The Role of Genetic Variation across IL-1β, IL-2, IL-6 and BDNF in Antipsychotic-Induced Weight Gain

by

Trehani Mary Fonseka

A thesis submitted in conformity with the requirements for the degree of Master of Science

> Institute of Medical Science University of Toronto

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Abstract

Background: Antipsychotics with high weight-inducing propensities influence the expression of immune and neurotrophin genes, which have been independently related to obesity indices. Thus, we investigated whether polymorphisms across interleukin (IL)-1 β , IL-2, IL-6, and brain-derived neurotrophic factor (BDNF) genes are associated with antipsychotic-induced weight gain (AIWG).

Methods: Nineteen polymorphisms were genotyped using Taqman® assays in 188 schizophrenia patients on antipsychotic treatment for up to 14 weeks. Mean weight change (%) from baseline was compared across genotypic groups using ANCOVA. A replication sample was used to validate findings.

Results: In Europeans, IL-1 β rs16944*GA (p=0.013), IL-1 β rs1143634*G (p=0.001), and BDNF Val66Met (Val/Val, p=0.004) were associated with greater AIWG, as were IL-1 β rs4849127*A (p=0.049), and IL-1 β rs16944*GA (p=0.012) in African Americans. Epistatic effects were observed between BDNF Val66Met and IL-1 β rs13032029 (Val/Met+TT, P_{Perm}=0.029), IL-6 rs2069837 (Val/Val+AA, P_{Perm}=0.021), and IL-1 β rs16944 (Val/Val+GA, P_{Perm}=0.006).

Conclusions: SNPs across IL-1 β and BDNF Val66Met may influence AIWG. Replication of these findings in larger, independent samples is warranted.

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List of Abbreviations

 α 7nAch: α 7-nicotinic acetylcholine α -MSH: α -melanocyte-stimulating hormone AgRP: agouti-related protein AIWG: antipsychotic-induced weight gain ANCOVA: analysis of covariance AP: antipsychotic APR: acute phase response ARC: arcuate nucleus BBB: blood-brain barrier BDNF: brain-derived neurotrophic factor BH₄: tetrahydrobiopterin BMI: body-mass index **BPRS: Brief Psychiatric Rating Scale** BSX: Brain-Specific Homeobox Factor CAN-BIND: Canadian Biomarker Integration Network in Depression CART: cocaine- and amphetamine-regulated transcript CATIE: Clinical Antipsychotic Trials of Intervention Effectiveness CCK: cholecystokinin CHI3L1: chitinase-3-like 1 CNS: central nervous system COX: cyclooxygenase CRH: corticotropin-releasing hormone CRP: C-reactive protein

CSF: cerebrospinal fluid

CSWG: clinically significant weight gain

DMH: dorsomedial hypothalamic nucleus

DSM-III-TR: Diagnostic and Statistical Manual of Mental Disorders, Third Edition, Revised

DSM-IV: Diagnostic and Statistical Manual of Mental Disorders, Fourth Edition

ENCODE: Encyclopedia of DNA Elements

EPA: eicosapentaenoic acid

EPS: extrapyramidal symptoms

EPUFAs: essential polyunsaturated fatty acids

FEP: first-episode patient

FGAs: first-generation antipsychotics

GABA: gamma-aminobutyric acid

GI: gastrointestinal

HAMD: Hamilton Rating Scale for Depression

HDL: high density lipoproteins

HIV: human immunodeficiency virus

¹H-MRS: proton magnetic resonance spectroscopy

HPA: hypothalamic-pituitary-adrenal

HWE: Hardy-Weinberg equilibrium

IDO: indoleamine 2,3 dioxygenase

IFITM: interferon-induced transmembrane

IFN: interferon

IL: interleukin

IL-1β: interleukin 1-beta

IL-2: interleukin 2

IL-6: interleukin 6

IL-1RA: interleukin-1 receptor antagonist

IL-1RI: interleukin 1 receptor, type I

IL-1RII: interleukin 1 receptor, type II

IL-2R: interleukin 2 receptor

IL-6R: interleukin 6 receptor

JAK: Janus kinase

KBP: kilobase pairs

KYN: kynurenine

KYNA: kynurenic acid

LD: linkage disequilibrium

LHA: lateral/perifornical hypothalamic area

LOD: logarithm of the odds

LPS: lipopolysaccharide

MADRS: Montgomery-Asberg Depression Scale

MAF: minor allele frequency

MAPK: mitogen activated protein kinase

MBMDR: Model-Based Multifactor Dimensionality Reduction

MCH: melanin-concentrating hormone

MCP-1: monocyte chemoattractant protein-1

MDD: major depressive disorder

MetS: metabolic syndrome

MHC: major histocompatibility complex

NF- κ B: nuclear factor- κ b

NK: natural killer

NMDA: N-methyl-D-aspartate NPY: neuropeptide-Y NSAIDs: non-steroidal anti-inflammatory drugs PAMPs: pathogen-associated molecular patterns PANSS: Positive and Negative Syndrome Scale PCR: polymerase chain reaction PET: positron emission tomography PGE₂: prostaglandin E2 PI-3-kinase: phosphoinositide-3-kinase Poly I:C: polyinosinic:polycytidylic acid POMC: proopiomelanocortin PVN: paraventricular nucleus QUIN: quinolinic acid **RNS:** reactive nitrogen species **ROS:** reactive oxygen species SERPINA3: serpin peptidase inhibitor, clade A, member 3 SGAs: second-generation antipsychotics sIL-2R: soluble interleukin 2 receptor sIL-6R: soluble interleukin 6 receptor SNAP: SNP Annotation and Proxy Search SNPs: single nucleotide polymorphisms SNPSpD: Single-Nucleotide Polymorphism Spectral Decomposition SPECT: single photon emission computed tomography SPSS: Statistical Package for the Social Sciences

STAT: signal transducer and activator of transcription

sTNFR: soluble tumor necrosis factor receptor TDO: tryptophan 2,3 dioxygenase TGF: transforming growth factor TH₁: type 1 T helper TH₂: type 2 T helper TNF-α: tumor necrosis factor-alpha TRH: thyrotropin-releasing hormone TrkB: tyrosine kinase receptor TSPO: translocator protein UCSC: University of California Santa Cruz VMN: ventromedial nucleus VTA: ventral tegmental area

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Chapter 1:

Literature Review

The purpose of this chapter is to review:

- ✤ Metabolic disturbances within schizophrenia
- Neuroinflammation within schizophrenia
- Effects of inflammation on metabolic processes

1.1. Introduction

Schizophrenia is a highly debilitating psychiatric condition with a chronic course, and according to diagnostic systems, a global lifetime prevalence rate of approximately 4 per 1000 persons¹. Clinical conceptualization of schizophrenia is predominantly defined by phenomenological heterogeneity across positive, negative, and cognitive symptom domains². Positive symptoms, which refer to the presence of abnormal mental functions and/or behaviours (e.g. delusions, hallucinations, bizarre or disorganized speech and behaviour), are clinically distinct from negative or deficit symptoms (e.g. blunted affect, amotivation, anhedonia, asociality, poverty of speech)³. The severity of cognitive symptoms, which can include disturbances in episodic and working memory, attention, concentration, information processing, learning, and executive function, may be influenced by the presence of affective symptoms^{4,5}.

Clinical improvement of schizophrenic symptoms is preferentially achieved through treatment with antipsychotic (AP) medication. Beginning with the advent of chlorpromazine in the early 1950s, typical or first-generation antipsychotics (FGAs) were the first class of psychotropic medication that efficaciously treated schizophrenia by primarily reducing positive symptoms and risk for relapse⁶. However, treatment benefits were limited by an adverse side effect profile which commonly included FGA-induced hyperprolactinemia, acute extrapyramidal

symptoms (EPS) (e.g. akathisia, dystonia, parkinsonism), and tardive dyskinesia⁷. A further disadvantage was a high rate of partial and full treatment resistance, particularly with regard to the persistence of negative and cognitive symptoms⁶. To address EPS concerns, atypical or second-generation antipsychotics (SGAs) were introduced with the advent of clozapine in the late 1960s. Clozapine showed considerable promise due to its superior efficacy in treating refractory schizophrenia relative to FGAs⁸. Additional SGAs such as risperidone, olanzapine, sertindole, and ziprasidone were subsequently developed⁹. Collectively, SGAs have been shown to therapeutically outperform FGAs across positive¹⁰, negative¹¹, cognitive^{12,13}, and affective¹⁴ symptoms, while maintaining a lower incidence of motor side effects and hyperprolactinemia¹⁵.

In spite of these therapeutic benefits, APs have been shown to cause substantial weight gain in patients. Meta-analyses have reported that weight gain occurs more often with SGAs relative to FGAs, and with greater probability for some SGAs, like clozapine and olanzapine, than others^{16,17}. Antipsychotic-induced weight gain (AIWG) is a leading contributor of AP non-compliance¹⁸, and a major risk factor for various medical conditions like obesity, metabolic (e.g. dyslipidemia, hyperglycemia, diabetes mellitus) and vascular (e.g. cardiovascular and cerebrovascular disease, arterial hypertension, ventricular arrhythmias) abnormalities, and premature mortality¹⁹. Inter-individual variability in the magnitude of weight gain susceptibility has been reported to depend on genetic factors^{16,20}. Previous studies have demonstrated an association between genetic variation in genes involved in inflammatory processes, such as tumor necrosis factor-alpha (TNF- α) and leptin, and weight change during AP treatment²¹⁻²³.

APs also yield partial treatment benefits by influencing expression of inflammatory cytokines, like interleukin 1-beta (IL-1 β), interleukin 2 (IL-2), and interleukin 6 (IL-6), to ultimately reduce the neuroinflammatory signatures observed within schizophrenia^{24,25}. Such alterations in cytokine levels can mediate changes in feeding behaviours and disturb metabolic parameters, with reduced inflammation leading to obesity²⁶⁻²⁸. Brain-derived neurotrophic factor (BDNF), a neurotrophin secreted by immune cells as a neuroprotective response to inflammation, is decreased in certain brain regions subsequent to AP treatment^{29,30}. At low levels, BDNF can contribute to metabolic disturbances like weight gain³¹. Genetic variation in pro-inflammatory cytokines and BDNF has also been associated with obesity³²⁻³⁵, and may therefore be implicated in the pharmacogenetics of AIWG.

PART I: METABOLIC DISTURBANCES IN SCHIZOPHRENIA

1.2. Metabolic Pathology and Schizophrenia

Schizophrenia and other severe mental disorders are characterized by a high prevalence of various physical health concerns. In particular, there is a clinically significant co-occurrence of schizophrenia with the metabolic syndrome (MetS) which occurs in approximately 9.8% to 12.9% of untreated schizophrenia patients³⁶⁻³⁸. MetS includes components such as obesity, glucose intolerance, atherogenic dyslipidemia, insulin resistance and hypertension, in addition to an increased risk of type II diabetes mellitus and cardiovascular disease^{39,40}. The metabolic pathology of schizophrenia has been documented in multiple case reports prior to the advent of APs (reviewed in Kohen, 2004)⁴¹. Studies of drug-naive and drug-free schizophrenia patients report central obesity, impaired glucose tolerance, insulin resistance, and elevated fasting plasma levels of glucose, insulin and cortisol relative to healthy controls⁴²⁻⁴⁴. However, these findings have not been consistently replicated⁴⁵⁻⁴⁷. Elevated rates of metabolic disturbances have also been observed in first-degree relatives of schizophrenic patients, suggesting a shared environmental and/or genetic component to metabolic outcomes in schizophrenia^{43,48}.

1.3. Metabolic Side Effects of Antipsychotic Medication

1.3.1. Antipsychotic-Induced Metabolic Disturbances

Metabolic abnormalities observed within untreated schizophrenia have been shown to worsen subsequent to AP treatment¹⁹. Zhang *et al.* $(2004)^{49}$ identified significant increases in subcutaneous and intra-abdominal fat, in addition to elevated levels of leptin, circulating lipids, and non-fasting glucose after 10 weeks of AP treatment in previously untreated schizophrenia patients. Similarly, a meta-analysis by Mitchell *et al.* $(2013)^{36}$ showed that metabolic irregularities like obesity (52.7% vs. 26.6%), elevated triglycerides (41.1% vs. 16.9%), low levels of high density lipoproteins (HDL) (44.7% vs. 20.4%), high blood pressure (39.7% vs.

24.3%), diabetes (12.8% vs. 2.1%), and hyperglycemia (27.8% vs. 6.4%) were elevated in treated as compared to untreated schizophrenic patients.

Weight gain is a common side effect of APs, and affects approximately 15% to 72% of schizophrenic patients receiving acute or maintenance treatment³⁷. AIWG has been documented since the introduction of chlorpromazine with reports of steadily increasing weight with treatment that rapidly declines upon drug cessation^{50,51}. AIWG often occurs within the first 4 to 12 weeks of treatment and may stabilize over time^{52,53}. AIWG has also been observed in other AP-treated psychiatric populations, such as bipolar disorder⁵⁴, treatment-resistant major depressive disorder (MDD)⁵⁵, mental retardation and autistic disorder⁵⁶, and Tourette's syndrome⁵⁷. However, the propensity to induce weight gain varies between APs. A meta-analysis by Lett *et al.* (2012)¹⁶ reported that SGAs carry a greater risk of weight gain compared to FGAs. with clozapine and olanzapine having the highest risk, quetiapine and risperidone having intermediate risk, and aripiprazole and ziprasidone having minimal risk, according to mean weight change values. Among FGAs, low-potency drugs such as chlorpromazine and thioridazine yield greater weight gain effects than high-potency drugs like haloperidol and fluphenazine (refer to Figure 1.1). Some studies also suggest that APs can induce clinically significant weight loss in approximately 10% of patients⁵⁸.





FIG 1.1: Antipsychotics are categorized according to a low, moderate or high propensity to induce weight gain in patients. Drugs are listed in order from highest to lowest weight-inducing potential, per category; *Second generation antipsychotic

Preliminary data have identified many potential predictors of AIWG which can influence the magnitude of treatment-induced weight change. Such risk factors typically pertain to patient, illness and/or treatment parameters (refer to Figure 1.2). *Patient Parameters*. Pediatric patients are particularly vulnerable to AIWG, as the amount of weight gained with AP treatment negatively correlates with age⁵⁹⁻⁶³. Elevated risk has been reported for women compared to men^{59,61}, but the reverse association has also been found^{64,65}. Other risk factors include non-white ethnicity⁶⁶, increased appetitive behaviours^{66,67}, and non-smoking status⁵⁹. Cannabis may also influence AIWG by acting on the endogenous endocannabinoid system to increase appetite and weight⁶⁸. An inverse relationship exists between baseline BMI and AIWG, where low pretreatment BMI correlates with greater weight gain^{60,61,69-71}. Low baseline BMI can also predict accelerated weight gain over the course of AP treatment⁵⁹. Patterns of accelerated weight gain, in addition to weight gain early in the course of treatment, predict greater long-term weight gain and a higher plateau for mean weight increase⁷². High parental BMI is predictive of weight gain, and suggests a shared environmental and/or genetic component to AIWG^{59,65}. The genetic basis of AIWG has received considerable support from candidate gene studies (refer to Section 1.4.4).

Illness Parameters. Although schizophrenia is an independent risk factor for weight gain (refer to Section 1.2), additional evidence suggests that the magnitude of AIWG differs between schizophrenic subtypes, with the undifferentiated and paranoid subtypes conferring the greatest risk⁷³⁻⁷⁵. First-episode patient (FEP) status, drug naivety, and high baseline levels of negative symptoms have also been identified as risk factors^{52,58,60,62}, as has symptomatic improvement which positively correlates with AIWG^{61,66,67,74}. *Treatment Parameters*. AIWG increases with the duration of AP treatment^{58,74}. Dose effects have been inconsistently reported, with some studies supporting a positive dose-dependent relationship for clozapine, olanzapine⁷⁶ and risperidone⁷⁷, while others suggest no relationship^{60,78}. As shown in Section 1.3.1, different APs confer varying risk of AIWG, with olanzapine and clozapine having the most robust outcomes. Polypharmacy can result in greater weight gain likely due to the combined effects of other weight-inducing drugs^{62,79}. For example, Casey *et al.* (2003)⁸⁰ observed a two-fold increase in weight during combined risperidone and valproate therapy relative to risperidone monotherapy.



FIGURE 1.2: Risk Factors for Antipsychotic-Induced Weight Gain

1.4. Mechanisms of Antipsychotic-Induced Weight Gain

1.4.1. Antipsychotic Pharmacodynamics and Weight Gain

The variability in weight gain propensities between APs may be attributed to differences in binding affinities at relevant receptors. FGAs are primarily characterized by pharmacological action at dopamine D₂ receptors but can include effects at muscarinic cholinergic, histamine H₁, and α 1-adrenergic receptors⁸¹. Low potency FGAs like chlorpromazine, loxapine, and thioridazine also interact with serotonin 5-HT_{2A} receptors⁸². Although all SGAs have affinity for D₂ receptors, they dissociate rapidly from these sites, with the majority achieving therapeutic effects through preferential occupancy of 5-HT_{2A} receptors⁸³. In addition to D₂ and 5-HT_{2A}, SGAs interact with serotonin and norepinephrine reuptake pumps, and one or more of the following receptors: D₁, D₃, D₄, 5-HT_{1A}, 5-HT_{2C}, 5-HT₃, 5-HT₆, 5-HT₇, α 1-adrenergic, α 2adrenergic, H₁, and muscarinic cholinergic receptors⁸². Since these receptors are differentially implicated in weight regulation (refer to Section 1.4.3), diversity in the number and combination of receptor binding sites between APs may contribute to divergent AIWG risk profiles.

1.4.2. Hypothalamic Regulation of Energy Homeostasis

AIWG results from AP-induced disruptions of central and peripheral energy homeostatic pathways, ultimately creating an imbalance favouring energy intake over energy expenditure⁸⁴. Increasing evidence has implicated different genetic, neuronal, and hormonal factors in mediating this association through effects on appetite and satiety signals⁸⁵. Of particular importance are hypothalamic homeostatic circuits which, in controlling food intake and thermoregulation⁸⁶, rely on peripherally-released hormones to monitor the body's energy stores and provide appetite-stimulating (orexigenic) or satiation (anorexigenic) signals to the central nervous system (CNS)⁸⁷. Although signals act at various CNS sites, the pathways converge onto the hypothalamus where they are integrated and cue central neurons to secrete relevant neuropeptides^{88,89}. Due to the necessity of maintaining adequate energy stores for survival, the most potent pathways signal for increased food intake and reduced energy expenditure⁸⁸.

Two primary anorexigenic hormones are leptin and insulin, secreted by adipocytes and pancreatic β -cells, respectively. Both hormones provide information on long-term energy stores, as their circulating concentrations are proportional to the degree of adiposity in the body⁹⁰. The primary CNS interface for these hormones is the arcuate nucleus (ARC) of the hypothalamus which, due to an anatomical position near the base of the brain and poor blood-brain barrier (BBB) insulation, can directly interact with peripheral regulatory factors⁹¹. The ARC is responsible for reciprocally regulating two types of first-order neurons: (1) anorexigenic neurons co-expressing proopiomelanocortin (POMC) and cocaine- and amphetamine-regulated transcript (CART), and (2) orexigenic neurons co-expressing neuropeptide-Y (NPY), and agouti-related protein (AgRP)⁹². These neuropeptides have action at second-order neurons which are localized to three primary hypothalamic sites: lateral/perifornical hypothalamic area (LHA) or 'hypothalamic hunger center', paraventricular nucleus (PVN) or 'hypothalamic satiety center', and the ventromedial nucleus (VMN) which is also involved in mediating satiation via signalling to the PVN in response to blood glucose levels⁹¹. POMC/CART stimulates the PVN, and inhibits the LHA via α-melanocyte-stimulating hormone (α-MSH). In contrast, NPY activates the LHA and inhibits the VMN, while AgRP inhibits the PVN and antagonizes α -MSH^{88,91}. Signals transmitted to the PVN, LHA, and VMN are subsequently translated into autonomic, endocrine

and behavioural responses^{89,93}. For example, activated PVN neurons secrete thyrotropinreleasing hormone (TRH) and corticotropin-releasing hormone (CRH) to decrease appetite and increase thermogenesis, whereas LHA neurons secrete orexins A and B and melaninconcentrating hormone (MCH) to increase appetite and decrease thermogenesis^{91,94}

In addition to leptin and insulin, inflammatory cytokines such as IL-1, IL-6, and TNF- α also function as adiposity signals⁹¹. In parallel with these long-term homeostatic controls, various other hormonal and neural signals (e.g. cholecystokinin [CCK], peptide YY, glucagon-like peptide-1, amylin, bombesin) are secreted by the gastrointestinal (GI) tract to provide short-term signals to the CNS and regulate GI function^{89,95}. For example, ghrelin is a short-term signalling factor that is secreted by the stomach to yield orexigenic effects by acting on NPY/AgRP neurons⁹⁶. Short-term signalling is important in regulating the size and timing of meals, but has limited effects on adiposity stores⁸⁷.

1.4.3. Monoamine Regulation of Energy Homeostasis

To date, a large body of research has investigated the role of monoamines and their APtargeted receptors in AIWG. Serotonin has been highly studied for its inhibitory effects on feeding behaviours⁹⁷, with particular attention paid toward the 5-HT_{2A}, 5-HT_{2C}, and 5-HT_{1A} receptor subtypes. The mechanism of action is based on serotonergic neurons in the mid-brain raphe nucleus projecting onto POMC hypothalamic neurons^{85,88,95}. Additional evidence suggests that serotonin yields anorexigenic effects by working in concert with leptin^{98,99}. Antagonism of 5-HT_{2A} and 5-HT_{2C} receptors yields increased food intake^{100,101}, while inconsistent effects of the 5-HT_{1A} receptor have been reported^{102,103}. Preferential affinity for 5-HT_{2C} receptors among SGAs relative to FGAs may partially explain their greater propensity to induce AIWG. Dopamine is also a key contributor to food intake, but its effects on weight are dependent on its site of action within the brain. For example, mesolimbic dopamine contributes to the rewarding nature of palatable foods (and therefore, the motivation to eat) while hypothalamic dopamine signals anorexigenic pathways⁹⁸. Evidence suggests that D₂ receptor antagonism by APs increases feeding behaviours, and these effects can be reversed using D₂ receptor agonists¹⁰⁴. D₂ receptor blockade can also disrupt reward mechanisms of taste¹⁰⁵. Histamine has been implicated in energy homeostasis and food intake across many studies. Histamine neurons originate in the tuberomamillary nucleus of the third hypothalamic ventricle and affect weight via dense projections to the hypothalamus¹⁰⁶. H₁ receptor agonism decreases food intake, and effects are reversible via H₁ receptor antagonism^{107,108}. Pharmacological evidence suggests that H₁ receptor affinities are positively correlated with weight gain across FGAs and SGAs¹⁰⁹. Norepinephrine (noradrenaline) neurons also have projections to the hypothalamus¹¹⁰. Chronic administration of norepinephrine into the PVN significantly increases daily food intake in rats¹¹¹. However, α 1- and α 2-adrenergic receptors yield functionally distinct effects on feeding, where agonism at each site decreases and increases food intake, respectively^{112,113}. Since all APs are α 1-adrenergic receptor antagonists¹¹⁴, this may contribute to their effects on AIWG.

