

Genetics of obesity: an overview of current approaches and advancement

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ABSTRACT

Elucidation of obesity susceptibility genes through genome wide approaches as well as candidate gene approaches provides great promise in ultimately determining the genetic underpinnings of obesity. The complex nature of human obesity stems from the multiple interaction of several genes that control the physiology of food intake, energy expenditure, development of the body, and behavioural patterns towards food intake, and the environment. According to twin, adoptees and family studies, genetic factors account for 40-70% of the variability observed in human adiposity. Twin studies supported that the heritability of adiposity is higher than other quantitative traits. The heritability of obesity traits has been further evidenced by identification of quantitative trait loci (QTL) and genes through methods such as genome-wide scans (studies conducted on unrelated obese individuals), linkage analyses (conducted in families), and association studies (investigating the correlation between obesity and polymorphisms). The number of contributing genes, however, is still unknown. Although research on the genetic basis of obesity has advanced, the mechanisms underlying the condition are still complex due to its heterogeneity even within families.

INTRODUCTION

Obesity is a multifactorial condition often associated with an excess of body fat. Nowadays obesity has emerged as second-most important leading cause of death yet, preventable as well as major public health issue. According to the National Center for Health Statistics reports, 61% of adult population in the United States are overweight (body-mass index 25–29.9) and 26% are obese (body-mass index 30); in fact it is no more a health hazard issue only in Western society, but it has also grown up throughout the world by >75% since 1980 (CDC; Cumming and Schwartz, 2003). Although Bangladesh suffers from under nutrition and underweight but there is steady rise of overweight and obesity (Shafique *et al.*, 2007; Balarajan and Villamor, 2009). Obesity became common issue and public health problem

in many countries of Asia (Pomerleau *et al.*, 1999; Mohamad *et al.*, 1996; Ismail *et al.*, 2002). Commonly BMI is used for measuring obesity in clinical and research settings, however, alternative anthropometric measures such as waist circumference (WC), and waist-hip-ratio (WHR) that indicates abdominal adiposity have been suggested to be the most accurate determinants and predictors of cardiovascular diseases (CVD) and type 2 diabetes (Wei *et al.*, 1997; Stevens *et al.*, 2001; Janssen *et al.*, 2004; Sailaja and Bhatnagar, 2010) This is based on the background that increased visceral adipose tissue is associated with decreased glucose tolerance, reduced insulin sensitivity and adverse lipid profiles, leading to risk factors for type 2 diabetes and CVD. Several studies also suggest the strong correlation between BMI with WC, and health risk indicator instead of using BMI alone (Chan *et al.*, 1994; Arden *et al.*, 2003; Janssen *et al.*, 2002; Bigaard *et al.*, 2003; Huzxley *et al.*, 2010). In support of this (Table 1), the National Institute of Health (NIH) guidelines indicate that the risk of acquiring CVD and type 2 diabetes increases in a graded fashion when moving from normal-weight through obese BMI categories, and that within each BMI category

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men and women with high WC values are at a greater health risk than are those with normal WC values (NIH 1998). The World Health Organization has announced obesity as a global epidemic (Cumming and Schwartz, 2003; WHO). Moreover, obesity predisposes to, or exacerbates, many clinical conditions such as hypertension, type-II diabetes, hyperlipidaemia, gout, gallbladder disease, osteoporosis, cancer and infertility (Digirolamo *et al.*, 2000; Helali *et al.*, 2013). It has been suggested that the obesity epidemic has a strong causal relation with our obesigenic lifestyle, mainly excessive caloric intake and less physical activity as well as increased reliance on mechanized inventing (Shuldiner and Munir, 2003). Furthermore, it has also been demonstrated that genetic factors play a dominant role in person susceptibility to obesity rather than the environmental cause and till date more than 200 candidate genes have been explored by gene mapping studies which have potential influence on developing obesity (Speakman, 2007). Hence, obesity results from gene- environment interaction and the individual's genetic tendency to become obese can be evident from the exposure to the modern environment (Speakman, 2007). Herein, the recent evidence of genes linked or related to obesity phenotypes has been reviewed.

