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Network pharmacology and *in vitro* validation of anti-adipogenic property of *Ipomoea mauritiana* Jacq.

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Muscle wasting during starvation or malnourishment is a major health concern. *Ipomoea mauritiana* Jacq. is a plant from the Convolvulaceae family commonly known as *Ksheera-vidari* in Ayurveda which is prescribed in malnourishment and is known for imparting strength. It is also used as a galactogogue in lactating mothers. The study explores the possible mechanism of action of this herb. *In silico* studies using network pharmacology revealed AMPK, PPAR, longevity-regulating, insulin related and adipocytokine pathways were affected by the phytochemicals of this plant. Methanolic extract of *Ipomoea mauritiana* tuber was used for *in vitro* studies. The extract reduced lipid content in 3T3-L1 derived adipocytes. Gene expression studies revealed down-regulation of some key adipogenic genes such as *PPARγ, Plin2, CD36 and FASN*. Interestingly, treatment reduces *RBP4* transcript level while an increase was observed in *Adiponectin* expression. This indicates that the extract reduces lipid content in adipocytes without increasing insulin resistance. This is the first report showing possible mechanism of action of *Ipomoea mauritiana*.

Keywords: Adipocyte, Ayurveda Biology, *Ksheer-vidaari*, Lipid metabolism

Obesity and malnutrition are two extremes of nutritional states in humans and both are associated with adverse outcomes[1]. In 2022, WHO reported that over 2 billion adults were overweight, and 390 million adults were underweight globally. It further reported that 149 million children under the age of five were stunted, 45 million wasted, and 37 million were either overweight or obese[2]. Underweight or malnourished children show a plethora of physiological, biochemical, and clinical abnormalities, including impaired growth, muscle wasting, micronutrient deficiencies, weakened immune function, and chronic diseases. There is an urgent need to deal with the dual problem, especially in India where we have increasing obesity and persistent malnutrition[3].

Ayurveda, one of the world's oldest traditional medicine systems, integrates herbal formulations, dietary changes and lifestyle modifications for a more holistic approach. *Ipomoea mauritiana* (IM), commonly called *Ksheera-vidari* is a perennial herb with glabrous or minutely muricate axial parts and large tuberous roots. It belongs to the Convolvulaceae family and is found in many parts of the world including India. The plant has several synonyms like *Ipomoea digitata, Ipomoea bignonioides, Ipomoea paniculatus* and *Ipomoea pentaloba*[4]. In Ayurveda it is described as a substitute for *Vidari* or *Pueraria tuberosa*[5]. The leaves of this plant are used to reduce obesity while the tuber is used to treat underweight individuals. Tuber is also used as galactagogue, with cardioprotective and wound healing properties, making it a desirable candidate for further pharmacological probing[6]. This plant is also known as "*Balya*" as per Ayurveda which means it imparts strength[6]. IM treatment has also been shown to decrease serum cholesterol and triglycerides in a diabetic rat model[7].

During starvation, malnutrition or cachexia, both skeletal muscle and adipose tissue are utilised for energy production. While the adipose tissue loss is easily reversed upon nutritional sufficiency, muscle wasting is much more difficult to reverse. Whether during starvation or planned weight loss for treatment

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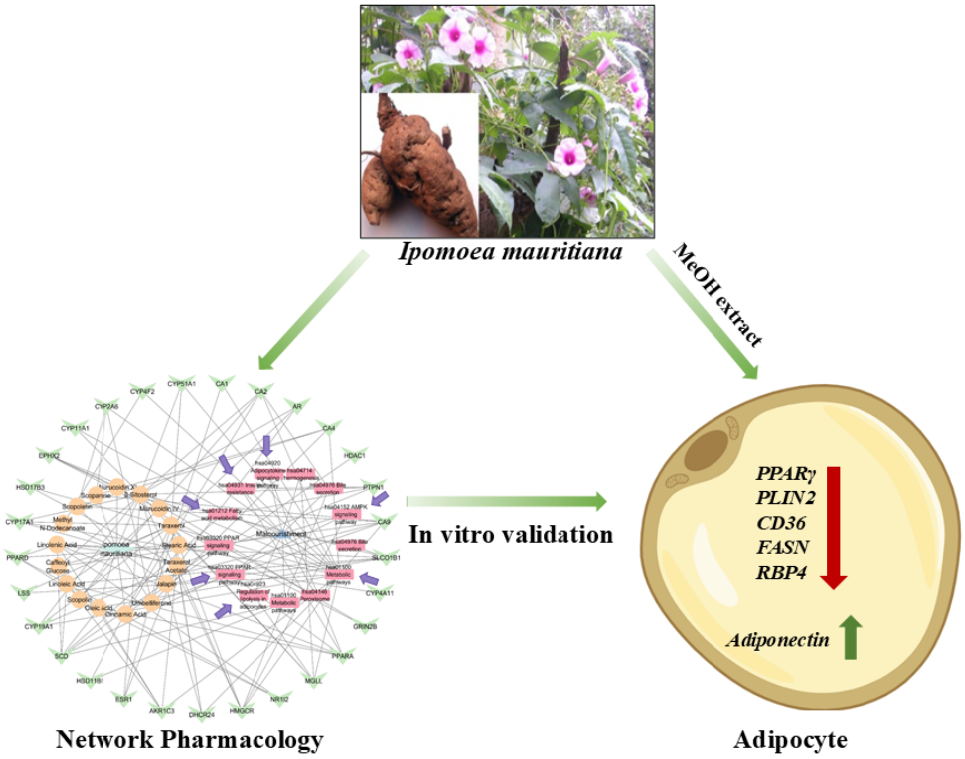
Suppl. data available on respective page of NOPR



Graphical abstract

of metabolic disorders, reduction in lean mass is a major concern. It has been shown that mobilizing lipids from adipose tissue can reduce muscle wasting[7]. Similarly, lipid mobilization from adipose tissue is low in children suffering from Kwashiorkor[8]. Fenofibrates which are activators of PPARα and induce lipolysis, have been suggested as a therapy for malnutrition induced liver steatosis[9]. Blocking lipolysis pharmacologically during starvation has been shown to increase protein degradation[10]. Therefore, therapies which stimulate lipid usage from adipose tissue can be useful in the conditions of nutrient starvation by providing much needed energy and protecting muscle degradation for gluconeogenesis.

