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Obesity research: Status quo and future outlooks

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Sleeve Gastrectomy, and other bariatric procedures are therefore under intense investigation. In this review, however, we will focus on obesity treatment, highlighting new insights and future trends of gut hormone research, the relation of obesity and cancer development *via* the obesity induced chronic state of inflammation, and new potential concepts of interventional and conservative obesity treatment.

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Key words: Obesity; Cancer; Gut hormones; Bariatric surgery

Core tip: This review focuses on the latest obesity research breakthroughs, current therapy options, future outlooks, also from a view of a surgeon as well as recently identified molecules that promote obesity and its comorbidities, outlining their great potential as new target molecules in the fight against the global pandemic, called "obesity".

Abstract

Obesity is a multifactorial disease showing a pandemic increase within the last decades in developing, and developed countries. It is associated with several severe comorbidities such as type II diabetes, hypertension, sleep apnea, non-alcoholic steatosis hepatitis and cancer. Due to the increasing number of overweight individuals worldwide, research in the field of obesity has become more vital than ever. Currently, great efforts are spent to understand this complex disease from a biological, psychological and sociological angle. Further insights of obesity research come from bariatric surgery that provides new information regarding hormonal changes during weight loss. The initiation of programs for obesity treatment, both interventional and pharmaceutical, are being pursued with the fullest intensity. Currently, bariatric surgery is the most effective therapy for weight loss and resolution of comorbidities in morbid obese patients. Reasons for weight loss and remission of comorbidities following Roux-en-Y-Gastric Bypass,

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INTRODUCTION

Obesity is a multifactorial disease caused by an energy sparing lifestyle on a predisposed polygenetic background. An obese person is defined as having a body mass index (BMI) greater than 30 kg/m². Within the last decades, there has been an extraordinary increase in the worldwide prevalence of obesity becoming a major human health threat especially in developing and developed countries with a tendency to rise. Being referred to as a global pandemic^[1], the number of overweight or obese

individuals increased up to 2.1 billion worldwide. Unfortunately, no single country announced decreasing numbers of obese individuals during the last three decades^[2]. Obesity is associated with several severe comorbidities (Figure 1) such as type II diabetes mellitus (T2DM), hypertension, sleep apnea, non-alcoholic steatosis hepatitis (NASH) and cancer. Obesity-related diabetes can lead to coronary heart disease, apoplex or kidney failure. Over 80% of all patients with type II diabetes in the United States are overweight and up to 20% of United States health expenditures are estimated to be spent on treating obesity-related diseases^[3].

It is expected that NASH will be the leading cause of liver transplantation within the next years^[4]. Additionally, obesity is associated with an increased risk of developing various cancer entities such as colorectal-, esophageal-, liver- and breast cancer^[5]. Visceral-, orthopedic or cardiac surgical treatment of obese patients is associated with higher complication rates^[6-9]. Subsequently, obesity is the origin of a wide spectrum of diseases and a confounding factor hindering adequate treatment. Due to this reasons, obesity and overweight are associated with an increased risk of death. Thus, therapy for obesity should be individually tailored and various factors such as sex, obesity degree, individual health risks should be taken into account^[10,11].

Secondary causes for obesity like endocrine disorders (*e.g.*, hypothyroidism, cushing disease), drug-induced obesity (*e.g.*, glucocorticoids, psychoactive drugs), inherited syndromes (*e.g.*, Prader-Willi syndrome, Bardet-Biedl syndrome) or monogenetic disorders (leptin receptor, melanocortin receptor) play a minor role or are cofactors in causation of obesity in daily practice. Therefore, identifying single reasons for obesity is a complex task. Intervention strategies for weight loss and maintenance at the individual and community level are strongly needed to reduce general health risks as well as health expenditures.

STATUS QUO

Due to the increasing number of overweight individuals worldwide, research in the field of obesity has become more vital than ever. As a multifactorial disease, research is conducted at a wide variety of areas. Currently, great efforts are spend to understand this complex disease from a biological, psychological and sociological angle. Further insights of obesity research come from bariatric surgery, which display new information regarding the hormonal changes during weight loss. The initiation of programs aiming to treat obesity, both interventional and pharmaceutical, are being pursued with the fullest intensity. There are various scopes of possible research activities. In this review, however, we will focus on obesity treatment, highlighting new insights into gut hormones and the relation of obesity and cancer development.

Multidisciplinary Treatment Modalities-or, how to lock the stable door after the horse had bolted

Among physicians there is consensus, to treat obese patients multidisciplinary. After diagnosis, the patient

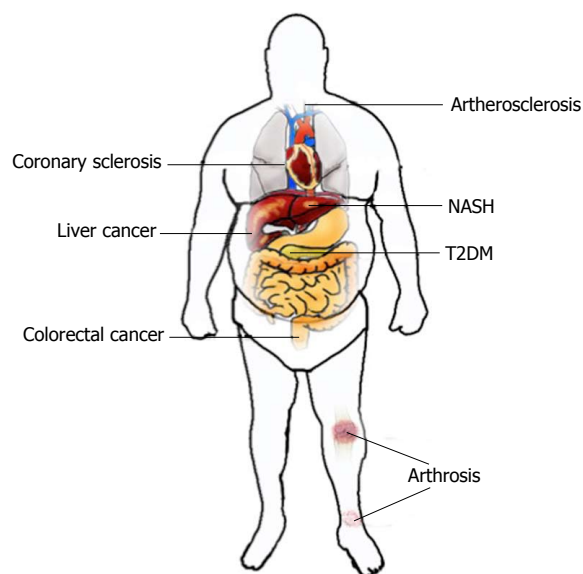


Figure 1 Obesity related diseases. T2DM: Type 2 diabetes mellitus; NASH: Non-alcoholic steatosis hepatitis.

should undergo a multimodal therapy concept based on individualized dietary education focusing on reducing energy intake, physical exercising, pharmacological therapy and psychological attendance with behavioral therapy. For the latter, many efforts to modify the behavior of obese individuals through encouragement of changes in dietary intake along with physical activity have not declined the obesity epidemic, unfortunately. The primary causes are high rates of therapy abandonment and poor patient compliance.

Patients who completed a comprehensive program including a low-calorie diet are able to lose approximately 15%-25% of their initial body weight during 3 to 6 mo of treatment. After therapy, most patients maintain a weight loss of 8% one year after treatment, 7% three years after treatment, and 5% four years after treatment^[12]. These results represent the best-case scenario, excluding patients who dropped out of their programs. It was already shown that patients who have completed structured weight loss programs, maintained their weight loss of less than 3 kg on average after 5 years; patients who accomplished more radical low-calorie diets had significantly higher weight loss of up to 20 kg and maintained more weight loss over time^[13]. In a randomized study, Jeffery *et al*^[14] evaluated the efficacy of long-term weight loss comparing one group with behavior therapy and an energy expenditure goal of 1000 kcal per week to a group of patients with high physical activity treatment and an energy expenditure goal of 2500 kcal per week. The high activity group showed significant higher weight loss and long term weight loss maintenance, reflecting that mobility is of high importance^[14].

Is bariatric surgery the best choice for long-term weight loss accompanied by remission of comorbidities in severe obese (BMI > 40 kg/m²) patients?

Bariatric surgery is more effective for weight loss and

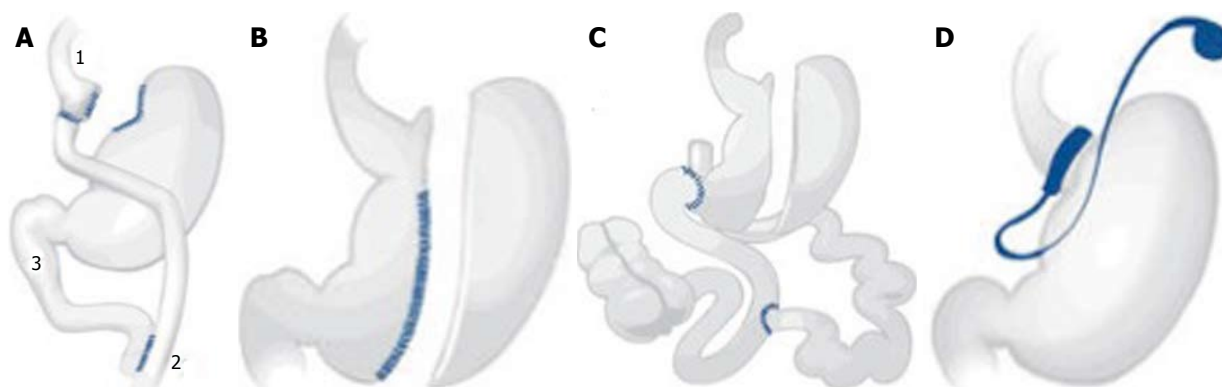


Figure 2 Bariatric surgical procedures. A: Roux-Y gastric bypass; B: Sleeve gastrectomy; C: Biliopancreatic diversion with duodenal switch; D: Gastric band.

resolution of comorbidities than conventional medical treatment modalities^[15,16]. A variety of procedures are described in the literature but only Roux-Y gastric bypass (RYGB) (46.6% of all bariatric procedures worldwide), sleeve gastrectomy (SG) (27.8%), adjustable gastric banding (GB) (17.8%) and in a smaller proportion biliopancreatic diversion with duodenal switch (BPD/DS) (2.2%) are performed in a notable quantity^[17].

Gastric bypass was first performed in the 1960s by Mason *et al.*^[18]. It was modified to a RYGB in the 1970s^[19]. It is still the most common bariatric surgical procedure. The combination of food-intake restriction by a small pouch and malabsorption through the smaller common channel (Figure 2A) leads to long-term weight loss^[15]. Also, hormonal changes after surgery may have a great impact on weight loss and diabetes remission.

SG (Figure 2B), includes the resection of the greater curve of the stomach. It is the first step of the BPD/DS (Figure 2C). BPD/DS can be performed by a two step procedure; a minority of patients do not need the second surgical step for weight loss^[20]. While SG is described as a primary restrictive procedure, including minor hormonal changes, BPD/DS causes malabsorption and leads to a higher rate of deficiencies^[21]. GB, which was developed in the 1970s, restricts food-intake by an inflatable, adjustable gastric band resulting in a small gastric pouch (Figure 2D). Since it is based on restriction only, it is the most insufficient bariatric surgical procedure regarding long-term weight loss^[22].

Overall, a preoperative multidisciplinary program is recommended. Our own clinical experiences and a review of the literature revealed that bariatric surgery for severe obese patients results in extensive weight loss and long-term comorbidity remission in a very short time frame.

There is no evidence for conventional treatment leading to sufficient excess weight loss in severe obese patients.

Padwal *et al.*^[23] performed an observational study of 500 patients with a two years follow-up. Three patient cohorts were included in which 200 patients received medical treatment, 150 patients received bariatric surgical treatment, and 200 patients received no therapy and were grouped as being waitlisted. Medically treated patients

received individualized and intensive medical management consisting of a 24-36 wk life style counseling (diet education, physical exercise, and behavioral therapy) and were observed by a multidisciplinary staff which is mandatory before bariatric surgery. Mean weight loss in the waitlisted group was 0.9%, 1.8% in the medically treated group and 22% in the surgery group. The proportion of patients who achieved at least 5% weight loss was 17% in the waitlisted group, 32% in the medically treated group and 75% in the surgery group. The prevalence of hypertension, diabetes and dyslipidemia was reduced in the surgical group, but remained unchanged or increased in the medically treated and waitlisted group^[23].

A large meta-analysis included 164 studies (37 randomized controlled trials and 127 observational studies). A total of 161756 patients were analyzed regarding effectiveness and outcome after bariatric surgery.

One year after surgery the patients showed 60% excess weight loss (EWL), and 57% EWL after 3 years. T2DM remission after surgery was 92%, hypertension remission was 75%, dyslipidemia remission was 76%, cardiovascular diseases remission was 58% and remission of sleep apnea was 96%, reflecting that surgical intervention may increase the long-term quality of life^[24].

Interestingly, 75.3% of patients that received bariatric surgery showed excess weight loss, whereas patients that had received conventional therapy showed only 11.3% excess weight loss. Moreover, remission of T2DM was reported in 63.5% of cases in surgery group, compared to 15.6% of patients in the conventional therapy group^[25]. Subsequently, there is no evidence for conventional treatment leading to sufficient EWL in obese patients with a BMI greater 40 kg/m². In fact, the only efficient treatment showing results in EWL and release of obesity associated diseases results from bariatric surgery. However, there is a strong recommendation to include the patients to a perioperative multidisciplinary medical treatment consisting of dietary changes, exercising and behavioral therapies. There is evidence that preoperative multidisciplinary preparation and education may lead to better long-term effects of bariatric surgery.

In sum, bariatric surgery is currently the only effective treatment for morbid obesity^[26]. Reasons for weight loss

Table 1 Gut hormones and their clinical relevance

Peptide	Production site	Effect	After bariatric surgery	Potential pharmaceutical intervention
Ghrelin	Stomach, mainly fundus	Appetite stimulating Growth hormone releasing	↓	Receptor antagonists GOAT inhibition Vaccination
GLP-1	L-cells of the distal small bowel	Postprandial insulin secretion Suppresses glucagon secretion Delays gastric emptying Suppresses appetite	↑	Weight loss in patients with diabetes Off-label use in obese patients
GIP	Duodenum, jejunum	Postprandial insulin secretion Energy expenditure	↓	GIP receptor antagonist
CCK	Duodenum, jejunum	Delays gastric emptying Suppresses appetite	↑	CCK analogue substance
PYY	Distal small bowel	Delays gastric emptying Suppresses appetite	↑	Long-acting analogue substance
PP	Distal small bowel	Suppresses appetite	↔	PP analogue substance
OXM	L-cells of the distal small bowel	Delays gastric emptying Suppresses appetite Increase energy expenditure	↑	Receptor agonist

Modified according to Kim *et al.*^[35]. GLP-1: Glucagon-like peptide-1; GIP: Glucose-dependent insulintropic polypeptide; CCK: Cholecystokinin; PYY: Peptide YY; PP: Pancreatic polypeptide; OXM: Oxyntomodulin; GOAT: Ghrelin O-acyltransferase.

and remission of comorbidities following RYGB, SG, and other bariatric procedures are therefore in a strong research focus.

Gut hormones and their impact on weight loss

Alterations of gut hormone serum levels after RYGB influence appetite, satiety, energy expenditure, and glucose homeostasis^[27-29]. Several hormones and peptides are considered to be involved in weight loss in bariatric patients (Table 1).

Incretins are gut-derived peptides that increase pancreatic insulin secretion. The Glucagon-like peptide (GLP-1) and Glucose-dependent insulintropic polypeptide (GIP) are well explored. GLP-1 and its analogues are used to treat diabetes. Beside its stimulating effects on β -cells of pancreatic Langerhans' islets, GLP-1 also suppresses glucagon secretion, delays gastric emptying and suppresses appetite^[30,31]. Therefore, GLP-1 is currently under intense discussion to become a potential therapeutic drug for obesity treatment^[32].