Table 1: Combined recommendations of body mass index and waist circumference cut-off points made for overweight or obesity classifications, and association with disease risk (NIH 1998).

Body weight category	Body Mass Index	Obesity Class	Disease risk (relative to normal weight and waist circumference)	
			Men < 102 cm Women < 88 cm	Men >102 cm Women >88 cm
Underweight	<18.5			
Normal	18.5–24.9			
Over weight	25.0–29.9		Increased	High
Obesity	30.0–34.9	I	High	Very High
	35.0–39.9	II	Very High	Very high
Extreme obesity	>40.0	III	Extremely High	Extremely High

GENETICS OF OBESITY

The common polygenic obesity in humans

Despite, the strong association of genetic component to human obesity, specific Mendelian mode of inheritance yet is not detected; suggestive of multiple genes' involvement in obesity (Shuldiner and Munir, 2003). Again, modern genetics researches offer two types of analytical approaches such as, genome wide (Chial and Craig, 2008; Chen *et al.*, 2008; Emilson *et al.*, 2008) and candidate gene analysis (Shuldiner and Munir, 2003; Clément *et al.*, 1996). In genome-wide approaches quantitative trait loci (QTL) are identified which in turns help to identify the regions of chromosome which are known to encode the genes associated with the Mendelian syndromes that possess obesity as one of the feature (Chagnon *et al.*, 2000). Afterwards, positional cloning can be done on the basis of information of human genome database; till date obesity prone genes in various chromosomal regions have been detected namely chromosome 10p, 11q24, 11q24, 16p, 18q21, 20q13, and Xq24 by attaining the genome-wide scan in different populations such as Caucasians, African Americans, Mexican Americans and Pima Indians (Bouchard and Perusse, 1993). In candidate gene approaches, genes those are potentially related to the pathophysiology of obesity are investigated and by comparing

the DNA sequences of these genes between obese and non-obese may help to discover the gene variants responsible for obesity vulnerability as well as linkage results of obesity and body fat phenotypes with candidate genes (Chagnon *et al.*, 2000). Two notable examples of candidate gene variants that might have some role in obesity susceptibility, include Trp64Arg β 3 adrenoceptor (Walston *et al.*, 1995; Widen *et al.*, 1995; Clement *et al.*, 1995) and Pro12Ala peroxisome proliferator activated Receptor- γ 2 (PPAR- γ 2) (Yen *et al.*, 1997; Beamer *et al.*, 1998). Recently 22 genes which have five or more positive associations of variants with obesity phenotypes have been explored (Table 2) and it mainly includes members of the leptin–melanocortin pathway, pro-inflammatory cytokines and uncoupling protein (Walley *et al.*, 2006). Meanwhile, it has been concluded by a majority of the study that most of them have a comparatively minor influence on obesity phenotype.

Monogenic obesity: Single – Gene- Mutation Rodent model

Animal models of obesity have been studied extensively in an effort to elucidate the mechanisms underlying human obesity, and currently there are several hundred genes that have evidenced the heritability of body weight (Rankinen *et al.*, 2006). Some of the popular genes implicated include leptin (*LEP*), leptin receptor (*LEPR*), agouti-related peptide (*AgRP*), tubby gene, POMC gene (Rankinen *et al.*, 2006; Brockmann and Bevova 2002). Spontaneous mutations in these genes has been detected being responsible for obesity in mouse models and by cloning the corresponding genes both in rodent and humans, their possible functions and pathways of body weight regulation has been identified (Inui 2000). Furthermore, the cognition of this pathway combined with modern genetic methods provides the new insights and paved a way of unraveling the complex nature of human obesity.

Leptin (*LEP*) Gene

The role of leptin in obesity was first explored in studies on severely obese ob/ob mice, which has a mutation in the gene encoding the leptin, which is a hormone secreted by adipose tissue and directly proportional to fat mass; leptin has significant impact on appetite and energy expenditure (Considine *et al.*, 1996; Maffei *et al.*, 1996; Farooqi *et al.*, 2005; Farooqi *et al.*, 2006; Farooqi *et al.*, 2007).