Network pharmacology (NP) integrates multiple disciplines of study such as basic biology, pharmacology, genomics and proteomics data to study possible drug targets[11]. NP approach is a valuable methodology for understanding the complex pharmacological mechanisms of medicinal herbs. In addition, various *in silico* analysis techniques combined with the NP approach can improve the understanding of therapeutic effects of natural products. The analysis provides us with hypothesis to be tested experimentally to verify targets and drug pairs. This substantially reduces the effort needed to work out the pharmacology of any unknown herb[11]. Therefore, the approach has been very useful in studying Ayurvedic formulations and herbs[12]. One such example is the target identification for improved synaptogenesis by *Withania somnifera*[13]. Known phytochemicals in IM were compiled from published literature and their potential targets were identified. Thereafter, genes affected during "malnourishment" were identified (Fig. 1). A protein-protein interaction (PPI) network was constructed which was utilised for pathway analysis. The findings were experimentally verified using methanolic extract of IM tubers. This study aims to bridge the gap between known effects of *Ipomoea mauritiana* and its molecular pharmacology.

Materials and Methods

Identification of phytochemicals from IM

PubMed Central (PMC), was used to retrieve and compile data on the phytochemical profile of IM. The repository was searched with the term "*Ipomoea mauritania"* and also synonyms "*Convolvulus paniculatus*", "*Ipomoea digitata*", "*Ipomoea eriosperma*" and "*Ipomoea paniculata*". Structure

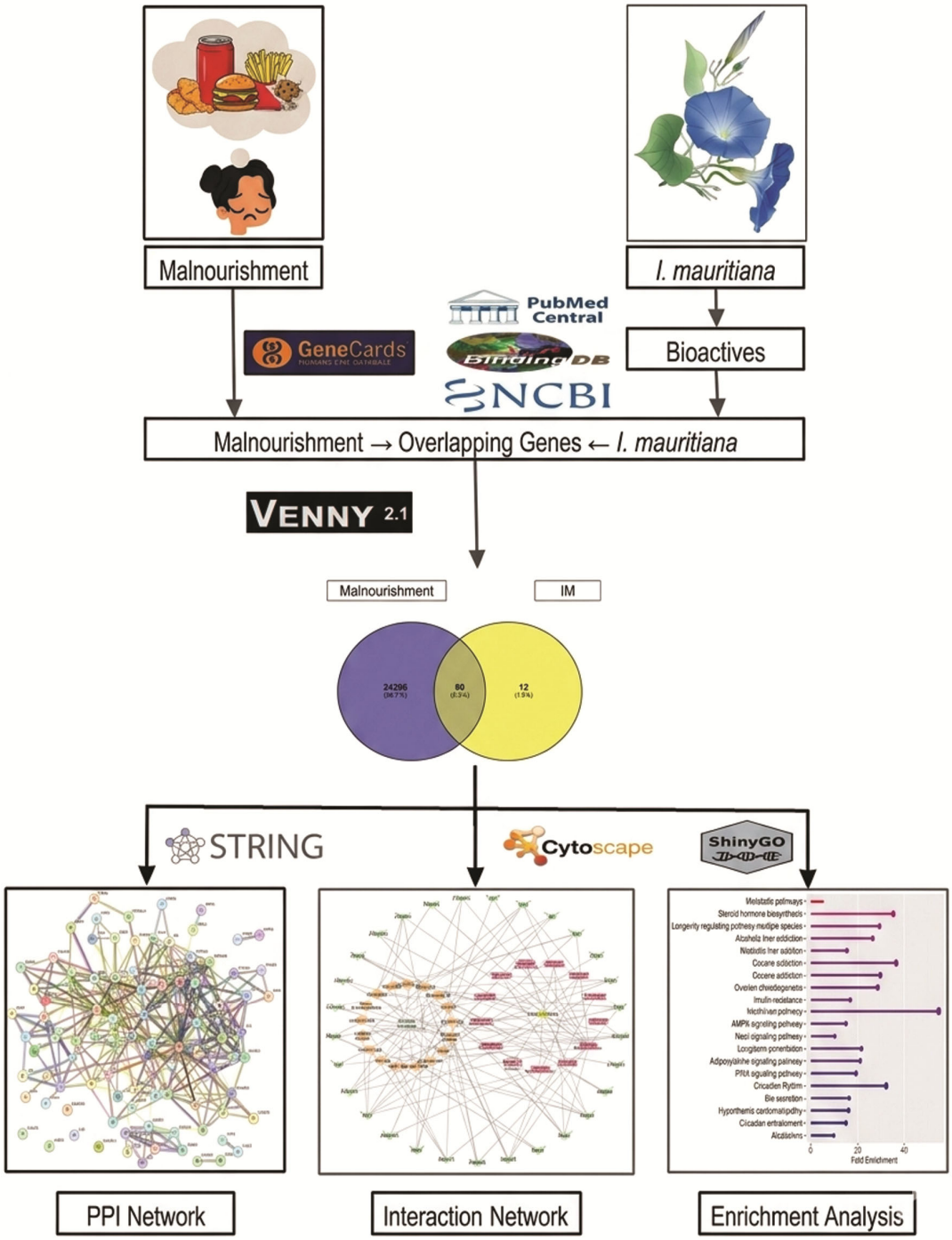


Fig. 1 — A diagrammatic representation of the *in silico* methodology used to investigate the potential molecular mechanism behind the action of IM in malnourishment

Data Files (SDF) of each compound were then downloaded from PubChem for use in the next step[14].

Target prediction of IM

Structure data files were uploaded to the Binding DB database[15], and the "Find my compound's targets" aid was run at a similarity parameter of 0.75. An exception was made for compounds yielding zero results *i.e.* "No compounds meet your criterion" and the canonical SMILES were used to confirm the results using SwissTarget Prediction[16] with a cut-off probability score of 0.06. Gene Names and Gene IDs

of targets were obtained from the NCBI Gene database. All target-associated information was exclusively collected for the species "*Homo sapiens*". Targets for malnourishment were also recovered from GeneCards. Search terms include keywords "malnourished", "underweight", "nourishment", "metabolism", "digestion", "appetite" and "weight gain". A Venn diagram was then constructed to identify the overlapping genes between the individual gene sets for nourishment-related terms and the IM gene set.

STRING-derived PPI network

The overlapping targets were imported into the STRING (Search Tool for the Retrieval of Interacting Genes) web resource[17] to construct a PPI (Protein-Protein Interaction) network showing both functional and physical interactions of the target set, searched under the species "*Homo sapiens*". The PPI network was then exported to Cytoscape (version 3.10.3)[18], and analysed to identify the top 10 hub genes based on the degree parameter. The use of hub genes for pathway prediction allows to concentrate on major determinants and reduce the noise in the system[19]. CytoHubba (version 0.1), and MCODE (version 2.0.3) plug-ins were used.