1.4.4. Pharmacogenetics of Antipsychotic-Induced Weight Gain

The high degree of inter-individual variability in AIWG has been previously described to be influenced by numerous risk factors (refer to Section 1.3.2). Of particular interest are genetic factors, as monozygotic twin studies suggest AIWG may be under strong genetic control. For example, Theisen et al. (2005)¹¹⁵ found greater similarity in AP-induced body-mass index (BMI) change among monozygotic twins (intrapair difference: $2.78 \pm 3.4 \text{ kg/m}^2$) than same-sex sibling pairs $(5.55 \pm 4.4 \text{ kg/m}^2)$. A case report also described similar clozapine-induced weight change between female monozygotic twins (Δ weight: 53.1 kg vs. 48.2 kg, final BMI: 38.1 kg/m² vs. 33.8 kg/m^2)¹¹⁶. To further examine genetic contributions, pharmacogenetic studies have tested the effects of polymorphisms on AIWG. As shown in Sections 1.4.2 and 1.4.3, many hormones and neuropeptides are implicated in energy homeostasis and food intake, and for this reason, are highly investigated within pharmacogenetic research. The serotonin system has been extensively studied, particularly the HTR2C gene, with multiple studies demonstrating protective effects of the -759T promoter variant allele against excessive AIWG¹¹⁷⁻¹²¹. Variant sites of the dopamine DRD2 gene, such as rs6277, rs1079598, rs1800497, and rs4436578, have also been implicated in AIWG^{122,123}. Other candidates that have been investigated include genes encoding leptin¹²⁴, NPY¹²⁵, α 2-adrenergic receptor¹²⁶, H₁ receptor¹²⁷, and ghrelin¹²⁸. For a review of the pharmacogenetic literature, refer to Lett *et al.* $(2012)^{16}$ and Mueller *et al.* $(2013)^{16,129}$.

PART II: NEUROINFLAMMATION IN SCHIZOPHRENIA

1.5. The Inflammatory Response System

1.5.1. The Peripheral Immune Response

The immune response can be broken down into two interconnected branches, (1) innate or non-specific immunity, and (2) adaptive or specific immunity. Innate immunity is the first line of host defence that rapidly mounts an inflammatory response upon detection of invading pathogens and physiological damage¹³⁰. This response is considered non-specific in that it broadly targets conserved microbial features, or pathogen-associated molecular patterns (PAMPs) (e.g. lipopolysaccharide [LPS], unmethylated DNA, peptidoglycan, flagellin), which are common to many pathogens but not present in the host¹³⁰⁻¹³². PAMPs bind to pattern recognition receptors expressed on the surface of phagocytic cells (e.g. toll-like receptors on macrophages and neutrophils) or as soluble receptors^{131,133}. The binding stimulates phagocytes to (1) engulf and degrade the pathogen, (2) initiate an inflammatory cascade, primarily via the nuclear factor-kb (NF-kB) pathway, to release immune factors (e.g. cytokines, prostaglandins, chemokines, leukotrienes), and (3) initiate an adaptive immune response by stimulating antigenspecific T and B lymphocytes^{130,132,134,135}. The adaptive immune response is a second line of defence which confers long-term protection against re-exposure to specific antigens by building immunological memory¹³⁶. Once the pathogen is contained, immune signalling shifts toward anti-inflammatory action to resolve inflammation and restore homeostatic balance¹³¹.

1.5.2. The Central Immune Response

In the CNS, there are two primary immune cells, microglia and astrocytes, which regulate the initiation and termination of the inflammatory response¹³⁷. Microglia are resident macrophages of the CNS that continuously survey the brain for neuronal damage, plaques, and microbes, and provide an immediate response to even minor central pathology¹³⁵. Once

activated, microglia engage in a variety of functions including phagocytosis and antigenpresentation of invading microbes, secretion of oxidative stress markers like reactive oxygen species (ROS) and reactive nitrogen species (RNS), and production of cyclooxygenase (COX)-2, prostaglandin E2 (PGE₂), and inflammatory cytokines (e.g. IL-1, IL-6, TNF- α , interferon [IFN]- γ)¹³⁸⁻¹⁴². Microglia can also confer neuroprotective benefits like enhanced neuronal survival through cellular maintenance and secretion of neurotrophic (e.g. BDNF) and anti-inflammatory factors, synaptic formation and pruning, developmental cell apoptosis, and axon remodelling ^{141,143,144}. Astrocytes have similar CNS functions including neuronal support, neurotransmission, synaptic formation, and BBB maintenance¹⁴². Although astrocytes can secrete pro-inflammatory mediators, they primarily produce anti-inflammatory factors^{142,145}. Astrocytes also have inhibitory and stimulatory effects on microglia depending on the internal immune state¹³⁵.

1.5.3. Neuroimmune Communication

There is evidence for the involvement of immune dysfunction in the etiopathogenesis of schizophrenia, particularly an up-regulation of pro-inflammatory signalling¹⁴⁶. This relationship is mediated though crosstalk between the immune system and CNS which is bidirectional under normal and pathological conditions^{147,148,149}. For example, cytokines and cytokine receptors, such as for IL-1, IL-2, and IL-6, are expressed within the brain and have action at central neurons, with particularly high densities localized to the hippocampus and hypothalamus^{149,150}. In addition to interleukins, other cytokines are present in the CNS such as IFNs and the tumor necrosis family¹⁵¹. Cytokines are reciprocally regulated by various centrally-released neurotransmitters and neuropeptides¹⁴⁹, and are produced in the CNS by neurons and glial cells^{149,151}.

Peripheral cytokines can also infiltrate the otherwise immune-privileged CNS through multiple humoral pathways that act in parallel, including: (1) passive transport at disrupted regions of the BBB¹⁵² or through the choroid plexuses and circumventricular organs which are BBB-deficient¹⁵³⁻¹⁵⁵, (2) active transport via saturable transport molecules, as observed for IL-1 α , IL-1 β , IL-1 receptor antagonist (IL-1RA), IL-6, and TNF- α ^{156,157}, and (3) binding to cerebral endothelial cells to stimulate release of secondary inflammatory messengers such as additional cytokines (e.g. IL-1 α , IL-1 β , IL-6), and PGE₂ via COX-2¹⁵⁸⁻¹⁶⁰. Immune information is also

directly transmitted to the brain using rapid neural pathways. Neural transmission involves activation of primary afferent nerve fibres in response to local cytokine release in the periphery, like the glossopharyngeal nerve during oral infections¹⁶¹ and vagal sensory ganglia during abdominal, visceral, and GI infections¹⁶²⁻¹⁶⁴. Once immune information from the periphery reaches the brain, it is reconstituted in the CNS via central cytokine release¹⁶⁵.

1.5.4. Neurotrophin-Immune Crosstalk

Neurotrophins, like BDNF, are involved in numerous processes that are critical for neuronal development and synaptic plasticity throughout development and in response to injury (refer to Table 1.1)¹⁶⁶⁻¹⁶⁹. Within this role, BDNF interacts with immune cells to mediate neuroimmune cross-talk^{168,170,171}. Although primarily secreted by neurons and astrocytes, BDNF and its tyrosine kinase receptor (TrkB) are produced by major peripheral immune cells (e.g. CD4⁺/CD8⁺ T lymphocytes, B lymphocytes, monocytes, macrophages)^{172,173}, and activated microglia¹⁴². BDNF is proposed to exert a neuroprotective role within the central immune response, as it is secreted by immune cells in response to inflammation to protect the brain from possible damage¹⁷⁴⁻¹⁷⁶. BDNF and TrkB, therefore, show inverse expression trends relative to inflammatory cytokines like IL-1 β , IL-6 and TNF- $\alpha^{177-179}$. In contrast, proBDNF, an immature isoform of BDNF, negatively regulates neuronal remodelling, synaptic transmission, and synaptic transmission via activation of the p75 neurotrophin receptor (p75^{NTR})¹⁸⁰.

1.5.5. Biological Properties of Cytokines

Cytokines are pleiotropic proteins involved in host regulation of both immunologic and non-immunologic processes (e.g. cell growth, migration, development, differentiation)¹⁸¹⁻¹⁸³. Cytokines are produced by a variety of cell types within the periphery (e.g. endothelial cells, monocytes, macrophages, dendritic cells, natural killer cells, and T cells) and CNS (e.g. astrocytes, microglia), and function as chemical messengers^{135,144,184}. The immune capabilities of different cytokines are highly redundant, and ultimately lead to the stimulation of multiple cell

types and the downstream production of inflammatory mediators^{37,185}. For example, IL-1 signals for the release of IL-2, IL-6 and TNF- α^{186} . Cytokines yield their effects by binding to specific cytokine receptors that are expressed on a variety of peripheral and central cells, and also exist in soluble form¹⁸⁷. Some receptor subtypes serve as non-functional decoys (e.g. interleukin 1 receptor, type II [IL-1RII], soluble interleukin 2 receptor [sIL-2R])^{184,188,189} while others enhance cytokine activity (e.g. soluble interleukin 6 receptor [sIL-6R])¹⁸⁴. Inhibitory effects are also achieved by non-functional receptor antagonists (e.g. IL-1RA) which compete with cytokines for receptor binding sites¹⁸⁸. Cytokine-receptor complexes are phosphorylated by Janus kinase (JAK) and Src kinases, and signal through pathways like (1) JAK-STAT (signal transducer and activator of transcription), (2) Ras/MAPK (mitogen activated protein kinase), and (3) phosphoinositide-3-kinase (PI-3-kinase) to activate gene transcription and cellular activity¹⁹⁰.

Cytokines are classified as either pro-inflammatory or anti-inflammatory in function. Proinflammatory cytokines, such as IL-1β, IL-2, and IL-6, augment the inflammatory cascade by recruiting leukocytes to sites of infection/injury, activating inflammatory cells, and assisting with the elimination of invading pathogens (refer to Table 1.1)^{135,184}. Anti-inflammatory cytokines, like IL-1RA, sIL-2R, IL-4, IL-5 IL-10, are reciprocally designed to down-regulate inflammation via immunosuppressive functions^{142,191}. Under certain conditions, cytokines can exert a dual role as both an inflammatory and anti-inflammatory signalling molecule. For example, IL-8 can function to either increase or decrease neutrophil recruitment¹⁸⁶. Cytokines can also be classified based on T cell origin sources. Type 1 T helper (TH₁) cells produce activators of cell-mediated immunity against intracellular antigens, and thus, typically secrete pro-inflammatory cytokines. Conversely, Type 2 T helper (TH₂) cells enhance humoral or antibody-based reactions against extracellular antigens and allergens, and thus, typically produce anti-inflammatory cytokines 134,142,184,190 . In addition to the traditional TH_1 and TH_2 branches, the more recently identified TH₁₇ cells (e.g. IL-17A, IL-17F, IL-21, IL-22) have been implicated in pro-inflammatory functions, particularly defence against extracellular bacterial infections, autoimmune diseases, and tissue immunity¹⁹². Disruptions of cytokine signalling can result in chronic inflammation that has been implicated in the onset of schizophrenia¹⁹³, and other psychiatric conditions, like panic disorder, obsessive-compulsive disorder, bipolar disorder, autism^{186,194}, and especially MDD^{177,195-197}. These inflammatory signatures are generally considered low-grade because they are modest in severity compared to primary inflammatory conditions like rheumatoid arthritis¹³⁵.

TABLE 1.1: Biological	Properties of C	ytokines and BDNF
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<u>Cytokine</u>	<u>Receptor</u> *	<u>Cell Source</u>	Biological Activity
IL-1β	IL-1RI	Monocytes, macrophages, fibroblasts, endothelial cells, dendritic cells, B lymphocytes, microglia, astrocytes	Stimulation of T, B and endothelial cells; induction of acute phase reaction; hematopoiesis; up-regulation of cytokines and cell adhesion molecules; neuronal depolarization/excitation; increase of NMDA receptor phosphorylation
IL-2	IL-2R	T cells, NK cells, microglia	Stimulation of T, B, and NK cells; generation of cytotoxic T cells; up- regulation of T-cell derived cytokines; facilitation of immunoglobulin synthesis; elimination of self-reactive T cells; T_{reg} cell maintenance
IL-6	IL-6R	Monocytes, macrophages, T cells, hepatocytes, osteoclasts, fibroblasts, microglia, astrocytes	Stimulation of T and B cells; induction of acute phase reaction; hematopoiesis; modulation of cytokine release; production of immunoglobulins
BDNF	TrkB	Neurons, astrocytes, microglia, T cells, B cells, monocytes, macrophages	Neuronal and glial survival, development, differentiation; synaptic/dendritic plasticity; influence production of T-cell derived cytokines; axonal/dendritic growth; neurotransmitter release; neuroprotection; increase survival of thermocyte precursors

*functional receptor; IL-1 β = interleukin 1-beta; IL-1RI = interleukin 1 receptor, type I; IL-2 = interleukin 2; IL-2R = interleukin 2 receptor; IL-6 = interleukin 6; IL-6R = interleukin 6 receptor; BDNF = brain-derived neurotrophic factor; TrkB = tyrosine kinase receptor; NK = natural killer cells; NMDA = *N*-methyl-D-aspartate ^{37,135,151,169,172,185,186,188,198}

1.6. Evidence of Immune Alterations in Schizophrenia

1.6.1. Prenatal Immune Activation Model of Schizophrenia

Maternal exposure to infection during a critical developmental (i.e. prenatal) period is proposed to increase the risk of schizophrenia in the offspring. This occurs when the maternal innate immune response leads to immune alterations in the fetal environment that disrupt early structural and functional neurodevelopment, with downstream implications for post-natal brain dysfunction that typically emerges after adolescence^{199,200}. Pre-natal immune challenges may also prime the fetus for post-natal immune hyperactivity toward both immunological and nonimmunological stimuli¹³⁵, and permanently alter the fetal peripheral immune system²⁰¹. These consequences may be the result of an influx of maternally-generated inflammatory mediators across the placenta and fetal BBB²⁰², in addition to stimulated expression of pro-inflammatory cytokines within the fetal brain²⁰⁰. In particular, there is strong support for increased IL-6, and possibly IL-1, IL-2, IFN- γ , and TNF- α , in mediating these effects^{200,203,204}. In addition to cytokine changes, maternal infection can alter neurogenesis and BDNF levels in offspring²⁰⁵⁻²⁰⁷.

Preclinical models of maternal exposure to immune-stimulating agents such as influenza^{208,209}, polyinosinic:polycytidylic acid (poly I:C)²¹⁰, LPS²¹¹, and turpentine²¹¹ have demonstrated the emergence of schizophrenia-like outcomes in behavioural, neurostructural and neurochemical domains. For example, immune models have shown alterations of dopamine, and dopamine-related metabolites, neurons, receptors and genes within offspring^{201,212,213}. Epidemiological studies also report higher rates of schizophrenia following prenatal exposure to influenza, rubella, measles, polio, herpes simplex, genital and/or reproductive infections, sinusitis, tonsillitis, pneumonia, and Toxoplasma gondii¹⁹⁹. Additional research suggests synergistic effects of CNS vulnerability from prenatal infection and pre-pubertal stress or environmental interactions (e.g. physical or psychological stress or exposure to pathogens) in the development of schizophrenia (i.e. 'two hit' model of schizophrenia) (refer to Figure 1.3)^{135,214}.

Several studies have found altered peripheral cytokine levels in schizophrenia (refer to Figure 1.3), with some discrepancy over which cytokines are elevated and which are lowered. Schizophrenia was initially characterized as an imbalance in TH₁ and TH₂ immune responses, observed as a shift toward exaggerated TH₂ cytokine production²¹⁵. The TH₁/TH₂ imbalance hypothesis received support from studies that found decreased levels of TH₁ cytokines (e.g. IL-2, II-6, IFN- γ)^{216,217}, and increased levels of TH₂ cytokines (e.g.IL-10) in schizophrenic patients²¹⁸. However, findings were later challenged by reports of increased pro-inflammatory mediators like IL-1, IL-2, IL-6, IL-8, IL-18, and TNF- α ²¹⁹⁻²²⁶, elevated levels of circulating monocytes²²⁷, and increased release of PGE₂ and COX-2²²⁸ in schizophrenia. This up-regulation of pro-inflammatory markers occurs within drug-naive, drug-free, and FEP, suggesting that these findings are independent of AP effects^{223,229-231}. Similar immune disturbances are observed in unaffected first-degree relatives of schizophrenic patients²³². A meta-analysis by Potvin *et al.* (2008)¹⁸⁴ confirmed that there is insufficient evidence to support a TH₂ cytokine shift. In addition to immune changes, reductions in serum levels of BDNF have been observed in drug-naive FEP, with levels negatively correlating with symptom severity (refer to Figure 1.3)^{233,234}.

This discrepant pattern of findings may have resulted from methodological differences between studies involving (1) biological sample type, (2) method of sample preparation and storage, (3) method of in vitro immune stimulation, and (4) method of cytokine quantification. Reliable quantification in serum can also be challenged by short cytokine half-lives and rapid turnover¹⁴². Other study parameters such as small sample size and variable diagnostic criteria should also be considered²³⁵. Many additional factors can affect cytokines levels but are not routinely controlled for across studies. Such factors include age²³⁶, ethnicity²³⁷, gender and menstrual cycle phase²³⁸, sleep²³⁹, BMI²⁴⁰, smoking status²⁴¹, alcohol use²⁴², medical comorbidities such as coronary artery disease, obesity, diabetes, osteoporosis, pain, and autoimmune diseases^{194,243,244}, exercise²⁴⁵, food consumption²⁴⁶, and stress²⁴⁷. This is in addition to the effects of clinical variables like duration and severity of schizophrenic illness, and use of medication²⁴⁸. Stage of schizophrenic illness is an additional factor to consider, as some cytokines have been identified as state markers of acute symptom exacerbations (e.g. IL-1β, IL-

6, transforming growth factor (TGF)- β) while others may be trait markers (e.g. IL-12, IFN- γ , TNF- α , sIL-2R)²⁴⁹.

The immunological profile of the periphery may also suggest that schizophrenia is associated with a concurrent increase in pro- and anti-inflammatory activity, evidenced by hyperproduction of both types of factors and immune cells^{250,251}. For example, Drexhage *et al.* $(2011)^{252}$ found higher percentages of pro-inflammatory monocytes, activated CD3⁺CD25⁺ T cells, and pro-inflammatory TH₁₇ cells in schizophrenic patients, in addition to elevated anti-inflammatory CD4⁺CD25^{high}FoxP3⁺ regulatory T cells, and IL-4⁺ lymphocytes. It has been proposed that increased anti-inflammatory signalling may be a protective response which develops subsequent to increased pro-inflammatory activity to limit the potentially damaging effects of chronic inflammation¹³⁵. Although the direction of these immune findings has not yet been clearly defined, peripheral cytokines and BDNF may be meaningful proxies of brain activity due to a high degree of correlation between circulating and central levels^{253,254}.

1.6.3. Central Cytokine Alterations in Schizophrenia

Numerous studies have provided evidence of central inflammation within schizophrenia (refer to Figure 1.3) by quantifying immune markers in cerebrospinal fluid (CSF). CSF investigations have shown elevations of pro-inflammatory mediators (e.g. IL-1 β , IL-2, IL-6) and their receptors (e.g. sIL-6R)^{135,255,256}, reductions of anti-inflammatory factors (e.g. sIL-2R, sIL-1RA, TGF- β receptor)^{135,257}, and increased numbers of monocytes and macrophages²⁵⁸. According to Meyer *et al.* (2011)¹³⁵, these patterns of CNS activity may reflect an enhanced inflammatory profile occurring in tandem with central immunosuppression, which differs from peripheral immune patterns in schizophrenia. CSF analyses have also suggested that neuroinflammation may only be present in a subgroup of schizophrenic patients²⁵⁹. Similar to in the periphery, CSF reductions in BDNF have been observed in drug-naive FEP, with levels negatively correlating with the severity of symptoms (refer to Figure 1.3)²⁵⁴.

S100B, a calcium- and zinc-binding protein, is a proxy for brain tissue damage and glial dysfunction, particularly astrocyte over-activation²⁶⁰. S100B can have harmful effects like

neuronal apoptosis, production of inflammatory factors (e.g. COX-2, PGE₂, IL-1 β) and NOS, and up-regulation of TNF- α secretion from monocytes and microglia¹⁴². CSF and serum levels of S100B are elevated within schizophrenia²⁶¹⁻²⁶³, with findings confirmed in drug-free patients²⁶⁴. Post-mortem investigations have observed S100B-imunoreactive astroglia in brain regions implicated in the pathophysiology of schizophrenia like the anterior cingulate cortex, dorsolateral prefrontal cortex, orbitofrontal cortex and hippocampus¹⁴². Reports of whether increased S100B occurs in the presence of astrogliosis have been inconsistent^{265,266}.

Microglia activation and enhanced densities, particularly in the temporal and frontal cortex, have also been implicated in schizophrenia according to post-mortem studies^{267,268}. Zhu *et al.* (2014)²⁶⁹ observed that intrahippocampal LPS injections into rats led to behavioural changes that were comparable to the schizophrenic phenotype (e.g. social and pre-pulse inhibition deficits) and to an elevated number of microglia in the hippocampus, cerebral cortex and thalamus. Positron emission tomography (PET) has confirmed enhanced microglia in schizophrenia, in real time, by quantifying translocator protein (TSPO) binding density activation²⁷⁰. TSPO is typically expressed at low levels in the brain but, in the presence of activated microglia are observable in the first 5 years of schizophrenia²⁷². Studies have also shown decreased BDNF concentrations within the cortex and hippocampus of schizophrenic patients, in addition to reduced TrkB and BDNF-positive neurons in the CNS²⁷³.

1.6.4. Immunogenetics and Schizophrenia

Many genes that have been implicated in conferring risk of schizophrenia are also involved in the inflammatory response (refer to Figure 1.3). Most significantly, genetic variants within the extended region of the major histocompatibility complex (MHC), which is an area of high immune relevance on chromosome 6p22.1, are the most likely susceptibility genes for schizophrenia^{274,275}. Similar findings have emerged for genes encoding the IL-1 cytokine family on chromosome $2q13^{191}$. Numerous cytokine polymorphisms are also associated with schizophrenia and its clinical features, such as variants localized to genes encoding IL-1 β (rs1143633, rs16944, rs4848306), IL-2 (rs2069762), IL-6 (rs1800795), IL-6R (rs8192284),
monocyte chemoattractant protein-1 (MCP-1, rs1024611), TNF-α (rs1800629, rs1799724, rs361525), IL-3RA (rs6603272), IL-4 (rs2243250), IL-8 (rs2227307), IL-10 (rs1800896), IL-18 (rs187238, rs1946518), and IL-28B (rs8099917) (for review, see Zakharyan & Boyajyan, 2014)¹⁹³. Adjunct imaging data have shown that the T, or high transcriptional, allele for IL-1β rs16944 is associated with brain volume reductions²⁷⁶ and differential brain activation²⁷⁷ in schizophrenia. Expression analyses have shown that several genes involved in immune response pathways, such as serpin peptidase inhibitor, clade A, member 3 (SERPINA3), interferon-induced transmembrane (IFITM) proteins, Chitinase-3-like 1 (CHI3L1), heat shock proteins, and CD14 antigen are up-regulated in schizophrenia, particularly within the prefrontal cortex^{278,279}. Expression of inflammatory cytokines (e.g. IL-1β, IL6, TNF-α) is also enhanced in circulating monocytes¹⁴⁴ and leukocytes ²⁸⁰ in schizophrenia.

Genetic variance in BDNF has also been associated with schizophrenia, particularly the Val66Met and C270T polymorphisms^{281,282}. However, findings have not been consistently replicated^{283,284}. A meta-analysis by Gratacos *et al.* (2007)²⁸⁵ confirmed the association between Val66Met and schizophrenia, reporting that homozygous carriers of the Met/Met genotype were at a 19% elevated risk compared to heterozygotes. Val66Met has also been associated with clinical features of schizophrenia, such as age of onset²⁸⁶, symptom severity²⁸⁶, cognitive difficulties^{287,288}, and alterations in brain morphology^{289,290}. Epigenetic alterations of BDNF, particularly DNA methylation signatures, may also contribute to schizophrenia^{291,292}



FIGURE 1.3: Immune and Neurotrophin Alterations in Schizophrenia

FIG 1.3: Maternal exposure to infection during prenatal development, in synergy with post-natal stress and schizophrenia susceptibility genes, lead to the development of the schizophrenic phenotype after adolescence. This phenotype is characterized by alterations in inflammatory factors, immune cells and BDNF within the periphery and CNS. Immune dysfunction is often normalized with antipsychotic treatment, while BDNF deficiency remains unchanged or may even undergo further reductions.