Leptin is highly similar among species and there are 83%-84% similarity reported between rodents and humans (O' Rahilly and Farooqi, 2006; Chagnon *et al.*, 1999). Treatment of ob/ob mouse with the recombinant leptin reduces the appetite as well as their body weight and corrects all their phenotypic abnormalities (Montague *et al.*, 1997; Kalra and Kalra, 2002; Iwaniec *et al.*, 2007). Similarly, after screening of thousands of obese individuals, mutations have been detected at three different families. Two cousins who were both normal weights at birth and afterwards suddenly gained weight and became obese were reported due to lack of circulating OB protein in their blood like OB protein deficient mice (Camfield and Smith, 2000). The causal

relation of obesity and ob gene mutation was also found in three members of another family of turkey (Camfield and Smith, 2000; David *et al.*, 2002). But, other attempts of finding associations between LEP mutation and human obesity have failed and it was suggested that obesity is more related to congenital deficiency in leptin production rather than leptin mutation (Montague *et al.*, 1997; Yang and Barouch, 2007). Besides this, a number of studies demonstrated that leptin deficiency leads to increase insulin resistance with age and thus causes obesity (Montague *et al.*, 1997; Martin *et al.*, 2008).

Another hypothesis established that, an absolute deficit of leptin does not underlie most cases of obesity. Instead, most obese individuals exhibit elevated circulating leptin levels (leptin resistance), which increase proportionally with their adipose mass (Considine *et al.*, 1996; Maffei *et al.*, 1996; Farooqi, 2005). A number of mechanisms have been proposed to explain leptin resistance, and these include the failure of circulating leptin to reach its target receptor within the brain, decreased expression of the leptin receptor within hypothalamic neurons, perturbations in developmental programming, etc (Bjørbaek and Kahn, 2004; Flier 2004; Remacle *et al.*, 2004).

Another mechanism that has received attention is the attenuation of the intracellular leptin signaling cascade (Bjørbaek *et al.*, 1998). The action of various cytokine receptors is negatively regulated by an intracellular protein, the suppressor of cytokine signaling-3 (Socs-3) (Starr *et al.*, 1997). Leptin is structurally related to cytokines and acts via a receptor that belongs to the cytokine receptor family. It is, therefore believed that Socs-3 limits leptin signalling, and mediates leptin resistance (Kievit *et al.*, 2006).

The Leptin-Receptor (LEPR) Gene

The rodent leptin-receptor *Lepr* gene encodes a protein of 1164 amino acids with a 22 amino acid secretory signal sequence, a predicted transmembrane domain and a cytoplasmic domain with variable length and constituent. In human *Lepr* is named LEPR and structure is very similar to those of rodents, with a similarity of 78% and 71% for extra and intracellular domains (Bouchard, 1995).

After deleting the signalling form of the leptin receptor in db/db mice were associated with unresponsiveness to endogenous or exogenous leptin and the result was the earlier development of hyperglycaemia (O'Rahilly and Farooqi, 2006; Zhang *et al.*, 1994). Similarly, a splice - mutation in the leptin receptor that produced truncated receptor lacking both transmembrane and intracellular portion of the receptor has been reported in a consanguineous family of Kabilian origin (O'Rahilly and Farooqi, 2006). Obese individuals were shown to be homozygotes for the mutation that produced an early-onset morbid obesity with hyperphagia and hypogonadotropic hypogonadism which is suggestive of the direct role of LEPR in the control of adiposity and human body composition and also a good manifest of DNA sequence variation in the LEPR directly contribute to the human obesity (Farooqi *et al.*, 2007; Clement *et al.*, 1998).

The Agouti Signalling-Protein (ASIP) Gene/Agouti-related peptide (AgRP)

Mutations in the agouti- signaling protein which acts through the melanocortin receptors to modulate eating behaviour are found to be associated with mouse obesity; the mouse AgRP gene is very similar to an ASIP gene in human. In humans the effect varies according to age, with loss of AgRP leading to a severe life threatening hypophagia in adults while in newborn babies it results in mild food suppression and body weight loss (Flier, 2006). But there have so far been no linkage and mutation studies of AgRP gene responsible for human obesity have been reported (Shuldiner and Munir, 2003; Chagnon *et al.*, 2000).