GO and KEGG enrichment analysis

GO (gene ontology) function and KEGG (Kyoto Encyclopaedia of Genes and Genomes) pathway analysis was performed using ShinyGO 0.82[20] to uncover the possible mechanisms. To perform this step, the intersecting genes were used as the input and run to obtain the biological processes (BP), molecular function (MF) and cellular component (CC) lollipop plots.

Network construction and visualisation

A Compound-Target-Pathway Network was constructed using Cytoscape, to help uncover the relationship between the phytochemical compounds, disease targets and signalling pathways shown to be most involved and affected by the gene set. Nodes falling under different categories were given unique attributes in the form of shapes, colours and labels to help distinguish them from others.

Preparation of methanolic extract of *Ipomoea mauritiana*

Ipomoea mauritiana tubers were sourced from the garden of The University of Trans-Disciplinary Health Sciences and Technology (TDU), Bangalore and authenticated by institutional herbarium. The tubers were thoroughly washed and dried, then ground coarsely and used for methanolic extraction (1:10 (*w/v*) tuber: methanol) using the Soxhlet apparatus for 7 h. Rotatory vaporization was used to remove the solvent and the extract was stored at -20°C for further use.

High performance liquid chromatography (HPLC)

The HPLC analysis was performed using a Shimadzu LC-20AT with SPD-M20 detector (D1/FIST/635), C18 column (250 × 4.6 mM, 5 µM). The mobile phase consisted of solvent A (0.1% Formic acid in water) and solvent B (acetonitrile) (95:5) with an isocratic elution program. The flow rate was maintained at 1.0 mL/min, injection volume was 20 µL, and detection was carried out at 344 nm.

Cell Culture

3T3-L1 (mouse fibroblast) cells were maintained in DMEM (high glucose, Gibco) supplemented with 10% FBS and Pen-Strep. For differentiation, cells were seeded in 6 well plate at 40000 cells/well. At 80% confluency (2 days after seeding), cells were induced with differentiation media containing 0.5 mM IBMX (3-Isobutyl-1-methylxanthine), 1 µM dexamethasone, and 2 µg/mL insulin for 48 h[21]. After 48 h, media was removed and cells were maintained in DMEM with 2 µg/mL insulin (Humulin, Eli Lilly) (maintenance media) with or without IM extract. Media was replaced every 2 days. Cells were harvested after 6 days in maintenance media.

Cell viability assay

5000 cells per well were seeded in a 96 well plate. After 24 h, cells were treated with various concentration of *Ipomoea mauritiana* (IM) for 24 h. Cell viability of cells was evaluated at concentrations 30, 10, 3, 1, 0.3, 0.1 µg/mL. After treatment, cells were incubated for 3 h in MTT (3- (4, 5-dimethylthiazol-2-yl)-2,5-diphenyltetrazolium bromide, SRL-33611) (0.5 mg/mL). Media was aspirated and formazan crystals were dissolved in DMSO. The absorbance was read at 570 nm in a Biotek Microplate Reader. The percentage of cell viability was calculated as % cell viability = 100 * (experimental well absorbance – negative control well absorbance) / (positive control well absorbance – negative control well absorbance).

Lipid staining: Oil Red O (ORO) staining

40 k cells were seeded in a 6 well plate and differentiation protocol was followed as mentioned

above. After 6 days of treatment, cells were taken out for lipid staining using ORO stain (Sigma)[21]. Briefly, cells were rinsed in PBS followed by fixing with 10% formalin for 1 h. Cells were then rinsed with distilled water, kept in 60% isopropanol for 10 min and dipped in Oil red O working solution for 15-20 min. The plate was visualised under a microscope to assess lipid droplets formation. For lipid quantification 400 µL of 100% isopropanol was used to dissolve the lipid content and absorbance was measured at 495 nm.

qRT-PCR

After 6 days of treatment of adipocytes, cells were harvested in TRIzol reagent. Total RNA was isolated using Krishgen RNA Fast PrepR-mini-RNA isolation kit. 2 µg of RNA was used for synthesizing cDNA using Applied biosystems cDNA synthesis kit and qPCR reaction was performed using iTaq SYBR green (Bio rad) following the manufacturer's instruction. Beta actin was used as internal reference gene. Relative expression was determined using ΔΔCt method. Primer sequences are in (Suppl. Table S1).

Statistical analysis

All *in vitro* experiments were repeated at least three times and statistical significance was calculated based on Student's *t*-test in Excel software. The data was called significant when p-value ≤ 0.05

Results

Phytochemicals and intersecting targets

Through literature reviews, 40 phytochemicals belonging to different classes of compounds were identified to be present in IM extract. Majority of the compounds were primary or secondary metabolites. Compounds from the following classes were present: fatty acids, coumarins, sterols, polyesters/resin glycosides, aromatic acids and derivatives, glycosides, alcohols, alkanes, aldehydes, methyl esters and miscellaneous compounds (Suppl. Table S2). Of the 40 compounds, structure data files for 36 could be found of which 22 had targets with reliable similarity score. Metabolites oleic acid, linoleic acid and linolenic acid were predicted to have 17 common targets. Beta-sitosterol, taraxerol, taraxerol acetate, umbelliferone, scopoletin and scoparone had 36, 30, 14, 15, 12, and 10 predicted targets respectively. A total of 95 unique targets were identified. Using specific keywords (mentioned in the methods section) GeneCards was searched for terms related to malnourishment, and filtered with a relevance score ≥1. Results were compared with the gene set associated with the phytochemicals of IM to identify the intersecting targets, of which a total of 80 were found to be common.

Analysis of the STRING PPI Network

Of all the genes involved in malnourishment 80 were predicted to be targets of phytochemicals from IM (Fig. 2a). These subset of intersecting targets were then used to construct PPI network. The emerging network had 80 nodes and 221 edges (Fig. 2b). The PPI enrichment p-value for the network was $<1.0e^{-16}$, indicating that the proteins are at least partially biologically connected as a group. Network analysis was performed to identify the hub genes with the help of CytoHubba (Fig. 3). *HMGCR, ESR1, PPARA,*