Ghrelin is mainly produced in the fundus of the stomach and plays an important role in satiety. When administered to humans, it increases food intake. Several studies showed that postprandial reduction of Ghrelin after bariatric surgery led to weight loss and T2DM remission^[33,34]. Therefore, lowering of Ghrelin plasma levels by non-surgical interventions might be a useful approach for obesity treatment. Different approaches already exist in the development of anti-obesity drugs. Pharmacological molecules like Ghrelin antagonists or Ghrelin receptor antagonists showed heterogeneous results in food intake reduction^[35]. Other strategies are the inhibition of Ghrelin O-acyltransferase (GOAT) that is required for activation of Ghrelin^[36] or lowering body weight by a vaccination targeting Ghrelin^[37].

Administration of Oxyntomodulin (OXM) decreases food intake and reduces body weight in rats^[38]. Further-

more, OXM has been shown to increase energy expenditure^[39]. The combination of decreasing energy intake and increasing energy consumption qualifies OXM to be a potential agent for bariatric treatment. Moreover, a plethora of other gut hormones and peptides are currently under intense investigation regarding weight loss. Interestingly, there is also evidence that various gut hormones are related to cancer growth and cancer development making their physiological understanding even more alluring^[40].

Obesity and cancer

Morbid obesity is associated with various types of cancer: Epidemiological studies identified an association of morbid obesity and several types of cancer disease, such as colorectal cancer, endometrium carcinoma, postmenopausal breast cancer, kidney cancer, esophageal cancer, pancreatic cancer, gallbladder cancer, liver cancer, and hematological malignancies^[41,42]. Obese patients have a tendency for worse prognosis and outcome after cancer treatment and an increased risk of cancer related morbidity^[43]. Calle *et al.*^[5] conducted a prospective study to examine the association of obesity and cancer related mortality. They concluded that increased body weight is associated with increased death rates for all cancers combined.

The link between obesity and cancer is still poorly understood. Several adipokines, growth factors, signaling pathways, inflammatory processes as well as the general demodulation of energy-balance and the lack of calorie restriction are being intensively discussed.

Adipokines are involved in cancer development: Traditionally, the adipose tissue was considered to be an energy storage organ. In recent years, however, it became evident that it also functions as an endocrine organ. Besides estrogen, it produces and secretes various adipokines and cytokines. Leptin and adiponectin, two well characterized adipokines, are associated with cancer development^[44].

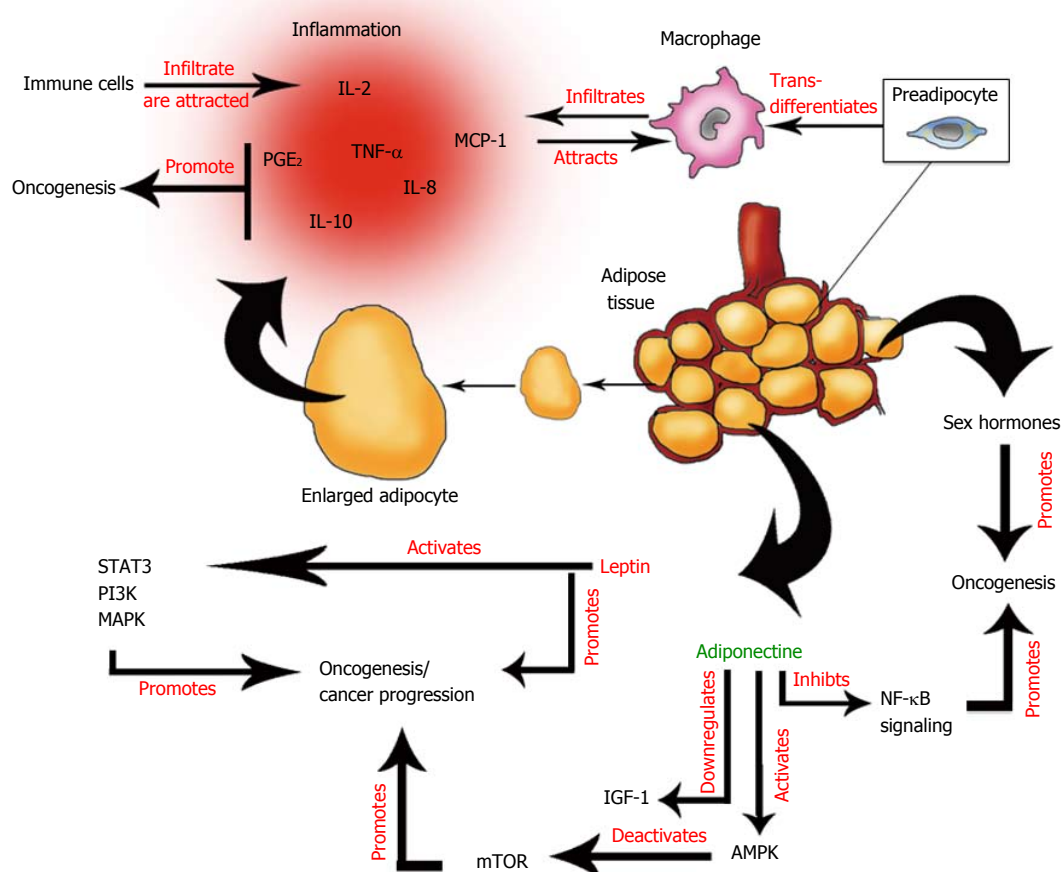


Figure 3 Endocrine, inflammatory, and cancer promoting effects of adipose tissue. IL-8: Interleukin 8; PGE₂: Prostaglandin E₂; TNF- α : Tumor necrosis factor- α ; MCP-1: Monocyte chemoattractant protein-1; STAT3: Signal transducer and activator of transcription 3; PI3K: Phosphatidylinositol-4,5-bisphosphate 3-kinase; MAPK: Mitogen-activated protein kinase; NF- κ B: Nuclear-factor-kappa-light-chain-enhancer activated B cells; IGF-1: Insulin-growth factor-1; AMPK: 5'AMP-activated protein kinase; mTOR: Mechanistic target of rapamycin.

Leptin concentration in serum correlates positively with the patients' adipose tissue reserves and their nutritional condition. Moreover, leptin has been identified to be a potential mediator of cancer development^[45], which is able to activate various key players of different signaling cascades like phosphatidylinositol-4,5-bisphosphate 3-kinase (PI3K), mitogen-activated protein kinase (MAPK) and signal transducer and activator of transcription 3 (STAT3). More interestingly, leptin signaling promotes the progression of different cancers^[46-48].

Adiponectin is mainly secreted by visceral fat cells and acts adversary to leptin. It is inversely associated with obesity, hyperinsulinemia, and inflammation and may have anti-cancer effects by decreasing insulin-growth factor-1 (IGF-1) and mechanistic target of rapamycin (mTOR) signaling by activation of 5'AMP-activated protein kinase (AMPK). Also anti-inflammatory actions of adiponectin are described through inhibition of nuclear-factor-kappa-light-chain-enhancer activated B cells signaling (NF- κ B)^[49].

Increased carcinogenesis in obese patients might be due to chronic inflammation

Recent studies suggest a causal link of obesity related

diseases (Figure 3) and low-grade/chronic inflammation (Figure 3)^[50-52].

In humans, the immune system is of major relevance, which in turn, is able to form a defence shield against bacteria, viruses, or injured cells. A hallmark of the immune system is its most powerful weapon, the "inflammatory response" which was already noticed by a German pathologist called Rudolf Virchow in 1863. Despite the fact that humans without a functional immune system are not able to survive, too much inflammation can have a great impact and may cause serious damage to the healthy individual. Well-known chronic inflammatory diseases occur in patients that suffer from psoriasis or rheumatoid arthritis. A possible link between infections and cancer already exists, since stomach cancer may result from *Helicobacter pylori* infections or liver cancer from hepatitis (B-, C-) virus infections. A unique feature of these infections is the chronic inflammation response, which is primarily mediated by specific immune cells, such as macrophages and granulocytes that infiltrate the tumor. The latter is known to be recruited by tumor-released attractants. Once leucocytes infiltrate the tumor, they start to secrete chemokines and thereby initiate blood vessel growth/angiogenesis to allocate oxygen and nutrients,

which are relevant for tumor growth.

Circulating immune cell recruitment is a crucial feature of immune response

Macrophages: In obese individuals, macrophages infiltrate and expand in adipose tissue. Quantitative and functional changes of these cells affect adipose tissue inflammation. Exposure of macrophages to cytokines promotes two different activation states inducing to divergent polarizations. M1 macrophages are activated by tumor necrosis factor- α (TNF- α), Interferon- γ (IFN- γ), and bacterial endotoxins such as lipopolysaccharides. They are characterized by high levels of interleukin (IL)-12 and IL-23, and low levels of IL-10 as well as inflammatory cytokines^[53]. Contrarily, M2 macrophages are attracted by IL-4, IL-13, IL-10, and glucocorticoid hormones. Both types are part of innate immune response. M1 macrophages may induce chronic inflammation, whereas M2 macrophages tend to act anti-inflammatory^[54]. It has been suggested, that a phenotypic switch from M2 to M1 occurs in fat tissue^[55], however, this model is discussed controversially.

Eosinophiles: Eosinophiles levels are negatively correlated with obesity and adipose tissue in mice. Wu *et al*^[54] could show, that eosinophiles promote an M2-polarization of macrophages by secreting IL-4 and IL-13 and a down regulation of M1 macrophages in adipose tissue.

Mast cells: Mast cell levels in adipose tissue are elevated in obese animals^[56]. Mast cell ablation reduces body fat and benefits glucose homeostasis in mice. This effect is induced by IL-6 and IFN- γ . Also, pro-angiogenic factors such as Cathepsins may influence mast cell levels^[56].

Myeloid-derived suppressor cells: In adipose tissue, Myeloid-derived suppressor cells (MDSCs) have an inhibitory effect on inflammation by suppressing CD8⁺-T cells and promoting M1 to M2 macrophage switch in favour for M2 macrophages^[57]. The state of chronic inflammation in adipose tissue leads to an accumulation of MDSCs^[58]. Being part of immune autoregulation by MDSCs suppress overt inflammatory immune response in chronic inflammation^[59].

CD4⁺-T cells: CD4⁺-T cell activation is mediated by class II major histocompatibility complex (MHC II) molecules presented by macrophages and dendritic cells. When activated, CD4⁺-T cells secrete cytokines, which attract pro-inflammatory cells. Three groups of T cells can be distinguished, namely T_{H1}, T_{H2}, and T_{H17}.

The ratio of T_{H1}/T_{H2} cells is significantly enhanced in high fat diet induced obesity, since T_{H2} cells are undermined by IFN- γ producing T_{H1} cells^[60]. CD4⁺-T cell substitution in immunodeficient mice eventuates in reduction of weight gain, adipocyte cell size, and improvement of glucose homeostasis^[60]. The STAT6 pathway is essential for T_{H2} differentiation, thus STAT6 deficient CD4⁺-T cells do not show any effect of reconstitution on glucose

homeostasis and body weight gain^[60].

Regulatory T cells: CD4⁺-T cells can transdifferentiate into immunosuppressive CD4⁺CD25⁺-regulatory T cells (T_{reg})^[61]. Obesity is associated with reduced levels of T_{reg} cells in visceral adipose tissue in mice and humans^[62,63]. T_{reg} cell depletion enhances circulating insulin levels and levels of pro-inflammatory cytokines in adipose tissue of lean mice^[62]. Up regulation of T_{reg} on the other hand improves insulin sensitivity and enhances anti-inflammatory cytokine IL-10 levels^[62]. Also, T_{reg} function to suppress pro-inflammatory immune response and promote macrophage M1 to M2 switch by secreting IL-4, IL-10, and IL-13^[64].

CD8⁺-T cells: CD8⁺-T cell activation is mediated by MHC I. Activated CD8⁺-T cells induce lysis of target cells by producing various cytokines and chemokines.

Adipose tissue of obese animals^[65] and humans^[60] show a significant increase of CD8⁺-T cell levels. CD8⁺-T cells lead to elevation of macrophages in adipose tissue and promote polarization into M1 macrophages^[63]. CD8⁺-T cell deficient mice have fewer levels of macrophages in adipose tissue and less levels of TNF- α and IL-6^[63].

Natural killer T cells: When activated by lipids, natural killer T (NKT) cells produce a significant amount of T_{H1}- and T_{H2}-responsive cytokines, such as IFN- γ and IL-4^[66]. NKT cells can either promote or suppress inflammatory response by promoting either T_{H1} or T_{H2} cell activation^[67,68]. Interestingly, NKT cell levels are reduced in human omental adipose tissue^[69]. The role of NKTs in obesity still remains unclear.

B cells: After high fat diet, accumulation of B cells can be detected in adipose tissue of mice. This accumulation is associated with high levels of pro-inflammatory immunoglobulin G2c^[70]. B cells promote T cell modulation and macrophage polarization by producing pathogenic Ig-G antibodies. Ig-G, however, increases inflammatory response^[70]. The specific role of B-cells and Ig-G in inflammatory response in obesity has yet to be further investigated.

Mediators of inflammatory response: Preadipocytes can transdifferentiate into macrophages^[71]. Also they tend to enlarge due to oxygen diffusion resulting in hypoxia, inflammation and increased macrophage infiltration. Enlarged adipocytes produce a variety of inflammatory cytokines and show greater insulin resistance than normal sized ones. Levels of prostaglandin E2, TNF- α , IL-2, IL-8, IL-10, and monocyte chemoattractant protein-1 (MCP-1) are elevated in the microenvironment of enlarged adipocytes. The inflammatory environment attracts macrophages and induces production of additional pro-inflammatory mediators^[71].

NF- κ B is a central transcription factor that is activated upon bacterial and viral stimuli. It activates gene

expression associated with apoptosis, cell proliferation, inflammation, tumorigenesis, metastasis, and angiogenesis^[72]. In addition, increased NF- κ B expression and activation is associated with insulin resistance.

The frequent up-regulation of NF- κ B in many cancers is already known^[73]. The increased expression and “uncontrolled” activation of NF- κ B may induce cancerogenesis^[74,75]. Interestingly, NF- κ B gets activated upon leptin stimulation in preneoplastic and neoplastic human colonic epithelial cells *in vitro*^[76,77].

Inflammasomes, by definition cytosolic multiprotein complexes, activate IL-1 β and IL-18 during infection or tissue damage^[78]. They can be sub-divided into different inflammasome sub-groups such as nucleotide-binding oligomerization domain-like receptors (NLR), NLR pyrin domain-containing 1 and 3 (NLRP1 and NLRP3), absent in melanoma 2, and caspase activation and recruitment domains domain containing 4 (NLRC4/IPAF)^[78]. Inflammasomes secrete caspase 1, which cleaves cytokine preforms, such as IL-1 β ^[79,80]. The activity of NLR is associated with autoimmune diseases, malignancies, inflammation, infection, and metabolic disorders^[59]. Inflammasome components expression levels are elevated in adipose tissue of obese mice^[81-83]. Conversely, NLRP3 and IL-1 β are decreased in low calorie dietary restriction^[83]. It seems therefore, that NLRP3 integrates multiple signals, causing pathogenic inflammation in obese subjects^[84]. Also NLRP6 has a critical role in gut homeostasis^[85,86]. Mice with non-functional NLRP6 develop an altered commensal system, preventing normal glycaemic control on a high fat diet and promoting NASH^[87].