POMC (Pro-opiomelanocortin) gene Deficiency

It is the first-order neuronal targets of leptin action in the brain which is anorectic (reducing food intake). Again, it has been reported that 40% of POMC neurons in the arcuate nucleus is responsible for the expression of the mRNA that is required for the long form of the leptin receptor and leptin is also associated with POMC expression (O'Rahilly and Farooqi 2006). The pro hormone processing enzyme, pro-hormone convertase 1 or PC-1 is required for post- translational processing of POMC for yielding biologic peptide.

However, a mutation in the gene for PC-1 was found to be related to obesity (Chagnon *et al.*, 2000). Besides this, hyperphagia and early onset obesity accompanied by adrenal insufficiency and red hair pigmentation have been reported due to direct homozygous or heterozygous mutations in POMC (Krude *et al.*, 1998).

Prohormone Convertase 1 Deficiency

In addition to the relation of PC-1 to POMC, PC 1 is also responsible for the cleavage of number of peptide such as GLP1, in the hypothalamus and GLP -1 is related to feeding behaviour. It has been demonstrated that early onset obesity which results from severe small-intestinal absorptive dysfunction as well as impaired pro-hormone processing and hypocortisolaemia is related to the maturation failure of pro-peptide that express PC1 throughout the gut (O'Rahilly and Farooqi, 2006).

The Tubby (TUB) gene

In tub mouse it has been found that there is a positive correlation between let onset obesity and also moderate type of obesity with tubby gene mutation (mutation in insulin signaling protein). However, no mutation in human equivalent to the gene has reported yet (Chagnon *et al.*, 2000).

MC4R mutations

Although currently no known *MC4R* obesity-causing mutation in animal models, in humans, *MC4R* defects are the most common causes of monogenic obesity with more than 100 mutations described in different ethnic groups and the most of the mutations are transmitted in an autosomal dominant manner (Krude *et al.*, 1998; Yeo *et al.*, 1998; Kobayashi *et al.*, 2002;

Table 2: Genes with five or more positive associations of variants with obesity or obesity-related phenotypes (Walley *et al.*, 2006).

Gene symbol	Full name	Chromosomal location	Number of studies	P-value
ACE	Angiotensin I-converting enzyme (peptidyl-dipeptidase A) 1	17q24.1	6	0.05–0.0023
ADIPOQ	Adiponectin, C1Q and collagen domain containing	3q27	11	0.05–0.001
ADRB2	Adrenergic, beta-2-, receptor, surface	5q31–q32	20	0.05–0.0001
ADRB3	Adrenergic, beta-3-, receptor	8p12–p11.2	29	0.05–0.001
DRD2	Dopamine receptor D2	11q23.2	5	0.03–0.002
GNB3	Guanine nucleotide binding protein (G protein), beta polypeptide 3	12p13.31	14	0.05–0.001
HTR2C	5-hydroxytryptamine (serotonin) receptor 2C	Xq24	10	0.05–0.0001
IL6	Interleukin 6 (interferon, beta 2)	7p21	6	0.03–0.003
INS	Insulin	11p15.5	7	0.05–0.0002
LDLR	Low density lipoprotein receptor (familial hypercholesterolaemia)	19p13.2	5	0.04–0.001
LEP	Leptin (obesity homologue, mouse)	7q31.3	10	0.05–0.003
LEPR	Leptin receptor	1p31	16	0.04–0.0001
LIPE	Lipase, hormone-sensitive	19q13.2	5	0.05–0.002
MC4R	Melanocortin 4 receptor	18q22	8	0.04–0.002
NR3C1	Nuclear receptor sub-family 3, group C, member 1 (glucocorticoid receptor)	5q31	10	0.05–0.001
PLIN	Perilipin	15q26	5	0.05–0.0008
PPARG	Peroxisome proliferative activated receptor, gamma	3p25	30	0.05–0.001
RETN	Resistin	19p13.2	5	0.048–0.001
TNF	Tumor necrosis factor (TNF superfamily, member 2)	6p21.3	9	0.05–0.004
UCP1	Uncoupling protein 1 (mitochondrial, proton carrier)	4q28–q31	10	0.05–0.001
UCP2	Uncoupling protein 2 (mitochondrial, proton carrier)	11q13.3	11	0.05–0.001
UCP3	Uncoupling protein 3 (mitochondrial, proton carrier)	11q13	12	0.049–0.0005

Mergen *et al.*, 2001; Vaisee *et al.*, 1998). Clinical heterogeneity and sometimes incomplete disease penetrance are the characterized features of these mutations.