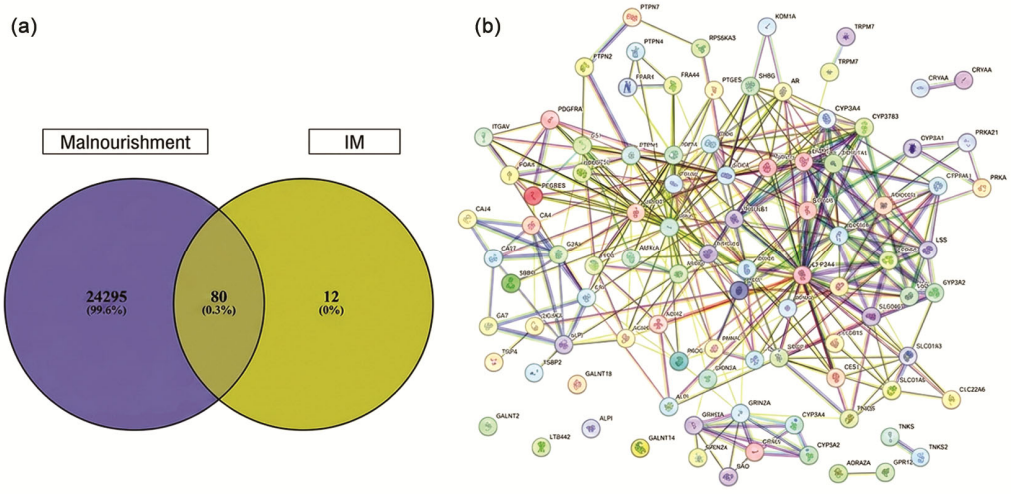


Fig. 2 — Intersecting gene set and STRING PPI network of gene set. (a) A venn diagram denoting 80 intersecting targets; and (b) STRING PPI network of the overlapping targets

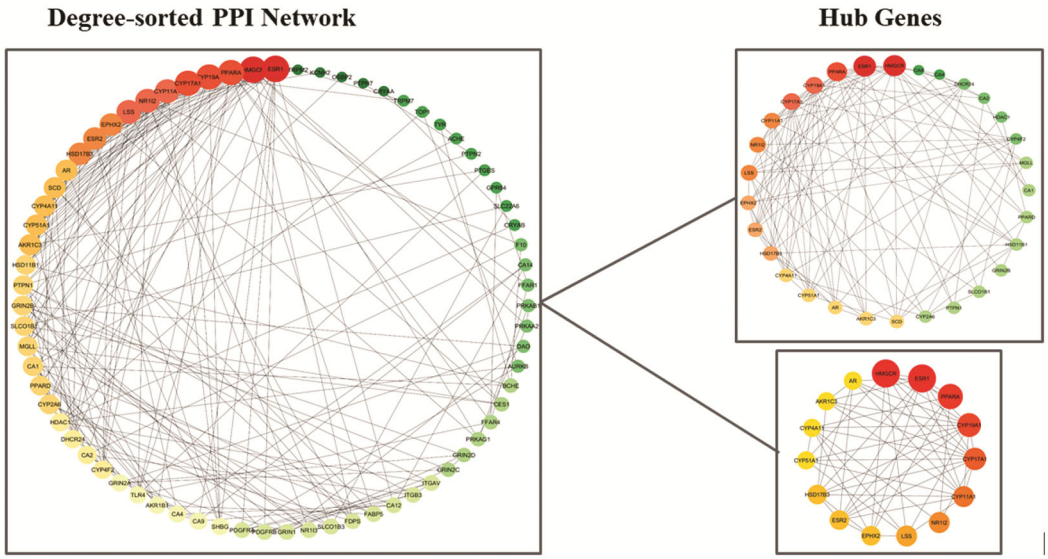


Fig. 3 — Degree-sorted network of targets, CytoHubba plug-in used to find hub genes. Left, degree-sorted network of targets overlapping between malnourishment and IM targets. Right, hub genes retrieved through use of CytoHubba plug-in

CYP19A1, NR1I2, CYP17A1, CYP11A1, LSS, EPHX2, ESR2, CYP51A1, CYP4A11, HSD17B3, AKR1C3, and *AR* were identified as core targets based on the degree parameter (Suppl. Table 3). Most of these genes are related to lipid metabolism.

GO and KEGG Enrichment Analysis

ShinyGO was used to map the hub genes to their known biological functions and pathways. Results showed that major relevant pathways were metabolic, AMPK signaling, PPAR signaling, longevity-regulating, insulin resistance and adipocytokine signaling pathways. Pathways were sorted in accordance to -log10 (FDR) and significance/size of term represented was based on fold enrichment of the term[20] and the top 20 terms for BP and MF are represented in the lollipop plots.

The gene ontology enrichment (Fig. 4a) shows biological processes such as lipid and steroid metabolism to be enriched. KEGG enrichment reinforces this notion and also identifies key pathways like AMPK and insulin resistance being affected (Fig. 4b).

Network Analysis

The results from previous steps were compiled and used to construct a network representing the data collectively. The network thus generated has a total of 61 nodes; 17 compound nodes, 29 target nodes, 13 pathway nodes, 1 IM node, and 1 malnourishment node (Fig. 5). Purple arrows indicate some of the top pathways relevant to our study.

Energy balance and nutritional status are key modulators of AMPK signaling, adipocytokine signaling and the regulation of lipolysis in adipocytes. These closely interconnected pathways are linked to malnourishment. Chronic energy deficiency activates AMPK, a sensor of cellular energy, thereby promoting catabolic processes such as lipolysis and inhibiting anabolic activities.

IM reduces lipid content in adipocytes:

A qualitative assessment of the extract was done to see a chemical fingerprint of IM extract. One of the major peaks coincided with that of scopoletin, which is a marker compound for this plant (Suppl. Fig. S1).

As per the enrichment and network analysis, IM appears to be affecting lipid metabolism and its associated pathways. To test the findings, we used an adipocyte cell line for *in vitro* experiments. 3T3-L1 cells are an established cell-based model to study adipose tissue physiology and function[22]. First, we checked safety profile of IM on 3T3L1 by cell viability assay at concentrations 30-0.1 µg/mL and found no significant change in viability (Suppl. Fig. S2).