IL = interleukin, IFN = interferon, TNF- α = tumor necrosis factor alpha, BDNF = brain-derived neurotrophic factor, MHC = major histocompatibility complex, MCP-1 = monocyte chemoattractant protein-1, PGE2 = prostaglandin E2, COX-2 = cyclooxygenase-2, CNS = central nervous system

1.6.5. Mechanisms of Cytokine-Induced Schizophrenia

Schizophrenia has been predominantly characterized by a highly interconnected disturbance of dopamine and glutamate neurotransmission. Dopamine dysregulation has been described by hyperactivity in the striatum (i.e. mesolimbic dopamine pathway) and hypoactivity

in the frontal cortex (i.e. mesocortical dopamine pathway), with the former contributing to positive symptoms and the latter to cognitive, negative and affective symptoms^{81,293}. Dopaminergic alterations are a possible consequence of glutamatergic hypofunction due to impaired synaptic signalling at the glutamate receptor, *N*-methyl-D-aspartate (NMDA)^{293,294}. Neurotransmitter disruptions can also occur for gamma-aminobutyric acid (GABA), serotonin, opioids, and acetylcholine²⁹³.

Inflammatory cytokines, like IL-1 β , IL-6, and TNF- α , may contribute to these disturbances, as they have been shown to affect glutamate release via activation of the enzyme, indoleamine 2,3 dioxygenase (IDO)²⁹⁵. IDO is found in immune cells (e.g. macrophages, dendritic cells), and in all organs including the brain¹⁶⁵. IDO degrades tryptophan, a serotonin precursor, into kynurenine (KYN) which is subsequently converted to kynurenic acid (KYNA) in astrocytes and quinolinic acid (QUIN) in microglia¹⁷⁷. Cortisol can also initiate this pathway via tryptophan 2,3 dioxygenase (TDO)¹⁶⁵. Increased KYNA inhibits signaling at NMDA and α 7-nicotinic acetylcholine (α 7nAch) receptors which leads to blockade of glutamate release^{135,142,296}. Studies confirm that KYN and KYNA are both elevated in the CSF ²⁹⁷⁻²⁹⁹ and post-mortem brain tissue³⁰⁰ of schizophrenic patients. Post-mortem analyses and studies employing various methodologies like PET/single photon emission computed tomography (SPECT), and proton magnetic resonance spectroscopy (¹H-MRS) have confirmed abnormalities in glutamatergic indices in both medicated and unmedicated patients^{105,301}.

Glutamate is the major excitatory neurotransmitter in the CNS, and its dysfunction has been implicated in positive, negative and cognitive symptoms, and changes in brain morphology in schizophrenia^{57,203,228,294,302}. *Positive Symptoms*. Corticobrainstem glutamate neurons inhibit dopamine release from mesolimbic neurons by signaling through an inhibitory GABA interneuron in the ventral tegmental area (VTA). NMDA hypoactivity within this projection would thus limit these capabilities, and lead to mesolimbic dopamine hyperactivity^{81,294}. Indeed, studies show that increased KYNA in schizophrenia leads to hyperactivity of dopamine neurons in the VTA³⁰³, and administration of NMDA receptor antagonists increases dopamine in the rat nucleus accumbens and striatum³⁰⁴. *Negative/Cognitive/Affective Symptoms*. Glutamate projections to the mesocortical dopamine pathway do not signal through GABA, and thus, can normally function to excite dopamine neurons. Thus, in the presence of NMDA hypoactivity,

mesocortical dopamine neurons are also hypoactive⁸¹. Similar dopaminergic effects may be achieved through cytokine-induced reductions in tetrahydrobiopterin (BH₄) bioavailability, an enzyme cofactor required for the dopamine synthetic pathway, through production of ROS and NOS³⁰⁵. Taken together, cytokines yield the dopaminergic profile found within schizophrenia by altering striatal and prefrontal dopamine levels^{201,212,213,227,306,307}. Negative symptoms may also be mediated by IDO-based reduction in tryptophan bioavailability leading to central serotonin deficiency¹³⁵. Cytokine-induced glutamatergic hypofunction may also mediate reductions in BDNF expression, as activation of NDMA receptors increases levels of BDNF mRNA, whereas NMDA antagonism has opposite effects^{308,309}. Another potential contributing factor is monoamine alterations, particularly serotonin, as 5-HT_{2A/2C} receptor agonists significantly elevate BDNF mRNA expression¹⁶⁶. Dopamine has also been shown to modulate levels of BDNF mRNA and protein through D₁ receptor activity³¹⁰.

1.6.6. Anti-inflammatory Properties of Antipsychotics

Several studies suggest that APs have immunomodulatory properties, particularly antiinflammatory effects. Long-term treatment with APs has been shown to increase expression of anti-inflammatory mediators (e.g. sIL-1RA, sIL-2R, and IL-10) while simultaneous reducing pro-inflammatory markers (e.g. IL-1 β , IL-2, IL-6, sIL-6R, IFN, and TNF- α) in the periphery and CNS^{25,135,186}. APs have also been shown to reduce levels of S100B³¹¹. Additional support is derived from reports of AP efficacy in treating tuberculosis/mycobacterial infections³¹², and rheumatoid arthritis³¹³. APs may mediate these effects by suppressing production of proinflammatory cytokines and nitric oxide from activated microglia^{134,138}. Among APs, SGAs have more potent anti-inflammatory properties relative to FGAs^{135,314}. The capacity of APs to normalize the inflammatory signatures of schizophrenia contributes to their clinical efficacy. For example, reduction of serum IL-2 subsequent to AP therapy correlates with greater improvement in symptom severity³¹⁴. Baseline levels of pro-inflammatory markers can serve as a predictive biomarker of treatment response, as it is shown to negatively correlate with clinical improvement³¹⁴. Genetic variation across immune genes also affects clinical response to APs, as observed for IL-1RA³¹⁵, MCP-1³¹⁶, and TNF- α ³¹⁷. Augmentation of APs with adjunctive anti-inflammatory compounds has shown superior treatment benefits in reducing positive and negative symptoms compared to AP monotherapy³¹⁸. Anti-inflammatory add-on therapy is also advantageous among AP-resistant patients^{319,320}. Various agents have been studied in schizophrenia including minocycline³²¹, and non-steroidal anti-inflammatory drugs (NSAIDs) like the COX-2 inhibitor celecoxib³²² and COX-1/2 inhibitor acetylsalicylic acid³²³. Essential polyunsaturated fatty acids (EPUFAs) like omega-3 eicosapentaenoic acid (EPA) and estrogens like 17β -estradiol have mild anti-inflammatory properties and show therapeutic benefits for schizophrenia^{324,325}. Similar findings have been reported for *N*-acetylcysteine which has both anti-inflammatory and antioxidant properties³²⁴.

Conversely, BDNF is not typically normalized with AP therapy. Instead, APs have been shown to cause a further reduction in BDNF, likely mediated through 5HT receptor inhibition¹⁷⁶. Numerous studies report decreased serum BDNF levels under FGA and SGA treatment relative to controls³²⁶⁻³²⁸. Pirildar *et al.* (2004)³²⁹ showed that untreated schizophrenic patients had lower baseline BDNF levels compared to controls, and levels were unchanged after 6 weeks of AP treatment. Rizos *et al.* (2010)³³⁰ reported similar findings after measuring serum BDNF in schizophrenic patients during relapse and again after 6 weeks of AP treatment. Pillai *et al.* (2006)³³¹ found that central levels of BDNF protein in the rat brain were unchanged by olanzapine, largely decreased by haloperidol and chlorpromazine, and moderately decreased by risperidone after 90 days of treatment, with levels continuing to decline for up to 180 days. However, findings are not consistently replicated, as some trials report AP-mediated improvements in BDNF levels³³².

PART III: INFLAMMATION AND METABOLIC PROCESSES

1.7. Cytokines and Anorexia of Infection

1.7.1. Anorexia of Infection and the Acute Phase Response

Inflammatory cytokines have been closely implicated in metabolic regulation, particularly a reduction in food-motivated behaviours, food intake, and body weight^{333,334}. Cytokines mediate these effects as part of the acute phase response (APR) of innate immunity³³⁵. The APR is an integrated set of immune, endocrine, metabolic, behavioural, and neural alterations that are mounted by the innate immune system upon immediate recognition of an immunological insult^{336,337}. In addition to anorexia, the APR can include reactions like fever, lethargy, altered plasma protein concentrations (e.g. C-reactive protein, CRP), and increased leukocyte counts³³⁸. APR reactions, including anorexia, form a critically adaptive defence strategy that takes priority over regular homeostatic controls to provide short-term survival benefits to the host^{335,339}. The survival benefits of anorexia can include: (1) reducing food scavenging behaviours to conserve energy and heat, (2) reducing access to food-derived micronutrients, such as iron and zinc, that can be used by pathogens to flourish, (3) limiting potentially harmful metabolic APR effects, and (4) promoting apoptosis of infected cells^{336,337,339}. In support of the adaptive effects of anorexia, Murray & Murray (1979)³⁴⁰ showed that force-feeding infected mice to a normal energy intake resulted in increased mortality and reduced survival time compared to infected mice fed ad libitum. Similarly, Wing & Young (1980)³⁴¹ found that acutely starved mice infected with Listeria monocytogenes showed significantly less mortality than fed mice.

1.7.2. Cytokines as Mediators of Anorexia

Inflammatory cytokines, such as IL-1 α , IL-1 β , IL-2, IL-6, IL-8, TNF- α , and IFNs have been shown to suppress food intake, both individually and synergistically, after peripheral and central administration³⁴²⁻³⁵⁰. Alterations in feeding behaviours are typically observed as reductions in meal size, duration, and frequency, and longer inter-meal intervals^{344,349,351}. Aubert *et al.* $(1995)^{352}$ showed that rats treated with IL-1 β had a reduced total caloric intake, and consumed relatively more carbohydrates and less protein. Taste aversion can also result from cytokine administration but this does not appear to be a major component of anorexic action^{336,353}. Studies have shown an attenuated anorexic response within cytokine and/or cytokine receptor gene knock-out models^{354,355}, and upon antagonism of cytokine action^{351,356-358}. However, chronic cytokine administration can eventually lead to tolerance toward their hypophagic effects, and thus, recovery of food intake^{359,360}. In addition to altering feeding behaviours, cytokines influence body weight through effects on energy expenditure (e.g. change in body temperature)^{361,362}.

1.8. Mechanisms of Cytokine-Induced Anorexia

1.8.1. Cytokines and Peripheral Satiety Signals

As shown in Section 1.5.3, peripheral cytokines have the ability to stimulate afferent nerve fibres, like the vagus nerve of the abdomen and GI tract which relay signals through the nucleus of the solitary tract to the PVN of the hypothalamus⁹¹. This neural route may be a potential mechanism through which cytokines mediate their anorexic effects, as subdiaphragmatic vagotomy can attenuate suppression of both food intake³⁶³ and food-motivated behaviour³⁶³ in some but not all cases³⁶⁴. Cytokines may work in concert with the peripheral satiety hormone CCK to stimulate the vagus nerve. Cytokines induce release of CCK, and activation of CCK_A receptors partially contributes to vagal-mediated hypophagic outcomes³³⁶. In addition, cytokines, like IL-1 and TNF- α , elevate plasma leptin levels to suppress food intake, and can act directly on adipocytes to stimulate leptin secretion^{309,365-368}. Cytokines can also influence levels of insulin and glucagon³⁶⁹. In further, IL-1 α , IL-1 β , IL-6, and TNF- α reduce stomach muscle contractions to yield gastric stasis (i.e. delayed gastric emptying) which contributes to anorexia by influencing meal size and length of inter-meal intervals³⁷⁰.

In the CNS, cytokines have direct action at hypothalamic neurons in the LHA, PVN, and VMN in mediating feeding behaviours³⁶⁹. In support, cytokine mRNA and protein (e.g. IL-1 β , TNF- α), and cytokine receptors have been found in multiple brain regions including the hypothalamus³⁷¹⁻³⁷³, with greatest concentrations in the VMH³³³. In anorexic tumor-bearing rats, IL-1 β and IL-1R mRNA are up-regulated in the hypothalamus, and CSF levels of IL-1 negatively correlate with food intake³³³. Kent *et al.* (1994)³⁷⁴ demonstrated that direct administration of recombinant IL-1 β into the VMN both time- and dose-dependently induced anorexia and weight loss, with food and water consumption reduced by 45% and 30%, respectively. VMN-injected cytokine antagonists have been shown to attenuate anorexic outcomes^{375,376}. For example, Laviano *et al.* (1995)³⁷⁵ showed that central injections of IL-1RA into the VMN improved food intake in anorexic tumor-bearing rats.

Cytokines can also mediate anorexic effects by influencing hypothalamic production of various neurotransmitters and neuropeptides that are relevant to the regulation of food intake. For example, central cytokine administration can reduce levels of NPY³⁷⁷. Sonti *et al.* (1996)³⁷⁸ observed that NPY administration blocks the anorexic effects of IL-1 β when both are administered together, and induces feeding in anorexic rats pre-treated with IL-1 β . A similar relationship exists between NPY and IFN- α^{346} . LPS and IL-1 β have been shown to decrease plasma ghrelin levels, an effect which can be blocked by administration of exogenous ghrelin, IL-1RA and the NSAID indomethacin³⁷⁹. Cytokines also interact with other neuropeptides like POMC-derived peptides (e.g. α -MSH), hypocretins/orexins, CART, MCH, and AgRP^{369,373}. Anorexic outcomes may also result from the ability of cytokines to influence the expression of hypothalamic neurotransmitters like dopamine, serotonin, histamine, and norepinephrine which, as shown in Section 1.4.3, are involved in regulating food intake^{369,380}.

In addition, prostaglandins, especially PGE₂, and their precursors have been shown to reduce food intake and influence GI motility³⁸¹⁻³⁸⁶. C-*fos* mRNA studies show that central injection of PGE₂ activates neurons within the PVN³⁸⁷. These anorexic effects are typically reversible by COX inhibitors like aspirin, flurbiprofen, indomethacin and paracetamol^{381,383}. In support, pre-treatment with COX-inhibitors can partially block the anorexic and gastric emptying

effects of IL-1α, IL-1β, and TNF³⁷⁰. COX gene knockout models suggest a greater involvement of COX-2 in cytokine-induced hypophagia than COX-1, although COX-1 may contribute to early-stage anorexic responses³⁸⁸⁻³⁹⁰. Furthermore, cytokines activate the hypothalamic-pituitaryadrenal (HPA) axis^{391,392}, and simulate release of CRH³⁹³⁻³⁹⁶ which then acts within the brain to reduce food intake³⁹⁷. Uehara *et al.* (1989)³⁹⁸ demonstrated that pre-treatment with CRHantiserum blocks reductions in food intake subsequent to IL-1β administration.

1.9. Cytokine Involvement in Weight Gain and Obesity

1.9.1. Inflammatory Feedback Response in Obesity

In Section 1.4.2, inflammatory cytokines were identified as a type of adiposity signal that, separate from their role in illness anorexia, convey information on long-term energy stores to the hypothalamus under normal conditions⁹¹. During fat accumulation and adipocyte enlargement, adipose tissue (particularly within visceral fat) becomes a site of active inflammation as it undergoes molecular and cellular changes, accumulates macrophages, and secretes various immune factors like inflammatory cytokines^{399,400}. These cytokines subsequently suppress feeding and induce energy expenditure (refer to Section 1.7.2) via a feedback loop to prevent obesity, and thus, maintain homeostatic balance (refer to Figure 1.4)⁴⁰¹. Therefore, once caloric restriction is achieved, it is accompanied by a potent anti-inflammatory effect which can include reduced production of inflammatory cytokines and prostaglandins, lowered blood lymphocyte counts, and reduced macrophage activation and infiltration into adipocytes^{400,402,403}. Perturbations of adiposity signalling may cause a shift in weight gain outcomes. For example, a developed resistance to inflammatory signalling leads to continued fat accumulation, and ultimately, obesity⁴⁰¹. In support, obesity (and MetS) is a condition associated with low-grade chronic inflammation⁴⁰⁴. Inflammation within obesity, particularly increased levels of TNF- α and IL-6, has also been shown to influence the insulin signalling pathway, thereby leading to insulin resistance⁴⁰⁵. This can, in turn, lead to hyperglycemia and type II diabetes, which may, through glucose excretion in the urine, be an extreme method to rid the body of surplus

energy⁴⁰¹. Similar to inflammation resistance, a deficit of inflammatory signalling in the face of increased adiposity would likely yield similar obesity outcomes. Supportive evidence may be derived from O'Rourke *et al.* (2006)⁴⁰⁶ who found decreased serum cytokine protein and mRNA levels in peripheral blood mononuclear cells of obese compared to lean patients, which occurred in spite of an intact capacity to up-regulate cytokine expression in response to leptin.





FIG 1.4: The adiposity signalling pathways of inflammatory cytokines (in blue) and BDNF (in green) are shown. Both markers, which are elevated during fat accumulation, act within the hypothalamus to initiate anorexigenic pathways, to ultimately decrease food intake and increase energy expenditure. Once caloric restriction is achieved, cytokine and BDNF levels are reduced. Perturbations of adiposity signalling by altering cytokine or BDNF levels may shift weight gain outcomes.

Various models have tested the association between deficit cytokine production and obesity outcomes using genetic knockout models. Wallenius et al. (2002)²⁷ observed that IL-6 deficient mice (IL-6^{-/-}) developed mature-onset obesity accompanied by increased food intake, altered carbohydrate and lipid metabolism, increased leptin levels, and reduced responsiveness to leptin treatment. IL-6 administration was able to partially reverse these effects by lowering body weight and leptin levels, and increasing energy expenditure. Investigations of IL-1 involvement have yielded similar findings. Garcia et al. (2006)⁴⁰⁷ found that IL-1RI deficient mice (IL-1RI^{-/-}) developed mature-onset obesity relative to wild-type mice by 5 to 6 months of age, with a 20% weight difference emerging by 9 months. $IL-1RI^{-/-}$ mice also developed a 1.5 to 2.5-fold increase in visceral and subcutaneous fat mass, insulin resistance, increased leptin levels and, prior to obesity onset, reduced locomotor activity and reduced suppression of body weight and food intake in response to leptin. Similar outcomes were observed by McGillicuddy et al. (2013)⁴⁰⁸ in IL-1R Γ^{-} mice which developed mature-onset obesity after 6 months despite being fed a low-fat diet. Netea et al. (2006)⁴⁰⁹ showed that deficiency of IL-18 (IL-18^{-/-}) in mice leads to higher leptin levels, hyperphagia, increased cholesterol and triglyceride concentrations, obesity, and insulin resistance, which can all be partly reversed with central administration of recombinant IL-18. Obesity differences, relative to control mice, first appeared at 6 months of age, with the greatest difference of 38.1% occurring at 12 months. Mice deficient for the IL-18 receptor (IL-18R^{-/-}) also displayed similar obesity and insulin resistance outcomes.

There is an observed synergy between cytokines in yielding weight change effects. Chida *et al.* $(2006)^{26}$ found that mice with a combined IL-1 and IL-6 deficiency $(IL-1^{-/-}/IL-6^{-/-})$ developed obesity by 10 weeks while mice with either a IL-1 or IL-6 knockout remained normal at this age. IL-1^{-/-}/IL-6^{-/-} mice also had significantly higher daily food intake and greater suppression of anorexic effects after peripheral IL-1 administration. Investigations of the effects of IL-1RA have also been conducted. Matsuki *et al.* $(2003)^{410}$ showed that IL-1RA^{-/-} mice, in which excess IL-1 signaling may occur, have a lean phenotype through impaired body fat accumulation and lipid storage, and resistance against the obesity-inducing effects of both monosodium glutamate and a high-fat diet. Similar results were obtained by Somm *et al.* $(2005)^{411}$ after studies of IL-1RA^{-/-} mice revealed a lean phenotype based on reduced fat mass,

dysfunctional adipogenesis, and increased energy expenditure. Horai *et al.* $(1998)^{412}$ also observed reduced body weight in IL-1RA^{-/-} mice relative to heterozygote IL-1RA^{+/-} littermates.

1.9.3. Cytokine Genetic Variants and Obesity

Polymorphisms in cytokine genes show an association with human obesity. Andersson et al. (2009)⁴¹³ found that the 3' untranslated region variant, rs4252041 (C>T), of the IL-1RA gene was associated with lower total and regional fat mass, total fat percent (%) and BMI in 1,068 young men. Um et al. (2011)⁴¹⁴ found two IL-1a polymorphisms, C-889T (rs1800587) and G+4845T (rs17561), that were associated with an increase in BMI in obese healthy women. Lee et al. $(2008)^{415}$ investigated the IL-1 β +3953 (rs1143634) variant site, finding a higher frequency of the T (CT/TT), or high transcriptional, allele among lean BMI (<25 kg/m²) versus overweight BMI (25-29 kg/m²) females. The same variant site was tested by Manica-Cattani *et al.* (2010)³² in 880 Caucasian subjects, similarly finding a higher T allele frequency in non-overweight than overweight and obese groups. Strandberg et al. (2006)⁴¹⁶ also tested the +3953 variant but against body fat mass in 1,068 young men. Results showed that carriers of the T allele had significantly lower total fat mass, in addition to reduced arm, leg, and trunk fat. Additional investigations by Strandberg *et al.* (2008)⁴¹⁷ found an association for both the IL-1 β -31T>C (rs1143627) and IL-6 -174 G>C (rs1800795) polymorphisms with total and regional fat mass in 3,014 elderly men. The IL-6 -174C variant has also been associated with higher BMI and risk of obesity-related metabolic indices like insulin resistance and high systolic blood pressure^{418,419}. while the -174G variant has been associated with a lean phenotype, low waist circumference, and low concentrations of insulin or glucose³³. Andersson et al. (2010)⁴²⁰ found the IL-6 polymorphism rs10242595 G>A to be associated with low BMI and total body fat mass, and smaller regional fat masses. In addition, the IL-6 promoter polymorphism rs2069827 G>T is associated with elevated early-adulthood BMI, baseline BMI, and waist circumference in men and women, separately⁴²¹. Wolford *et al.* $(2003)^{422}$ studied multiple polymorphisms across the IL-6R gene (rs4845623 T>C, c 1981308 10 T>C, rs2228145 T>G, c 1158918 10 G>C, rs2229328 T>C) finding that carriers of the variant allele for these sites had a higher mean BMI compared to those with the wild-type allele when tested among 700 non-diabetic Pima Indians.

BDNF has been implicated in the regulation of feeding and energy metabolism (refer to Figure 1.4). The highest levels of BDNF protein are within the hippocampus and hypothalamus⁴²³, and BDNF mRNA has been isolated within these brain regions¹⁶⁶. In particular, although both BDNF and TrkB are expressed in the VMN, LHA, PVN, and dorsomedial hypothalamic nucleus (DMH), BDNF is greatest in the VMN⁴²⁴. BDNF has also been shown to affect NPY and POMC expression⁴²⁵⁻⁴²⁷, and the serotonin system within the hypothalamus^{428,429}. The suggested role of BDNF within feeding is anorexigenic, with reports of central BDNF administration suppressing food intake^{428,430,431} and increasing energy expenditure⁴³¹ leading to weight loss. Central BDNF protein has been shown to decrease subsequent to food deprivation, and increase with re-feeding⁴³⁰. Serum BDNF levels are positively correlated with body weight and BMI⁴³². Investigations of BDNF gene mutations provide further support for this association. Kernie et al. (2000)⁴³³ found that approximately 50% of BDNF^{+/-} heterozygous mice develop obesity, evidenced by a 300% increase in fat by 9 months, in addition to leptin resistance and hyperinsulinemia. Lyons *et al.* $(1999)^{429}$ observed that $BDNF^{+/-}$ mice develop chronic hyperphagia and obesity by 2 to 4 months of age, with a 34% higher body weight than wild-type littermates by 12 to 18 months. The literature further suggests that polymorphisms within the BDNF gene, particularly Val66Met, are associated with obesity, with variable reports on the causal allele. Gunstad *et al.* $(2006)^{35}$ first identified that the Met/Met genotype was associated with a lower BMI than Val allele carriers in 481 healthy adults. This finding was subsequently replicated in other studies⁴³⁴⁻⁴³⁶. However, some studies report the reverse association linking the 66Met allele to obesity^{437,438}, while others report no association⁴³⁹. Reduced BDNF levels have also been noted within eating disordered patients^{440,441}, while elevated BDNF is observable in obese individuals⁴³².