In summary, there are at least two inflammasome types and substrates that can imbalance metabolism and inflammation in obesity^[85].

Linking obesity to cancer-inflammation is a double-edged sword

The role of chronic inflammation as a precursor of tumorigenesis can be observed in various cancers. A gastritis can give rise to gastric cancer, inflammatory bowel disease may promote colorectal cancer and patients suffering from a chronic pancreatitis may have a higher risk to develop pancreatic cancer^[88]. The inflammatory effect of adipose fat tissue might therefore be a general precursor of cancerogenesis. Like adipose tissue, tumor microenvironment is composed of multiple cell types like fibroblasts, epithelial cells, mast cells, and cells of innate and adaptive immune system that favor a pro-inflammatory, pro-tumorigenic environment^[89-91].

Contribution to the pro-inflammatory environment is the presence of macrophages that are attracted by MCP-1. Tumor tissue classically contains a high amount of M2 polarized macrophages^[92]. Macrophages activated by obese states, infiltrate tumors and amplify the inflammatory tumor environment through NF- κ B dependent cytokine production and angiogenic factors^[88]. Malignancies may be initiated or exacerbate by inflammation, and increased levels of inflammation may be a cause and/or a

consequence of malignancy^[88,93].

Steroid hormones

Production of steroid hormones in the adipose tissue are also relevant for various cancers: Steroid hormones such as progesterone, estrogen, androgens and adrenal steroids are associated with energy balance level and obesity associated development of several cancer types^[94]. In women, the BMI correlates with the incidence of breast cancer, endometrium cancer and other cancer entities that are associated to sexual hormone levels. The relative contribution of adipose tissue steroid hormone production to the whole steroid metabolism is about 100% in postmenopausal women^[44]. The risk of developing breast cancer in post-menopausal women enhances with an increase of circulating levels of steroid hormones such as dehydroepiandrosterone, testosterone, estradiol and estrogen, and low levels of sex hormone binding globuline. There is evidence that estrogens are mitogenic, regulating the expression of insulin, and inducing DNA damage by free radicals, genetic instability and gene mutations in cells^[95]. Increased estradiol levels can induce endometrial cell proliferation rates while inhibiting apoptosis and activating the IGF-1 synthesis in endometrial tissue^[5].

In men, testosterone has been the focus of most studies on sex hormones, obesity and metabolic complications. Evidence indicates that most tissues, including adipose tissue, express steroid converting enzymes necessary for the local production of androgens and/or estrogens^[96]. Up to 40% of the active androgen production (dihydrotestosterone) is accounted for by tissue conversion of adrenal precursors^[96]. In men, obesity has generally been associated with reduction of testosterone levels in plasma and elevated estrogen concentrations^[97-99]. It has also been reported, that men with visceral adiposity have decreased levels of testosterone^[100,101]. A growing body of interest suggests, that obese men are more likely to be diagnosed with aggressive prostate cancer and high tumor volumes^[102]. Furthermore, obese patients show a higher risk of cancer recurrence, as well as an increase in disease related deaths compared to lean patients^[103,104].

Hyperinsulinemia and insulin growth factors

Increased insulin levels and insulin growth factor-1 signaling enhance cancer development^[105]. Other observational studies reported an increased mortality of obese cancer patients with T2DM due to hyperinsulinemia and elevated IGF-1 serum levels. In contrast, patients with lower insulin, IGF-1, and IGF-2 levels showed a lower risk to develop cancer^[105-107].

Patients treated with insulin or drugs stimulating insulin secretion showed a significantly higher incidence of developing malignancies than those patients treated with anti-diabetic drugs like metformin. Therefore, metformin might be a potential anticancer agent^[108].

Caloric restriction, which causes down-regulation of circulating insulin and IGF-1 levels is a potent suppressor in carcinogenesis^[74]. Insulin and IGF-1 can trigger cell

growth and proliferation, while inhibiting cell survival *via* protein kinase B (Akt)/PI3K/mTOR (Akt/PI3K/mTOR) pathway^[73]. This signaling pathway is not only the most frequently mutated pathway in human cancers, it is also a signal mediator of leptin, adiponectin and pro-inflammatory cytokines^[46,109,110].

Caloric restriction reduces cancer incidence by inhibiting the Akt/PI3K/mTOR pathway *via* AMPK activation^[111-113]. In contrast, Kalaany *et al.*^[110] could show that tumors with PI3K activation do not respond to the anti-cancerous effects of caloric restriction.

Interestingly, mTOR activity is increased in obese patients. It plays a central role in obesity related inflammation. Multiple risk factors for cancer development in obesity have been identified, such as the insulin-IGF-1 axis, leptin/adiponectin, and pro-inflammatory cytokines like IL-6, IL-7 and TNF- α . These factors can activate multiple pathways including PI3K/Akt, MAPK and STAT3, resulting in increased mTOR activity. mTOR, however, inhibits the insulin-PI3K pathway by stimulating the STAT3 pathway^[46].

IL-6 and TNF- α play a major role in obesity associated hepatocellular carcinoma by activating the STAT3 pathway^[114]. The STAT3 pathway is involved in the regulation of various gene expressions including IL-17, IL-23, B-cell lymphoma 2, and vascular epithelial growth factor to promote cell survival, proliferation, invasion, angiogenesis, and metastasis^[115]. Consistent activation of STAT3 increases tumor cell proliferation, survival and invasion in suppressing anti-tumor immunity. STAT3 activation also leads to activation of further pro-oncogenic pathways, such as NF- κ B and the IL-6/Janus kinase pathways^[115].

FUTURE OUTLOOKS

As time passes, advancement of technologies proceeds

In 2003, the Human Genome Project was accomplished. After 13 years and estimated costs of 2.7 billion USD, the first human genome was sequenced. In contrast, the human genome of an individual was sequenced over a 5 mo period of time at costs of 1.5 million United States-Dollars in 2008^[116].

An overall trend in the public health sector is the tendency towards “individualized therapy” in order to tailor specific therapy options that are currently available for a given patient which is further supported by usage of sophisticated mouse models.

Without doubt, mouse models have helped to understand relevant pathways that are important in the regulation of human body fat on the molecular level^[117-123]. Initial insights into molecules that are important in regulating body fat, resulted primarily from genetic mouse screenings^[117,124-126]. The identification of specific inactivating gene mutations accompanied by an obese phenotype, have revealed that leptin, leptin receptor and melanocortin-4 receptor play central roles in the regulation of body fat^[127-132]. Interestingly, these three obesity phenotypes as a result of inactivating mutations, are also

relevant in humans, suggesting that knockout mouse models are a powerful tool to gain new insights into obesity relevant human genes and proteins.

A clinical approach might further support the *in vivo* findings that resulted from former obesity mouse models. Extensive tissue banking combined with collected clinical data may open up new perspectives in translational medicine as well.

There already exist several methods for screening large patient cohorts such as next generation sequencing. Also, established methods (*e.g.*, Fluorescence *in situ* hybridization or immunohistochemistry) became powerful tools when featured with high-throughput methods such as tissue microarrays to gain knowledge in the distribution of potential obesity relevant proteins. Tools such as laser mass spectrometry combined with a large tissue database in a microarray format might enable the initiation of virtual protein expression profiling of cells in their natural tissue environment. Further development in this field and others will open up new possibilities to identify causal links between gene expression levels, RNA modification, protein expression levels, post translational modification of proteins, intrinsic enzyme activity, and initiation and progression of diseases on a molecular level.

Automated chip technologies for detection of structural variation discoveries on a DNA- and RNA-level may decrease sequencing time, streamline sample preparations and reduce costs in future studies.

Acquiring great amounts of patient cohorts' data in large databases combined with blood and tissue sampling will move clinical applicability of new gained knowledge into focus. New potential risk factors and/or therapy targets will be identified by high throughput tissue and blood screenings. Especially the combination of organ-tissue samples with respective blood samples, body fluids, and visceral/subcutaneous fat samples will help to understand complex causal connections between obesity and organ function failure and carcinogenesis on a molecular basis. The novel knowledge will be centralized and digitally organized, accompanied by its' access that will be provided to health care units and hospitals for data reconciliation.

Preclinical and clinical patient screening will provide the basis for individualized digital patient DNA-, RNA-, protein-, post translational modification-, and enzyme activity profiles that automatically may be compared to already identified risk factors or therapy targets in centralized data bases.

In the present, there already exist research projects that might serve as landmarks for individualized obesity research in the future.

Interestingly, the TG and HDL Working Group were able to identify rare mutations that disrupt apolipoprotein C3 function by sequencing the protein-coding regions of 18666 genes in each of 3734 participants. By correlating loss of function studies with clinical data, carriers of these mutations were found to have a reduced risk of

coronary heart disease^[133].

In the future, these mutations might serve as clinical risk-markers for coronary heart disease in obese patients. Blood samples of obese patients could be easily tested for gene mutations and the presence of a mutation might then be interpreted as a protective factor in favor of the patients' health.

Another study conducted an association analysis of single nucleotide polymorphisms, identifying genetic variants that predispose to T2DM^[134]. Testing blood or tissue samples right after birth for these genetic variants might probably change the way of clinical diagnostics entirely.

In the future, patients with genetic predisposition for *e.g.*, diabetes might be diagnosed before the onset of disease. This knowledge could then lead to an individualized treatment in terms of dietary intake, physical exercise, or to earlier elective surgical intervention in obese patients.

Also, gut hormone and adipokine serum levels could be screened on regular basis in obese individuals. When out of balance, pharmaceutical intervention with suitable drugs such as GOAT- inhibitors, GIP-Receptor antagonists, inhibitors of the mTOR-, STAT3- and MAPK-, PI3K-pathways or even Metformin might be applicable in the future to prevent relevant comorbidities such as cancer.

Morbid obesity is already a widespread problem not only in first-, but also in second world countries. It causes various major chronic diseases such as coronary heart disease, diabetes, hypertension, and cancer. As living standards in second and third world countries enhance, morbid obesity will proceed to be a huge challenge for health institutions and national health systems. Obesity is a potential human health threat and is likely to become even more present in the future. The relevance and possible long-terms effects of maternal obesity to the health of the offspring are not fully understood. Studies that deal with this issue are of high relevance to precisely understand the long-term adverse health outcomes for the upcoming new generations.

In conclusion, there is an urgent need for obesity research with a straightforward concentration on new studies that aim to identify and interpret the complex, multifactorial variables in order to develop new therapy approaches and prevention programs for patients suffering from this disease.

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Pathophysiological responses from human gut microbiome

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Abstract

The human gastrointestinal tract harbors a vast collection of symbiotic microorganisms-collectively termed as "gut microbiome". This microbiota has important effect in immune system and other host activities. Recent studies have suggested that alterations of the normal gut microbiota are associated with various human diseases and psychological disorders. The underlying cause, once proven, may provide novel insights into the importance of gut flora in human health. In this review, we give an attempt to describe how the alteration in the microbial community causes the development of certain widespread pathophysiological disorders; focusing on inflammatory bowel disease, colorectal cancer, obesity and autism. Proper knowledge about the host-microbiota interaction and linkage could be essential for the development of future personalized strategies of therapeutics.

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Key words: Human gut microbiome; Inflammatory bowel disease; Colorectal cancer; Obesity; Autism

Core tip: This review is an endeavor to provide an ac-

count about the human gut microbiome, their diversity, and disease causing capability. Till date, so many diseases have been associated with the alteration of gut microbiota. In this review we talk about four of the major diseases/disorders, viz., inflammatory bowel disease, colorectal cancer, obesity and autism.

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INTRODUCTION

The topic of human microbiome is pretty trendy in the present world of science. Human body is inhabited by more microbial cells than our own cell numbers. The term "microbiome" refers to the whole number of microorganisms residing in human body and their genetic material^[1-3]. It is different from the term "microbiota", which describes the microbial population present in different niches in the body. Resident microbes contain ten times more cells than our own somatic and germ cells and hence more number of genes than present in a human body-as a consequence they represent a combined microbial genome with a size bigger than human genome itself^[1,4]. Collectively, the flora has a metabolic action equal to a virtual organ within an organ^[5]. Researchers at human microbiome project, NIH are sampling and exploring data from few specific sites of human body, viz., airways, nasal passages, oral cavities, skin, blood, gastrointestinal tract, and urogenital tract^[2]. The microbial density starts increasing in the distal small intestine, and in the large intestine it rises to an estimated of 10^{11} - 10^{12} microbes per gram of colonic content, which contributes to 60% of the fecal mass. However, this is to bear in mind, since so many factors affect our body's ecosystem, the microbiota composition is different for every individual regardless of their age and sex.

Usually this microbiota is commensal and represents a healthy asset of our body, helping us to digest food and maintain immunity. Our typical understanding about a disease causing event states us that whenever a pathogenic organism enters our body, the disease takes shape. Introduction to the era of human microbiome enlightens us about a more susceptible way of causing disease—the imbalance of the microbiota within our body. Therefore human microbiome can be considered as a therapeutic drug target^[6].

The organisms from this microbiome are hard to culture. Metagenomics, the study of the genetic material extracted directly from environmental samples in a given environment, has been applied to the studies of the human microbiome, since it can be used to investigate various microbes simultaneously, without cultivation. This approach gathers speed in studies of human microbiome and their medical relevance. Studies about diverse microbes from the human body site-specific microbiota, and the correlations between their composition and disease have rapidly increased our understanding towards the importance of the human microbiome and its roles in health and disease^[3,7]. This bang of human microbiome data holds the promise of managing personal health, based on the genome and microbiome information of an individual.

HUMAN GUT MICROBIOME

A new chapter in medical science has emerged with the recognition of the crucial role of the gut microbiota in health and disease. At the time of birth human gut is completely sterile. However, immediately after birth the colonization of mammoth variety of microorganisms including bacteria, archaea, fungi and viruses starts within the body. The colonization of these microbial species within a body depends upon the mode of delivery, hygiene level, infant diet, and medication^[8].