We treated 3T3-L1 derived adipocytes with methanolic extract of *Ipomoea mauritiana* at 1 µg/mL (Fig. 6a), previously shown to be effective[23]. We estimated the lipid content within adipocytes by ORO staining. Lipid droplets accumulation was clearly observed in differentiated adipocytes as compared to preadipocytes, and IM treatment lowered the lipid

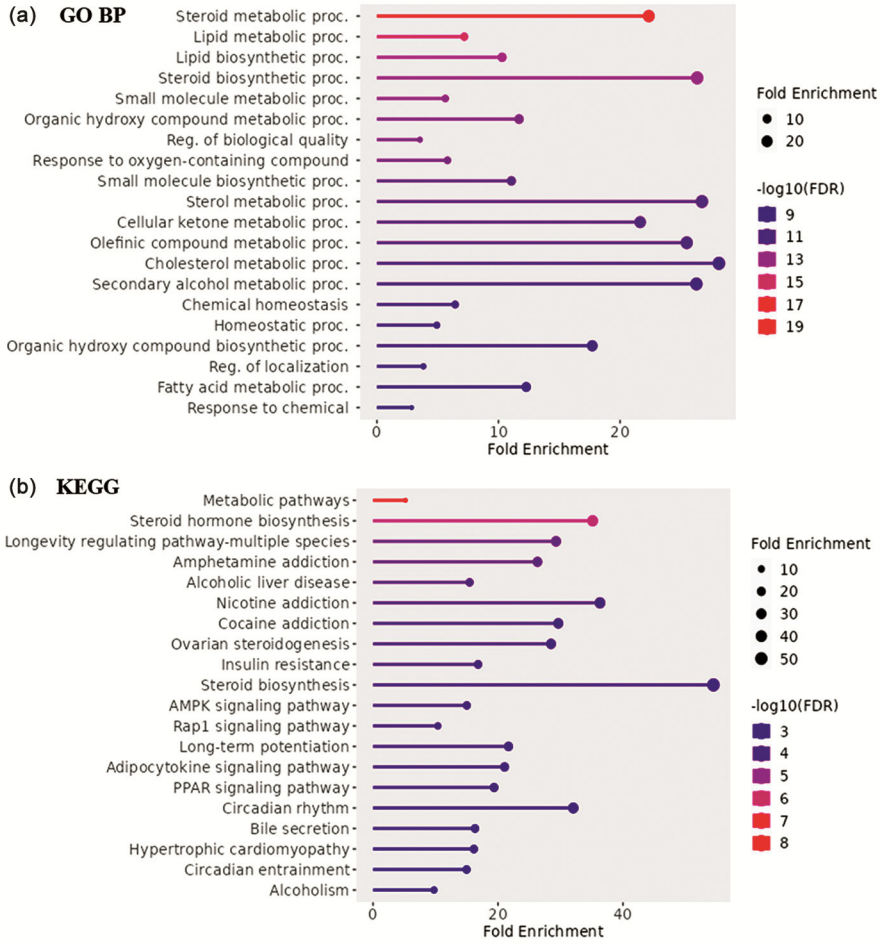


Fig. 4 — Gene enrichment lollipop plot of the GO Biological Process (a) KEGG pathway enrichment analysis showing top pathways associated with the gene set; and (b) The colour of the bar corresponds to FDR (false discovery rate)

accumulation (Fig. 6b). We used GW9662, which is a known PPARγ antagonist as a positive control. Upon quantification we found that IM treatment reduces lipid content by over 20% (Fig. 6c) comparable to the control compound.

IM modulates expression of key adipogenesis markers

To further understand the molecular pathways, we checked the gene expression of *PLIN2* (perilipin 2). *PLIN2* is also known as adipose differentiation related protein (ADRP) and is a ubiquitously present on lipid droplets[24]. Reduction in expression level of *PLIN2* (Fig. 7a) after treatment is in line with the observed reduction in in ORO staining upon IM treatment. We then, studied some key transcriptionally regulated genes involved in adipocyte differentiation.

PPARs are one such group of transcription factors belonging to the superfamily of ligand activated nuclear receptors[25]. These receptors were also found to be major targets in our network analysis. They control the expression of several genes involved in adipogenesis, lipid metabolism, inflammation and maintenance of metabolic homeostasis[26]. *PPARγ* is prominently expressed in white adipose tissue (WAT), where it is a master regulator of adipogenesis[27]. We found that IM treatment lowered *PPARγ* expression (Fig. 7b) suggesting the key mechanism of IM lowering the lipid accumulation. *PPARγ* controls adipogenesis and lipolysis through genes having PPAR response elements such as *C/EBPα, CD36, FATP1, FASN* and adipokines.

CEBPα is a critical transcription factor along with *PPARγ* during adipogenesis[28]. Its level was also decreased upon IM treatment (Fig. 7c). Two key genes responsible for fatty acid uptake are *CD36* and *FATP1*. Treatment of IM shows significant decrease in *CD36* (Fig. 7d) without any change in *FATP1* expression (Fig. 7e). *FASN*, also known as fatty acid synthase expression level was decreased upon treatment (Fig. 7f). Lower expression of *CD36* is

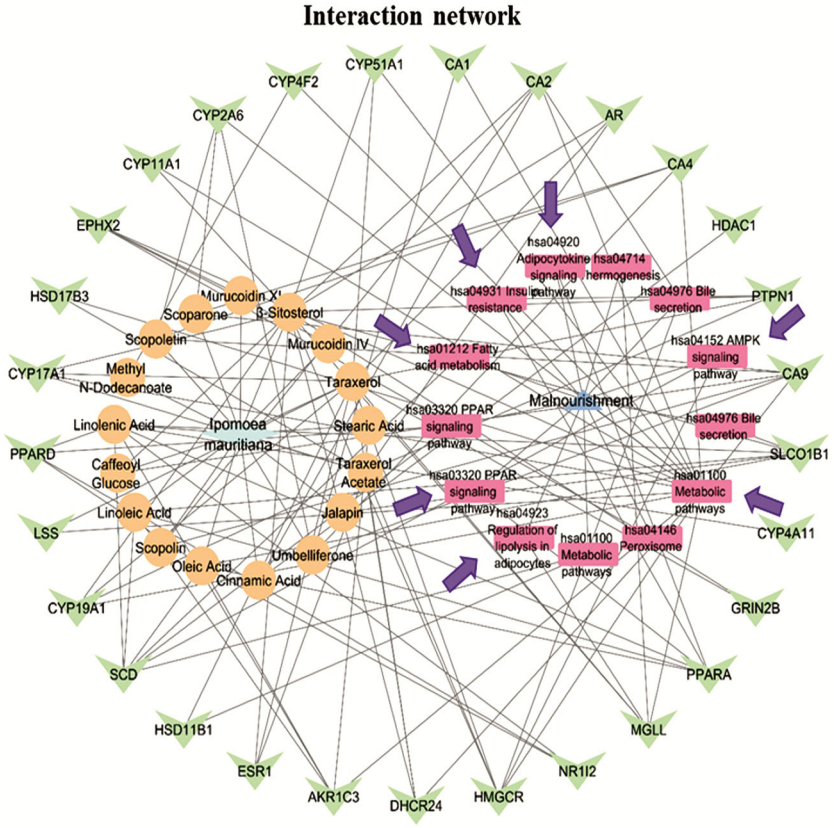


Fig. 5 — Interaction network with IM and Malnourishment as central nodes, bioactives, targets, and associated pathways as other nodes. The green diamond represents the botanical node, orange circles – phytochemical compounds, blue triangle – disease/condition, pink rectangles – pathways and green arrowheads – targets