1.10. Conclusions

There is a growing body of evidence that supports the role of cytokine and neurotrophin

(BDNF) dysfunction in both schizophrenia and metabolic disturbances like weight gain. In considering the proposed immunomodulatory properties of APs, in addition to their effects on BDNF, it is plausible that these factors contribute to AIWG. This theory has received some attention in recent years, starting with Klunge et al. (2009)⁴⁴² who proposed that the effects of clozapine and olanzapine on weight gain may be closely related to their effects on cytokine networks after finding that levels of TNF- α , soluble tumor necrosis factor receptor (sTNFR)-1, sTNFR-2, and sIL-2R correlated with BMI after 6 weeks of treatment. Similarly, Song et al. $(2014)^{443}$ observed significant alterations in serum levels of IL-1 β , IL-6, and TNF- α , in addition to body weight, over 6 months of risperidone treatment in drug-naïve FEPs. In fact, patients who experienced clinically significant (>7%) weight gain by the end of treatment had higher levels of all cytokine markers compared to patients who gained <7% of weight. Klemettila *et al.* (2014)⁴⁴⁴ tested similar associations in 190 treatment-resistant schizophrenia patients on clozapine and found that levels of IL-1RA and CRP were associated with obesity, as was IL-6 within females. However, no studies, to the author's knowledge, have investigated the effects of cytokine polymorphisms on AIWG. BDNF has also been tested within AIWG with various lines of evidence suggesting involvement of reduced serum levels, and polymorphisms such as rs11030101, rs1519480, and Val66Met in mediating weight gain⁴⁴⁵⁻⁴⁴⁸. In spite of this work, there are no studies, to the author's knowledge, that have tested the epistatic effects between cytokine and BDNF polymorphisms on AIWG. At this stage, details of these associations have yet to be clearly elucidated and require further research.

Chapter 2:

Research Aims and Hypotheses

The purpose of this chapter is to outline:

- Research aims of the proposed study
- Research hypotheses of the proposed study

2.1. Research Aims

- <u>Aim 1</u>: To investigate whether variants in the genes encoding IL-1β, IL-2, and IL-6, in addition to BDNF Val66Met, are associated with:
 - A. AIWG
 - B. Clinically significant (≥7% weight change from baseline) AIWG (herein referred to as *clinically significant weight gain, CSWG*)
- <u>Aim 2:</u> To investigate whether variants in the genes encoding IL-1β, IL-2, and IL-6 have epistatic (or synergistic) effects with BDNF Val66Met in their association with AIWG.
- <u>Aim 3:</u> To determine whether variants from *Aim 1* that are significantly associated with AIWG replicate in an independent sample (CATIE sample).

2.2. Research Hypotheses

Based on the aforementioned research aims, the following hypotheses were formulated:

- <u>Hypothesis 1:</u> If antipsychotics decrease expression of IL-1β, IL-2, and IL-6, and either further antagonize or do not improve already reduced BDNF levels, and low levels of inflammatory cytokines and BDNF are associated with hyperphagia and weight gain, then genetic variation across IL-1β, IL-2, and IL-6, in addition to BDNF Val66Met, will be associated with:
 - A. AIWG
 - B. CSWG
- <u>Hypothesis 2</u>: If pro-inflammatory cytokines and BDNF show inverse expression trends within schizophrenia, and cytokines and neurotrophins interact as part of neuroimmune crosstalk, then variants across IL-1β, IL-2, and IL-6 will interact with BDNF Val66Met to yield AIWG.
- <u>Hypothesis 3:</u> If variants that were identified as being significantly associated with AWIG from *Aim 1* are informative of a true causal relationship, then these associations will replicate in an independent sample (CATIE sample).

Chapter 3:

Methodology

The purpose of this chapter is to:

- Provide an overview of data collection parameters
- Describe SNP selection and genotyping procedures
- Describe statistical analyses

3.1. Study Design

To determine the genetic basis of AIWG, study participants were administered AP medication and monitored for weight change outcomes. Participants had the following information collected:

- Demographic information including age, sex, and ethnicity
- Clinical information including baseline symptom severity, type of AP medication received, and duration of AP treatment
- Weight change information including baseline weight (in kilograms, kg), and weight (in kg) at the end of AP treatment. Information was used to determine the amount of weight gained over the course of AP treatment, as a percentage (%) of baseline weight (herein referred to as *weight change (%) from baseline*).
- 10-20mL of venous blood for genetic analysis

The effect of genetic variance on AIWG was determined by comparing weight change (%) from baseline across genotypic groups for each SNP of interest. Study parameters are described in further detail in the below-listed sections.

3.2. Study Participants

Participants were 188 English-speaking males (n=126) and females (n=62), 18 to 60 years of age, with a Diagnostic and Statistical Manual of Mental Disorders, Third Edition, Revised (DSM-III-TR) or Fourth Edition (DSM-IV) diagnosis of chronic schizophrenia or schizoaffective disorder. Analyses were not restricted to schizophrenia participants because these cases could not be isolated from schizoaffective disorder participants due to lack of available information. Participants with a diagnosis of schizoaffective disorder comprised approximately 10% of the total sample. Participants were primarily of European (n=128) or African descent (n=50), with ethnicity ascertained using self-reported ancestry over three generations. Additional demographic and clinical characteristics are presented in Table 3.1. All participants provided written informed consent. The study was approved by all participating institutional ethics review boards. Participants were recruited across three primary sites:

Sample A. Charite University Medicine in Berlin, Germany (DJ Mueller, I Puls, n=70). Inclusion criteria included a Positive and Negative Syndrome Scale (PANSS)^a score of \geq 60, and either first manifestation or relapse of schizophrenic symptoms with significant deterioration. Participants were treated with one of nine AP medications, which primarily included clozapine, haloperidol, olanzapine or risperidone, for up to six weeks.

Sample B. Case Western Reserve University in Cleveland, Ohio (HY Meltzer, JA Lieberman, n=69). Eligible participants were treatment refractory or intolerant to FGAs. Participants did not have prior exposure to SGAs and, where clinically possible, were drug-free for two to four weeks prior to the start of the study. Participants were treated with clozapine for six weeks. Clozapine dosing was variable and serum levels were monitored to confirm compliance.

^aThe PANSS is a 30-item, clinician-rated instrument which assesses the severity of schizophrenic illness using a 7point rating scale (from 1=absent to 7=extreme) across the following domains: positive symptoms, negative symptoms, and global psychopathology. The PANSS is an adaptation of 18 items from the Brief Psychiatric Rating Scale (BPRS) and 12 items from the Psychopathology Rating Schedule⁴⁴⁹.

Samples A and B had additional exclusionary criteria. Participants were excluded from the study if any of the following criteria were endorsed:

- Pregnancy or breast feeding
- Organic brain disorder or severe head injury
- Severe or unstable medical condition requiring treatment including hepatitis C, human immunodeficiency virus (HIV), thyroid disorder or diabetes mellitus
- Substance dependence
- Mental retardation
- Severe personality disorder

Sample C. Hillside Hospital in Glen Oaks, New York (JA Lieberman, n=49). Eligible participants had a PANSS score of ≥ 60 , and showed poor response to FGAs as evidenced by persistent positive symptoms and reduced functioning over the past two years. Participants did not have prior exposure to SGAs. Participants were randomly assigned to clozapine (500mg/day), haloperidol (20mg/day), olanzapine (20mg/day), or risperidone (8mg/day) for up to 14 weeks. Dosing was adjusted in response to clinical status. Exclusionary criteria were an intolerance or failure to attain clinical improvement during past trials of the study medications, and/or receipt of depot antipsychotics ≤ 1 month prior to the start of the study (for more details, see Volavka *et al.* 2002)⁴⁵⁰.

<u>Characteristics</u>	Sample A	<u>Sample B</u>	<u>Sample C</u>	<u>Total Sample</u>
	n=70	n=69	n=49	n=188
Sex				
Female	32 (45.7%)	24 (34.8%)	6 (12.2%)	62 (33.0%)
Male	38 (54.3%)	45 (65.2%)	43 (87.8%)	126 (67.0%)
Age (years)	35.04 ± 11.9	33.04 ± 8.0	40.74 ±7.5	35.80 ± 10.0
Baseline Weight (kg)	82.31 ± 16.4	74.54 ± 13.1	84.86 ± 18.3	80.07 ± 16.3
Weight Change (kg)	3.48 ± 3.8	3.60 ± 4.4	4.76 ± 6.6	3.85 ± 4.9
Weight Change (%)	4.09 ± 4.3	5.11 ± 6.3	6.18 ± 8.6	5.01 ± 6.4
CSWG				
<7%	52 (74.3%)	44 (63.8%)	32 (65.3%)	128 (68.1%)
<u>≥</u> 7%	18 (25.7%)	25 (36.2%)	17 (34.7%)	60 (31.9%)
Baseline BPRS †	50.81 ± 15.7	50.98 ± 14.5	53.74 ± 7.5	51.89 ± 12.9
Study Duration (weeks)	5.23 ± 1.4	6.00 ± 0.0	12.02 ± 3.6	7.26 ± 3.5
Ethnicity				
European	69 (98.6%)	49 (71.0%)	10 (20.4%)	128 (68.1%)
African	1 (1.4%)	20 (29.0%)	29 (59.2%)	50 (26.6%)
Other ‡			10 (20.4%)	10 (5.4%)
Study Medications				
Clozapine	8 (11.4%)	69 (100%)	10 (20.4%)	87 (46.3%)
Haloperidol	6 (8.6%)		9 (18.4%)	15 (8.0%)
Olanzapine	14 (20.0%)		18 (36.7%)	32 (17.0%)
Risperidone	19 (27.1%)		12 (24.5%)	31 (16.5%)
Others	22 (31.4%)			22 (11.7%)
Values represent number (percent) or mean ± standard deviation; †For comparability across samples, BPRS				

TABLE 3.1: Demographic and Clinical Sample Characteristics

Values represent number (percent) or mean \pm standard deviation; †For comparability across samples, BPRS information was used to assess severity of schizophrenic illness. BPRS total scores were extracted from the PANSS for Samples A and C; ‡Includes Hispanic, Asia Pacific, American Indian; IIncludes quetiapine, fluphenazine, aripiprazole, ziprasidone, amisulpride; CSWG = clinically significant weight gain, BPRS = Brief Psychotic Rating Scale

3.3. SNP Selection

A total of 19 putative functional (13) and tag (6) single nucleotide polymorphisms $(SNPs)^b$ were selected for analysis across IL-1 β , IL-2, IL-6 and BDNF (listed below). For the purpose of this study, functional properties (denoted by *) refer to SNPs that have been shown to either (i) affect gene expression directly, (ii) be in high linkage disequilibrium (LD, $r^2 \ge 0.8)^c$ with a secondary SNP known to affect gene expression, or (iii) reside within or in close proximity to a regulatory region of the gene (e.g. promoter region, transcription factor binding site, insulator region). Tagger properties refer to SNPs that capture variation across the gene from being in high LD with other SNPs in the gene region. The following SNPs were selected for genetic analysis:

• Interleukin 1 β (IL-1 β) (located on chromosome 2, refer to Figure 3.1):

rs4849127, rs13032029 (*), rs16944 (*), rs3136558, rs1143634 (*), rs1143643 (*)

• Interleukin 2 (IL-2) (located on chromosome 4, refer to Figure 3.2):

rs2069762 (*), rs2069778, rs2069779, rs2069772, rs2069776 (*)

• Interleukin 6 (IL-6) (located on chromosome 7, refer to Figure 3.3):

rs2069827 (*), rs1800795 (*), rs2069837 (*), rs2066992 (*), rs2069840 (*), rs2069861, rs10242595 (*)

• **Brain-Derived Neurotrophic Factor** (BDNF) (located on chromosome 11, refer to Figure 3.4):

Val66Met (rs6265*)

^bA SNP refers to a type of genetic variation which occurs when a nucleotide (A, T, C, G) at a given locus in the DNA sequence differs between individuals of a population⁴⁵¹.

^cLinkage disequilibrium (LD) refers to the non-random association of alleles at different loci. The r² statistic, which is a measure of LD, is the squared correlation between allele frequencies at two loci. The value of the r² statistic ranges from 0 (loci are randomly associated, and thus, in perfect equilibrium) to 1 (loci provide identical genetic information, and thus, are in perfect disequilibrium)⁴⁵¹. An r² cut-off of 0.8 between SNPs implies that the genotype of SNP1 can be reliably predicted 80% of the time if the genotype of SNP2 is known. The use of r²≥0.8 between loci is a general cut-off to identify SNPs that do not need to be investigated separately.

Putative functional SNPs were selected based on functional evidence in the literature and through use of Encyclopedia of DNA Elements (ENCODE)⁴⁵² data which were visualized via University of California Santa Cruz (UCSC) Human Genome Browser⁴⁵³, and further explored using HaploReg⁴⁵⁴ version 1.0, and RegulomeDB⁴⁵⁵.

The International HapMap Project⁴⁵⁶ database of human genetic variation was used in conjunction with Haploview⁴⁵⁷ version 4.2 to identify tag SNPs ($r^2 \ge 0.8$, minor allele frequency (MAF)^d \ge 0.05) that were 10 kilobase pairs (kbp) upstream and 2kbp downstream of each interleukin gene. No tag SNPs were selected for BDNF. Haploview⁴⁵⁷ version 4.2 was also used to assess Hardy-Weinberg equilibrium (HWE)^e and MAFs for all SNPs. The selected SNPs covered $\ge 90\%$ of the common genetic variation of IL-1 β , IL-2 and IL-6.

^dA minor allele frequency (MAF) is the lowest allele frequency at a given variant site within a specified population. In this study, MAFs for tag SNP selection were based on subjects of European ancestry from the International HapMap Project⁴⁵⁶. The MAF was set at 5% to ensure that SNPs would be adequately polymorphic.

^eThe Hardy-Weinberg equilibrium (HWE) law states that allele and genotype frequencies will remain constant across generations in a given population in the absence of evolutionary influences like non-random mating, mutation, migration, and natural selection^{458.} A departure from HWE may indicate selection pressure effects or, more likely, a genotyping error⁴⁵¹.



FIGURE 3.1: IL-1β Gene Diagram of Polymorphisms

FIGURE 3.2: IL-2 Gene Diagram of Polymorphisms



FIGURE 3.3: IL-6 Gene Diagram of Polymorphisms



FIGURE 3.4: BDNF Gene Diagram of Polymorphisms



FIG 3.1 to 3.4: The structure of each gene from the present study is depicted, with the full gene region highlighted. Green boxes represent coding exon regions, light green boxes represent non-coding exon regions, and intermediate green boxes represent alternate splicing regions. Study SNPs are tagged based on their location within their respective gene region.

3.4. Genotyping Procedures

Genotype information was determined using polymerase chain reaction (PCR). Venous blood (10-20mL) was obtained from all study participants. Genomic DNA was extracted at the Centre for Addiction and Mental Health using the high-salt method⁴⁶⁰. DNA samples were stored between 2°C to 8°C. All samples were centrifuged using the AllegraTM X-22 Centrifuge (Beckman CoulterTM Inc, Indianapolis, IN) at 2000rpm for 1 minute prior to PCR preparations. Genotyping was performed blind to weight change status. Of the 19 study SNPs, 16 were genotyped using Taqman[®] OpenArray[®] technology, while the remaining three were genotyped using Taqman[®] SNP genotyping assays.

3.4.1. Taqman® OpenArray® Genotyping

SNPs were genotyped using the format-16 Taqman® OpenArray® Genotyping Plate (Applied Biosystems Inc, Foster City, CA). Taqman® assays for 16 SNPs were pre-loaded onto the arrays. Arrays were stored at -20°C to 5°C, and thawed at room temperature prior to use. The quantity of DNA per sample was measured using NanoDrop 8000 spectrophotometer, in conjunction with NanoDrop 8000 Software version 2.0.0 (Thermo Scientific Inc, Wilmington, DE). Spectrophotometer readings were performed according to the manufacturer's protocol. Samples had nucleic acid concentrations in the range of 20-100ng/µL.

PCR was performed using the following reagents: 1.5µL of DNA, and 1.5µL Taqman® OpenArray® Genotyping Master Mix, with a total volume of 3µL per subject. Reagent mixtures were centrifuged at 2000rpm for 1 minute prior to being loaded onto the array using the OpenArray® AccuFill[™] System in conjunction with the OpenArray® AccuFill[™] System Software version 1.1 (Applied Biosystems Inc). Each array held 144 samples and four negative controls^f. DNA target sequences were immediately amplified using the QuantStudio[™] 12K Flex Real-Time PCR system in conjunction with the QuantStudio[™] 12K Flex Software version 1.2.1 (Applied Biosystems Inc), according to the following conditions: (Stage 1) 93°C for 10 minutes,

^f Negative controls are included to ensure that samples are free from contamination. In the absence of contamination, negative controls should not amplify.

(Stage 2) 50 cycles of 95°C for 45 seconds, 94°C for 13 seconds, and 53°C for 2 minutes and 14 seconds, and (Stage 3) 25°C for 2 minutes.

SNPs IL-1 β rs3136558, IL-2 rs2069779, and IL-6 rs2069861 did not successfully plate onto OpenArray® technology and were re-genotyped using Taqman® SNP assays (Applied Biosystems Inc) according to the protocol described in Section 3.4.2.

3.4.2. Taqman® SNP Genotyping

IL-2 rs2069776, IL-6 rs1800795, and BDNF Val66Met (rs6265) were genotyped using Taqman® SNP genotyping assays (Applied Biosystems Inc). Assays were stored between -15°C to -25°C. Each assay was separately mixed using the Vortex Genie® 2 (Thermo Scientific Inc) prior to use in the PCR experiments. Taqman® assays included forward and reverse primers specific to the DNA target sequence of interest, and two fluorescent-dye-labelled probes to differentiate each allele of the target SNP. PCR was performed using the following reagents: 1µL of DNA, 5µL of Taqman® Genotyping Master Mix, 0.25µL of Taqman® SNP assay, and 3.75µL of Qiagen nuclease-free water, with a total volume of 10µL per subject. MicroAmp® Optical 96-Well Reaction Plates (Applied Biosystems Inc) were used in the PCR experiments. Plates included a minimum of four negative controls. All genotyping procedures were carried out according to the manufacturer's protocol. Once added to the plate, reagent mixtures were centrifuged at 2000rpm for 1 minute prior to amplification. The DNA target sequence was immediately amplified using 2720 thermal cyclers (Applied Biosystems Inc), according to the following conditions: (Stage 1) 95°C for 10 minutes, and (Stage 2) 50 cycles of 92°C for 15 seconds and 60°C for 1 minute.

3.4.3. Genotype Calls

SNP genotyping calls were based on allelic discrimination and genotype cluster plots. For Taqman® SNP genotyping, allele-specific fluorescence was measured on the ViiATM 7 using the ViiATM 7 RUO Software version 1.2.2 (Applied Biosystems Inc). For Taqman® OpenArray®

genotyping, allele-specific fluorescence was measured directly on the QuantStudio[™] 12K Flex Real-Time PCR system using the Taqman® Genotyper Software version 1.3. Genotyping calls were confirmed by two independent researchers after visual inspection of allelic discrimination plots (refer to Figure 3.5). To verify genotyping accuracy, 10% of the total sample was regenotyped. The concordance rate was 99.9%. Discordant genotypes were removed, and entered as missing values for statistical analysis. The SNP genotyping rate was >97% and subject genotyping rate was >89% in this study.





FIG 3.5: An allelic discrimination plot is a visual representation of genotype clusters for a given SNP, as determined by allele-specific fluorescence. Red dots represent individuals homozygous for Allele 1. Blue dots represent individuals homozygous for Allele 1 and Allele 2. A high quality PCR reading presents clearly defined, well-separated clusters. Negative controls (black squares) show zero or minimal fluorescence in the absence of PCR contamination. Individuals with undetermined genotypes are represented by an 'X' (not shown).

3.5. Statistical Analysis

In association testing, categorical variables (CSWG, $\geq 7\%$) were compared using Pearson χ^2 , and continuous variables (weight change, %) were analyzed using analysis of covariance (ANCOVA). Pearson's correlation coefficients, Pearson's χ^2 , and Student t-tests were used to determine any confounding associations between each weight change outcome variable and age, sex, duration of treatment, baseline weight, and baseline Brief Psychotic Rating Scale (BPRS)^g score. To determine the association between genetic variation and AIWG, two major association analyses were conducted (described below in Sections 3.5.1 and 3.5.2). Within each major analysis, we tested the association of SNPS with AIWG in (i) total, (ii) race-stratified, and (iii) race- and treatment-stratified samples. Statistical analyses were performed using Statistical Package for the Social Sciences (SPSS; SPSS Inc, Chicago, III) version 20.0.

3.5.1. Association Analysis I: Weight Change (%) from Baseline

The dependent variable of weight change (%) from baseline was compared across genotypic groups using ANCOVA. Baseline weight and duration of treatment were identified as confounding variables (described in further detail in Section 4.1.2) and entered into the model as covariates. Post-hoc analyses were carried out for all significant SNPs. The effect of each genotype was investigated separately, where possible. However, where there were fewer than five individuals homozygous for the minor allele of a given SNP, these participants were merged with heterozygotes and assessed according to a dominant model of genetic inheritance. If n<5 in the merged group, the SNP analysis was not tested for an association with weight change (%). Effect size estimates were reported using eta squared values. Despite the fact that 67% of the total sample was male, gender sub-analyses were not conducted as this variable was not associated with weight change (refer to Section 4.1.2).

^gThe Brief Psychotic Rating Scale is an 18-item, clinician-rated instrument which assesses the severity of both psychotic and non-psychotic symptom dimensions associated with schizophrenia or other psychotic illnesses using a 7-point rating scale (from 1=not present to 7=extremely severe)⁴⁶¹.

The dependent variable was assessed for normality using the Shapiro-Wilk test. Where p<0.05, data were visually inspected using normality plots. Visual calls were confirmed by two independent researchers. Homogeneity of variances between genotypic groups was determined using Levene's F statistic. Where testing assumptions were violated, the non-parametric Kruskal-Wallis test was performed. Statistical tests were considered significant at the p<0.05 level.

3.5.2. Association Analysis II: Clinically Significant Weight Gain

The variable of weight change (%) from baseline was dichotomized to reflect clinically significant weight change, where patients at or above 7% weight change ('clinically significant weight gain' or CSWG, n=60) were compared against the remainder of the sample ('nonclinically significant weight gain' or non-CSWG, n=128). Weight gain of 7% or more was considered clinically significant, as defined according to the Food and Drug Administration⁴⁶². Pearson χ^2 was used to determine the effect of genotype on CSWG status. No statistical covariates were entered. To ensure an adequate number of individuals across factor space, all investigations were carried out according to a dominant model of inheritance. If any of the *expected cell counts* were 5>n≥1, the Fisher Exact test was performed. If n=0 for any cells of factor space, the SNP analysis was not tested for an association with CSWG. Statistical tests were considered significant at the p<0.05 level.

3.5.3. Haplotype and Allelic Analyses

Unphased⁴⁶³ version 3.1.5 was used to investigate haplotype and allelic effects of IL-1 β , IL-2, IL-6, and BDNF^h. Three-marker haplotypes were constructed and analyses were carried out to identify any associations with weight change (%) from baseline. Investigations were restricted to the subset of patients treated with either clozapine or olanzapine. Analyses were performed separately for patients of European and African ancestry. Haplotypes with frequencies less than 5% were excluded from analysis. Where tests of overall association were significant at the

^hHaplotypes were not tested for BDNF

p<0.05 level, post-hoc comparisons were reviewed. Allelic analyses were performed under the same conditions and examined individual allele effects at each locus.