Among all the niches, human GI tract contains the most number of microorganisms. The density of the microbiota increases from the proximal to the distal gut, reaching its maximum at the colon. In the different habitats of the gut, ecological sorting and competitive exclusion between microbes are the key factors influencing microbial diversity^[9,10]. Stochastic factors during colonization and in situ evolution cause the diversity of gut microbiota between individuals^[11]. The intestinal microbiota of infants lacks diversity and the major constituents are the phyla *Proteobacteria* and *Actinobacteria*. The microbiota attains diversity with age with the addition of *Fusobacteria*, *Cyanobacteria*, *Verrucomicrobia* and *Actinobacteria* amongst others and the dominance of *Firmicutes* and *Bacteroidetes* characterizes the adult microbiota^[12-14]. The gut microbiota is mainly a collection of anaerobes, which outnumber facultative anaerobes and aerobic microbes by approximately 2-3 orders of magnitude^[15]. In human, after the age of 2.5 years the gut microbiota remains almost the same throughout the adult age of that individual^[16,17]. The

actual adult human gut microbiota composition is diverse and differs from person to person in a significant way. Therefore it has been suggested that it can be used as a substitute to fingerprinting^[18]. In this regard three enterotypes have been found, *viz.*, *Prevotella*, *Ruminococcus* and *Bacteroids* that are independent of age or sex. The normal human gut flora composition is subject to age, diet, medication and socioeconomic conditions. In a recent study of gut microbiota in elderly individuals, the associations with diet and age was documented^[19].

It is a prominent fact that, although there is great variety in the composition of the gut microbiota among individuals, there still lays a conserved set shared between individuals, and this set of microbiota is called the core gut microbiome^[20]. The functions and pathways encoded by the core gut microbiome offer the greatest benefit to the host and are essential for the correct functioning of the healthy gut. The gut microbiota helps the host in various ways, including protection against probable pathogens, production of essential vitamins, digestion of polysaccharides, regulation of fat storage and modulation of the host's immune system^[21]. Latest studies have also revealed that the gut microbiota influences brain and the gut-brain axis configures the stress related symptoms such as anxiety and pain tolerance and few other psychological condition^[22].

ROLE OF GUT MICROBIOTA IN HUMAN DISEASE/DISORDER

It has been well established that the human gut microbiota is essential for human health. However, an alteration of the normal composition of the gut microbiome leads to formation of various types of diseases. Therefore it is reasonable to conclude that modulation of the gut microbiota can be used as a therapeutic target in treating these chronic diseases. Before properly utilizing the gut microbiota as a therapeutic tool, it is necessary to understand the role of these microbes in shaping disease. Till date, a great number of physical and psychological disorders have been associated with the alteration of gut flora; addressing all can be quite unfeasible task for this review. Thus, in this review, brief overviews of the current understanding about the role of microbiota in four common disease and disorders have been discussed.

INFLAMMATORY BOWEL DISEASE

Inflammatory bowel disease (IBD) is chronic, relapsing, immunologically mediated disorder that affects the digestive tract, mainly colon and small intestine. IBD majorly includes ulcerative colitis (UC) and Crohn's disease (CD). There is considerable evidence suggesting the importance of gut microbiota in IBD^[23-25]. Recent studies imply that an unbalanced microbial community composition is associated with a dysregulated immune response^[26]. Although the exact mechanism of IBD is not yet being

fully elucidated, four broad mechanisms are proposed to explain the complex relationship between the commensal microbiota and IBD: (1) dysbiosis of conventional microbiota; (2) induction of intestinal inflammation by pathogens and functionally altered commensal bacteria; (3) host genetic defects in containing commensal microbiota; and (4) defective host immunoregulation^[27]. The net result of these effects is continuous antigenic stimulation that activates pathogenic T cells, ultimately causing chronic intestinal inflammation. In case of patients suffering from CD, intestinal T lymphocytes have shown to be hyperactive against bacterial antigens as local tolerant mechanism is found to be abolished in them^[28]. In addition, they have increased intestinal secretion of IgG antibodies against a broad spectrum of commensal bacteria that, unlike IgA, activate complement cascade and inflammatory mediators^[29,30].

There are various hypothesis of how microbial composition in human gut plays vital role in the pathogenesis of IBD. Recent studies have shown that reduction of dominant commensal bacteria, such as *Firmicutes* and *Bacteroidetes*, and an increased number of *Proteobacteria* and *Actinobacteria*, may lead to this pathophysiological condition of human gut^[31,32]. A wide variety of gut microbial species have directly being linked with IBD. Among Firmicutes, *Faecalibacterium prausnitzii* is shown to have anti inflammatory activity and is found to be significantly decreased in CD^[33,34]. Furthermore, Joossens *et al.*^[35] have shown that reduction of *Faecalibacterium prausnitzii*, *Bifidobacterium adolescentis*, *Dialister invisus*, an unknown species of *Clostridium* clusters XIVA and increase of *Ruminococcus gnavus* are characteristic features in patients suffering from CD. A number of studies have shown that a wide variety of probiotic microorganisms, including *Escherichia coli*, *Saccharomyces boulardii*, and *Bifidobacterium* are involved in treating UC, although these are not always supported by high quality clinical trials^[36-42]. Also the role of microbiota in fecal transplantation, efficiently utilized in severe *Clostridium difficile* infection, have shown to be effective in IBD^[43,44].

COLORECTAL CANCER

Colorectal cancer (CRC) is one of the most common malignancies in the world, which accounts for about half million deaths annually^[45]. Although the prevalence of CRC is higher in the western world but it is found to be increasing in the developing countries at an alarming pace. Two principle mechanisms are mainly involved for the development of CRC-molecular genetics mechanisms and environmental factors^[46]. Dietary and genetic factors interact with each other *via* events taking place in the lumen of the large intestine^[47].

The genetic mechanisms of CRC are well established^[48]. A number of oncogenes and tumor-suppressor genes, such as *APC*, *KRAS*, *p53* and other regulatory genes are mutated in CRC patients. Together with DNA-methylation and chromatin-structure changes, the mutations

act to dysregulate conserved signaling networks that play vital role on cell phenotypes, including the regulation of cellular metabolism, proliferation, differentiation, and survival. Beside genes, environmental factors also influence the occurrence of CRC. Dietary carbohydrate and fat play critical roles in the development of colon tumorigenesis^[49]. Studies suggested that dietary fat and high consumption of red meat are associated with high risk of CRC^[50]. By contrast, a high intake of complex carbohydrate or dietary fibers, such as cellulose, lignin and pectin, that undergo bacterial fermentation in the colon, has been associated with reduced CRC risk^[51-53].

The effect of diet on carcinogenic process is mediated by changes in metabolic activity and composition of the colonic microbiome that accounts for over 100 trillion bacteria grouped in about 1000 species in human gut^[54,55]. Various studies have shown significant association between abundance of different bacterial species, particularly *Fusobacterium nucleatum*, with the prevalence of CRC^[56,57]. CRC risk was found to be associated with decreased bacterial diversity of Gram-positive, fiber-fermenting Clostridia; and increased presence of Gram-negative, pro-inflammatory genera such as *Fusobacterium* and *Porphyromonas*^[58]. The bacterial gut population can be shifted to a healthier composition by dietary fiber that provides substrates for bacterial fermentation^[55]. On the other hand, diet rich in fat and meat but poor in vegetables increases the concentration of N-nitroso compounds, a group of genotoxic substances that are known initiators of colon cancer^[59]. Another group of carcinogens are heterocyclic aromatic amines that are found in meat and some intestinal bacteria leads to DNA damage in colon cells due to the presence of such compounds^[60]. A more descriptive human study highlighted that high risk of CRC is associated with the presence of *Bacteroides vulgatus* and *Bacteroides stercoris*, whereas presence of *Lactobacillus acidophilus*, *Lactobacillus S06* and *Eubacterium aerofaciens* are associated with low risk of CRC^[61]. Although there is no conclusive evidence, gut microbiome seems to be a significant contributing factor that modulates risk of CRC in human beings.

OBESITY

Obesity is a medical disorder in which excess body fat accumulates over body. It is only recently that the problem of obesity has achieved global acknowledgment, in contrast to the problem of underweight and malnutrition-which have always conquered clinical attention. World Health Organization describes obesity as one of the major public health concern that threatens the modern world civilization and of late has become a global epidemic. A person is categorized as overweight when the body-mass index (BMI) is around 25 kg/m² or higher and people are classified as obese when the BMI is 30 kg/m² or more^[62]. A plentiful of studies has demonstrated that obese individuals are lazy, lack self-discipline. There is a social disgrace and discrimination against obese people

in various fields of life, which in turn creates numerous consequences for their psychological and to some extent physical health^[63]. However, obesity is not only a cosmetic concern. It has serious health concerns including increased risk for type 2 diabetes, cardiovascular diseases, non alcoholic fatty liver disease, pulmonary hypertension, asthma, sleep apnea, osteoarthritis, gall-bladder disease, a number of cancers, and most importantly an increased risk of mortality^[64].

Numerous studies have suggested that the gut microbiota plays a crucial role in the development of fat mass and altered energy homeostasis^[65]. Obese gut microbiota increases both the capacity to harvest energy from the diet and the accumulation of fat in adipose tissue and liver, by altering host metabolism. Studies in germ-free and conventionalized mice revealed that the microbiota helps in absorbing the monosaccharides from the gut lumen and adipocyte hypertrophy by suppressing fasting-induced adipocyte factor in the intestine, and this suggests that the gut microbiota is an important factor that affects energy harvest from the diet and energy storage in the host^[66,67]. The gut microbial community is diverse; consisting of bacterial species, archaea and various microbial eukaryotes. Therefore competitive interactions among these species might also play crucial roles in promoting obesity. In this regard, methane producing archaea *Methanobrevibacter smithi* has been found to be present in greater abundance in obese mice and humans when compared with lean individuals^[68,69]. Obesity and diet could be associated with altered gut microbiota characterized by a high *Firmicutes* to *Bacteroidetes* ratio and a dramatic fall in overall microbial diversity^[70].

It has been proposed that the composition of the gut microbiota during childhood predicts the following development of obesity in humans. In this regard some studies were conducted to compare between the fecal samples from overweight/obese and normal weight children^[68,71]. It shows that during infancy, a significantly higher number of *Bifidobacterial* species was observed in children who maintain a normal weight at age 7 years, while significantly greater numbers of *Staphylococcus aureus* were detected in children who became obese afterward. Therefore, it is hypothesized that an early modulation of gut microbiota can actually prevent obesity^[72,73]. Interestingly, another study found that the microbiota composition is different in case of pregnant women also, with relatively higher numbers of *Bacteroides* and *Staphylococcus* found in overweight pregnant women^[74]. Obese human twins also have different gut microbial composition as compared to their lean twin. The obese one has reduced levels of *Bacteroidetes* and also less bacterial diversity^[69].

AUTISM

The brain is strongly coupled with the gut *via* 200-600 million neurons^[75]. Currently, a growing number of clinical data and experimental observations suggest the presence of bidirectional gut-brain axis, implying that there

are probably many a type of neuro-atypical symptoms; including stress, depression, anxiety, associated with the alteration of the normal composition of gut microbial flora^[76,77]. In this review we would like to restrict ourselves to one neuropsychiatric disorder-Autism. The Autism Spectrum Disorder (ASD) is an assemblage of neuro-developmental disorders characterized by obscurity in social interaction and communication in affected children. It is typically associated with limited, repetitive, and stereotypic behavior and is noticeable within the first 3 years of life^[78,79]. Until 1990, Autism was treated as a rare psychological disorder. Today it is a major health concern, big emotional burden for families, and large financial burden for the government worldwide.

Though the principal cause of this disorder is yet to be known; gastrointestinal disorders have frequently been reported in the children with autism-suggesting the probable link between the atypical compositions of human gut microbiome with ASD^[80]. The hypothesis regarding the gut microbiota and ASD linkage was first coined by Bolte^[81]. Their study showed that interruption in the normal composition of native gut flora resulted colonization of some neurotoxin producing bacteria, contributing to the autistic symptom^[82]. As the importance of gut microbiota in gut-brain function came emerging; probable role of diet, bacteria, and enzyme became a field of important study in autism research^[83]. It has been proved that there is a significant difference between the stool sample from autistic and normal children in terms of frequency of occurrence of four bacterial phyla specifically, *viz.*, *Firmicutes*, *Bacteroids*, *Actinobacteria* and *Proteobacteria*. Further studies have shown higher count and diversity of *Clostridia* (mainly *Clostridium tetani*, *Clostridium perfringens* and *Clostridium botteae*) and *Desulfovibrio* (mainly *D.desulfuricans*, *D.fairfieldensis*, *D.piger*) in fecal samples of children with autistic behavior as compared to the normal healthy children with same sex and age^[81,84-91]. Evidence suggests that high occurrence of *Bifidobacterium* and *Lactobacillus* species is a biological indicator for healthy gut microbiota in breast-fed infants as they serve important probiotic function in the gut^[92-94]. As expected, these organisms are frequently reported to be lower in patients with ASD. People are working with several animal models to investigate the expected link between gut microbiota and autism like disorders. One recent paper on maternal immune activation (MIA) mouse model has revealed gastrointestinal abnormalities and changes in the gut microbial community in offspring of MIA animals with autism-like symptoms^[95].

Till date, several studies have demonstrated the presence of a perturbed intestinal microbiota composition in children with ASD compared to normal control children. However, caution should be applied while drawing conclusion from these results, as patients with ASD have probable history of using high antibiotic dosage and different diets compared with neuro-typical individuals, either of these can influence the normal composition of the gut microbiota^[96,97]. Fortunately enough, a recent study demonstrated that the alteration in the concentra-

tions of short-chain fatty acids in the fecal sample of children with ASD^[98]. This suggests that atypical production of such microbial metabolites may have a direct effect on our brain function and thus bacteria can modulate the brain function in a straight line.

CONCLUSION

It is well established fact that the gut microbiota influences host metabolism, immune function, and host homeostasis. Interruption in this balanced community may generate very serious health troubles for the host. Advancement of next-generation genomic technology will pave the way to the development of experimental models of representative examples from the human gut microbiome. This will consecutively accelerate the discovery, testing, and validation of novel drug targets. Future metagenomic research is also expected to focus on the complex relationships of the gut microbiome composition and host metabolism so that in time their actual importance to human health will also be understood better. More in depth understanding of the specific relationships between the gut microbiota and disease will enlighten us about the potential therapeutic targets. The issue of intelligent modulation of the intestinal community is a topic of great interest nowadays. The gut microbiome is expected to contribute immensely to the delivery of personalized healthcare strategies that are already being applied into the clinical environment for the benefit of patients. It can open new door to treating disease and potential modulation of human disease risk factors.

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Pharmacogenetics of type 2 diabetes mellitus: An example of success in clinical and translational medicine

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responsible for the interindividual variability of drug response to sulfonylureas in patients with T2DM. Instead, genetic variants in the genes that encode for the organic cation transporters of metformin have been related to changes in both pharmacodynamic and pharmacokinetic responses to metformin in metformin-treated patients. Thus, based on the individual's genotype, the possibility, in these subjects, of a personalized therapy constitutes the main goal of pharmacogenetics, directly leading to the development of the right medicine for the right patient. Undoubtedly, this represents an integral part of the translational medicine network.

