontology of the 22 potential therapeutic target genes

Term	p value	Genes		
Biological process GO: 0000122~negative	0.05878410987680528	HDAC1 IARID2		
regulation of transcription	0.03676410967060326	HDAC1, JARID2, TCF3, CHD4		
from RNA polymerase II				
promoter				
GO:	0.08869262932347735	HIF1A, HDAC1, JARID2,		
0006351~transcription,		CBX3, TCF3, CHD4		
DNA-templated GO: 0045892~negative	0.12784550606541756	HDAC1,		
regulation of transcription,	0.12101000000011100	JARID2, CBX3		
DNA-templated				
GO: 0045893~positive	0.1345965033431493	HIF1A,		
regulation of transcription, DNA-templated		HDAC1, TCF3		
GO: 0006355~regulation	0.2893336322416595	HIF1A, HDAC1,		
of transcription,		TCF3, CHD4		
DNA-templated				
GO: 0004672~protein	0.07263251481178587	EGFR,		
kinase activity GO: 0098641~cadherin	0.00530635145361415	MAP3K5, TBK1 HSP90AB1,		
binding involved in	0.00000000140001410	PKM, EGFR, ANXA2		
cell-cell adhesion				
GO: 0005913~cell-cell	0.0057898661163517506	HSP90AB1, PKM,		
adherens junction	0.0400445500000005	EGFR, ANXA2 HSP90AB1, EGFR, ANXA2		
GO: 0016323~basolateral	0.01801155022396305			
plasma membrane		LOT N, ANVAZ		
GO: 0098609~cell-cell	0.04454764908303356	HSP90AB1,		
adhesion		PKM, ANXA2		
GO: 0044822~poly[A]	0.16227798926506184	HSP90AB1, PKM, YTHDF2, ANXA2		
RNA binding GO: 0001934~positive	0.010848600290442318	EGFR,		
regulation of protein	0.010010000200112010	MMP9, ANXA2		
phosphorylation				
Cellular component	0.0007400740070040	110000404 111544 110404		
GO: 0005654~nucleoplasm	0.08871697106273643	HSP90AB1, HIF1A, HDAC1, JARID2, TEAD1, TCF3, CHD		
GO:	0.08871697106273643	HSP90AB1, HIF1A, HDAC1,		
0005654~nucleoplasm		JARID2, TEAD1, TCF3, CHD		
GO: 0000790~nuclear	0.0205301891902419	HDAC1,		
chromatin	0.00074600005704000	TCF3, CHD4		
GO: 0043234~protein complex	0.08074688825784038	HDAC1, TCF3, CHD4		
GO: 0016020~membrane	0.47395510617554676	HSP90AB1, EGFR,		
		CHD4, ANXA2		
GO: 0005886~plasma	0.8850254366828423	PKM, EGFR,		
membrane GO:	0.1996517577718779	TGM2, ANXA2 EGFR, MMP9,		
0005615~extracellular	0.1000011011110110	SLIT1, ANXA2		
space				
GO: 0016021~integral	0.9915053828035031	CPT1C,		
component of membrane	0.4000044665064570	EGFR, ATAD3A HSP90AB1,		
GO: 0009986~cell surface	0.1280244665061579	EGFR, ANXA2		
Molecular function		2011,71170		
GO: 0008270~zinc ion	0.17459658423852453	MMP9, TNFAIP3,		
binding	0.0405004047044054	CHD4, USP44		
GO: 0003677~DNA binding	0.3465861347844654	TEAD1, TNFAIP3, TCF3, CHD4		
GO:	0.11416783095336286	HIF1A, HDAC1,		
0003700~transcription		TEAD1, TCF3		
factor activity,				
sequence-specific DNA				
binding GO:	0.0480050925831412	HIF1A,		
0008134~transcription	5.5-0000002000 IT IZ	HDAC1, TCF3		
factor binding				
GO: 0005524~ATP	2.63E-04	HSP90AB1, PKM, EGFR,		
binding		MAP3K5, ATAD3A, ATAD3B,		
GO: 0042826~histone	0.007044468809860209	TBK1, TGM2, CHD4 HSP90AB1,		
deacetylase binding	0.00 <i>1</i> 0 444 00009000209	HSP90AB1, HIF1A, HDAC1		
GO: 0000978~RNA	0.009259543919357753	HDAC1, TEAD1,		
polymerase II core		TCF3, CHD4		
promoter proximal region				
sequence-specific DNA				