3.5.4. Gene-Gene Interaction Analyses

The association between bi-locus genotypes and weight change (%) from baseline was investigated using Model-Based Multifactor Dimensionality Reduction (MBMDR)⁴⁶⁴ operated through R version 3.0.2 (R Foundation for Statistical Computing, Vienna, Austria). Epistatic effects were modelled between BDNF Val66Met and variant sites across IL-1 β , IL-2, and IL-6. Significance was calculated using a permutation test based on 1000 permutations. Investigations were restricted to the subset of patients treated with either clozapine or olanzapine. Analyses were performed separately for patients of European and African ancestry. Epistatic effects were considered significant at the p<0.05 level.

3.5.5. Multiple Testing Corrections

Single-Nucleotide Polymorphism Spectral Decomposition (SNPSpD)⁴⁶⁵ was used to correct for multiple comparisons across association analyses. Adjusted p-values were derived from a variation of the Nyholt correction using the Li and Ji method⁴⁶⁶. The Li and Ji method more accurately estimates the effective number of independent tests (M_{eff}) to control the type I error rate without lowering statistical power. To avoid excessively conservative results, the Li and Ji method was applied wherever its proposed M_{eff} (i.e. M_{eff} Li) was lower than the standard M_{eff} , as recommended⁴⁶⁵. Gene-wide corrections were calculated for each of IL-1 β ($p_{IL-1\beta}$), IL-2 (p_{IL-2}), and IL-6 (p_{IL-6}); a gene-wide correction was not applicable for BDNF. A hypothesis-wide correction (p_{corr}) was applied by multiplying unadjusted p-values by a summation of M_{eff} Li values for each of the four genes.

For haplotype and gene-gene interaction analyses, Bonferroni corrections were applied. For haplotype investigations, gene-wide corrections were applied to tests of overall association, based on the number of three-marker haplotypes examined across each gene. Hypothesis-wide corrections were not applied. Allelic analyses were corrected for the number of SNPs tested. For gene-gene interaction effects, corrections were based on the number of pair-wise interactions investigated. Since corrections were applied to statistics of overall association, none were applied to post-hoc comparisons.

3.5.6. Power Calculations

Power calculations were performed using Quanto⁴⁶⁷ version 1.2.4. Assuming a MAF of 0.05 and a sample size of n=188, we had more than 80% power to detect a mean difference of 4.2% between carriers and non-carriers of the risk genotype (explains 4.1% of the variance) in an additive model of genetic inheritance or a mean difference of 4.4% between carriers and non-carriers of the variance) in a dominant model of genetic inheritance.

Chapter 4:

Results

The purpose of this chapter is to review results from:

- Descriptive Statistics
- ✤ Association Analysis I Weight Change (%) from Baseline
- ✤ Association Analysis II Clinically Significant Weight Gain
- Haplotype and Allelic Analyses
- Gene-Gene Interaction Analyses

4.1. Descriptive Statistics

4.1.1. Clinical and Demographic Sample Characteristics

One hundred and eighty-eight individuals, consisting of 126 males and 62 females, were included in the study. All participants had a DSM-III-TR or DSM-IV diagnosis of chronic schizophrenia or schizoaffective disorder. Participants were 18 to 60 years of age, with a mean age of 35.8 ± 10 years. Participants were primarily of European (n=128) or African descent (n=50), with ten participants reporting Hispanic, Asian Pacific or American Indian ancestry.

Participants were primarily treated with one of four APs including clozapine (n=87), olanzapine (n=32), risperidone (n=31) or haloperidol (n=15). All remaining participants (n=22) were treated with quetiapine, fluphenazine, aripiprazole, ziprasidone or amisulpride. The average length of AP treatment was 7.26 ± 3.5 weeks. Mean baseline weight was 80.07 ± 16.3 kg, and mean weight change subsequent to AP treatment was 3.85 ± 4.9 kg. Refer to Table 3.1 for further demographic and clinical characteristics.

4.1.2. Statistical Covariates of AIWG

Weight change (%) from baseline did not significantly differ between recruitment sites (p=0.214). However, significant site-specific differences were observed for baseline weight (p=0.001) and duration of treatment (p<0.001). Among the total sample, confounding associations were observed between weight change (%) and duration of treatment (p=0.006) but not participant age (p=0.953), gender (p=0.557), baseline weight (p=0.069) or baseline BPRS score (p=0.819). In the subset of patients of European ancestry treated with clozapine or olanzapine, no associations were found between any of the aforementioned variables (p>0.3). In the subset of patients of African ancestry treated with clozapine or olanzapine, an association was observed between weight change (%) and baseline weight (p=0.047), while all other associations were non-significant (p>0.06). Since baseline weight and treatment length influenced the amount of weight gained with AP treatment, they were entered as statistical covariates for Association Analysis I.

The same variables were re-assessed to determine confounding associations with CSWG, as variable dichotomization may yield different covariates. None were found to be associated with CSWG status for the total sample or among patients of European or African ancestry treated with clozapine or olanzapine (p>0.09). We elected not to force include covariates identified for Association Analysis I (e.g. baseline weight, duration of treatment) because controlling for variables that are not significantly associated with the outcome measure can increase statistical noise. Thus, no variables were entered as statistical covariates for Association Analysis II.

4.1.3. Linkage Disequilibrium, Hardy Weinberg Equilibrium and Minor Allele Frequencies

None of the 19 SNPs analyzed in this study were in high LD with each other ($r^2 < 0.8$, refer to Figure 4.1 to 4.3). All SNPs maintained HWE (p > 0.05) (refer to Table 4.2 and 4.3) except IL-2 rs2069779 (p=0.026, European sub-sample). IL-2 rs2069779 was also monomorphic in patients of African ancestry and was, therefore, excluded from further analyses. All remaining SNPs had a MAF greater than 5% in patients of European ancestry (refer to Table 4.2). In

patients of African ancestry, IL-2 rs2069778, IL-6 rs2069827, and IL-6 rs2069861 had a MAF less than 5% (refer to Table 4.3) but were still analyzed to maintain procedural consistency.



FIGURE 4.1: IL-1 β Linkage Disequilibrium Plots





FIGURE 4.3: IL-6 Linkage Disequilibrium Plots



ⁱD' is a second measure of LD between loci with statistics ranging from 0 (indicative of no LD) to 1 (indicative of complete LD). Logarithm of the odds (LOD) is a measure of confidence in the value of D^{,451}.

FIG 4.1 to 4.3:

Linkage disequilibrium (LD) plots are based on data obtained from study participants of European (left) ancestry and African ancestry (right) separately (Haploview⁴⁵⁷ v4.2). LD plot values represent r^2 statistics. LD plots are formatted according to the following color scheme: 'bright red' represents D'=1 and logarithm of $(LOD)^i \geq 2,$ the odds 'shades of pink/red' D'<1 represents and LOD >2. 'blue' represents D'=1 and LOD <2, and 'white' represents D'<1 and LOD <2.

4.2.1. Total Sample Analyses

Weight change (%) from baseline was compared across genotypic groups, with baseline weight and duration of treatment entered as statistical covariates. In the total sample, four genotypic associations involving IL-1 β and BDNF with weight change (%) were observed. No associations were observed for variants across IL-2 or IL-6 (refer to Table 4.1).

Finding #1: A significant genotypic association was found for IL-1 β rs4849127 where carriers of the A-allele gained approximately 4% more weight than individuals homozygous for the G-allele (p=0.001, refer to Figure 4.4), according to a dominant model of genetic inheritance. Under this model, IL-1 β rs4849127 explains approximately 5.9% of the variance in weight change (%) from baseline. This finding remained significant after a gene-wide (p_{IL-1 β}=0.004) and hypothesis-wide (p_{corr}=0.014) correction. However, with approximately 93% of A-allele carriers having the heterozygous GA genotype, results may be driven by an over-dominance model.

Finding #2: A significant genotypic association was found for IL-1 β rs16944 where individuals with the heterozygous GA genotype gained approximately 4% more weight than individuals with either homozygous genotype (p=0.001, refer to Figure 4.5). Under this model, IL-1 β rs16944 explains approximately 7.3% of the variance in weight change (%) from baseline. This finding remained significant after a gene-wide (p_{IL-1 β}=0.004) and hypothesis-wide (p_{corr}=0.014) correction. Post-hoc comparisons confirmed that individuals with the GA genotype significantly differed from both the AA (p=0.008) and GG (p=0.001) genotype groups.



FIGURE 4.4: Weight Change (%) Distribution for IL-1β rs4849127 in the Total Sample

FIGURE 4.5: Weight Change (%) Distribution for IL-1β rs16944 in the Total Sample



Finding #3: A significant genotypic association was found for IL-1 β rs1143634 where individuals with the heterozygous GA genotype gained more weight than individuals with either homozygous genotype (p=0.010, refer to Figure 4.6). Under this model, IL-1 β rs1143634 explains around 5.0% of the variance in weight change (%) from baseline. This finding remained significant after a gene-wide (p_{IL-1 β}=0.04) but not a hypothesis-wide (p_{cor}=0.14) correction.





Post-hoc comparisons revealed that individuals with the GA genotype only statistically differed from the AA (p=0.003) but not the GG (p=0.226) genotype group. A re-analysis of the data was performed with G-allele carriers merged. Results showed that individuals homozygous for the A-allele gained approximately 6% less weight than G-allele carriers (AA vs. GA + GG; - 0.84 ± 8.2 vs. 5.28 ± 6.2 ; p=0.005). Under this model, IL-1 β rs1143634 explains approximately 4.3% of the variance in weight change (%) from baseline. This finding remained significant after a gene-wide (p_{IL-1 β}=0.02) but not a hypothesis-wide (p_{corr}=0.07) correction.
Finding #4: A significant genotypic association was found for BDNF Val66Met where individuals with the Val/Val genotype gained more weight than individuals with the Val/Met or Met/Met genotype (p=0.007, refer to Figure 4.7). Under this model, BDNF Val66Met explains about 5.4% of the variance in weight change (%). This finding did not remain significant after a hypothesis-wide correction ($p_{corr}=0.098$).



FIGURE 4.7: Weight Change (%) Distribution for BDNF Val66Met in the Total Sample

Post-hoc comparisons revealed that the Val/Val genotype group did not significantly differ from the Met/Met group (p=0.184). In fact, the Met/Met group did not differ from the Val/Met genotype group either (p=0.968). This may have resulted from the genetic model being underpowered due to low numbers in the Met/Met group (n=6). A re-analysis of the data using a dominant model of inheritance was performed with Met allele carriers merged. Results showed that carriers of the Met allele gained approximately 4% less weight than individuals homozygous for the Val allele (Met/Met + Val/Met vs. Val/Val; 2.36 ± 5.8 vs. 5.92 ± 6.5 , p=0.002). Under this model, BDNF Val66Met still explains about 5.4% of the variance in weight change (%). This finding remained significant after a hypothesis-wide correction (p_{corr}=0.028).

SNP	<u>Genotype</u>	<u>Frequency</u> ^a	$\Delta Weight (\%)^{a}$	χ^2 / F Value	<u>P Value</u> ^b	<u>p</u> _{corr} ^c
	AA	3 (1.6%)	4.18 ± 4.8			
IL-1β rs4849127	GA	41 (21.8%)	8.50 ± 7.4	11.1	‡ *0.001	*0.014
	GG	144 (76.6%)	4.04 ± 5.8			
	CC	63 (34.2%)	5.40 ± 6.2			
IL-1β rs13032029	СТ	86 (46.7%)	5.20 ± 6.9	0.61	0.545	1.00
	TT	35 (19.0%)	3.22 ± 5.1			
	AA	27 (14.4%)	3.34 ± 4.3			
IL-1β rs16944	GA	78 (41.5%)	7.29 ± 7.0	13.6	 *0.001	*0.014
	GG	82 (43.6%)	3.39 ± 5.8			
	AA	116 (62.7%)	5.45 ± 6.4			
IL-1β rs3136558	GA	57 (30.8%)	4.60 ± 6.7	0.98	0.376	1.00
	GG	12 (6.5%)	2.39 ± 4.8			
	AA	9 (4.8%)	-0.84 ± 8.2			
IL-1β rs1143634	GA	65 (34.9%)	5.69 ± 6.6	4.73	*0.010	0.140
	GG	112 (60.2%)	5.04 ± 6.0			
	CC	75 (40.8%)	5.46 ± 7.2			
IL-1β rs1143643	СТ	84 (45.7%)	4.70 ± 6.0	0.09	0.918	1.00
	TT	25 (13.6%)	4.45 ± 5.6			
	AA	98 (53.0%)	5.60 ± 6.3			
IL-2 rs2069762	CA	74 (40.0%)	4.39 ± 5.7	1.75	0.177	1.00
	CC	13 (7.0%)	2.61 ± 9.4			
	AA	1 (0.5%)	1.66			
IL-2 rs2069778	GA	34 (18.6%)	4.64 ± 5.3	0.16	ŧ0.686	1.00
	GG	148 (80.9%)	5.11 ± 6.7			
	CC	12 (6.5%)	4.27 ± 4.0			
IL-2 rs2069772	СТ	62 (33.7%)	4.35 ± 5.8	0.32	0.723	1.00
	TT	110 (59.8%)	5.36 ±7.0			
	CC	6 (3.3%)	7.32 ± 6.2			
IL-2 rs2069776	СТ	61 (33.3%)	5.39 ± 6.8	0.74	0.478	1.00
	TT	116 (63.4%)	4.72 ± 6.3			

TABLE 4.1: Results from Association Analysis of SNPs with AIWG in the Total Sample

	GG	156 (83.9%)	5.18 ± 6.7			
IL-6 rs2069827	GT	28 (15.1%)	4.14 ± 5.0	0.22	ŧ0.638	1.00
	TT	2 (1.1%)	1.85 ± 2.6			
	CC	87 (47.5%)	6.15 ± 6.4			
IL-6 rs1800795	CG	70 (38.3%)	4.49 ± 6.3	2.35	0.099	1.00
	GG	26 (14.2%)	2.71 ± 6.6			
	AA	153 (82.7%)	4.83 ± 6.6			
IL-6 rs2069837	GA	29 (15.7%)	5.05 ± 5.6	0.19	ŧ0.664	1.00
	GG	3 (1.6%)	7.23 ± 1.3			
	GG	157 (86.7%)	4.93 ± 6.5			
IL-6 rs2066992	GT	23 (12.7%)	5.42 ± 6.6	0.10	ŧ0.753	1.00
	TT	1 (0.5%)	5.10			
	CC	101 (54.6%)	4.96 ± 6.6			
IL-6 rs2069840	CG	66 (35.7%)	4.82 ± 6.1	0.20	0.821	1.00
	GG	18 (9.7%)	5.77 ± 7.1			
	CC	155 (83.8%)	5.31 ± 6.3			
IL-6 rs2069861	СТ	29 (15.7%)	3.17 ± 7.0	1.46	ŧ0.229	1.00
	TT	1 (0.5%)	4.37			
	AA	31 (16.8%)	6.58 ± 6.8			
IL-6 rs10242595	GA	74 (40.0%)	4.73 ± 5.8	0.70	0.499	1.00
	GG	80 (43.2%)	4.66 ± 6.9			
	Val/Val	137 (74.9%)	5.92 ± 6.5			
BDNF Val66Met	Val/Met	40 (21.9%)	2.44 ± 6.0	5.04	*0.007	0.098
	Met/Met	6 (3.3%)	1.85 ± 4.2			
	1	1		1	1	1

Covariate information was missing for two participants; ^aValues represent number (percent) or mean \pm standard deviation; ^bUncorrected p-values; ^cP-value after a hypothesis-wide correction; *Value significant at p<0.05 level; \ddagger P-value calculated under a dominant model of genetic inheritance; IValue calculated using Kruskal-Wallis; AIWG = antipsychotic-induced weight gain, SNP = single nucleotide polymorphism, IL-1 β = interleukin 1 beta, IL-2 = interleukin 2, IL-6 = interleukin 6, BDNF = brain-derived neurotrophic factor

Participants were mainly of European (n=128) or African ancestry (n=50), and SNP allele frequencies differed between ethnic groups (refer to Table 4.2 and 4.3). To avoid a population stratification bias, a race-stratified sub-analysis was tested using parameters from Section 4.2.1.

4.2.2.1. Sub-Analysis of Patients of European Ancestry

In patients of European ancestry, three genotypic associations involving IL-1 β and BDNF with weight change (%) from baseline were observed. No associations were observed for variants across IL-2 or IL-6 with weight change (%) (Refer to Table 4.2).

Finding #1: A significant genotypic association was found for IL-1 β rs16944 where individuals with the heterozygous GA genotype gained more weight than individuals with either homozygous genotype (p=0.013, refer to Figure 4.8). Post-hoc comparisons confirmed that heterozygote individuals significantly differed from the AA (p=0.017) and GG (p=0.019) genotype groups. Under this model, IL-1 β rs16944 explains about 6.9% of the variance in weight change (%). However, this finding did not remain significant after a gene-wide (p_{IL-1 β}=0.052) or hypothesis-wide (p_{corr}=0.182) correction.

Finding #2: A significant genotypic association was found for IL-1 β rs1143634 where individuals with the heterozygous GA genotype gained more weight than individuals with either homozygous genotype (p=0.004, refer to Figure 4.9). Under this model, IL-1 β rs1143634 explains about 8.7% of the variance in weight change (%). This finding remained significant after a gene-wide (p_{IL-1 β}=0.016) but not a hypothesis-wide (p_{corr}=0.056) correction. Post-hoc comparisons for IL-1 β rs1143634 revealed that individuals with the GA genotype only statistically differed from the AA (p=0.001) but not the GG (p=0.441) genotype group. A reanalysis of the data was performed with G-allele carriers merged. Results showed that individuals homozygous for the A-allele gained about 7% less weight than G-allele carriers (AA vs. GA + GG; -2.17 ± 7.7 vs. 4.42 ± 5.2, p=0.001). Under this model, IL-1 β rs1143634 explains around 8.3% of the variance in weight change (%). This finding remained significant after a gene-wide (p_{IL-1 β}=0.004) and hypothesis-wide (p_{corr}=0.014) correction.



FIGURE 4.8: Weight Change (%) Distribution for IL-1β rs16944 in Europeans

FIGURE 4.9: Weight Change (%) Distribution for IL-1β rs1143634 in Europeans



Finding #3: A significant genotypic association was found for BDNF Val66Met where individuals with the Val/Val genotype gained more weight than individuals with the Val/Met or Met/Met genotype (p=0.014, refer to Figure 4.10). Under this model, BDNF Val66Met explains about 6.8% of the variance in weight change (%). This finding did not remain significant after a hypothesis-wide correction (p_{corr} =0.196). Post-hoc comparisons revealed that the Val/Val genotype group did not significantly differ from the Met/Met group (p=0.073). In fact, the Met/Met group did not differ from the Val/Met genotype group either (p=0.508). This may have resulted from the model being underpowered due to low numbers in the Met/Met group (n=5). A re-analysis of the data was performed with Met allele carriers merged. Results showed that carriers of the Met allele gained approximately 4% less weight than individuals homozygous for the Val allele (Met/Met + Val/Met vs. Val/Val; 1.97 ± 5.9 vs. 5.01 ± 5.2 , p=0.004). Under this model, BDNF Val66Met explains approximately 6.5% of the variance in weight change (%). This finding did not remain significant after a hypothesis-wide correction (p_{corr} =0.056).





		<u>∆Weight (%)</u> ^a			Δ Weight (%) ^a				HWE
<u>SNP</u>	<u>Genotype</u>	<u>All Drugs</u>	<u>P Value</u> ^b	<u>p</u> _{corr} ^c	CLZ or OLZ	<u>P -Value</u> ^b	<u>p</u> _{corr} ^c	$\underline{\mathbf{MAF}}^{\mathrm{d}}$	P-Value ^d
		<u>(n= 128)</u>			<u>(n= 74)</u>				<u>1 vuiue</u>
	AA								
IL-1β rs4849127	GA	5.92 ± 4.6 (17)	0.141	1.00	6.64 ± 5.1 (12)	0.282	1.00	0.07	1.00
	GG	3.71 ± 5.6 (111)			4.39 ± 5.9 (62)				
	CC	4.09 ± 5.3 (31)			4.66 ± 5.8 (21)				
IL-1β rs13032029	СТ	4.00 ± 5.6 (62)	0.828	1.00	5.01 ± 5.4 (32)	0.654	1.00	0.49	0.967
	TT	3.35 ± 5.2 (33)			3.50 ± 5.9 (19)				
	AA	0.96 ± 2.5 (9)			1.12 ± 3.0 (6)				
IL-1β rs16944	GA	5.65 ± 5.1 (51)	*0.013	0.182	6.52 ± 5.6 (33)	0.056	0.784	0.27	1.00
	GG	3.13 ± 5.9 (67)			3.72 ± 5.8 (35)				
	AA	3.94 ± 5.2 (76)			4.64 ± 6.1 (45)				
IL-1β rs3136558	GA	4.46 ± 6.3 (43)	0.616	1.00	5.31 ± 5.7 (23)	0.850	1.00	0.24	0.509
	GG	2.34 ± 3.9 (9)			3.51 ± 4.3 (6)				
	AA	-2.17 ± 7.7 (8)			0.84 ± 1.9 (4)				
IL-1β rs1143634	GA	4.92 ± 5.7 (45)	*0.004	0.056	5.59 ± 6.0 (27)	ŧ0.757	1.00	0.24	0.857
	GG	4.12 ± 4.9 (75)			4.60 ± 5.8 (43)				
	CC	3.86 ± 6.6 (37)			5.09 ± 5.7 (27)				
IL-1β rs1143643	СТ	3.86 ± 4.9 (66)	0.859	1.00	4.35 ± 5.6 (32)	0.903	1.00	0.44	0.648
	TT	4.50 ± 5.8 (23)			5.10 ± 7.0 (14)				

TABLE 4.2: Results from Association Analysis of SNPs with AIWG in Europeans

	AA	3.91 ± 4.8 (54)			3.85 ± 4.8 (34)				
IL-2 rs2069762	CA	4.43 ± 5.1 (64)	0.321	1.00	5.66 ± 6.2 (33)	0.377	1.00	0.33	0.200
	CC	1.83 ± 10.5 (10)			4.92 ± 8.3 (7)				
	AA	1.66 (1)			1.66 (1)				
IL-2 rs2069778	GA	4.52 ± 5.1 (27)	ŧ0.649	1.00	4.57 ± 5.4 (18)	ŧ0.773	1.00	0.12	0.984
	GG	3.90 ± 5.8 (97)			4.96 ± 6.1 (53)				
	CC	4.27 ± 4.0 (12)			3.15 ± 3.5 (8)				
IL-2 rs2069772	СТ	3.91 ± 5.6 (52)	0.986	1.00	4.66 ± 6.4 (31)	0.530	1.00	0.30	0.911
	TT	3.97 ± 5.8 (63)			5.14 ± 5.8 (34)				
	CC	4.34 ± 4.6 (4)			2.15 ± 1.9 (3)				
IL-2 rs2069776	СТ	4.37 ± 5.2 (47)	ŧ0.582	1.00	5.10 ± 5.9 (29)	ŧ0.940	1.00	0.22	0.466
	TT	3.86 ± 5.9 (75)			4.93 ± 6.0 (40)				
	GG	3.92 ± 5.7 (103)			4.70 ± 5.8 (61)				
IL-6 rs2069827	GT	4.58 ± 4.9 (23)	ŧ0.683	1.00	5.45 ± 5.7 (12)	ŧ0.746	1.00	0.11	0.825
	TT	1.85 ± 2.6 (2)			0E-14 (1)				
	CC	4.67 ± 4.3 (41)			4.44 ± 4.8 (21)				
IL-6 rs1800795	CG	4.07 ± 6.0 (60)	0.524	1.00	5.22 ± 6.5 (39)	0.967	1.00	0.44	0.823
	GG	3.08 ± 6.4 (25)			4.56 ± 5.4 (12)				
	AA	4.10 ± 5.9 (107)			5.06 ± 6.1 (63)				
IL-6 rs2069837	GA	3.32 ± 3.5 (20)	ŧ0.719	1.00	3.00 ± 2.9 (11)	10.479	1.00	0.09	1.00
	GG	7.92 (1)							
	GG	3.96 ± 5.7 (111)			4.85 ± 6.0 (62)				
IL-6 rs2066992	GT	4.88 ± 5.2 (13)	0.624	1.00	5.01 ± 5.5 (9)	0.941	1.00	0.05	1.00
	TT								

IL-6 rs2069840	CC CG	3.70 ± 5.7 (64) 4.32 ± 5.7 (49)	0.835	1.00	$4.15 \pm 5.6 (37) \\ 5.92 \pm 6.1 (31)$	0.299	1.00	0.31	0.315
	GG	4.29 ± 4.4 (15)			2.44 ± 4.3 (6)				
	CC	4.29 ± 5.2 (99)			4.82 ± 5.9 (56)				
IL-6 rs2069861	СТ	2.83 ± 6.7 (27)	ŧ0.257	1.00	4.58 ± 5.7 (17)	ŧ0.933	1.00	0.11	1.00
	TT	4.37 (1)			4.37 (1)				
	AA	4.48 ± 4.0 (14)			4.88 ± 3.4 (8)				
IL-6 rs10242595	GA	3.74 ± 5.5 (48)	0.883	1.00	4.01 ± 6.1 (29)	0.691	1.00	0.30	0.342
	GG	4.16 ± 5.9 (65)			5.32 ± 6.0 (37)				
	Val/Val	5.01 ± 5.2 (87)			5.95 ± 5.7(50)				
BDNF Val66Met	Val/Met	2.23 ± 6.2 (34)	*0.014	0.196	2.82 ± 5.5 (20)	**0.025	0.350	0.18	0.624
	Met/Met	0.25 ± 1.7 (5)			-0.74 ± 1.1 (2)				

^aValues represent mean \pm standard deviation (number); ^bUncorrected p-values; ^cP-value after a hypothesis-wide correction; ^dValues calculated among all patients of European ancestry; [‡]P-value calculated under a dominant model of genetic inheritance; **I**Value calculated using Kruskal-Wallis; *Value significant at p<0.05 level; SNP = single nucleotide polymorphism, CLZ = clozapine, OLZ = olanzapine, MAF = minor allele frequency, HWE = Hardy-Weinberg equilibrium, IL-1 β = interleukin 1 beta, IL-2 = interleukin 2, IL-6 = interleukin 6, BDNF = brain-derived neurotrophic factor

4.2.2.2. Sub-Analysis of Patients of African Ancestry

In the sub-sample of patients of Africa ancestry, two genotypic associations involving IL- 1β with weight change (%) were observed. No genotypic associations were observed for variants across IL-2, IL-6 or BDNF with weight change (%) (refer to Table 4.3).