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Key words: Type 2 diabetes; Anti-diabetic drugs; Personalized therapy; Genetic variants; Genome-wide association study

Abstract

The pharmacological interventions currently available to control type 2 diabetes mellitus (T2DM) show a wide interindividual variability in drug response, emphasizing the importance of a personalized, more effective medical treatment for each individual patient. In this context, a growing interest has emerged in recent years and has focused on pharmacogenetics, a discipline aimed at understanding the variability in patients' drug response, making it possible to predict which drug is best for each patient and at what doses. Recent pharmacological and clinical evidences indicate that genetic polymorphisms (or genetic variations) of certain genes can adversely affect drug response and therapeutic efficacy of oral hypoglycemic agents in patients with T2DM, through pharmacokinetic- and/or pharmacodynamic-based mechanisms that may reduce the therapeutic effects or increase toxicity. For example, genetic variants in genes encoding enzymes of the cytochrome P-450 superfamily, or proteins of the ATP-sensitive potassium channel on the beta-cell of the pancreas, are

Core tip: Type 2 diabetes mellitus (T2DM) is a heterogeneous complex disorder, in which predisposing genetic variants (polymorphisms) and precipitating environmental factors interact synergistically in the development of the disease. Besides being useful in identifying individuals at risk for T2DM, knowledge of the polymorphisms associated with T2DM is also useful in pharmacogenetics for correlating individual variants with individual responses to anti-diabetic drugs. To date, a wide variety of genes that influence pharmacogenetics of anti-diabetic drugs have been identified. However, with few exceptions, drug therapy has not taken into account the individual genetic diversity of treated patients, representing, this, a substantial limitation of pharmacogenetics. This review focuses on clinically important polymorphisms affecting a patient's response to diabetic medications.

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INTRODUCTION

The common observation that patients with type 2 diabetes mellitus (T2DM) show a great variability in the individual response to the same drug treatment suggests the importance of a personalized care approach, in which the most appropriate treatment is indicated by the genetic peculiarities of each individual^[1]. The introduction, in 2007, of genome-wide association study (GWAS) has greatly enhanced the number of genes that are known to be associated with common diseases. Applied to millions of people, this method has allowed the identification of several genetic variants which are associated with T2DM^[2]. However, similarly to other complex diseases, none of the individual variants identified so far is in itself sufficient to cause the disease, but most of the genetic risk for T2DM is mediated by the combined influence of more genetic variants that individually have only a small degree of risk^[3,4]. This combination (haplotype) defines the genetic profile of the individual. The fact that the pathogenesis of T2DM requires the involvement of multiple genes in different combination is in line with the assumption that T2DM, far from being a disease genetically identifiable in a few specific forms, actually consists of a large number of rather different disorders^[3,4], each of which is associated with a specific disease phenotype only apparently identical to one another, and in which inter-individual variability in drug response can be identified both in terms of drug efficacy and undesired drug reactions.

Therefore, clarifying the molecular mechanisms by which genetic variations may cause differences in phenotypic traits and in individual drug response is essential not only to determine the etiological role of gene variants, but also to identify new personalized medical solutions. Personalized therapy, based on the genetic diversity of each individual, is one of the most fascinating challenges of modern medicine, representing an integral part of the translational medicine effort, whose ultimate goal is to translate advances in biomedical research into new medical treatments and improvements in patient care (Figure 1). Herein, we provide an overview of this area and its relevance to clinical practice in T2DM.

PHARMACOGENETICS AND GENE POLYMORPHISMS

Pharmacogenetics is defined as the influence of variations in DNA sequence on drug response (www.ema.europa.eu). Its relevance arises from the clinical observation that patients suffering from the same disease do not necessarily respond to the same drug treatment in terms of therapeutic efficacy as well as adverse effects. The principal aim of pharmacogenetics is to provide

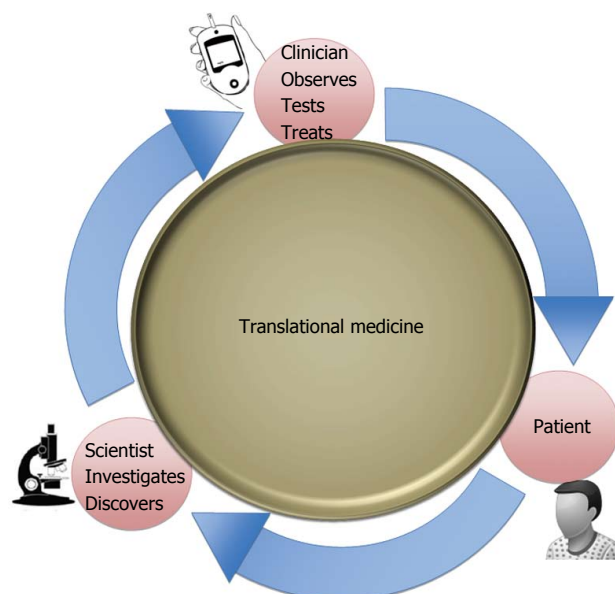


Figure 1 From bench to bedside. Translational medicine is a discipline of biomedical research that attempts to connect basic research with clinical care.

personalized medicine, tailored to an individual's genetic makeup, in order to optimize the effectiveness and safety of drug treatment. Although elements of pharmacogenetics can be traced back to ancient Greece (510 years BC), when it was already known the risk of hemolytic anemia in certain individuals in response to the ingestion of uncooked fava beans^[5], the term “pharmacogenetics” was first coined by Vogel^[6] in 1959 to indicate the importance of genetic polymorphisms on the disposition and action of drugs. The first evidence on the role of genetic variants in drug response back to the ‘70s and refers to cytochrome P-450 2D6 (CYP2D6), an enzyme of the hepatic P-450 microsomal enzyme system, which is involved in the metabolism of numerous drugs. Studies of the genetic variations within the P-450 family of enzymes provided the first direct evidence for the genetic contributions to drug therapy and efficacy, and these studies continue to be an active part of the basic and clinical research performed today. In fact, numerous other genetic variations have been identified in subsequent years, within the P-450 family of enzymes, including the biotransformation enzymes CYP3A4/5 and the CYP2C9 enzyme. It has been shown that individuals carrying genetic variants of *CYP2D6* (and other P-450 isoforms resulting in poor enzymatic activity), who are concomitantly taking medications that are influenced by these enzymes, are at risk for increased or prolonged drug effect, influencing the speed and effectiveness of drug metabolism^[7]. However, there is no doubt that the greatest contribution to pharmacogenetics has come from the sequencing of the entire human genome in 2003, showing that over 99% of DNA is identical in all humans and that, therefore, phenotypic differences among individuals, as well as differences in disease susceptibility and the inter-individual variability in drug response, are the result of sequence polymorphisms that

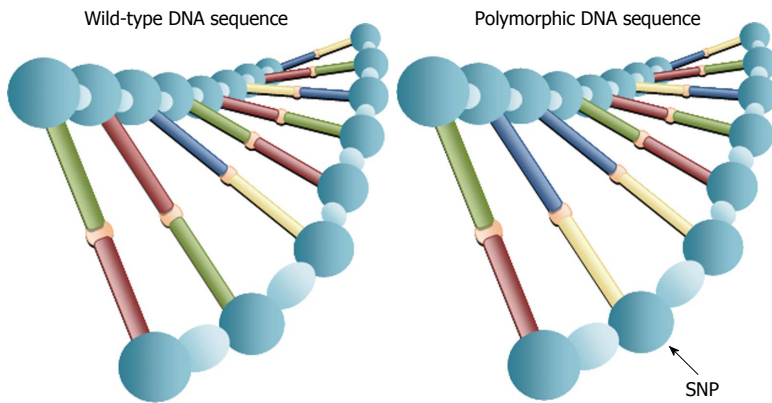


Figure 2 Single nucleotide polymorphism. As the most common type of variant, a single nucleotide polymorphism is characterized by a single DNA base pair substitution at a specific location in a gene. SNP: Single nucleotide polymorphism.

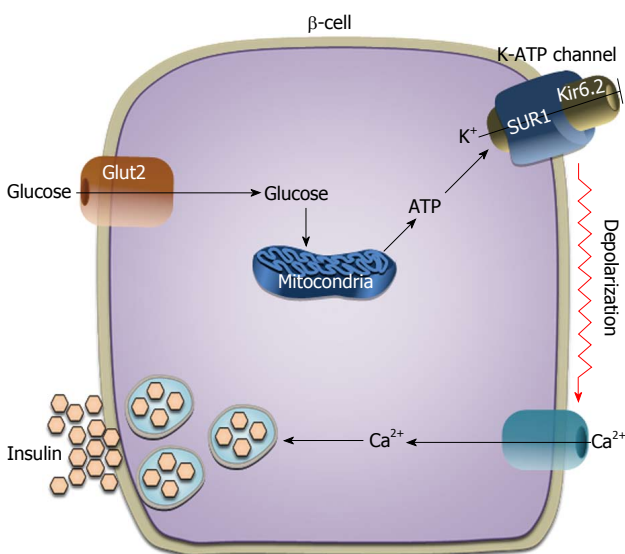


Figure 3 The ATP-sensitive K⁺ channels regulate insulin release in beta-cells. Single nucleotide polymorphism in *SUR1* and/or *Kir6.2* genes may cause functional abnormalities of the ATP-sensitive K⁺ channel on the pancreatic β -cell membrane, leading to abnormalities in insulin secretion.

affect less than 1% of 3 billion bases of human DNA. In most cases, these variants consist of the exchange of single nucleotides in both coding and noncoding DNA regions and are defined as single nucleotide polymorphisms (SNPs) (Figure 2). The ability of the SNP to influence drug response and therapeutic efficacy may rely on the capacity of the variant to induce changes in the expression of proteins that may influence either the pharmacokinetic and/or pharmacodynamic profile and hence the clinical efficacy of the drug. On the basis of these acquisitions, recent GWAS have identified several SNPs that can affect both the therapeutic efficacy and the occurrence of adverse reactions after drug intake^[8-10].

PHARMACOGENETICS IN T2DM TREATMENT

Pharmacogenetics of sulfonylureas

In Caucasians, sulfonylureas are metabolized primarily

in the liver by CYP2C9 to active metabolites, which are ultimately excreted by the kidney^[11]. In previous work, it was demonstrated that polymorphisms of the *CYP2C9* gene significantly affect the pharmacological response of diabetic patients to sulfonylureas^[12], due to the reduction of the catalytic activity in the metabolism of these drugs^[13-16], with a consequent increase in drug bioavailability. In particular, in certain diabetic patients with the variants Ile359Leu (isoleucine changes to leucine in exon 7 position 359) and Arg144Cys (arginine changes to cysteine in exon 3 position 144) in the *CYP2C9* gene, the clearance of glibenclamide was reduced by 30%-80%, allowing the use of lower doses of this drug to limit the risk of hypoglycemia^[12,17-20]. The risk of hypoglycemia in sulphonylurea treated patients was confirmed in a study with a larger population, in which the simultaneous presence (or the presence in homozygosity) of the variants Ile359Leu and Arg144Cys in the *CYP2C9* gene was associated with the improvement in markers of glycemic control, including glycated hemoglobin A1c (HbA1c)^[21]. Therefore, genotyping of the *CYP2C9* gene may provide important additional information in predicting the adverse effects of these drugs and to assist physicians in prescribing oral hypoglycemic agents.

The ATP-sensitive potassium [ATP-sensitive K⁺ (K-ATP)] channel plays a central role in mediating glucose-stimulated insulin release from pancreatic beta-cells (Figure 3). In physiological conditions, the rapid entry of glucose into the beta-cell results in an increase in the intracellular concentration of ATP, which promotes the closure of the K-ATP channel with consequent opening of the voltage-dependent calcium channel, elevation of intracellular calcium ion concentration and insulin secretion. The K-ATP channel is composed of two subunits: the sulphonylurea receptor (SUR1) and the pore-forming inward rectifier K⁺ channel Kir6.2^[22,23]. Genetic variants inactivating the *KCNJ11* (potassium inwardly-rectifying channel, subfamily J, member 11) gene, which encodes for the protein Kir6.2, and the ATP-binding cassette, subfamily C (CFTR/MRP), member 8 (*ABCC8*) gene, which encodes the SUR1 protein, are responsible for neonatal diabetes mellitus; conversely, activating mutations of

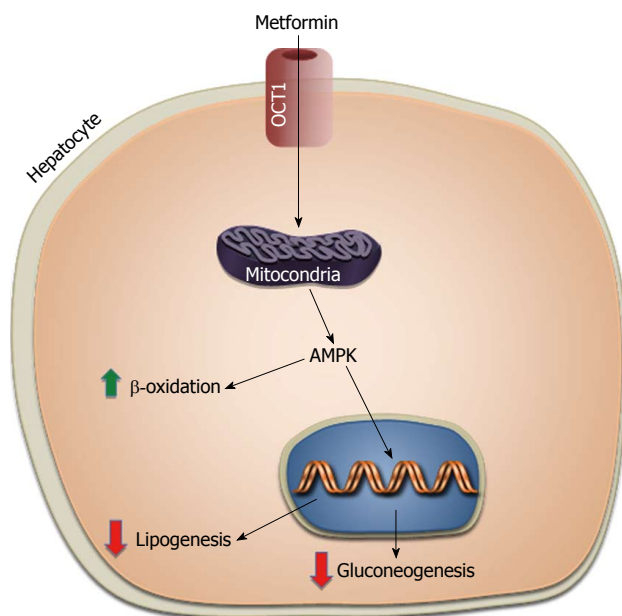


Figure 4 Organic cation transporter 1 plays a major role in drug uptake across the liver cell membrane. Single nucleotide polymorphism associated with organic cation transporter 1 may contribute to variation in response to metformin. AMPK: Adenosine 5'-monophosphate (AMP)-activated protein kinase; OCT1: Organic cation transporters 1.

these two genes lead to hyperinsulinism and neonatal hypoglycemia^[24]. As an example of pharmacogenetics with important clinical implications, recent studies have found that diabetic patients carrying mutations in the *KCNJ11* gene respond better to treatment with sulfonylureas than to treatment with insulin^[25-27].

Association of the polymorphism Ser1369Ala (serine 1369 to alanine substitution) in *ABCC8* with the antidiabetic efficacy of gliclazide was found in patients with T2DM, after two months of treatment^[28]. In particular, patients with the genotype alanine/alanine had a greater reduction in either fasting plasma glucose or 2 h postload plasma glucose during oral glucose tolerance test, and a greater decrease in HbA1c levels compared to patients with the Serine/Serine genotype^[28]. The variant Ser1369Ala in *ABCC8* is often associated in linkage disequilibrium with a variant, Glu23Lys (glutamine to lysine variant at position 23), in the *KCNJ11* gene, forming a haplotype that increases the risk of developing T2DM^[29]. It has been observed that this haplotype displays large differences to the therapeutic effects of various sulfonylureas: greater to gliclazide, less apparent to tolbutamide, chlorpropamide and glimepiride, invariable in the glipizide and glibenclamide treatment group^[30].