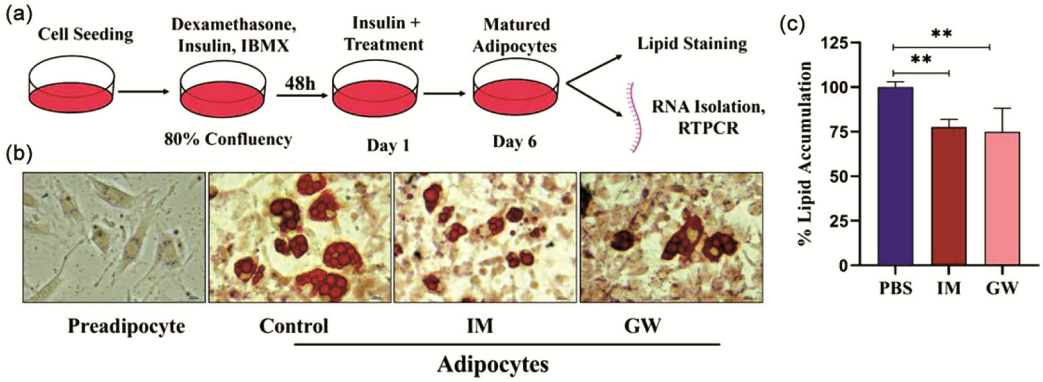


Fig. 6 — IM reduces lipid accumulation in differentiated 3T3L1 cells. (a) Treatment protocol, (b) Representative images of ORO staining of cells and (c) quantification of lipid accumulation in differentiated adipocytes. Treatment-1 µg/mL *Ipomoea mauritiana*, GW9662-1 µM. Data- Mean±SD (n=3). p-value, (*t*-test, two tailed), **<0.01

known to be metabolically protective[29], while increased *FASN* expression is linked with development of obesity and type 2 diabetes[30].

Role of adipokines is well established in adipocyte as an autocrine and paracrine signal affecting adipose homeostasis. Adiponectin is known to stimulate insulin sensitivity and lipid turnover in adipocytes[31]. It is very interesting to note that IM treatment increased *adiponectin* levels (Fig. 7g) indicating increase in insulin sensitivity. Similarly, Retinol binding protein-4 (RBP4) is an adipokine marker of insulin resistance (IR) and metabolic diseases[32]. Treatment with IM decreased its expression levels suggesting improvement in insulin sensitivity

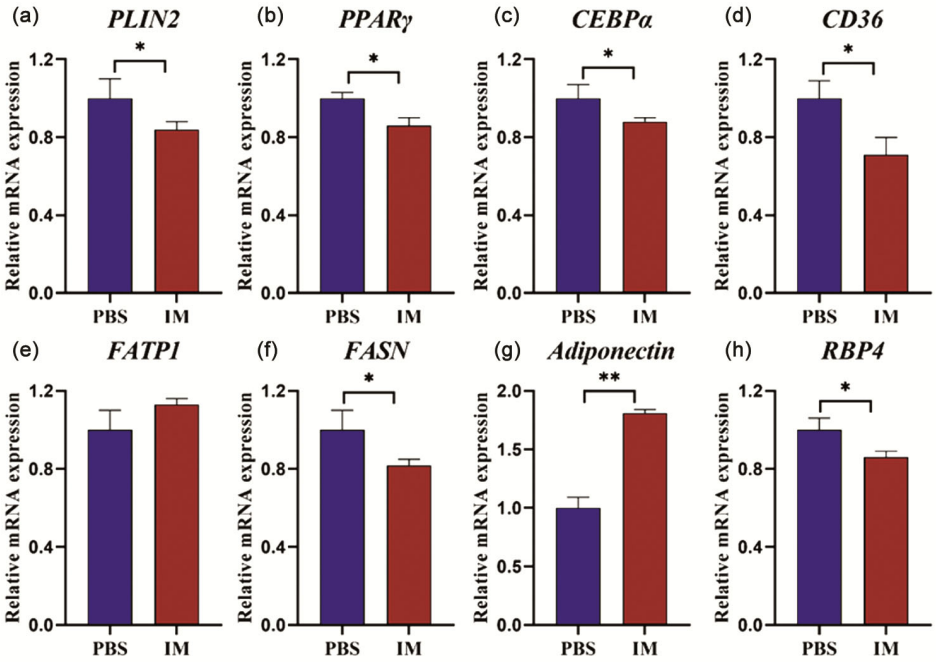


Fig. 7 — The effect of IM (1 µg/mL) on the relative gene expression of adipogenesis markers (a) *Plin2*; (b) *PPARγ*; (c) *CEBPα*; (d) *CD36* (e) *FATP1*; (f) *FASN*; (g) *Adiponectin*; and (h) *RBP4* by RT-PCR, β-actin as reference gene. Treatment-1 µg/mL *Ipomoea mauritiana*. Data- Mean±SD (n=3). p-value (*t*-test, two tailed), *<0.05,**<0.01

(Fig. 7h). Taken together, our findings suggest that the methanolic extract of IM has lipid lowering ability in differentiated adipocytes and it does so by transcriptionally regulating some key genes. The changes in adipokines support its effect in improving insulin sensitivity.

Cell-based studies validate the observations of network pharmacology.

Discussion

The number of overweight and malnourished individuals is really large and without scientific intervention, the number will continue to grow. Therefore, there is an urgent need to address both the conditions using dietary and therapeutic interventions. One step in the direction, is to scientifically understand the mode of action of several botanicals and formulations mentioned in Ayurvedic texts. Our study aims to evaluate the mechanism of action of *Ipomoea mauritiana* for the potential treatment of malnourishment, as it is described as imparting strength in weak individuals.

Traditionally, the tubers are extensively used by local communities in different parts of the Indian sub-continent, for various conditions like increasing milk production in lactating mothers, increasing body strength, improving sperm count and to control tuberculosis[6]. In all these conditions mobilization of fat deposit is a key event. Our computational analysis helped identify key bioactives and their potential target interactions. Pathway analysis pointed towards involvement of lipid metabolism and therefore, we studied changes in adipocytes.

A clinical study by S.R. Parija *et al.,* on underweight children, clearly shows administration of *Ipomoea mauritiana* leads to an increase in body weight and a reduction in weakness along with increased appetite. This study also shows increased serum protein and haemoglobin levels and reduced morbidity in children[33].