Finding #1: A significant genotypic association was found for IL-1 β rs4849127 where carriers of the A-allele gained approximately 4% more weight than individuals homozygous for the G-allele (p=0.049, refer to Figure 4.11), according to a dominant model of inheritance. However, with around 92% of A-allele carriers having the heterozygous GA genotype, results may be driven by an over-dominance model. Under this model, IL-1 β rs4849127 explains approximately 8.5% of the variance in weight change (%). This finding did not remain significant after a gene-wide (p_{IL-1 β}=0.245) or hypothesis-wide (p_{corr}=0.784) correction.





Finding #2: A significant genotypic association was found for IL-1 β rs16944 where individuals with the heterozygous GA genotype gained more weight than individuals with either homozygous genotype (p=0.012, refer to Figure 4.12). Post-hoc comparisons confirmed that individuals with the GA genotype significantly differed from both the AA (p=0.006) and GG (p=0.037) genotype groups. Under this model, IL-1 β rs16944 explains approximately 18.1% of the variance in weight change (%). This finding did not remain significant after a gene-wide (p_{IL-1 β}=0.06) or hypothesis-wide (p_{corr}=0.192) correction.



FIGURE 4.12: Weight Change (%) Distribution for IL-1β rs16944 in Africans

<u>SNP</u>	Genotype	<u>∆Weight (%)</u> ª <u>All Drugs</u> <u>(n=50)</u>	<u>P</u> <u>Value</u> ^b	p _{corr} ^c	<u>∆Weight (%)</u> ^a <u>CLZ or OLZ</u> <u>(n=37)</u>	<u>P-Value</u> ^b	<u>p</u> _{corr} ^c	MAF ^d	<u>HWE</u> <u>P-Value</u> ^d
	AA	6.89 ± 1.6 (2)			6.89 ± 1.6 (2)				
IL-1β rs4849127	GA	10.16 ± 8.6 (23)	‡*0.049	0.784	11.79 ± 8.9 (18)	‡*0.027	0.432	0.27	0.458
	GG	6.22 ± 6.8 (23)		7.19 ± 7.5 (16)					
	CC	7.60 ± 6.4 (27)			8.07 ± 7.3 (20)				
IL-1β rs13032029	СТ	9.23 ± 9.3 (20)	ŧ0.415	1.00	11.22 ± 9.3 (16)	0.525	1.00	0.24	0.312
	TT	0.84 (1)							
	AA	4.73 ± 3.4 (15)			4.68 ± 3.9 (11)				
IL-1β rs16944	GA	11.88 ± 8.7 (23)	 *0.012	0.192	13.46 ± 8.7 (19)	 *0.008	0.128	0.47	0.741
	GG	5.13 ± 5.8 (12)			5.98 ± 6.4 (7)				
	AA	9.07 ± 7.4 (35)		1.00	10.49 ± 7.6 (28)		1.00	0.14	1.00
IL-1β rs3136558	GA	5.28 ± 8.6 (12)	ŧ0.409		5.89 ± 10.1 (8)	0.655			
	GG	9.83 (1)							
	AA	9.83 (1)							
IL-1β rs1143634	GA	8.18 ± 7.9 (17)	ŧ0.272	1.00	8.99 ± 8.1 (14)	0.252	1.00	0.19	0.885
	GG	8.05 ± 7.9 (30)			9.78 ± 8.5 (22)	1			
	CC	8.18 ± 7.4 (31)			9.26 ± 8.0 (23)				
IL-1β rs1143643	СТ	8.62 ± 8.9 (15)	ŧ0.917	1.00	10.09 ± 9.4 (12)	ŧ0.773	1.00	0.20	1.00
	TT	3.85 ± 4.3 (2)			6.86 (1)				

TABLE 4.3: Results from Association Analysis of SNPs with AIWG in Africans

	AA	8.08 ± 7.46 (39)			9.13 ± 8.1 (30)				
IL-2 rs2069762	CA	6.56 ± 9.5 (7)	ŧ0.784	1.00	9.35 ± 9.8 (5)	0.727	1.00	0.09	0.663
	CC	9.29 (1)							
	AA								
IL-2 rs2069778	GA	6.18 ± 2.9 (4)			6.86 (1)			0.04	1.00
	GG	8.31 ± 8.0 (44)			9.54 ± 8.4 (35)				
	CC								
IL-2 rs2069772	СТ	8.09 ± 6.1 (8)	0.664	1.00	10.24 ± 5.4 (6)	0.555	1.00	0.08	1.000
	TT	8.13 ± 8.2 (39)			9.34 ± 8.9 (29)				
	CC	13.29 ± 4.9 (2)			16.75 (1)				
IL-2 rs2069776	СТ	10.20 ± 10.2 (11)	∥ ‡0.341	1.00	13.09 ± 10.6 (8)	ŧ0.079	1.00	0.15	0.587
	TT	7.23 ± 6.8 (36)			8.18 ± 7.5 (26)				
	GG	8.22 ± 7.9 (46)			9.47 ± 8.3 (36)				
IL-6 rs2069827	GT	6.19 ± 4.4 (2)						0.02	1.00
	TT								
	CC	8.06 ± 7.7 (40)			9.17 ± 8.0 (32)				
IL-6 rs1800795	CG	8.78 ± 9.3 (7)	0.545	1.00	13.63 ± 13.5 (3)			0.08	1.00
	GG								
	AA	7.68 ± 7.9 (36)			8.91 ± 8.5 (27)				
IL-6 rs2069837	GA	8.89 ± 7.5 (9)	ŧ0.863	1.00	11.09 ± 8.2 (6)	ŧ0.847	1.00	0.14	0.465
	GG	6.89 ± 1.6 (2)			6.89 ± 1.6 (2)				

	GG	8.23 ± 7.5 (39)			9.52 ± 7.9 (30)				
IL-6 rs2066992	GT	6.93 ± 9.3 (8)	0.500	1.00	8.23 ± 11.6 (5)	0.956	1.00	0.08	1.00
	TT								
	CC	8.17 ± 7.3 (32)			9.33 ± 7.6 (26)				
IL-6 rs2069840	CG	6.90 ± 7.4 (13)	ŧ0.917	1.00	8.39 ± 9.1 (7)	ŧ0.925	1.00	0.19	0.452
	GG	13.17 ± 14.2 (3)			13.17 ± 14.2 (3)				
	CC	8.15 ± 7.7 (46)			9.57 ± 8.2 (34)				
IL-6 rs2069861	СТ	7.80 ± 12.7 (2)			7.80 ± 12.7 (2)			0.03	1.00
	TT								
	AA	9.52 ± 7.9 (15)			11.09 ± 8.0 (12)				
IL-6 rs10242595	GA	6.79 ± 5.6 (24)	10.717	1.00	8.05 ± 6.0 (16)	10.658	1.00	0.46	0.979
	GG	9.09 ± 10.6 (11)			9.68 ± 11.6 (9)				
	Val/Val	8.42 ± 8.1 (42)			9.81 ± 8.3 (34)				
BDNF Val66Met	Val/Met	4.78 ± 4.4 (4)	ŧ0.518	1.00	-0.61 (1)			0.06	0.300
	Met/Met	9.83 (1)							

Covariate information was missing for two participants. Where p-value not shown, analysis not performed due to <2 genotypic groups for comparison or <5 subjects in merged comparison group. ^aValues represent mean \pm standard deviation (number); ^bUncorrected p-values; ^cP-value after a hypothesis-wide correction; ^dValues calculated among all patients of African ancestry; [‡]P-value calculated under a dominant model of genetic inheritance; IValue calculated using Kruskal-Wallis; *Value significant at p<0.05 level; SNP = single nucleotide polymorphism, CLZ = clozapine, OLZ = olanzapine, MAF = minor allele frequency, HWE = Hardy-Weinberg equilibrium, IL-1 β = interleukin 1 beta, IL-2 = interleukin 2, IL-6 = interleukin 6, BDNF = brain-derived neurotrophic factor

4.2.3. Race-and Treatment-Stratified Analyses

Participants were administered AP treatment that primarily included clozapine (46.3%), haloperidol (8.0%), olanzapine (17.0%) or risperidone (16.5%) (refer to Table 3.1). Of these APs, the greatest weight change (%) from baseline was observed for clozapine (5.55 ± 6.3) and olanzapine (8.01 ± 8.1) compared with haloperidol (0.70 ± 7.0) or risperidone (3.87 ± 3.8). This is consistent with the literature which has identified olanzapine and clozapine as high-risk drugs for AIWG¹⁶. Thus, a sub-analysis restricted to individuals on clozapine or olanzapine was performed. To maintain sample homogeneity, race stratification was applied.

4.2.3.1. Sub-Analysis of Patients of European Ancestry on Clozapine or Olanzapine

In the sub-sample of patients of European ancestry on clozapine or olanzapine, only BDNF Val66Met was associated with weight change (%) from baseline. Results showed that Met allele carriers gained approximately 3% less weight than individuals homozygous for the Val allele (p=0.025, refer to Figure 4.13). Under this model, BDNF Val66Met explains about 7.2% of the variance in weight change (%). However, this finding did not remain significant after a hypothesis-wide correction ($p_{corr}=0.35$). No genotypic associations were observed for variants across IL-1 β , IL-2 or IL-6 with weight change (%) (refer to Table 4.2).



FIGURE 4.13: Weight Change (%) Distribution for BDNF Val66Met in Europeans on CLZ/OLZ

4.2.3.2. Sub-Analysis of Patients of African Ancestry on Clozapine or Olanzapine

In the sub-sample of patients of Africa ancestry on clozapine or olanzapine, two genotypic associations involving IL-1 β with weight change (%) were observed. No associations were observed for IL-2, IL-6 or BDNF with weight change (%) (refer to Table 4.3).

Finding #1: A significant genotypic association was found for IL-1 β rs4849127 where carriers of the A-allele gained approximately 4% more weight than individuals homozygous for the G-allele (p=0.027, refer to Figure 4.14), as assessed according to a dominant model of genetic inheritance. However, with approximately 90% of A-allele carriers having the heterozygous GA genotype, results may be driven by an over-dominance model. Under this model, IL-1 β rs4849127 explains around 14.3% of the variance in weight change (%). This finding did not remain significant after a gene-wide (p_{IL-1 β}=0.135) or hypothesis-wide (p_{corr}=0.432) correction.





Finding #2: A significant genotypic association was found for IL-1 β rs16944 where individuals with the heterozygous GA genotype gained more weight than individuals with either homozygous genotype (p=0.008, refer to Figure 4.15). Under this model, IL-1 β rs16944 explains approximately 26.8% of the variance in weight change (%). Post-hoc comparisons confirmed that individuals with the GA genotype significantly differed from the AA group (p=0.003) but, unlike in previous analyses, not the GG genotype group (p=0.069). In fact, the GG group did not differ from the AA group either (p=0.821). This may have resulted from the genetic model being underpowered due to low numbers in the GG group (n=7), as merging G allele carriers weakened the genotypic association (p=0.061). This finding remained significant after a gene-wide (p_{IL-16}=0.04) but not a hypothesis-wide (p_{corr}=0.128) correction.





4.3. Haplotype and Allelic Analyses

Three-marker haplotypes were tested for an association with weight change (%) from baseline in patients treated with clozapine or olanzapine. Analyses were performed separately for patients of European and African ancestry. Among all analyses performed, only one significant haplotype on the IL-1 β gene was identified in the subset of patients of African ancestry between the following variant sites: rs1143643, rs1143634, rs3136558 (p<0.001, refer to Table 4.4). The overall test of association remained significant after a gene-wide correction ($p_{IL-1\beta}$ =0.002). Posthoc comparisons revealed that the T-A-G haplotype was responsible for this association (χ^2 =6.06, p=0.014). However, an examination of the LD plot for this haplotype (refer to Figure 4.1) revealed that the rs1143643 and rs1143634 loci are not in high LD with each other (D'=0.37, LOD=0.04). LD information for the remaining pairwise combinations includes: rs1143643 and rs3136558 (D'=1, LOD=0.27), and rs1143634 and rs3136558 (D'=0.61, LOD=2.73). This indicates that this haplotypic combination has a low likelihood of existing in nature. No haplotypes were identified for IL-2 or IL-6 in this sub-sample (refer to Table 4.4). No haplotypes were identified across IL-1 β , IL-2 or IL-6 in patients of European ancestry on clozapine or olanzapine (refer to Appendix A).

Allelic investigations were performed for all SNPs under the same testing conditions. Among all analyses, an allelic association was observed for BDNF Val66Met in patients of European ancestry on clozapine or olanzapine, where the Met allele was associated with lower weight gain (%) from baseline as compared to the alternate Val allele (χ^2 =6.76, p=0.009). This result did not remain significant after a hypothesis-wide correction (p_{corr}=0.162). This finding is supported by results from Association Analysis I (refer to Section 4.2.3.1, Figure 4.13). BDNF Val66Met could not be tested in patients of African ancestry on clozapine or olanzapine due to less than five patients in the minor allele group. No allelic associations were observed for variants across IL-1 β , IL-2 or IL-6 in patients of European or African ancestry on clozapine or olanzapine or olanzapine or olanzapine (refer to Table 4.5).

Tost Morkors	<u>Overall</u>	Hanlatyna	Froquonev ^a	× ²	Haplotype
<u>1 est Markers</u>	P-Value ^b	<u>Haplotype</u>	<u>Frequency</u>	X	P-Value ^b
II -18 rs1143643		C-A-A	8 (12.1%)	2.72	0.099
$II = 1\beta rs 1143634$	*~0.001	C-G-A	44 (66.7%)	1.88	0.171
IL-10 m2126559	~~~~	T-A-G	4 (6.1%)	6.06	* 0.014
IL-1p 185150558		T-G-A	10 (15.2%)	3.76	0.053
II -18 rs1143634		A-A-G	7 (10.6%)	3.63	0.057
$II_{10} = 10^{-10} = 126558$	0.054	A-G-G	5 (7.6%)	3.29	0.070
IL-10 m16044	0.034	G-A-A	36 (54.6%)	0.64	0.424
IL-1p rs16944		G-A-G	18 (27.3%)	0.43	0.513
II_18_rs3136558		A-A-C	37 (54.4%)	0.43	0.512
$IL - 1\beta rs 16044$	0.672	A-G-C	11 (16.2%)	0.12	0.726
IL-10 m12022020	0.073	A-G-T	15 (22.1%)	1.57	0.210
IL-1p f815052029		G-G-C	5 (7.4%)	0.06	0.805
II = 1.8 rs 16044		A-C-A	22 (29.7%)	1.04	0.309
IL - 10 IS10944	0 101	A-C-G	19 (25.7%)	3.98	0.046
IL-10 is13032029	0.191	G-C-G	16 (21.6%)	< 0.01	0.978
IL-16 rs4849127		G-T-G	17 (23.0%)	0.88	0.347
IL-2 rs2069776	0.150	C-T-G	9 (13.2%)	3.68	0.055
IL-2 rs2069772	0.139	T-C-G	6 (8.8%)	0.04	0.848
IL-2 rs2069778		T-T-G	53 (77.9%)	2.89	0.089
IL-2 rs2069772		C-G-A	6 (8.8%)	0.10	0.748
IL-2 rs2069778	0.949	T-G-A	57 (83.8%)	0.08	0.784
IL-2 rs2069762		T-G-C	5 (7.4%)	< 0.01	0.969
IL-6 rs2069827		G-C-A	54 (84.4%)	0.08	0.780
IL-6 rs1800795 IL-6 rs2069837	0.781	G-C-G	10 (15.6%)	0.08	0.780

TABLE 4.4: Haplotype Analysis in Patients of African Ancestry on CLZ/OLZ

IL-6 rs1800795		C-A-G	49 (79.0%)	0.20	0.652
IL-6 rs2069837	0.611	C-A-T	4 (6.5%)	0.83	0.361
IL-6 rs2066992		C-G-G	9 (14.5%)	0.01	0.908
II -6 rs2069837		A-G-C	44 (62.9%)	0.02	0.881
II -6 rs2066992	0.672	A-G-G	13 (18.6%)	0.63	0.426
II -6 rs2069840	0.072	A-T-C	4 (5.7%)	0.93	0.335
		G-G-C	9 (12.9%)	< 0.01	0.967
IL-6 rs2066992		G-C-C	51 (75.0%)	0.50	0.480
IL-6 rs2069840	0.587	G-G-C	12 (17.7%)	1.07	0.302
IL-6 rs2069861		T-C-C	5 (7.4%)	0.11	0.737
IL-6 rs2069840		C-C-A	39 (57.4%)	0.18	0.670
IL-6 rs2069861	0.354	C-C-G	19 (27.9%)	1.56	0.212
IL-6 rs10242595		G-C-G	10 (14.7%)	0.97	0.325

^aValues refer to frequency among haplotype options for the specified test markers; ^bUncorrected p-values; *Value significant at p<0.05 level; IL-1 β = interleukin 1 beta, IL-2 = interleukin 2, IL-6 = interleukin 6

TABLE 4.5: Allelic Analysis in Patients of Euro	opean and African Ancestry on CLZ/OLZ
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		European Ancestry (n=74)			African Ancestry (n=37)			
<u>Test Marker</u>	Allele	<u>Frequency</u> ^a	χ^2	<u>P-</u> <u>Value</u> ^b	Frequency ^a	χ^2	<u>P-</u> <u>Value</u> ^b	
IL-1ß rs4849127	А	12 (8.1%)	1.40	0.237	22 (29.7%)	1.04	0.309	
	G	136 (91.9%)			52 (70.3%)			
IL-1β rs13032029	C	74 (51.4%)	0.45	0.502	57 (77.0%)	0.88	0.347	
IL-10 1313032027	Т	70 (48.6%)			17 (23.0%)			
IL-1β rs16944	A	45 (30.4%)	0.21	0.650	41 (55.4%)	0.67	0.413	
	G	103 (69.6%)			33 (44.6%)			
IL-1β rs3136558	A	113 (76.4%)	0.01	0.939	66 (89.2%)	1.74	0.187	
12 1p 133130330	G	35 (23.7%)			8 (10.8%)			
IL-1β rs1143634	A	35 (23.7%)	0.09	0.765	14 (18.9%)	0.05	0.817	
	G	113 (76.4%)			60 (81.1%)			

$II_{-1}\beta$ rs11/36/3	C	86 (58.9%)	0.01	0.907	60 (81.1%)	0.01	0.010
11-10131145045	Т	60 (41.1%)	0.01	0.907	14 (18.9%)	0.01	0.919
II -2 rs2069762	А	101 (68.2%)	0.98	0 323	67 (93.1%)	<0.01	0.950
12 2 132009 702	С	47 (31.8%)	0.70	0.525	5 (6.9%)	<0.01	0.750
IL-2.rs2069778	А	20 (13.9%)	0.20	0.654			
	G	124 (86.1%)	0.20	01001	72 (100%)		
IL-2.rs2069772	C	47 (32.2%)	0.68	0.411	6 (8.3%)	0.06	0 806
	Т	99 (67.8%)	0.00	0.111	66 (91.7%)	0.00	0.000
II -2 rs2069776	C	35 (24.3%)	0.12	0 733	10 (13.9%)	3 25	0.071
12 2 132003 7 70	Т	109 (75.7%)	0.12	0.755	62 (86.1%)	5.25	0.071
IL -6 rs2069827	G	134 (90.5%)	< 0.01	<0.01 0.953	74 (100%)		
12-0 132009027	Т	14 (9.5%)	(0.01				
II_6 rs1800795	C	81 (56.3%)	0.03	0.873	66 (100%)		
	G	63 (43.8%)	0.05	0.075			
IL-6 rs2069837	А	137 (92.6%)	1 12	0.291	62 (86.1%)	0.01	0 908
	G	11 (7.4%)	1.12		10 (13.9%)		0.900
IL-6 rs2066992	G	133 (93.7%)	0.01	0 941	67 (93.1%)	0.09	0 758
	Т	9 (6.3%)	0.01	01911	5 (6.9%)	0.07	0.750
IL-6 rs2069840	C	105 (71.0%)	0.07	0 790	61 (82.4%)	0 33	0 567
	G	43 (29.1%)	0.07	01770	13 (17.6%)	0.00	0.507
IL-6 rs2069861	C	129 (87.2%)	0.03	0.869	70 (100%)		
	Т	19 (12.8%)	0.05	0.009			
IL-6 rs10242595	А	45 (30.4%)	0.38	0 539	40 (54.1%)	0.26	0.608
	G	103 (69.6%)	0.20	0.007	34 (46.0%)	0.20	0.000
BDNF Val66Met	Met	24 (16.7%)	6.76	*0.009	1 (1.4%)		
	Val	120 (83.3%)	0.70	0.007	71 (98.6%)		_

Where p value is not shown, analysis could not be performed due to n<5 in minor allele group. ^aValues refer to frequency among allelic options for the specified test marker; ^bUncorrected p-values; *Value significant at p<0.05 level; IL-1 β = interleukin 1 beta, IL-2 = interleukin 2, IL-6 = interleukin 6, BDNF = brain-derived neurotrophic factor

4.4. Association Analysis II: Clinically Significant Weight Gain

SNPs were tested using Pearson χ^2 for an association with CSWG status, defined by a weight change (%) from baseline equal to or greater than 7%. No covariates were entered into the statistical model. Among the total sample, two genotypic associations were observed involving IL-1 β and IL-6 with CSWG status. No associations were observed for variants across IL-2 or BDNF (refer to Table 4.6)

Finding #1: For IL-1 β rs4849127, an association was observed between CSWG and carriers of the A-allele (OR=2.17, CI: 1.08 – 4.35, p=0.028), where the A-allele conferred risk for CSWG. This finding did not remain significant after a gene-wide (p_{IL-1 β}=0.112) or hypothesis-wide (p_{corr}=0.392) correction. However, with about 93% of A-allele carriers having the heterozygous GA genotype, results may be driven by an over-dominance model, as observed in Section 4.2.1.