Interesting results, in this context, have been obtained from the study of the transcription factor 7-like 2 (*TCF7L2*) gene, which encodes a nuclear transcription factor that appears to play a role in beta-cell function. Genetic variants of *TCF7L2* are associated with increased risk of T2DM^[3]. Recently, two variants of the *TCF7L2* gene, rs7903146 (G > T), and rs7903146 (C > T), have been shown to influence the therapeutic efficacy of sulfonylureas^[31-33]. In particular, the reduction in both

HbA1c and fasting plasma glucose was higher in diabetic patients carrying either GG or CC genotypes^[31-33]. In contrast, diabetic patients with the TT genotype in both the rs7903146 (G > T) and the rs7903146 (C > T) variants showed a lower response to sulfonylureas and appeared to be more prone to therapeutic failure^[31-33].

Pharmacogenetics of metformin

Metformin, in use for control of diabetes since 1950s, is the first-line pharmacological therapy for T2DM. After oral administration, the drug is absorbed into the blood *via* the gastrointestinal tract, rapidly distributed in body tissues by travelling through specific transport proteins [including the organic cation transporters 1 (OCT1) and OCT2, the multidrug and toxin extrusion 1 (MATE1) transporters and MATE2-K, and the plasma membrane monoamine transporter (PMAT)] located on the cytoplasmic membrane of many cells, especially intestinal cells, liver cells and kidney cells^[34], and excreted in the urine almost unchanged from the original drug. The individual's response to metformin is highly variable with less than 2/3 of treated patients achieving glycemic control^[35]. Thus, identification of genetic variants that may influence the interindividual variability to metformin would be of major importance for the effective treatment of these patients. However, studies on the pharmacogenetics of metformin are relatively limited, mainly because its mechanism of action is still poorly defined. So far, most of the studies on this topic have involved the solute carrier family 22A1 (*SLC22A1*) gene, which by coding for the OCT1 transport protein, plays a key role in the cell absorption of the drug^[36], and is essential for the anti-gluconeogenic effect of metformin into the liver^[37] (Figure 4). It has been shown that polymorphisms of this gene (rs12208357; rs34130495; rs72552763; rs34059508), by reducing the functional capacity of OCT1, can alter the bioavailability of metformin and mitigate its hypoglycemic response in healthy people carrying these gene variants^[37-39]. Recently, two polymorphisms of *SLC22A1* (rs628031 and rs36056065) have been associated with gastrointestinal side effects in diabetic patients treated with metformin^[40]. At the same time, other authors^[41,42] have also reported that the bioavailability of metformin was increased in healthy individuals carrying mutations of the *SLC22A2* gene, which encodes for the OCT2 transport protein. Variants of this gene, by adversely affecting OCT2 function, may decrease the renal clearance of metformin, and may contribute to increased plasma metformin levels with increased risk of hypoglycemic events.

Interindividual variation in metformin response has been recently reported in subjects with genetic variations in *SLC47A1* and *SLC47A2* genes coding for MATE1 and MATE2-K, respectively, which play important roles in the urine excretion of metformin. A better glycemic response to metformin, with lower HbA1c levels, has been reported in association with the *SLC47A1* gene variant rs2252281^[43-46]. In contrast, the therapeutic response to metformin was reduced in diabetic patients

carriers of the variant rs12943590 in the *SLC47A2* gene^[45,46]. Therefore, these observations imply that genetic variants of MATE1 and MATE2-K are important determinants of the therapeutic efficacy of metformin in patients treated with this drug. The first GWAS on the efficacy of metformin on glycemic control in diabetic patients resulted in the demonstration that a gene variant near ataxia telangiectasia mutated (*ATM*), rs11212617, is significantly associated with metformin treatment response in T2DM, more frequently with HbA1c levels < 7%^[47]. The explanation of this phenomenon lies in the role *ATM*, the protein product of the *ATM* gene, plays in the context of insulin signaling and insulin action^[48].

Thus, genetic variants of *SLC22A1* and *SLC22A2* may be determinant in the therapeutic efficacy of metformin. Furthermore, genotyping of *SLC22A1* and *SLC22A2* is useful in the management of diabetic patients under metformin therapy.

Pharmacogenetics of thiazolidinediones

Genetic variants that can influence the pharmacogenetics of oral antidiabetic medications were also assessed in diabetic patients treated with pharmacogenetics of thiazolidinediones (TZDs) (pioglitazone and rosiglitazone). As agonists of peroxisome proliferator-activated receptor gamma (PPAR- γ), TZDs act as insulin-sensitizing, thus reducing the release of glucose from the liver and increasing glucose uptake in muscle^[49]. The *PPAR- γ* gene has been extensively investigated in pharmacogenetic studies of TZDs, especially because genetic variants of this gene have been associated with an increased risk of T2DM^[3]. However, pharmacogenetic studies with TZDs have shown conflicting results, probably due to insufficient sample size and low levels of statistical power^[50]. Furthermore, it is worthy noting that the retrospective study design used in the majority of studies on pharmacogenetics has its own drawbacks, being able to expose to a variety of confounding and bias, including age, gender, ethnicity, lifestyle, concomitant use of other medications, *etc.* A similar discrepancy has emerged from studies on the genetic variants of the *CYP2C8* gene, which is responsible for metabolizing pioglitazone^[50]. A reduction in the blood glucose-lowering effect of pioglitazone was recently observed in diabetic patients carriers of the truncation variant, Ser447X, of the lipoprotein lipase gene^[51]. Another study has reported that the -420 C/G variant of the *resistin* gene promoter can also be used as an independent predictor of the reduction of fasting plasma glucose and insulin resistance by pioglitazone in T2DM^[52]. As it is known, side effects of TZDs therapy include fluid retention and peripheral edema, worsening heart failure^[53]. In this context, various genetic variations have been discovered in genes known to be involved in sodium and water reabsorption. Among these, the aquaporin 2 (*AQP2*) rs296766 variant and the *SLC12A1* rs12904216 variant, both of which have been associated with edema in T2DM patients treated with a TZD^[54]. *AQP2* gene codes aquaporin-2, which function as a water channel in the

collecting duct of the kidney^[55]. *SLC12A1* encodes the kidney-specific sodium-potassium-chloride cotransporter (NKCC2), which plays an important role in both urine concentration and NaCl reabsorption^[54,56]. Therefore, it is quite evident that these variants may represent both a risk factor for the development of edema in diabetic patients during treatment with TZDs.

Pharmacogenetics of metiglinides

Metiglinides (repaglinide and nateglinide) are a class of rapid-acting, short duration insulin secretagogues that act in a manner similar to that of the sulfonylureas^[57]. Nateglinide is also metabolized by the *CYP2C9* enzyme of the cytochrome P-450 system, and gene variants of *CYP2C9* are associated with variability in glucose-lowering effect of nateglinide^[58]. Repaglinide is metabolized by *CYP2C8* and to a lesser degree by *CYP3A4*^[59]. Also in this case, gene variants of *CYP2C8* have been associated with increased clearance of repaglinide, although with contradictory results^[60]. The solute carrier organic anion transporter family member 1B1 (*SLCO1B1*) gene encodes for the organic anion transporting polypeptide, OATP1B1, which regulates cellular uptake of various drugs, including statins by the liver. Recent studies have reported the role of some variants of *SLCO1B1* in the pharmacokinetics of metiglinides^[61-64]. For example, a more effective hypoglycemic effect of repaglinide was observed in diabetic patients carrying the Glu23Lys (E23K) polymorphism in the *KCNJ11* gene^[65], and the rs13266634 variant in the *SLC30A8* gene^[66]. Similarly, polymorphisms of neurogenic differentiation 1 (*NEUROD1*), also called beta2 (*NEUROD1/BETA2*), paired box gene 4^[67] and uptake control 2^[68] genes were also found to be associated with the hypoglycemic efficacy of repaglinide. An association of the variant G2677 T/A in the multidrug resistance gene, which encodes a multidrug efflux pump, with the variability in the pharmacokinetics of repaglinide was found recently in a Chinese study in healthy volunteers^[69].

Pharmacogenetics of incretins

Glucagon-like peptide-1 (GLP-1) is part of the group of incretin hormones that are secreted from endocrine cells in the intestinal mucosa in response to meals. It mediates insulin secretion in a glucose-dependent manner and is easily inactivated after being secreted by the enzyme dipeptidyl peptidase-IV (DPP-IV). Recent pharmacological research has led to the development and synthesis of medications that are capable of acting at this level as both GLP-1 agonists (exenatide and liraglutide) and DPP-IV inhibitors (gliptins)^[70]. Variants of the GLP-1 receptor gene have been shown to be associated with altered sensitivity to GLP-1^[71]. Furthermore, whereas variants in the *TCF7L2* (rs7903146) and wolfram syndrome 1 (rs10010131) genes have been associated with a reduced response to exogenous GLP-1, variations in the *KCNQ1* (rs151290, rs2237892, and rs2237895) gene appear to alter the secretion of endogenous GLP-1^[72]. The only significant study on the pharmacogenetics of gliptins

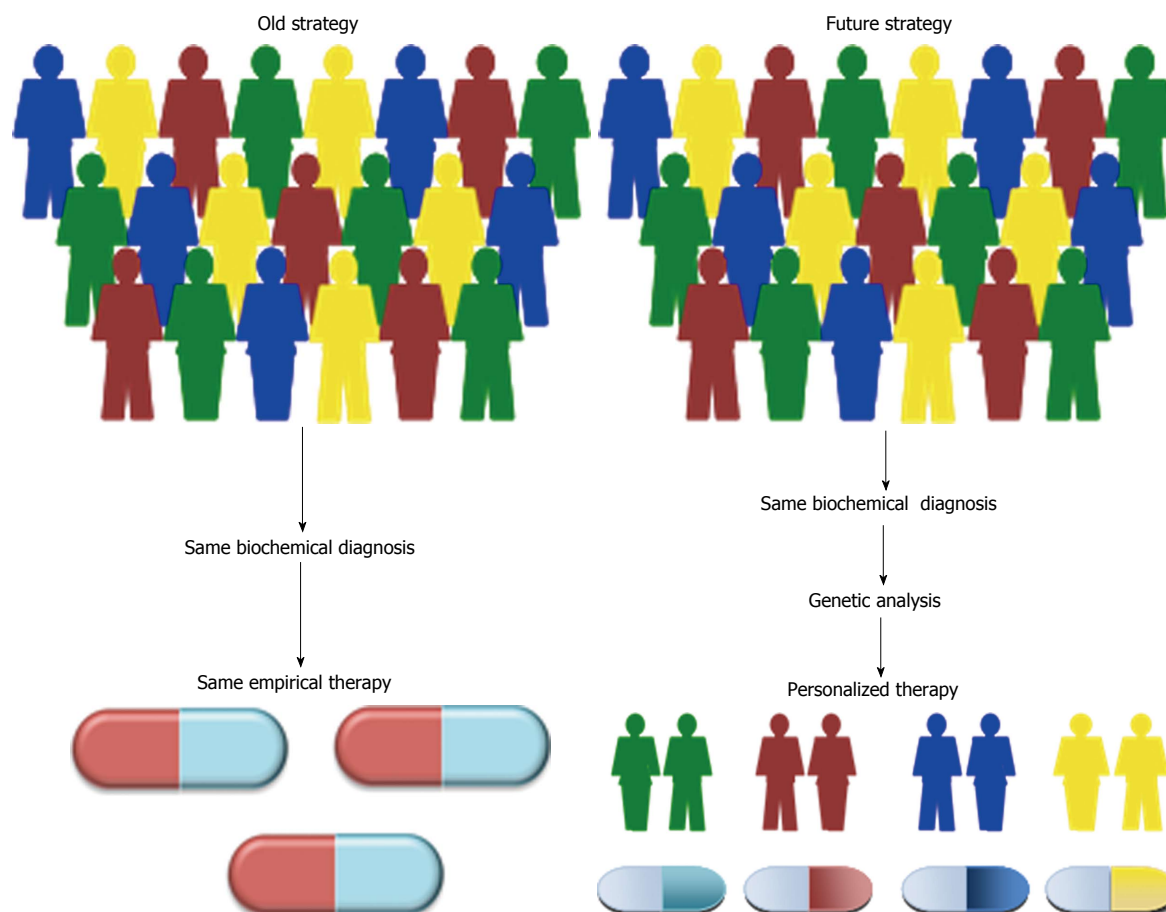


Figure 5 Pharmacogenetic testing. The pharmacogenetic test has the potential to provide personalized therapy based on individual genetic variability.

showed that three novel genetic loci (transmembrane protein 114, carbohydrate sulfotransferase 3 and Chymotrypsinogen B1/2) were identified, which affect GLP-1-induced insulin release during hyperglycemic clamp in nondiabetic Caucasian subjects^[73].

CONCLUSION

Pharmacogenetics is an expanding area of research which seeks to understand how variations in the genome influence medication response. Pharmacogenetics has gained increasing attention in the context of translational medicine, providing an opportunity for personalized treatment strategies based on an individual's genetic makeup. The results obtained so far with the study of genetic variants in patients with T2DM (and other common diseases) may be used for the realization of a pharmacogenetic test, which can assist in making treatment decisions on the basis of each patient's genetic profile, thus improving the overall management of the disease and ensuring better results in terms of safety and therapeutic efficacy. The clinical use of pharmacogenetics, through the identification of individual genetic variants (genetic polymorphisms), can contribute to move to a more evidence-based and less empiric clinical management of patients, thereby avoiding treatment failures, while reducing the incidence of adverse drug reactions (Figure 5).

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Psychotherapy in anorexia nervosa: What does the absence of evidence mean?

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Core tip: This paper presents an alternative explanation conspicuously lacking in the literature as to the scarce evidence concerning the efficacy of psychotherapy in anorexia nervosa. The absence of data supporting a particular treatment undermines the basic tenets underlying the theory on which it is grounded, or is at least a defective translation of the theory into the “dos” and “don’ts” of manualized treatment. This assertion is elucidated by recent research on a placebo and non-specific treatment that was found to be more effective than a number of specialized treatments.

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Abstract

Psychological treatment in anorexia nervosa (AN) is disheartening. Psychotherapy is the “treatment of choice” for adults though this recommendation is grounded on the absence of good quality clinical studies. This paper seeks to address the question of why improvements in the psychological treatment of AN have been thwarted, and why one of the best treatments available for adult patients is specialist supportive clinical management that has entered the stage through the backdoor of nonspecific supportive treatments originally serving as a placebo treatment assigned in randomized clinical trials to control for non-specific aspects of true psychosocial treatments. The possibility that most of the psychopathological features that characterise the AN symptoms profile could be best understood as the direct consequences of emaciation would enhance the utility of research with animal models for generating new hypothesis to improve AN treatment.