Development of breast tissue during late pregnancy and lactation shows various physiological changes as white adipose tissue trans-differentiates into pink adipose tissue with milk secreting potential. Lipid mobilization is one of the key events which help cells to gain their secretory function[34]. Reduction in lipids explains the galactogogue (increased breast milk production) property of *Ipomoea mauritiana*. Increased serum RBP4 levels in pregnant women makes them more prone to gestational diabetes[35]. Subdued expression of *RBP4* after treatment makes IM a good galactogogue for lactating mothers who are often at risk of gestational diabetes.

CD36 being a downstream signal of *PPARγ* and its decrease after IM treatment is interesting, as ablation of *CD36* in animal models has been linked to reduced

inflammation and improved insulin resistance[36]. Reduction in *FASN* upon IM treatment is also in line with reduced *PPARγ*. Inhibition of *FASN* is shown to alleviate diet-induced obesity and diabetes type 2 in animal models[37]. Reduction in muscle *FASN* improves insulin resistance and increases contraction strength[38]. This is very significant in our study as IM is known to impart strength (*Balya*) as per Ayurveda. There is increasing evidence of mutually exclusive development of adipose and muscle fibres from a common progenitor cell[39]. This opens up a new possibility to explore the effect of IM in muscle regeneration.

In a mouse model of muscular dystrophy, moderate exercise leads to reduction in adipocyte cross-sectional area while increased serum adiponectin level results in improved muscle performance[40]. Decreased adipocytes with increased adiponectin expression after IM treatment supports this observation. A glycoside isolated from tubers of *Ipomoea digitata* showed stimulant effect on myocardium and respiration[41], supporting the usage of *Ipomoea* for imparting strength.

Lipid metabolism is known to be closely related to spermatogenesis[42]. The tuber of *Ipomoea* increases spermatogenesis and hence it is used in management of male infertility[43]. Our findings are in line with these studies. The logical next step would be to fractionate the extract further and possibly identify the active ingredient(s). Furthermore, any pharmacological finding needs to be validated in animal model and subsequently in clinical studies.

Conclusion

This study for the first time reports a possible mechanism of action of *Ipomoea mauritiana* for use in common indications mentioned in Ayurveda. Network pharmacology approach identified lipid metabolism as key pathway modulated by phytochemicals present in IM. *In vitro* experiments using adipocytes revealed that the tuber extract reduces lipid content associated with changes in key molecular modulators. This lipid lowering ability of IM can be a possible reason for its known therapeutic indications. However, isolation of key active ingredients and performing *in vivo* studies will further improve our understanding of IM pharmacology.

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Conflict of interest

All authors declare no conflict of interest.

References

1 UNICEF, WHO & The World Bank, Levels and trends in child malnutrition: UNICEF / WHO / World Bank Group Joint Child Malnutrition Estimates: Key findings of the 2023 edition, (UNICEF, New York), (2023).

2 Jindal H, Suresh V, Agarwal S, Vyas P & Bari N, Understanding the dynamics of malnutrition dichotomy in India: Trends and insights from the National Family Health Surveys. *Dialogues Health*, 6 (2025) 100209.

3 WFO: Ipomoea mauritiana Jacq. Published on the Internet; http://www.worldfloraonline.org/taxon/wfo-0001298779 (Accessed on June 3, 2025).

4 Padma V, Kumar S & Venugopal SN, Use of Ksiravidari as a Substitute for Vidari as per Ayurvedic Descriptions. *Indian J Tradit Knowl*, 8 (2009) 310.

5 Bharti R, Chopra BS, Raut S & Khatri N, *Pueraria tuberosa*: A Review on Traditional Uses, Pharmacology, and Phytochemistry. *Front Pharmacol,* 11 (2021) 582506.

6 Goncalves MD, Hwang SK, Pauli C, Murphy CJ, Cheng Z, Hopkins BD, Wu D, Loughran RM, Emerling BM, Zhang G, Fearon DT & Cantley LC, Fenofibrate prevents skeletal muscle loss in mice with lung cancer. *Proc Natl Acad Sci U S A*, 115 (2018) E743.

7 Badaloo A V, Forrester T, Reid M & Jahoor F, Lipid kinetic differences between children with kwashiorkor and those with marasmus. *Am J Clin Nutr*, 83 (2006) 1283.

8 van Zutphen T, Ciapaite J, Bloks VW, Ackereley C, Gerding A, Jurdzinski A, de Moraes RA, Zhang L, Wolters JC, Bischoff R, Wanders RJ, Houten SM, Bronte-Tinkew D, Shatseva T, Lewis GF, Groen AK, Reijngoud DJ, Bakker BM, Jonker JW, Kim PK & Bandsma RH, Malnutrition-associated liver steatosis and ATP depletion is caused by peroxisomal and mitochondrial dysfunction. *J Hepatol*, 65 (2016) 1198.

9 Nørrelund H, Nair KS, Nielsen S, Frystyk J, Ivarsen P, Jørgensen JOL, Christiansen JS & Møller N, The Decisive Role of Free Fatty Acids for Protein Conservation during Fasting in Humans with and without Growth Hormone. *J Clin Endocrinol Metab*, 88 (2003) 4371.

10 Muthuramalingam P, Jeyasri R, Varadharajan V, Priya A, Dhanapal AR, Shin H, Thiruvengadam M, Ramesh M, Krishnan M, Omosimua RO, Sathyaseelan DD & Venkidasamy B, Network pharmacology: an efficient but underutilized approach in oral, head and neck cancer therapy—a review. *Front Pharmacol*, 15 (2024) 1410942.

11 Chandran U, Mehendale N, Tillu G & Patwardhan B, Network Pharmacology of Ayurveda Formulation Triphala with Special Reference to Anti-Cancer Property. *Comb Chem High Throughput Screen*, 18 (2015) 846.

12 Mitra S, Munni YA, Dash R, Sultana A & Moon IS, Unveiling the effect of *Withania somnifera* on neuronal cytoarchitecture and synaptogenesis: A combined *in vitro* and network pharmacology approach. *Phytother Res*, 36 (2022) 2524.