Finding #2: For IL-6 rs1800795, an association was observed between CSWG and carriers of the G-allele (OR=0.53, CI: 0.28 - 0.98, p=0.042), where the G-allele was protective against CSWG. This finding did not remain significant after a gene-wide (p_{IL-6}=0.252) or hypothesis-wide (p_{corr}=0.588) correction.

No genotypic associations were observed for IL-1 β , IL-2, IL-6 or BDNF with CSWG among patients of European ancestry (refer to Appendix B), patients of African ancestry (refer to Appendix C), patients of European ancestry on clozapine or olanzapine (refer to Appendix D), or patients of African ancestry on clozapine or olanzapine (refer to Appendix E).

However, since heterozygosity at IL-1 β rs16944 has consistently shown an association with AIWG, the GA group was tested for an association with CSWG. An examination across genotypes revealed a significant association in the total sample ($\chi^2 = 9.47$, p=0.009, p_{IL-1 β}=0.036, p_{corr}=0.126) and in patients of African ancestry ($\chi^2 = 9.19$, p=0.010, p_{IL-1 β}=0.05, p_{corr}=0.16). Analyses could not be computed for patients of European ancestry or among Europeans or Africans on clozapine or olanzapine due to expected cell counts less than five.

<u>SNP</u>	<u>Genotype</u>	$\frac{CSWG}{(n=60)^a}$	$\frac{\text{Non-CSWG}}{(n=128)^{a}}$	<u>OR</u>	<u>95% CI</u>	<u>χ</u> ²	<u>P-Value</u> ^b	D corr ^c
II18_rs4849127	AA/GA	20 (33.3%)	24 (18.8%)	2 17	1 08 – 4 35	4 85	*0.029	0 302
1L-1013+0+9127	GG	40 (66.7%)	104 (81.2%)	2.17	1.00 4.55	4.05	0.020	0.372
II -18 rs13032029	TT/CT	37 (63.8%)	86 (67.2%)	0.86	0.45 - 1.65	0.21	0.650	1.00
12 1p 1815052027	CC	21 (36.2%)	42 (32.8%)	0.00	0.45 1.05	0.21	0.050	1.00
II -18 rs16944	AA/GA	38 (63.3%)	67 (52.8%)	1 55	0 82 – 2 91	1 85	0.174	1.00
IL-101310744	GG	22 (36.7%)	60 (47.2%)	1.55	0.02 2.71	1.05		
IL-1β rs3136558	GG/GA	21 (35.0%)	48 (37.8%)	0.89	0 47 – 1 68	0.14	0.712	1.00
	AA	39 (65.0%)	79 (62.2%)		0.47 1.00	0.14	0.712	
II -18 rs1143634	AA/GA	28 (46.7%)	46 (35.9%)	1.56	0.84 - 2.91	1 97	0.160	1.00
IL-10 1311+505+	GG	32 (53.3%)	82 (64.1%)			1.97		
II -1B rs1143643	TT/CT	31 (52.5%)	79 (62.2%)	0.67	0.36 1.26	1 56	0.212	1.00
1L-101311+30+3	CC	28 (47.5%)	48 (37.8%)	0.07	0.50 - 1.20	1.50		1.00
II2 rs2069762	CC/CA	23 (39.0%)	64 (50.0%)	0.64	0.34 - 1.20	1 97	0 160	1.00
11-2 132007702	AA	36 (61.0%)	64 (50.0%)	0.04	0.34 1.20	1.97	0.100	1.00
II2 rs2069778	AA/GA	11 (18.3%)	24 (19.2%)	0.95	0.43 - 2.08	0.02	0 888	1.00
11-2 132007770	GG	49 (81.7%)	101 (80.8%)	0.75	0.45 - 2.08	0.02	0.000	1.00
II -2 rs2069772	CC/CT	22 (37.9%)	52 (40.6%)	0.80	0 47 - 1 69	0.12	0.728	1.00
11-2 132007772	TT	36 (62.1%)	76 (59.4%)	0.09	0.47 - 1.09			1.00

TABLE 4.6: Genetic Predictors of Antipsychotic-Induced CSWG in the Total Sample

IL -2 rs2069776	CC/CT	24 (40.0%)	43 (34.4%)	1 27	0.67 - 2.40	0.55	0.458	1.00
	TT	36 (60.0%)	82 (65.6%)	1.27	0.07 2.10	0.00	0.100	1.00
IL-6 rs2069827	TT/GT	8 (13.3%)	22 (17.2%)	0.74	0.31 – 1.78	0.45	0.501	1.00
	GG	52 (86.7%)	106 (82.8%)	0.71	0.01 11/0	0.15	0.001	1.00
IL-6 rs1800795	GG/CG	25 (41.7%)	72 (57.6%)	0.53	0.28 - 0.98	4.13	*0.042	0.588
	CC	35 (58.3%)	53 (42.4%)	0.00	0.20 0.90		0.012	0.200
II -6 rs2069837	GG/GA	13 (22.0%)	20 (15.6%)	1 53	0.70 - 3.33	1.14	0.285	1.00
12 0 132009037	AA	46 (78.0%)	108 (84.4%)	1.55				1.00
П. 6 то 2066002	TT/GT	7 (11.9%)	17 (13.7%)	0.85	0.33 – 2.17	0.12	0 730	1.00
112 0 132000772	GG	52 (88.1%)	107 (86.3%)	0.05		0.12	0.750	1.00
II -6 rs2069840	GG/CG	26 (43.3%)	58 (45.7%)	0.91	0.49 - 1.69	0.09	0 764	1.00
12 0 132009040	CC	34 (56.7%)	69 (54.3%)	0.71		0.07	0.704	1.00
II -6 rs2069861	TT/CT	8 (13.6%)	23 (18.0%)	0.72	0.30 - 1.71	0.57	0.451	1.00
12 0 132009001	CC	51 (86.4%)	105 (82.0%)	0.72				1.00
II -6 rs10242595	AA/GA	38 (63.3%)	69 (54.3%)	1 45	0.77 - 2.73	1 35	0 245	1.00
112-01810242393	GG	22 (36.7%)	58 (45.7%)	1.45	0.77 - 2.75	1.55	0.245	1.00
BDNE Val66Met	Met/Met + Val/Met	10 (16.9%)	36 (28.6%)	0.51	0.23 - 1.12	2.91	0.088	1.00
	Val/Val	49 (83.1%)	90 (71.4%)	0.51	0.25 - 1.12			1.00

^aValues represent number (percent) or mean \pm standard deviation; ^bUncorrected p-values; ^cP-value after a hypothesis-wide correction; *Value significant at p<0.05 level; SNP = single nucleotide polymorphism; CSWG = clinically significant weight gain, \geq 7% weight change from baseline, OR = odds ratio, CI = confidence interval, IL-1 β = interleukin 1 beta, IL-2 = interleukin 2, IL-6 = interleukin 6, BDNF = brain-derived neurotrophic factor

4.5. Gene-Gene Interaction Analyses

Epistatic effects were modelled between variant sites across each of IL-1 β , IL-2, and IL-6 and the BDNF Val66Met locus for an association with weight change (%) from baseline. Analyses were restricted to patients treated with either clozapine or olanzapine, and performed separately for patients of European and African ancestry. Among these sub-samples, three interactions were observed involving IL-1 β and IL-6 with BDNF Val66Met.

Interaction #1: In patients of European ancestry, an interaction was observed between IL-1 β rs13032029 and BDNF Val66Met (β =-7.63, Wald=9.70, Permutation P=0.029, refer to Table 4.7). This finding did not remain significant after a gene-wide ($p_{IL-1\beta}$ =0.174) or hypothesis-wide (p_{corr} =0.493) correction. Carriers of the TT genotype at IL-1 β rs13032029 and the Val/Met genotype at BDNF Val66Met were identified as low risk (least weight gain) for AIWG compared to individuals with any other genotypic combination at these two loci. A re-analysis of the data using ANCOVA to compare patients with the combined TT + Val/Met genotype against all other patients confirmed this finding (TT + Val/Met vs. CC or CT + Val/Val or Met/Met; -2.44 ± 3.9 vs. 5.19 ± 5.4; p=0.004, refer to Table 4.9 and Figure 4.16).

Interaction #2: In patients of European ancestry, an interaction was observed between IL-6 rs2069837 and BDNF Val66Met (β =3.95, Wald=9.12, Permutation P=0.021, refer to Table 4.7). This finding did not remain significant after a gene-wide (p_{IL-6} =0.147) or hypothesis-wide (p_{corr} =0.357) correction. Carriers of the AA genotype at IL-6 rs2069837 and the Val/Val genotype at BDNF Val66Met were identified as high risk (greatest weight gain) for AIWG compared to individuals with any other genotypic combination at these two loci. A re-analysis of the data using ANCOVA to compare patients with the combined AA + Val/Val genotype against all other patients confirmed this finding (AA+ Val/Val vs. GG or GA + Val/Met or Met/Met; 6.60 ± 6.0 vs. 2.65 ± 4.7; p=0.006, refer to Table 4.9 and Figure 4.17).

Interaction #3: In patients of African ancestry, an interaction was observed between IL-1 β rs16944 and BDNF Val66Met (β =8.59, Wald=13.06, Permutation P=0.006, refer to Table 4.8). This finding remained significant after a gene-wide ($p_{IL-1\beta}$ =0.036) but not a hypothesis-wide (p_{corr} =0.102) correction. Carriers of the GA genotype at IL-1 β rs16944 and the Val/Val genotype at BDNF Val66Met were identified as high risk (greatest weight gain) for AIWG compared to individuals with any other genotypic combination at these two loci. A re-analysis of the data using ANCOVA to compare patients with the combined GA + Val/Val genotype against all other patients confirmed this finding (GA + Val/Val vs. GG or AA + Val/Met or Met/Met; 13.77 \pm 8.8vs. 5.01 \pm 5.0; p=0.002, refer to Table 4.9 and Figure 4.18).

CND	Construns ^a	Dick Croup ^b	Data	Wold	D Volue	Perm
<u>SINP</u>	Genotype	KISK Group	Deta	<u>vvalu</u>	<u>P-value</u>	<u>P-Value</u> ^c
IL-1β rs4849127	GG + Val/Met	Low	-3.40	4.49	*0.038	0.156
IL-1β rs13032029	TT + Val/Met	Low	-7.63	9.70	*0.003	*0.029
IL-1β rs16944	GA + Val/Val	High	3.90	7.94	*0.006	0.063
IL-1β rs3136558	AA + Val/Met	Low	-3.93	4.50	*0.038	0.310
IL-1β rs1143634	GG + Val/Met	Low	-3.93	4.50	*0.038	0.322
IL-2 rs2069762	CC + Val/Met	Low	-8.39	4.25	*0.043	0.273
IL-2 rs2069778	GG + Val/Val	High	2.80	4.13	*0.046	0.305
IL-2 rs2069772	TT + Val/Val	High	2.76	3.78	0.056	0.394
IL-6 rs2069827	GT + Val/Val	High	4.65	4.24	*0.043	0.28
IL-6 rs1800795	CG + Val/Val	High	3.06	4.75	*0.033	0.28
IL-6 rs2069837	AA + Val/Val	High	3.95	9.12	*0.004	*0.021
IL-6 rs2066992	GG + Val/Val	High	2.88	4.17	*0.045	0.193
IL-6 rs2069840	CG + Val/Val	High	2.87	3.88	0.053	0.316
IL-6 rs10242595	$\overline{GG + Val/Val}$	High	3.28	5.42	*0.023	0.175

TABLE 4.7: Gene-Gene Interaction against BDNF Val66Met in Europeans on CLZ/OLZ

All interactions were performed against BDNF Val66Met. An interaction model was not found between BDNF Val66Met and IL-1 β rs1143643, IL-2 rs2069776 or IL-6 rs2069861. ^aValues represent the respective interleukin + BDNF genotype; ^bHigh risk represents greatest change in weight (%) from baseline, and low risk represents least change in weight (%) from baseline; ^cUncorrected p-values based on 1000 permutations; *Value significant at p<0.05 level; SNP = single nucleotide polymorphism; IL-1 β = interleukin 1 beta, IL-2 = interleukin 2, IL-6 = interleukin 6, BDNF = brain-derived neurotrophic factor

<u>SNP</u>	<u>Genotype</u> ^a	<u>Risk Group</u> ^b	<u>Beta</u>	<u>Wald</u>	<u>P-Value</u>	<u>Perm</u> <u>P-Value</u> ^c
IL-1β rs4849127	AG+ Val/Val	High	4.62	2.97	0.094	0.274
IL-1β rs16944	GA+ Val/Val	High	8.59	13.06	*0.00097	*0.006

TABLE 4.8: Gene-Gene Interaction against BDNF Val66Met in Africans on CLZ/OLZ

All interactions were performed against BDNF Val66Met. An interaction model was not found between BDNF Val66Met and all remaining SNPs. ^aValues represent the respective interleukin + BDNF genotype; ^bHigh risk represents greatest change in weight (%) from baseline, and low risk represents least change in weight (%) from baseline; ^cUncorrected p-values based on 1000 permutations; *Value significant at p<0.05 level; SNP = single nucleotide polymorphism, IL-1 β = interleukin 1 beta, IL-2 = interleukin 2, IL-6 = interleukin 6, BDNF = brain-derived neurotrophic factor

TABLE 4.9: ANCOVA Analysis of Gene-Gene Interaction Effects against BDNF Val66Met inPatients of European and African Ancestry on CLZ/OLZ

Gene	<u>Gene</u> <u>Genotype</u> ^a		<u>Frequency</u> ^b	$\Delta Weight$	<u>P-</u>
				<u>(%)</u> °	Value
	GG or AA +		17 (48.6%)	5.01 ± 5.0	
IL-1β rs16944	Val/Met or Met/Met	African	17 (48.0%)	5.01 ± 5.0	 *0.002
	GA + Val/Val		18 (51.4%)	13.77 ± 8.8	
	CC or CT +		65 (02 0%)	5.19 + 5.4	
IL-1β rs13032029	Val/Val or Met/Met	European	05 (72.770)	5.17 ± 5.4	*0.004
	TT + Val/Met		5 (7.1%)	-2.44 ± 3.9	
IL-6 rs2069837	GG or GA +		31 (43 1%)	2.65 ± 4.7	
	Val/Met or Met/Met	European	51 (+5.170)	2.03 - 4.7	*0.006
	AA + Val/Val		41 (56.9%)	6.60 ± 6.0	

All interactions were performed against BDNF Val66Met. Only subjects with genotypic information for both loci were included in the analysis. Covariates included duration of antipsychotic treatment and baseline weight. Covariate information was missing for 1 person; ^aValues represent the respective interleukin + BDNF genotype; ^bValues represent number (percent) or mean \pm standard deviation; IValue calculated using Kruskal-Wallis; *Value significant at p<0.05 level; IL-1 β = interleukin 1 beta, IL-6 = interleukin 6, BDNF = brain-derived neurotrophic factor

FIGURE 4.16: Weight Change (%) Distribution within an Interaction Model for IL-1 β rs13032029 and BDNF Val66Met in Europeans on CLZ/OLZ



FIGURE 4.17: Weight Change (%) Distribution within an Interaction Model for IL-6 rs2069837 and BDNF Val66Met in Europeans on CLZ/OLZ



FIGURE 4.18: Weight Change (%) Distribution within an Interaction Model for IL-1 β rs16944 and BDNF Val66Met in Africans on CLZ/OLZ



Chapter 5:

CATIE Replication

The purpose of this chapter is to:

- Provide an overview of the CATIE sample
- Describe SNP selection and data extraction
- Describe statistical analyses

5.1. Replication Design

To validate findings from Chapter 4, a replication analysis was performed using genetic information extracted from the Clinical Antipsychotic Trials of Intervention Effectiveness (CATIE) sample (described in Section 5.2). AIWG parameters differed from our discovery sample, as information was collected for change in BMI over the course of AP treatment, as a percentage (%) of baseline BMI (herein referred to as *BMI change (%) from baseline*). Despite these methodological differences, the CATIE sample was chosen to evaluate our findings further and because this was the only available replication sample. CATIE participants had the following clinical information collected: age, sex, ethnicity, baseline PANSS, and type of AP medication received including dose and duration of treatment. The effect of genetic variance on AIWG was determined by comparing BMI change (%) from baseline across genotypic groups for each SNP of interest. Study parameters are described in further detail in the below-listed sections.

5.2. CATIE Sample

CATIE was a double-blind clinical trial designed to determine the efficacy of AP treatment. Patients were randomly assigned to one of four SGAs which included olanzapine (7.5

to 30 mg/day), quetiapine (200 to 800 mg/day), ziprasidone (40 to 160 mg/day) or risperidone (1.5 to 6.0 mg/day) or the FGA perphenazine (8 to 32 mg per day), for up to 18 months. Medication dosing was flexible and based on clinical response.

A total of 1,493 patients were recruited between 2001 and 2004 across 57 U.S. sites. Patients were between 18 to 65 years of age with a DSM-IV diagnosis of chronic schizophrenia. Participants were excluded from the study if any of the following criteria were endorsed:

- Diagnosis of schizoaffective disorder
- Mental retardation or other cognitive disorder
- Prior adverse reactions or treatment resistance to the study medications
- Only one past episode of schizophrenic illness

All participants provided written informed consent. The study was approved by all participating institutional ethics review boards. For further details, see Lieberman *et al.* $(2005)^{468}$. For the purpose of this study, analyses were performed on a refined subset of the CATIE sample (n=318). Refinement criteria included the following restrictions:

- No prior exposure to high risk medications for AIWG (e.g. olanzapine or clozapine) lasting longer than 30 days
- No marked obesity (BMI \geq 40) at baseline
- No exposure to low risk medications for AIWG (e.g. ziprasidone or perphenazine) during the CATIE trial
- CATIE treatment duration between 14 to 190 days
- No familial relatedness to other CATIE participants
- Only patients of self-reported European or African ancestry^j
- Heterozygosity of less than four standard deviations from the mean^k

Demographic and clinical characteristics for this sub-sample are presented in Table 5.1.

^jAncestry was further confirmed using genetic markers

^kHeterozygosity refers to the frequency of heterozygotes for a specified locus. If the level of heterozygosity is higher than would be expected under HWE, this may indicate sample contamination or genotyping error.

5.3. Statistical Covariates of AIWG

Among the total sample, confounding associations were observed between BMI change (%) and baseline BMI (p=0.001) but not participant age (p=0.138), gender (p=0.843), medication dose (p=0.375), duration of treatment (p=0.325) or baseline PANSS score (p=0.147). In the subset of patients of European ancestry treated with olanzapine, no associations were found between any of the aforementioned variables (p>0.05). In the subset of patients of African ancestry treated with olanzapine, an association was observed between BMI change (%) and baseline PANSS score (p=0.047), while all other associations were non-significant (p>0.1). Since baseline BMI and baseline PANSS score influenced the amount of weight gained with AP treatment, they were entered as statistical covariates.

<u>Characteristics</u>	<u>Total Sample</u> <u>(n=318)</u>	<u>Characteristics</u>	<u>Total Sample</u> <u>(n=318)</u>
Sex		Duration (days)	132.84 ± 53.4
Female	76 (23.9%)	Ethnicity	
Male	242 (76.1%)	European	207 (65.1%)
Age (years)	41.07 ± 11.1	African	111 (34.9%)
Baseline BMI	28.58 ± 5.4	Study Medications	
BMI Change	0.72 ± 2.0	Olanzapine	109 (34.3%);
			$25.94\pm49.4~mg/day$
BMI Change (%)	2.78 + 7.5	Quetiapine	108 (34.0%);
		2	557.09 ± 171.5 mg/day
Baseline PANSS	75 29 + 17 2	Risperidone	101 (31.8%);
	15.29 ± 11.2	Risperidone	3.95 ± 1.2 mg/day

TABLE 5.1 : Demographic	and Clini	cal Sample	Characteristics
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Values represent number (percent) or mean \pm standard deviation

5.4. SNP Extraction

Genetic information was extracted from CATIE using Plink⁴⁶⁹ version 1.07. Where genetic information was available, original study SNPs were directly investigated using CATIE data. Since genetic data were not available for all original SNPs, high LD proxies were identified 50kbp upstream and 50kbp downstream of each gene region of interest. Variants within the extended gene regions of IL-1 β , IL-2 and IL-6 were assessed for pairwise LD with original study SNPs (r² \ge 0.7) using the SNP Annotation and Proxy Search (SNAP)⁴⁷⁰ version 2.2. Final SNPs selected for replication are listed in Table 5.2. The SNP genotyping rate for the replication panel was >96%, and the subject genotyping rate was >83%.

5.5. Hardy-Weinberg Equilibrium and Minor Allele Frequencies

Of the 12 SNPs analyzed in this study, all maintained HWE (p>0.05) except IL-6 rs1800795 (p=0.040, African sub-sample) which was, therefore, excluded from further analyses. All remaining SNPs had a MAF equal to or greater than 5% in patients of European ancestry. In patients of African ancestry, BDNF Val66Met had a MAF less than 5% but was still analyzed to maintain procedural consistency between ethnic subgroups.

5.6. Statistical Analyses for Replication

BMI change (%) from baseline was compared across genotypic groups according to the testing parameters described in Section 3.5.1. For ANCOVA analyses, baseline BMI and baseline PANSS score were entered as statistical covariates. Gene-gene interaction analyses followed the procedures outlined in Section 3.5.4. Treatment-stratified analyses included only olanzapine cases, as clozapine treatment data were not available from CATIE. Since analyses were performed to replicate findings from Chapter 4, only data pertaining to SNPs (or their high LD proxies) that were significant in our discovery sample (herein referred to as *primary replication SNPs*) are shown. Replication p-values were not corrected for multiple comparisons.

TABLE 5.2: CATIE Replication SNPs

Original SNP	In CATIE (Y/N)	Highest LD Proxy*	Origin
IL-1β rs4849127	Ν	IL-1β rs17042517	IL-2 rs206
IL-1β rs13032029	N	IL-1β rs4447608	IL-6 rs206
IL-1β rs16944	N	IL-1β rs2723152	IL-6 rs180
IL-1β rs3136558	N	IL-1β rs11674397	IL-6 rs200
IL-1β rs1143634	Y	IL-1β rs1143634	IL-6 rs200
IL-1β rs1143643	N		IL-6 rs206
IL-2 rs2069762	N	IL-2 rs11724582	IL-6 rs200
IL-2 rs2069778	N		IL-6 rs102
IL-2 rs2069772	N	IL-2 rs17388568	BDNF Va
IL-2 rs2069779	N		1

Original SNP	<u>In CATIE</u> (Y/N)	Highest LD Proxy*
IL-2 rs2069776	Ν	IL-2 rs1479923
IL-6 rs2069827	Ν	
IL-6 rs1800795	Y	IL-6 rs1800795
IL-6 rs2069837	Y	IL-6 rs2069837
IL-6 rs2066992	Y	IL-6 rs2066992
IL-6 rs2069840	Ν	
IL-6 rs2069861	Ν	
IL-6 rs10242595	N	
BDNF Val66Met	Y	BDNF Val66Met

Bold font represents primary replication SNPs. Where an original SNP is analyzed in CATIE, its highest LD proxy is itself; Where a high LD proxy is not listed, $r^2<0.6$; *Highest LD proxies were included in replication analyses; CATIE = Clinical Antipsychotic Trials of Intervention Effectiveness, SNP = single nucleotide polymorphism, LD = linkage disequilibrium, IL-1 β = interleukin 1 beta, IL-2 = interleukin 2; IL-6 = interleukin 6; BDNF = brain-derived neurotrophic factor

5.7. Results from Association Analyses

5.7.1. Total Sample Analyses

In the total sample, none of the primary replication SNPs were associated with AIWG in the CATIE sample (refer to Table 5.3). Additional exploratory analyses across all remaining SNPs identified a significant association involving IL-2 rs11724582 where individuals with the heterozygous GA genotype had the greatest BMI change compared with individuals with either homozygous genotype (GA: 4.13 ± 7.9 , AA: 1.90 ± 6.8 , GG: 1.96 ± 9.4 , p=0.048). Under this model, IL-2 rs11724582 explains around 2.0% of the variance in BMI change (%) from baseline. Post-hoc comparisons revealed that the GA group only statistically differed from the AA (p=0.016) but not the GG (p=0.187) group. A re-analysis of the data was performed with Gallele carriers merged. Results showed that carriers of the G-allele experienced an AP-induced BMI change that was approximately 2% greater than individuals homozygous for the A-allele (GA + GG vs. AA; 3.70 ± 8.2 vs. 1.90 ± 6.8 , p=0.037). Under this new model, IL-2 rs11724582 explains around 1.4% of the variance in BMI change (%) from baseline.