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INTRODUCTION

According to successive state-of-the-art reviews, contemporary treatment of anorexia nervosa (AN) is discouraging^[1]. This pessimistic view is all the more disturbing when we consider the high rates of relapse after successful weight restoration in specialist inpatient settings^[2]. With regard to pharmacological treatment, several reviews have reached a similar conclusion: No efficacy documented. “In general, studies have not consistently shown favourable results when pharmacotherapy is used for the treatment of anorexia” (p.114)^[3]; and: “No pharmacological intervention for AN has a significant impact on weight gain or the psychological features of AN. Although mood may improve with tricyclic antidepressants, this outcome is not associated with improved weight

gain. Moreover, medication treatment for AN is associated with high dropout rates, suggesting that the currently available medications are not acceptable to individuals with AN^[4]. Furthermore, “In summary, at present, there is no convincing evidence of efficacy for any drug treatment for AN in either the acute or chronic phase of the illness; AN is one of the few psychiatric disorders of which this may be said”^[5].

For example, in the case of antipsychotics, one of the drugs most extensively administered to AN patients, chlorpromazine, has not made much progress since it was deemed to be ineffective and toxic when administered to AN patients five decades ago^[6]. In combination with supportive psychotherapy and bed rest (to avoid possible fractures due to episodes of hypotension), chlorpromazine was no better in the follow-up with respect to control patients not receiving the drug, although it caused severe extrapyramidal effects in up to 50% of cases^[7]. With the advent of the so-called atypical antipsychotics, patients are free of these serious side effects, but still with no substantial positive effects, as concluded in a recent meta-analysis: “Compared with placebo, atypical antipsychotics were associated with a nonsignificant increase in body mass index (BMI), and a nonsignificant effect on the drive for thinness and body dissatisfaction. Compared with placebo or active control, these medications led to an increase in anxiety and overall eating disorder symptoms” (p.1)^[8]. In spite of the poor response to the core symptoms of AN, pharmacotherapy continues to be frequently employed as part of a comprehensive treatment plan in an attempt to alleviate negative emotions and obsessive ruminations^[9].

According to current clinical practice guidelines on psychosocial treatments^[10,11], family therapy is recommended for medically stable adolescents [a practice that is supported by the findings of several randomized clinical trials (RCTs) excellently reviewed elsewhere^[12,13]], whereas generic psychotherapy is the recommended “treatment of choice” for adults. However, this later recommendation is based on poor scientific evidence, that is, an expert’s clinical confidence, consensus or opinion (Grade C), which indicates the absence of good quality clinical studies. Thus, the panoply of recommended therapeutic approaches spans the entire theoretical spectrum of psychotherapy, namely cognitive analytic therapy, cognitive behaviour therapy (CBT), Interpersonal Therapy (IPT), Focal Psychodynamic Therapy, and Family Therapy. However, although the philosophy inherent in these Guidelines is that not “everything-is-worth-the-same”, the fact is that these recommendations lack any specific indications or specificity for selecting among them. This gloomy panorama was described some years ago with a succinct “Barely” to the question “Is evidence-based treatment of anorexia nervosa possible?” with the author concluding that: “New forms of treatment are needed for adults with anorexia nervosa, and the true value of family-based treatment for adolescents has yet to be established”^[14].

Attempts at explaining the limited evidence on AN treatment efficacy have enumerated several factors responsible either for the lack of research, or the difficulties in performing more randomized controlled treatment trials. For instance, it is claimed that AN is an uncommon disorder with a relatively low prevalence in the general population. This hinders efforts to collect data from large patient samples, which consequently limits the methodological strength both in terms of the internal validity of most RCTs performed up to date (*e.g.*, randomization procedures, adequate control groups), and in terms of external validity as the lack of replication is the overriding norm. Furthermore, the ego-syntonic nature of AN symptomatology and the ambivalence of AN patients about recovery hinder their enrolment, participation, and the acceptability of treatments in clinical studies, which paves the way to the high dropout rates characteristic of AN clinical trials.

Though there may be sound reasons for understanding the lack of evidence regarding effective AN treatments, there is an alternative explanation conspicuously lacking in the literature, namely that the absence of documented efficacy is related to the current conceptualization of AN. In contrast to pharmacological treatments for AN, where the expected action of drugs are loosely connected to any aetiological or maintenance theory of a disorder, psychological treatments are supposed to be more committed with a particular conceptualization of AN. According to this stronger theoretical link, the absence of data supporting a particular AN treatment would be indicative of a failure in the basic tenets underlying the theory on which it is founded, or at least a defective translating of the theory into the “dos” and “don’ts” of manualized treatment.

A plausible hypothesis is that the lack of documented efficacy is related to the current conceptualization of AN, a view which has been reinforced by the outcomes of a new treatment originally termed as “Nonspecific Supportive Clinical Management”^[15], which later, in the light of its unexpected efficacy, has lost its disconcerting “Nonspecific” qualification which has been euphemistically rebranded with the more reassuring label of “Specialist Supportive Clinical Management”^[16]. However, the truth behind this relabeling reinforced by its abbreviation (SSCM) is that a placebo and non-specific treatment was found to be more effective than two specialized treatments, *i.e.*, CBT or IPT, and was as effective as these treatments at 5-year follow-up^[17]. Moreover, in a further randomized controlled trial, SSCM was found to be as efficacious as the Maudsley Model of Anorexia Nervosa Treatment for Adults (MANTRA)^[18,19], which was specifically devised to address the disorder according to a rather complex rationale in comparison to SSCM as illustrated in Table 1.

Furthermore, in a third RCT with a good retention rate (85%), SSCM was again similar to CBT at the end of the study^[20]. Similar to differences with MANTRA shown in Table 1, differences between CBT and SSCM treatment manuals modified for treating a group of chronic

Table 1 Descriptive characteristics of two “novel” treatments for Anorexia Nervosa

SSCM (previously, nonspecific supportive clinical management ^[16])	MANTRA ^[19]
“Nonspecific supportive clinical management was developed for the present study, and its aim was to mimic outpatient treatment that could be offered to individuals with anorexia nervosa in usual clinical practice. It combined features of clinical management and supportive psychotherapy. Clinical management includes education, care, and support and fostering a therapeutic relationship that promotes adherence to treatment. Supportive psychotherapy aims to assist the patient through use of praise, reassurance, and advice. The abnormal nutritional status and dietary patterns typical of anorexia nervosa were central to nonspecific supportive clinical management, which emphasized the resumption of normal eating and the restoration of weight and provided information on weight maintenance strategies, energy requirements, and relearning to eat normally. Information was provided verbally and as written handouts” (p. 742)	“MANTRA, aims to tackle maintaining factors related to rigid thinking styles (<i>e.g.</i> , perfectionism and obsessive-compulsive personality traits), avoidance of strong emotion, pro-anorectic beliefs and responses of close others. The modularised treatment that has resulted from this model maintains a focus on specific changes required in eating and weight within a motivational interviewing and cognitive behavioural therapy frame-work, including individualised case conceptualisation, in addition to summary letters from the therapist to the patient. Due to its modularized nature, it results in a targeted treatment of AN that is matched to the clinical symptoms, personality traits and neuropsychological profile of participants” (pp. 2-3)

SSCM: Specialist supportive clinical management; MANTRA: Maudsley model of anorexia nervosa treatment for adults; AN: Anorexia nervosa.

anorexia nervosa patients were significant. Thus, while CBT sessions were highly structured and included motivational enhancement strategies to improve motivation and willingness for change with the therapist adopting a directive stance, SSCM treatment was less structured and mostly circumscribed to what the patient brought to the session. In CBT psychoeducational material was discussed with the patients to increase their motivation, and their eating behaviours were confronted through the use of cognitive strategies and behavioural experiments, while patients receiving SSCM were encouraged to change their eating behaviours using advice and education about nutrition but they were not taught specific strategies. Finally, homework assignments and reviewing of the content of each session was systematically employed with patients receiving CBT, but no homework was employed in the SSCM, and when patients were provided with some educational material it was not necessarily reviewed in the next session.

Although the authors reported significant effects for CBT in the Weissman Social Adjustment Scale at the 6-mo follow-up, the better Eating Disorder Examination global scores and higher readiness for recovery at 12-mo follow-up were comparable to SSCM, these differences were not confirmed by sensitivity analysis using complete case data. In short, as the authors report: “both groups experienced significant changes on all primary and secondary measures of outcome at EOT, 6- and 12-mo follow-ups... The magnitude of improvements for health-related quality of life, depression and social adjustment were somewhat larger for SSCM, whereas those for ED symptoms and readiness for change were generally larger for CBT” (p.7)^[20].

Thus, for the fourth time consecutively, SSCM has yielded a better or similar outcome in comparison to sophisticated treatments that presumably have sound theoretical foundations. Bearing in mind the constitutive non-specific nature of SSCM, it is rather paradoxical that SSCM should be the first AN treatment for adults to attain the distinction of a “well established psychosocial intervention” according to the criteria of the American Psychological Association Task Force for the Promotion

and Dissemination of Psychological Procedures^[21].

The aim of treatment such as SSCM was to control for nonspecific therapeutic influences inherent in CBT, IPT, and MANTRA, as illustrated in their original conception in Table 1. In contrast to these highly structured, directive and modular treatments, SSCM is nondirective, *i.e.*, the patient meets the therapist in an unstructured setting with an emphasis on patient self-exploration and understanding. According to conventional practice in the psychotherapy research literature, SSCM is a non-psychotherapy control placebo condition^[22]. Its two components, clinical management with a strong component in education and supportive psychotherapy only retain the contextual and relationship elements of any therapeutic encounter and it is devoid of any further specific ingredient^[23]. Thus, clinical management and supportive therapy are the pragmatic baseline elements of SSCM that stand in contrast with the efficacy of theory driven specific treatments built according to an explicit focus on specific cognitive, behavioural and interpersonal domains which are highly structured, and introduced by the therapist in a directive way according to a manualized protocol. As in previous RCTs^[24], SSCM was intended to be a routine type of outpatient treatment.

The unexpected good outcome of patients receiving SSCM has not led to any critical reappraisal of presumably “genuine” treatments, but instead the fundamental nature of SSCM as a non-specific placebo treatment has been called into questioned. Thus, some have argued the possibility of hidden specific active ingredients in SSCM^[12], or even more astonishing is the recommendation that “it would have been desirable to have included a third treatment arm, such as ‘treatment as usual’ (TAU). Such a group would have controlled for non-specific therapy factors (of SSCM)” (p. 9)^[20]. Hence, the burden of proof is placed on attesting that a non-specific treatment is truly non-specific instead of questioning the theory underlying MANTRA, CBT or IPT.

As for the employment of “TAU” as a control condition, the authors of the recent Anorexia Nervosa Treatment of OutPatients (ANTOP) study^[25] in Germany should be congratulated as they have undertaken an am-

bitious multicentre randomized clinical trial in AN adults, whose methodological quality will be quite difficult to match in the coming years. However, as the authors themselves have acknowledged, once again the results were not as expected, *i.e.*, two manual-based specialized treatments- focal psychodynamic therapy (FPT), and enhanced CBT (CBT-E)-were not superior to an optimized treatment as usual.

In short, the list of specialized brand name treatments (CBT, IPT, MANTRA, FPT, CBT-E) with a “non-superiority” score over non-specific treatments initially conceived as a control condition continues to grow. Remarkably, the unfulfilled expectations regarding the efficacy of these specialized AN treatments have not prompted any reappraisal of theoretical assumptions underpinning these treatments, but rather has led to the euphemistic renaming of Nonspecific Supportive Clinical Management, as SSCM. However, as long as the aims of treatment are a logical corollary of the basic understanding of the disorder, the reluctance to critically reappraise the current conceptualization of AN is quite disturbing, bearing in mind that the parity with nonspecific treatments has been the norm since the first RCT in AN twenty six years ago^[26]. In that study, a nonspecific form of individual therapy was already found to be more beneficial than family therapy in older patients, and the authors’ proposed improving individual supportive therapy by incorporating: “more specific therapeutic components in the individual therapy” (p. 1056)^[26]. Notwithstanding, the evidence-base for AN treatments gathered since the recommendation was proposed would suggest this goal is far from being accomplished.

This recurrent pattern of failed attempts at developing a successful treatment for AN challenges established beliefs underlying failed treatments and their specific components. In other words, the parity between nonspecific treatments (not based on any singular trait of AN), and specialized brand type treatments that have been the primary focus of research in recent decades cannot continue to be overlooked, which compels one to consider the possibility that conceptualizations of the disorder may be misleading, and research on AN treatment developed over the last four decades may have been on a misguided path^[27].

Furthermore, with the publication of the ANTOP study the full spectrum of theoretical assumptions underlying treatments (cognitive, interpersonal, psychodynamic) have been encompassed, yet the outcomes of these treatments remain similar or marginally better than SSCM nonspecific treatment, or optimized treatment as usual. Strikingly, it makes no difference whatever the theoretical foundations of treatments are when compared with nonspecific treatments mimicking treatment as usual. This applies regardless of whether treatments are founded on theories aligned with weight and shape concerns prevalent in current AN diagnosis, as is the case of different cognitive behaviour treatments^[28-30], or if they depart significantly from this mainstream thinking^[31], or still if

they are derived from treatments developed for other disorders such as depression, as in the case of IPT^[32].

Several options are open for overcoming the virtual impasse in current treatments for AN. To date the most common strategy has been to try to enhance^[29] and/or refine existing treatments^[33]. However this “more-of-the-same” solution fails to take into account that the similar efficacy of SSCM derives from what SSCM “lacks” in comparison to specialized treatment. For example, despite SSCM lacking specific techniques for addressing complex problems and psychological needs in AN patients, which frustrated more the therapists than the patients themselves^[34], SSCM instilled hope in these patients^[35]. Likewise, the process evaluation of the Maudsley Outpatient Study of Treatments for Anorexia Nervosa and Related conditions (MOSAIC) has revealed the relative unstructured agenda of SSCM, except from its focus on weight restoration and target symptoms, which was addressed in a supportive therapeutic atmosphere, and its slower pace and time to listen the patients were helpful characteristics in developing a positive therapeutic relationship. In the same line, the authors involved in the comparison of SSCM and CBT reported that: “there were no significant differences in patient ratings of therapeutic alliance of the two treatments. Although CBT-AN and SSCM use unique intervention strategies to achieve therapy aims, both were able to promote moderate therapeutic alliance in early treatment, increasing to strong therapeutic alliance in late treatment, to relatively the same degree” (p. 787)^[36]. However, this common therapeutic alliance factor across the two treatments was affected by the absence of an emphasis on weight gain owing to these treatments administered to “severe and enduring anorexia nervosa”^[20] patients. Under different circumstances, where the pressure to gain weight arouses anxiety, early therapeutic alliance seems not to be associated “with either the likelihood of completing treatment or subsequent weight gain. In contrast, both early and later weight gain were associated with the strength of subsequent alliance. These findings indicate that it might be advisable to focus on techniques to drive weight gain rather than rely on the therapeutic alliance to bring about therapeutic change” (p. 216)^[37], which highlight the golden rule in AN treatment, *i.e.*, psychotherapy only works after the starvation process has been properly managed.