PHARMACOLOGICAL INTERVENTIONS

Obesity potentially increases the risk of cardiovascular diseases, type II diabetes, dyslipidemia, arthritis, and some type of cancers and also reduces both quality of life and average life expectancy (Haslam and James, 2005). The effective treatment of obesity will reduce the load of disease as personally and also for the community (Hainer *et al.*, 2008). Anti-obesity drugs have abuse potential also (Kroll, 2013). Researchers found at Columbia University College New York that ‘anti-obesity drug that turns off the same brain circuits which trigger the marijuana-induced hunger pangs appears to produce sustained weight loss among patients’. This finding probably delayed the approval of the world first blockbuster anti-obesity medicine Rimonabant (News Medical, 2006). Rimonabant is not now considered as safe drug as it is reported to cause increased number of psychiatric diseases in otherwise normal individual (Soyka, 2008). Obesity is a multifactorial chronic medical disorder. Again there is almost no short cut way to treat the condition instantly. Physicians need to educate their patients about obesity and available pharmacological interventions (Wyatt and Hill, 2004). Again it is always no medication is absolutely free from adverse drug reactions. Henceforth, anti-obesity drug is not answer (Wyatt and Hill, 2004). ‘Life-threatening safety issues led to the withdrawal of number of antiobesity drugs from the US market, including a multibillion dollar settlement by the manufacturers of these drugs’ (Elangbam, 2009). Orlistat is considered as a safe agent for obesity. Hence, National Institute of Health Care Excellence (NICE), UK also suggests orlistat because it’s higher efficacy and also cost-effective (Hampp *et al.*, 2008). Orlistat has quite free drug interactions especially with drugs of low therapeutic index or

drugs usually need for these patients like antihypertensive, anti-diabetics, and cardio-tonics (Al-Suwailem *et al.*, 2006). Therefore in current context low-calorie diet and low-calorie diet in combination with or listat shows higher efficacy cost-effectiveness (van Baal *et al.*, 2008). Researchers expect that in near future more effective and well tolerated drug will be developed soon with ‘a better understanding of the multiple mechanisms and complex physiological systems is targeting appetite’. It is estimated medical cost of obesity is more 150 billion per year in USA (Finkelstein *et al.*, 2009). Henceforth, scholars and patients also expect that beside scientific and regulatory issues researches will also consider patents’ financial burden as obesity is not only a trouble of rich country but also of the developing countries. There are also need appropriate policies for ‘social intervention as a means of managing obesity because obese patients often return to toxic environments and behaviours’ (Kang and Park, 2012).

CONCLUSION

The substantial advances have been achieved in the last few years through the cloning of the genes those are responsible for the obesity and comorbidities in the single-gene rodent models of obesity. It can be assumed that several genes have the potential for human obesity and obesity genotype to cause obesity in humans. It seems likely that the obesity genotype is a complicated multi-genic system; possibly the more severe individuals carry the mutation at multiple loci and less severe cases may carry only one mutated genes. However, clarification of obesity susceptibility genes through the genome wide approaches or candidate gene approaches can provide powerful tool for identifying the genetics beneath the obesity. Eventually, the new insight for the pathogenesis of obesity then contribute to the new medicines and diagnostic tools and hopefully within the next few years these innovations will be applied to the clinical field; for instance with the single blood test the health professionals will be able to

demonstrate the individual's genetic burden to obesity genes as well as genetic elements associated with co-morbid risks. In conclusion, there is an emergent call for effective research for the development of effective and safe treatment modalities to combat global threat of obesity and related issues for developed and developing countries.

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