13 Kim S, Chen J, Cheng T, Gindulyte A, He J, He S, Li Q, Shoemaker BA, Thiessen PA, Yu B, Zaslavsky L, Zhang J &

Bolton EE, PubChem 2025 update. *Nucleic Acids Res*, 53 (2025) D1516.
14 Liu T, Lin Y, Wen X, Jorissen RN & Gilson MK, BindingDB: a web-accessible database of experimentally determined protein-ligand binding affinities. *Nucleic Acids Res*, 35 (2007) D198.
15 Daina A, Michielin O & Zoete V. SwissTargetPrediction: updated data and new features for efficient prediction of protein targets of small molecules. *Nucleic Acids Res*, 47 (2019)W357.
16 Szklarczyk D, Kirsch R, Koutrouli M, Nastou K, Mehryary F, Hachilif R, Gable AL, Fang T, Doncheva NT, Pyysalo S, Bork P, Jensen LJ & von Mering C, The STRING database in 2023: protein–protein association networks and functional enrichment analyses for any sequenced genome of interest. *Nucleic Acids Res*, 51 (2023) D638.
17 Shannon P, Markiel A, Ozier O, Baliga NS, Wang JT, Ramage D, Amin N, Schwikowski B & Ideker T, Cytoscape: A Software Environment for Integrated Models of Biomolecular Interaction Networks. *Genome Res*, 13 (2003) 2498.
18 Barabási AL & Oltvai ZN, Network biology: understanding the cell's functional organization. *Nat Rev Genet*, 5 (2004) 101.
19 Ge SX, Jung D & Yao R, ShinyGO: a graphical gene-set enrichment tool for animals and plants. *Bioinformatics*, 36 (2020) 2628.
20 Bhatia K, Tiwari S, Gupta VK, Sapariya NM & Upadhyay SK, An *in vitro* model of adipose tissue-associated macrophages. *J Biosci*, 49 (2024) 79 .
21 Ruiz-Ojeda F, Rupérez A, Gomez-Llorente C, Gil A & Aguilera C, Cell Models and Their Application for Studying Adipogenic Differentiation in Relation to Obesity: A Review. *Int J Mol Sci*, 17 (2016) 1040.
22 Sapariya NM, Bhatia K, Gupta VK, Godbole A & Upadhyay SK, Ksheer vidari or Ipomoea mauritiana increases M2 macrophage population. *J Ayurveda*, 19 (2025) 357.
23 Itabe H, Yamaguchi T, Nimura S & Sasabe N, Perilipins: a diversity of intracellular lipid droplet proteins. *Lipids Health Dis*, 16 (2017) 83.
24 Evans RM, Barish GD & Wang YX, PPARs and the complex journey to obesity. *Nat Med*, 10 (2004) 355.
25 Ahmadian M, Suh JM, Hah N, Liddle C, Atkins AR, Downes M & Evans RM, PPARγ signaling and metabolism: the good, the bad and the future. *Nat Med*, 19 (2013) 557.
26 Tontonoz P & Spiegelman BM, Fat and Beyond: The Diverse Biology of PPARγ. *Annu Rev Biochem*, 77 (2008) 289.
27 Rosen ED, Hsu CH, Wang X, Sakai S, Freeman MW, Gonzalez FJ & Spiegelman BM, C/EBPα induces adipogenesis through PPARγ: a unified pathway. *Genes Dev*, 16 (2002) 22.
28 Love-Gregory L & Abumrad NA, CD36 genetics and the metabolic complications of obesity. *Curr Opin Clin Nutr Metab Care*, 14 (2011) 527.
29 Berndt J, Kovacs P, Ruschke K, Klöting N, Fasshauer M, Schön MR, Körner A, Stumvoll M & Blüher M, Fatty acid synthase gene expression in human adipose tissue: association with obesity and type 2 diabetes. *Diabetologia*, 50 (2007) 1472.
30 Nguyen TD, Adiponectin: Role in physiology and pathophysiology. *Int J Prev Med*, 11 (2020) 136.
31 Fan J, Yin S, Lin D, Liu Y, Chen N, Bai X, Ke Q, Shen J, You L, Lin X, Li F, He F, Yan L, Chen C & Xia M, Association of Serum Retinol-Binding Protein 4 Levels and the Risk of Incident Type 2 Diabetes in Subjects with Prediabetes. *Diabetes Care*, 42 (2019) 1574.
32 Parija SR, Harichandan BK & Jayasingh BK, Clinical Study on underweight Children with Kshiravidari (Ipomia digitata Linn.). *J Res Ayur Sci*, 32 (2011) 149.
33 Kothari C, Diorio C & Durocher F, The Importance of Breast Adipose Tissue in Breast Cancer. *Int J Mol Sci*, 21 (2020) 5760.
34 Mousavi SN, Bahramfard T, Rad EY, Hosseinikia M & Saboori S, Association of Leptin and Retinol Binding Protein 4 with the Risk of Gestational Diabetes: A Systematic Review and Meta-Analysis of Observational Studies. *Indian J Endocrinol Metab*, 27 (2023) 96.
35 Kennedy DJ, Kuchibhotla S, Westfall KM, Silverstein RL, Morton RE & Febbraio M, A CD36-dependent pathway enhances macrophage and adipose tissue inflammation and impairs insulin signalling. *Cardiovasc Res,* 89 (2011) 604.
36 Kumar MV, Shimokawa T, Nagy TR & Lane MD, Differential effects of a centrally acting fatty acid synthase inhibitor in lean and obese mice. *Proc Natl Acad Sci U S A*, 99 (2002) 1921.
37 Funai K, Song H, Yin L, Lodhi IJ, Wei X, Yoshino J, Coleman T & Semenkovich CF, Muscle lipogenesis balances insulin sensitivity and strength through calcium signaling. *J Clin Invest*, 123 (2013) 1229.
38 Chen W, You W, Valencak TG & Shan T, Bidirectional roles of skeletal muscle fibro-adipogenic progenitors in homeostasis and disease. *Ageing Res Rev*, 80 (2022) 101682.
39 Zelikovich AS, Quattrocelli M, Salamone IM, Kuntz NL & McNally EM, Moderate exercise improves function and increases adiponectin in the mdx mouse model of muscular dystrophy. *Sci Rep,* 9 (2019) 5770.
40 Matin MA, Tewari JP & Kalani DK, Pharmacological Effects of Paniculatin—a Glycoside Isolated from *Ipomoea Digitata* Linn. *J Pharm Sci*, 58 (1969) 757.
41 Yang CF, Liu WW, Wang HQ, Zhang JL, Li K, Diao ZY, Yue QL, Yan GJ, Li CJ & Sun HX, Gonadal white adipose tissue is important for gametogenesis in mice through maintenance of local metabolic and immune niches. *J Biol Chem*, 298 (2022) 101818.
42 Mahajan G, Mahajan R & Mahajan A, Improvement of sperm density in neem-oil induced infertile male albino rats by Ipomoea digitata Linn. *J Intercult Ethnopharmacol*, 4 (2015) 125.