Moreover, as the authors involved in the MOSAIC project recognized: “The overlaps between MANTRA and SSCM remind us of the significance of the most basic features of any psychological treatment, such as regularity and predictability of appointments, being given time to talk, and above all the importance of a solid therapeutic relationship.., (Furthermore) two thirds of the patients interviewed about their experience in the process evaluation, embedded in the MOSAIC study, reported external factors that had influenced therapy outcome positively or negatively” (p. 137)^[35], which underscores that being involved in an RCT does not exclude external interferences that may outweigh any involvement in an RCT.

Thus, the lack of any greater efficacy as compared to SSCM, profoundly undermines the conceptualization of AN underlying CBT, IPT, MANTRA, FPT and CBT-E. Either these fundamentals do not represent the essence of AN itself or there are flaws in the way the theory translates into treatment. And, by the same token, these elements purportedly reflecting the essence of the AN disorder might be epiphenomena with respect to its true essence and its maintenance factors, and are therefore irrelevant for the purposes of making them targets for treatment development. Should the latter assertion be correct, it would follow that treatments based on flawed assumptions may be not only ineffective, which is currently the norm, but worse still by being counterproductive and iatrogenic in preventing spontaneous remission: *i.e.*, by requiring patients to work on motives that are not so much in the patients' minds as in the minds of clinicians.

This assertion, which will undoubtedly prove unsettling in some quarters, and runs along the lines of a previous warning against firmly grounded beliefs governing routine treatment of AN patients: "an over-emphasis on weight/BMI and targets is inappropriate, misleading and potentially harmful. Although this view is not always greeted with enormous enthusiasm by some, others are relieved that this particular 'holy cow' is at last being challenged. It is important that we should all have an open mind to the possibility that one of the main tenets of our practice may actually be unhelpful"^[38].

To contend that AN is an elusive, multifactorial disorder refractory to treatment should not preclude fresh avenues of research that may eventually generate alternative AN conceptualizations and treatment, *e.g.*, assessing concurring circumstances in spontaneous remissions, considering psychopathology as an epiphenomenon of malnutrition, and researching the signs of the AN disorder such as hyperactivity and its link to starvation. Anorexia nervosa is extreme in many ways, low incidence, high mortality, and a detrimental impact on health and quality of life, but it is the mental disorder with more objective signs that may serve to guide diagnosis. However, the diagnosis of AN has been primarily based on psychopathology (symptoms), and in the DSM-5^[39] two of the three criteria for AN diagnosis involve symptom complexes of unobservable aspects, *e.g.*, body image disturbance or fear of fatness, whilst the only sign referring to the low bodyweight criterion lacks any clear standard of reference^[40]. The DSM-5 not only discards a previously included sign such as amenorrhea, but also continues to ignore hyperactivity as a relevant sign^[41]. However, as the developers of MANTRA have judiciously pointed out, the unexpected efficacy of SSCM has underscored that treatment: "that does not focus specifically on weight and shape concerns may just (if not more) effective treatments that do" (p. 357)^[31]. It follows that the next step should be to further simplify AN treatment by removing the unnecessary and by incorporating new facets to it.

Much remains to be improved concerning existing AN treatments, as "contemporary etiological hypotheses

have not produced informative research for predictably effective treatments" (p. 163)^[42]. Nevertheless, animal research with analogous models of the human disorder, as is the case of Activity-based anorexia (ABA)^[43], and semi-starvation induced hyperactivity^[44] may be helpful in circumventing the assumption of an internal agency organized around a core motive (weight and shape concerns) underlying restrictive eating and excessive exercising in AN, an assumption which unfortunately has not advanced the treatment of this serious disorder^[45].

The utility of these animal models in generating new hypothesis or for improving AN treatment is further enhanced by the possibility that most of the psychopathological features that characterise AN patients are best understood as the direct consequences of emaciation. The semi-starvation study of Minnesota^[46] has shown that typical symptoms in AN patients (elation and sense of liveliness, irritability, obsessive thinking, depression, anxiety, decreased libido, decreased sociability, and a feeling of personal inefficiency) were associated to a state of starvation. The young men volunteers who lost 25% of body weight suffered insomnia, complained of cold hands and feet and showed an increased tolerance to heat. As their weight loss progressed bizarre food rituals began to show up including cutting food into small pieces, increased gum chewing, food hoarding and an inordinate interest in cooking, and the collection of food recipes^[47,48].

Likewise, the recommendations by members of the Keys' research team may prove to be instructive with respect to the attitude and behaviour patterns of those who have experienced starvation: "One of the more profound changes which took place was the decreased sociability of the men (p. 30)... You are working with people who are living in a narrow world of their own interests and concerns, who must be patiently dealt with as individuals. They are similar to normal people, but have most of the peculiarities and sensitivities of normal people in a greatly exaggerated form" (p. 71)^[49]. Further recommendations have been proposed for one of the signs of AN, *i.e.*, hypothermia: "The lowering of body temperature is more serious than it sounds, for it makes the starving very sensitive to cold weather. This means it is necessary to provide warm clothing, warm blankets, and some warm place where people can spend their day-time hours" (p. 62)^[49]. Due to this hypothermia, the influence of ambient temperature and protection from the cold should be taken into consideration: "the fact that the starving are emotionally affected by the weather (p. 66)^[49], and bad weather is a sufficient cause to explain" the frequent irritability and mood swings: "Such cyclic tendencies were markedly influenced by the weather; warm, sunny days brightened the spirits immeasurably, while cold, damp, cloudy days lowered the men further in their abyss of dejection"^[49]. Notwithstanding, the role of ambient temperature (AT) and climate on the course of AN has been unduly overlooked in research^[50].

Surprisingly most of these recommendations have gone unnoticed so far in spite of being explicitly men-

tioned in Gull's seminal paper, in which he coined the term "anorexia nervosa", and stated: "I have observed that in the extreme emaciation, when the pulse and respiration are slow, the temperature is below the normal standard. This fact together with the observation made by Chossat on the effect of starvation on animals, and their inability to digest food in the state of inanition, without the aid of external heat, has direct clinical bearings- it being often necessary to supply external heat as well as food to patients" (p.24)^[51].

It is worth noting that the first recommendation for the treatment for AN was translational from findings on animal studies. Since Gull's time, however, successive "too human" conceptualizations of AN treatment have evolved that have, with some notable exceptions^[52], relegated animal research as unworthy.

Twelve years ago a paper entitled "Ambient temperature: A neglected factor in Activity-based Anorexia"^[53] brought to the forefront the deficient control and even the absence of reports of AT in research performed with the ABA animal models analogous to anorexia nervosa. This oversight of ambient temperature in studies with the ABA procedure -in which rats on a restricted feeding schedule can exercise freely in a running wheel- violated a well-established recommendation that "one cannot study food intake without specifying or controlling the conditions of temperature regulation"^[54]. Accordingly, AT mishandling has been widespread in ABA research as self-starvation was acknowledged to be the core element in the conceptualization of ABA.

However, research performed in recent years has established the paramount importance of AT on the development^[45,55], and more importantly on the reversal of exhausting running activity, severe weight loss and self-starvation of rats exposed to the ABA experimental procedure^[56-58]. The manipulation of AT in animals exposed to ABA was an attempt to prevent hypothermia resulting from weight loss due to constraints in adequate energy replenishment exerted by the restricted feeding schedule. Together, these studies demonstrated that under the ABA experimental conditions the increase in AT over the thermoneutral range reversed excessive running and favoured weight gain.

The effect of ambient temperature on body weight gain was illustrated in a study where food restricted (1.5 h/d) sedentary rats were housed at either 21 °C or 32 °C^[59]. Under this arrangement cumulative food ingestion of rats housed at 21 °C for a 2-wk period was a 21.5% higher than that of rats maintained at 32 °C, but rats housed at 21 °C gained even less weight than the rats housed at 32 °C. This study also included two additional pair-fed groups of rats housed either at 21 °C or 32 °C that were fed according to the amount of food ingested the previous day by the animals housed at a different AT. Thus, under food restricted conditions, a warmer environment was more influential for body weight gain than food availability, and that under a given fixed food intake only increased AT enhanced body weight gain.

The absence of evidence-based efficacy in AN treat-

ment, and the parity of efficacy compared with a placebo nonspecific treatment such as SSCM are a clear red flag that something has gone awry in the development of treatments for a disorder mostly prevalent in young women that has remained unchanged for centuries. A promising alternative may be to look towards clues provided by animal research, but in the words of John Maynard Keynes: "The difficulty lies not so much in developing new ideas as in escaping from old ones".

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GENERAL INFORMATION

World Journal of Translational Medicine (World J Transl Med, WJTM, online ISSN 2220-6132, DOI: 10.5528) is a peer-reviewed open access (OA) academic journal that aims to guide clinical practice and improve diagnostic and therapeutic skills of clinicians.

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WJTM publishes articles that report the results of translational medicine-related applied and basic research in fields such as immunology, physiopathology, cell biology, pharmacology, medical genetics, and pharmacology of Chinese herbs. The current columns of WJTM include editorial, frontier, diagnostic advances, therapeutics advances, field of vision, mini-reviews, review, topic highlight, medical ethics, original articles, case report, clinical case conference (Clinicopathological conference), and autobiography. Priority publication will be given to articles concerning diagnosis and treatment of translational medicine diseases. The following aspects are covered: Clinical diagnosis, laboratory diagnosis, differential diagnosis, imaging tests, pathological diagnosis, molecular biological diagnosis, immunological diagnosis, genetic diagnosis, functional diagnostics, and physical diagnosis; and comprehensive therapy, drug therapy, surgical therapy, interventional treatment, minimally invasive therapy, and robot-assisted therapy.

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Acknowledgments

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Format

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- 1 **Jung EM**, Clevert DA, Schreyer AG, Schmitt S, Rennert J, Kubale R, Feuerbach S, Jung F. Evaluation of quantitative contrast harmonic imaging to assess malignancy of liver tumors: A prospective controlled two-center study. *World J Gastroenterol* 2007; **13**: 6356-6364 [PMID: 18081224 DOI: 10.3748/wjg.13.6356]

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- 2 **Lin GZ**, Wang XZ, Wang P, Lin J, Yang FD. Immunologic effect of Jianpi Yishen decoction in treatment of Pixu-diar-rhoea. *Shijie Huaren Xiaohua Zazhi* 1999; **7**: 285-287

In press

- 3 **Tian D**, Araki H, Stahl E, Bergelson J, Kreitman M. Signature of balancing selection in Arabidopsis. *Proc Natl Acad Sci USA*

2006; In press

Organization as author

- 4 **Diabetes Prevention Program Research Group**. Hypertension, insulin, and proinsulin in participants with impaired glucose tolerance. *Hypertension* 2002; **40**: 679-686 [PMID: 12411462 PMCID:2516377 DOI:10.1161/01.HYP.00000035706.28494.09]

Both personal authors and an organization as author

- 5 **Vallancien G**, Emberton M, Harving N, van Moorselaar RJ; Alf-One Study Group. Sexual dysfunction in 1, 274 European men suffering from lower urinary tract symptoms. *J Urol* 2003; **169**: 2257-2261 [PMID: 12771764 DOI:10.1097/01.ju.0000067940.76090.73]

No author given

- 6 21st century heart solution may have a sting in the tail. *BMJ* 2002; **325**: 184 [PMID: 12142303 DOI:10.1136/bmj.325.7357.184]

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- 7 **Geraud G**, Spierings EL, Keywood C. Tolerability and safety of frovatriptan with short- and long-term use for treatment of migraine and in comparison with sumatriptan. *Headache* 2002; **42** Suppl 2: S93-99 [PMID: 12028325 DOI:10.1046/j.1526-4610.42.s2.7.x]

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- 8 **Banit DM**, Kaufer H, Hartford JM. Intraoperative frozen section analysis in revision total joint arthroplasty. *Clin Orthop Relat Res* 2002; **(401)**: 230-238 [PMID: 12151900 DOI:10.1097/00003086-200208000-00026]

No volume or issue

- 9 Outreach: Bringing HIV-positive individuals into care. *HRS A Careaction* 2002; 1-6 [PMID: 12154804]

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Personal author(s)

- 10 **Sherlock S**, Dooley J. Diseases of the liver and biliary system. 9th ed. Oxford: Blackwell Sci Pub, 1993: 258-296

Chapter in a book (list all authors)

- 11 **Lam SK**. Academic investigator's perspectives of medical treatment for peptic ulcer. In: Swabb EA, Azabo S. Ulcer disease: investigation and basis for therapy. New York: Marcel Dekker, 1991: 431-450

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- 12 **Breedlove GK**, Schorheide AM. Adolescent pregnancy. 2nd ed. Wicczorek RR, editor. White Plains (NY): March of Dimes Education Services, 2001: 20-34

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- 13 **Harnden P**, Joffe JK, Jones WG, editors. Germ cell tumours V. Proceedings of the 5th Germ cell tumours Conference; 2001 Sep 13-15; Leeds, UK. New York: Springer, 2002: 30-56

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- 14 **Christensen S**, Oppacher F. An analysis of Koza's computational effort statistic for genetic programming. In: Foster JA, Lutton E, Miller J, Ryan C, Tettamanzi AG, editors. Genetic programming. EuroGP 2002: Proceedings of the 5th European Conference on Genetic Programming; 2002 Apr 3-5; Kinsdale, Ireland. Berlin: Springer, 2002: 182-191

Electronic journal (list all authors)

- 15 Morse SS. Factors in the emergence of infectious diseases. *Emerg Infect Dis* serial online, 1995-01-03, cited 1996-06-05; 1(1): 24 screens. Available from: URL: <http://www.cdc.gov/ncidod/eid/index.htm>

Patent (list all authors)

- 16 **Pagedas AC**, inventor; Ancel Surgical R&D Inc., assignee. Flexible endoscopic grasping and cutting device and positioning tool assembly. United States patent US 20020103498. 2002 Aug 1

Statistical data

Write as mean \pm SD or mean \pm SE.

Statistical expression

Express *t* test as *t* (in italics), *F* test as *F* (in italics), chi square test as χ^2 (in Greek), related coefficient as *r* (in italics), degree of freedom as *ν* (in Greek), sample number as *n* (in italics), and probability as *P* (in italics).

Units

Use SI units. For example: body mass, *m* (B) = 78 kg; blood pressure, *p* (B) = 16.2/12.3 kPa; incubation time, *t* (incubation) = 96 h; blood glucose concentration, *c* (glucose) 6.4 ± 2.1 mmol/L; blood CEA mass concentration, *p* (CEA) = 8.6 24.5 $\mu\text{g/L}$; CO₂ volume fraction, 50 mL/L CO₂, not 5% CO₂; likewise for 40 g/L formaldehyde, not 10% formalin; and mass fraction, 8 ng/g, *etc.* Arabic numerals such as 23, 243, 641 should be read 23 243 641.

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Italics

Quantities: *t* time or temperature, *c* concentration, *A* area, *l* length, *m* mass, *V* volume.

Genotypes: *gyrA*, *arg 1*, *c myc*, *c fos*, *etc.*

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