5.7.2. Race-Stratified Analyses

In race-stratified sub-samples which separately included patients of European and African ancestry, none of the primary replication SNPs were associated with AIWG in the CATIE sample (refer to Table 5.4 and Table 5.5). Additional exploratory analyses across all remaining SNPs identified a significant association involving IL-2 rs11724582 in patients of African ancestry. Results showed that carriers of the G-allele experienced an AP-induced BMI increase that was approximately 4% greater than individuals homozygous for the A-allele (GA + GG vs. AA; 5.76 ± 8.3 vs. 2.08 ± 7.4 , p=0.018). Under this model, IL-2 rs11724582 explains approximately 5.2% of the variance in BMI change (%) from baseline.

In olanzapine-restricted, race-stratified sub-samples which separately included patients of European and African ancestry, none of the primary replication SNPs were associated with AIWG in the CATIE sample (refer to Table 5.4 and Table 5.5). Additional exploratory analyses across all remaining SNPs identified a significant association involving IL-1 β rs11674397 in the African sub-sample. Results showed that individuals with the heterozygous CT genotype experienced an AP-induced BMI increase that was approximately 6% greater than individuals homozygous for the C-allele (CT vs. CC; 10.65 ± 8.7 vs. 5.05 ± 8.0, p=0.025). Under this model, IL-1 β rs11674397 explains around 12.6% of the variance in BMI change (%) from baseline.

<u>SNP</u>	<u>Genotype</u>	Frequency ^a	<u>ΔBMI (%)</u> ^a	F Value	P-Value ^b
	AA	278 (87.7%)	2.87 ± 7.7		
IL-1β rs17042517	GA	38 (12.0%)	1.95 ± 6.1	0.26	ŧ0.610
	GG	1 (0.3%)	8.39		
	CC	172 (54.3%)	3.09 ± 7.7		
IL-1β rs2723152	СТ	118 (37.2%)	2.71 ± 7.0	0.55	0.576
	TT	27 (8.5%)	1.11 ± 8.3		
	GG	205 (65.3%)	2.68 ± 7.2		
IL-1β rs1143634	GA	91 (29.0%)	3.13 ± 8.4	0.20	0.822
	AA	18 (5.7%)	2.81 ± 6.5		
	Val/Val	243 (76.9%)	2.93 ± 7.5		
BDNF Val66Met	Val/Met	63 (19.9%)	2.64 ± 7.5	0.16	0.851
	Met/Met	10 (3.2%)	0.63 ± 7.9		

TABLE 5.3: Results from Replication Analysis of SNPs with AIWG in the Total Sample

Covariate was information missing for one participant; ^aValues represent mean \pm standard deviation (number); ^bUncorrected p-values; [‡]P-value calculated under a dominant model of genetic inheritance; SNP = single nucleotide polymorphism, BMI = body-mass index, IL-1 β = interleukin 1 beta, BDNF = brain-derived neurotrophic factor
SNP	<u>Genotype</u>	<u>∆BMI (%)</u> ^a <u>All Drugs</u> <u>(n=207)</u>	<u>P-Value</u> ^b	<u>∆BMI (%)</u> ^a <u>OLZ</u> <u>(n=67)</u>	<u>P-Value</u> ^b	MAF ^c	<u>HWE</u> <u>P-Value</u> ^c
IL-1β rs17042517	AA	2.65 ± 7.5 (181)		5.49 ± 7.3(56)			
	GA	1.83 ± 6.1 (25)	0.702	$1.22 \pm 6.1(10)$	0.092	0.06	0.925
	GG						
IL-1β rs2723152	CC	2.56 ± 7.1 (124)		4.66 ± 7.4 (42)			
	СТ	2.84 ± 7.2 (73)	0.542	5.92 ± 6.8 (21)	+0.611	0.22	0.813
	TT	0.11 ± 11.0 (9)		-0.14 ± 8.8 (3)			
IL-1β rs1143634	GG	2.41 ± 6.7 (126)	0.806	4.32 ± 6.9 (38)	0.624	0.23	0.636
	GA	2.68 ± 8.6 (68)		6.06 ± 8.3 (23)			
	AA	3.29 ± 5.6 (12)		3.2 ± 4.5(5)			
BDNF Val66Met	Val/Val	2.74 ± 7.3 (135)		4.59 \$ 6.6 (48)			
	Val/Met	2.54 ± 7.4 (60)	0.908	6.30 ‡ 8.6 (17)	ŧ0.732	0.20	0.466
	Met/Met	0.63 ± 7.9 (10)		-7.65 (1)			

TABLE 5.4: Results from Replication Analysis of SNPs with AIWG in Europeans

Covariate information was missing for one participant; ^aValues represent mean \pm standard deviation (number); ^bUncorrected p-values; ^cValues calculated among all patients of European ancestry; [‡]P-value calculated under a dominant model of genetic inheritance; SNP = single nucleotide polymorphism, BMI = body-mass index, OLZ = olanzapine, MAF = minor allele frequency, HWE = Hardy-Weinberg equilibrium, IL-1 β = interleukin 1 beta, BDNF = brain-derived neurotrophic factor

<u>SNP</u>	<u>Genotype</u>	<u>∆BMI (%)</u> ^a <u>All Drugs</u> <u>(n=111)</u>	<u>P Value</u> ^b	<u>ΔBMI (%)</u> ^a <u>OLZ</u> <u>(n=42)</u>	<u>P -Value</u> ^b	<u>MAF</u> ^c	<u>HWE</u> <u>P-Value</u> ^c
IL-1β rs17042517	AA	3.29 ± 8.0 (97)		6.42 ± 8.6 (36)			
	GA	2.18 ± 6.3 (13)	ŧ0.827	2.41 ± 4.7 (6)	0.428	0.07	0.795
	GG	8.39 (1)					
IL-1β rs2723152	CC	4.48 ± 9.0 (48)		6.52 ± 10.2 (22)			
	СТ	2.49 ± 6.6 (45)	0.313	4.76 ± 6.2 (15)	0.926	0.37	0.244
	TT	1.61 ± 7.0 (18)		6.20 ± 2.9 (5)			
IL-1β rs1143634	GG	3.11 ± 7.9 (79)		5.62 ± 8.6 (32)			
	GA	4.46 ± 7.8 (23)	0.661	6.88 ±z7.9 (9)	ŧ0.167	0.16	0.063
	AA	1.85 ± 8.6 (6)		3.85 (1)			
BDNF Val66Met	Val/Val	3.17 ± 7.8 (108)		5.63 ± 8.3 (40)			
	Val/Met	4.69 ± 11.0 (3)		10.24 ± 7.7 (2)		0.014	1.000
	Met/Met						

TABLE 5.5: Results from Replication Analysis of SNPs with AIWG in Africans

Where p-value not shown, analysis not performed due to <5 subjects in merged comparison group; ^aValues represent mean \pm standard deviation (number); ^bUncorrected p-values; ^cValues calculated among all patients of African ancestry; [‡]P-value calculated under a dominant model of genetic inheritance; SNP = single nucleotide polymorphism, BMI = body-mass index, OLZ = olanzapine, MAF = minor allele frequency, HWE = Hardy-Weinberg equilibrium, IL-1 β = interleukin 1 beta, BDNF = brain-derived neurotrophic factor

5.8. Results from Gene-Gene Interaction Analyses

Epistatic effects were modelled between variant sites across each of IL-1 β , IL-2, and IL-6 and the BDNF Val66Met locus for an association with BMI change (%) from baseline. Analyses were restricted to patients treated with olanzapine, and performed separately for patients of European and African ancestry. In the European sub-sample, none of the primary replication SNPs were found to significantly interact with BDNF Val66Met to predict BMI change (%) from baseline (refer to Table 5.6). No interactions models were found in the African sub-sample. Additional exploratory analyses across all remaining SNPs did not yield any significant findings.

TABLE 5.6: Gene-Gene Interaction against BDNF Val66Met in Europeans on OLZ

<u>SNP</u>	<u>Genotype</u> ^a	<u>Risk Group</u> ^b	<u>Beta</u>	<u>Wald</u>	<u>P-Value</u>	<u>Perm</u> <u>P-Value</u> ^c
IL-1β rs17042517	GA + Met/Met	Low	-12.63	3.10	0.083	0.325
IL-1β rs2723152	CC + Met/Met	Low	-12.63	3.10	0.083	0.391
IL-1β rs1143634	GA + Met/Met	Low	-12.63	3.10	0.083	0.463

All interactions were performed against BDNF Val66Met. ^aValues represent the respective interleukin + BDNF genotype; ^bHigh risk represents greatest change in BMI (%) from baseline, and low risk represents least change in BMI (%) from baseline; ^cUncorrected p-values based on 1000 permutations; SNP = single nucleotide polymorphism, OLZ = olanzapine, $IL-1\beta = interleukin 1$ beta, BDNF = brain-derived neurotrophic factor

Chapter 6:

Discussion

The purpose of this chapter is to:

- Review main study findings and their relation to study hypotheses
- ✤ Discuss how findings integrate into the current literature
- Review study strengths and limitations
- Discuss clinical implications of study findings
- Propose areas for future research

6.1. Main Study Findings

In this sample of chronic schizophrenia patients on AP medication, the authors set out to address four primary study aims pertaining to the pharmacogenetic testing of IL-1 β , IL-2, IL-6, and BDNF variants in AIWG. The data revealed the following main findings:

IL-1ß variants and BDNF Val66Met are associated with AIWG

In the present study, IL-1 β SNPs rs16944 and rs1143634 were significantly involved in mediating the effects of FGA and SGA treatment on weight gain in patients of European ancestry, with the latter SNP remaining significant after correcting for multiple comparisons. Similarly, IL-1 β SNPs rs16944 and rs4849127 were associated with AIWG in patients of African ancestry, and remained significant in the African subset treated with olanzapine or clozapine; however, these findings did not remain significant after correction. IL-1 β is a critically important inflammatory cytokine that is the proposed 'gatekeeper' of inflammation,

having numerous and diverse roles in regulating injury and infection⁴⁷¹. Genetic variation at the rs16944 (G/A) locus has been implicated in several diseases that have an inflammatory component including, but not limited to, gastric cancer⁴⁷², type II diabetes mellitus⁴⁷³, osteoarthritis⁴⁷⁴, cervical cancer⁴⁷⁵, and gastroesphageal reflux disease⁴⁷⁶. Genetic association studies have also provided evidence on the involvement of rs16944 in schizophrenia, with reports that implicate the A-allele in illness endophenotypes like elevated brain activation and brain volume reductions^{276,277}, and the G-allele in overall disease risk^{477,478}. Similarly, the rs16944 variant has been associated with non-remission and impaired emotion processing in MDD, which is another psychiatric condition characterized by aberrant inflammatory signatures⁴⁷⁹.

According to functional investigations, rs16944 is a promoter polymorphism involved in the regulation of gene expression, where the A-allele is responsible for high transcriptional activity relative to the G-allele⁴⁸⁰. In this study, genotype effects were observed for rs16944 where GA heterozygotes gained the most weight relative to individuals with either homozygous genotype. The genetic involvement of IL-1 β in AIWG is supported by its biological role in regulating food intake^{333,374}. Other studies have also identified a relationship between heterozygosity at rs16944 and disease phenotypes. For example, Tanaka *et al.* (2014)⁴⁸¹ found that individuals with the GA genotype had a significantly reduced risk of periodontal disease compared with a GG genotype reference group. Similarly, Zheng *et al.* (2013)⁴⁸² found that individuals with the GA genotype had a significantly decreased risk of esophageal squamous cell carcinoma relative to GG homozygous subjects. Based on these findings, we hypothesize that heterozygosity at rs16944 may lead to reduced expression of the IL-1 β gene relative to either homozygous genotype. Reduced expression would consequently lower the risk of inflammatory conditions, and increase metabolic disturbances via impaired adiposity signalling.

According to HaploReg⁴⁵⁴, rs16944 is in high LD ($r^2 = 0.98$) with a second variant, rs6735739 (T>C), that is approximately 15kbp upstream. The rs6735739 polymorphism serves as a binding site for a hypothalamic transcription factor known as Brain-Specific Homeobox Factor (BSX) which regulates expression of NPY and AgRP⁴⁸³. Studies of the adult mouse brain have shown that BSX expression is localized to the hypothalamus, with greatest expression in the ARC and DMH, and some expression in the LHA. Additional evidence indicates that

NPY/AgRP neurons in the ARC express BSX, while POMC neurons do not⁴⁸³. BSX mRNA expression is up-regulated in the ARC subsequent to acute ghrelin administration and in response to fasting, while re-feeding decreases expression^{484,485}. Overall, various lines of evidence suggest that BSX is involved in hypothalamic control of hyperphagia and locomotor activity⁴⁸³.

BDNF Val66Met (rs6265) was also significantly involved in mediating AP effects on weight gain in this study, both among patients of European ancestry, and the European subset treated with either clozapine or olanzapine; however, findings did not remain significant after correcting for multiple comparisons. Results showed that carriers of the Met (or T) allele (Met/Met + Met/Val) were protected against excessive AIWG. These findings are consistent with the general obesity literature which has reported on the association between the Met/Met genotype and a lower BMI relative to Val allele carriers^{35,434-436}. Investigations of Val66Met and AIWG within the pharmacogenetic literature have yielded mixed findings. In concordance with our results, Lane *et al.* (2006)⁷⁴ showed that the Met/Met genotype was associated with lower body weight than the Val allele in acutely exacerbated schizophrenia patients treated with risperidone. However, Zhang et al. (2008)⁴⁴⁶ showed that the Met/Met genotype was associated with a significantly higher BMI relative to Val allele carriers in schizophrenia patients on longterm AP treatment. Other studies have found no relationship between Val66Met and AIWG in schizophrenia^{445,447}. The discrepant susceptibility allele between our study and Zhang *et al.* (2008)⁴⁴⁶ may suggest that the risk of AIWG conferred by Val66Met may differ between ethnic groups, as their study sample was exclusively comprised of Chinese patients, while our findings were relevant to patients of European ancestry. Additional support for our findings is derived from reports of the Val/Val genotype being associated with clinical response to APs⁴⁴⁷ which, as mentioned in Section 1.3.2, is a risk factor for AIWG. There are also reports of 66Met being associated with eating disorders such as restricting anorexia nervosa⁴⁸⁶.

IL-1β and IL-6 variants are associated with CSWG

In our secondary analysis, IL-1 β rs4849127 and IL-6 rs1800795 SNPs were associated with CSWG in the total sample. In particular, IL-1 β rs4849127*A conferred risk for CSWG, whereas IL-6 rs1800795*G was protective against CSWG. Genotypic analysis of IL-1 β rs16944

revealed a significant association between heterozygosity at this locus and risk of CSWG in both the total sample and patients of African ancestry treated with clozapine or olanzapine. These results strengthen the roles of rs4849127 and rs16944 in mediating the genetic risk of AIWG by IL-1 β . Significant SNPs from our previous investigations (IL-1 β rs1143634 and BDNF Val66Met) may not have been associated with CSWG due to reduced analytic power through dichotomization of the weight change (%) variable.

IL-1 β and IL-6 variants interact with BDNF Val66Met among patients treated with clozapine and olanzapine

IL-1 β rs13032029 and IL-6 rs2069837 SNPs demonstrated a genetic interaction with BDNF Val66Met in patients of European ancestry. In particular, individuals with the TT genotype at IL-1 β rs13032029 and the CT genotype at Val66Met were at low risk for AIWG, whereas carriers of the AA genotype at IL-6 rs2069837 and the CC genotype at Val66Met were at high risk for AIWG. Since these SNPs did not show any significant association with AIWG when analyzed individually, these results suggest that their genetic effects may be mediated through BDNF-dependent pathways. Epistatic effects were also observed among patients of African ancestry between IL-1 β rs16944 and Val66Met. Within this interaction, individuals with the GA genotype at IL-1 β rs16944 and the Val/Val genotype at Val66Met were identified as high risk for AIWG. The observed genetic interactions between cytokine SNPs and BDNF further support their biological interaction within neuroimmune crosstalk¹⁷⁷⁻¹⁷⁹.

The association of IL-1 β variants and BDNF Val66Met did not replicate in the CATIE sample

None of the primary replication SNPs, which included IL-1 β rs17042517, rs2723152, and rs1143634 and BDNF Val66Met, had their association with AIWG replicated using the CATIE data across total or subscale analyses. This may have been the result of methodological differences between CATIE and our own study design that may have ultimately led to a loss of power. *AP Treatment*. Our discovery sample included clozapine as a treatment of interest, while

the CATIE study opted for the non-inclusion of clozapine treatment. This may be a major contributor to the observed difference in study results considering that different APs have variable weight-inducing propensities, with clozapine being a high-risk medication^{16,17}. Our discovery sample primarily consisted of individuals who had no prior exposure to SGAs. However, SGA-naivety was not an inclusionary criterion for CATIE. At best, the data extracted from CATIE could only be restricted to subjects that had no prior exposure to olanzapine or clozapine that lasted longer than 30 days. In considering that SGAs have considerable weight inducing propensities^{16,17}, any weight gained outside of the study had the potential to limit within-study weight change, according to the inverse relationship between baseline BMI and AIWG^{61,70,71}. Study subjects. Our discovery sample allowed for the inclusion of patients with both chronic schizophrenia and schizoaffective disorder whereas CATIE excluded patients with the latter diagnosis. This diagnostic difference could have affected study outcomes as the magnitude of AIWG can differ between schizophrenic subtypes⁷³⁻⁷⁵. In the same regard, the inclusion of clozapine-treated, and thus, treatment-refractory patients within the discovery sample may have further influenced results. Weight analysis. Although the consequences of this methodological difference may be minor, our discovery sample used weight change (%) from baseline as a measure of AIWG, while CATIE used BMI (%) change.

6.2. Strengths and Limitations

To the author's knowledge, this is the first study to demonstrate an association between the IL-1 β polymorphisms rs4849127, rs16944, and rs1143634 and increased risk of AIWG. This is also believed to be the first study that has demonstrated epistatic effects between both IL-1 β and IL-6 polymorphisms and BDNF Val66Met in mediating AIWG. Investigating interactive effects is highly important in considering that AIWG is a complex, polygenic trait. Our genetic methodology has greater accuracy in assessing cytokine involvement in AIWG since the DNA sequence is not perturbed by the numerous confounds that readily alter cytokine expression in the periphery (refer to Section 1.6.2). Our main AP analyses were also advantageously conducted in a sample of schizophrenic patients that were predominantly SGA, and even clozapine, naive prior to the onset of the study. In addition, pre-selecting SNPs with a known or predicted

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immune function increased our statistical power to detect an association compared to employing a hypothesis-free approach. Overall, the goal of identifying peripherally accessible and efficiently analyzed biomarkers of AIWG holds considerable promise for its application in clinical practice (for further details, refer to Section 6.3)

However, our study design is not without limitations. The relatively small sample size and low MAF for some polymorphisms, particularly within race and treatment stratified subanalyses, may have limited our statistical power to be able to detect small effect sizes. Loss of power would have also resulted from dichotomization of the weight change (%) variable during analysis of CSWG. It is, therefore, possible that we did not have sufficient power to test specific hypotheses within the large number of sub-analyses conducted. This may be a major contributor to the lack of significant relationships between some of our cytokine SNPs and AIWG, and possibly even the over-dominance effect observed for IL-1 β rs16944. Despite this consideration, the predominance of sub-analyses that were conducted in this study were secondary investigations that were exploratory in design. In addition, since participants were recruited across three different centers, this may have increased within-sample heterogeneity. In recruiting patients with chronic schizophrenia, duration of illness and possible weight gain from previous treatments may have affected AIWG outcomes. To avoid a population stratification bias, we performed sub-analyses separately restricted to patients of European and African ancestry. However, ancestry was self-reported and not verified genetically. Another limitation is that information on potential risk factors of AIWG (e.g. AP dose, cigarette or cannabis use, dietary status, level of physical activity) was not collected, and therefore, the possible confounding effects of these factors cannot be ruled out. In addition, with inclusion of a placebo-controlled group, we cannot say with absolute certainty that weight gain outcomes are due to AP effects. Finally, a major limitation of our replication analysis was that 74% of all CATIE participants discontinued AP therapy before 18 months. Of these participants, 64% were receiving olanzapine and discontinued treatment predominantly due to AIWG or metabolic outcomes⁴⁶⁸.

6.3. Clinical Implications

Although APs offer symptomatic relief for patients diagnosed with schizophrenia or other psychotic disorders, therapeutic benefits may be offset by AIWG. This adverse side effect not only increases the risk of obesity and various metabolic and vascular conditions, but it can also lead to premature mortality and AP non-compliance^{18,19}. If patients become non-compliant with treatment or stop treatment prematurely, they put themselves at an elevated risk for symptom recurrence or illness relapse, and both an increased rate and duration of hospital admission⁴⁸⁷. AIWG is quite common, affecting approximately 15% to 72% of schizophrenic patients receiving acute or maintenance treatment³⁷. AIWG is also one of the most distressing side effects experienced by patients, particularly females⁴⁸⁸. In recognition of these facts, the American Diabetes Association issued a consensus statement in 2004 which recommended baseline and ongoing metabolic monitoring for all patients receiving high-risk APs⁴⁸⁹. In spite of this recommendation, metabolic screening for AP-treated patients is still alarmingly infrequent, as baseline rates of glucose and lipid testing are only 23% and 8%, respectively⁴⁹⁰. Even metabolic parameters that are relatively simple to assess such as blood pressure and correlates of obesity (e.g. weight, waist circumference) are insufficiently monitored¹⁹. Although there are numerous factors that can contribute to non-adherence of clinical practice guidelines⁴⁹¹, metabolic monitoring may be improved by minimizing the burden it places on clinicians and patients. This may be partly achieved through the use of more efficient pharmacogenetic paradigms, which would essentially only require a one-time genetic screening for AIWG susceptibility at baseline.

Pharmacogenetic testing can be used to identify inter-individual genetic variation that is associated with, and thus has clinical utility in predicting, patient risk of adverse drug reactions such as AIWG⁴⁹². Isolating relevant genetic variants is critically important when considering that 50% of adverse drug reactions can be attributed to genetic factors, as can 25% to 50% of inappropriate drug responses⁴⁹³. Based on the results of this study, variability at IL-1 β SNPs rs4849127, rs16944, and rs1143634, and BDNF Val66Met can both individually and, in some cases, synergistically predict AIWG outcomes in AP-treated patients with chronic schizophrenia. These genetic biomarkers offer a potential platform for the design of predictive treatment algorithms that can personalize drug therapy by providing patient-specific information on the relative safety of a given AP prior to its initial administration⁴⁹⁴. The ultimate goal of pharmacogenetic testing is to therefore optimize treatment outcomes by using an algorithmbased approach to rapidly prescribe APs to patients at a high likelihood of drug tolerability rather than simply using inefficient and costly 'trial and error' methods⁴⁹⁵.

The long-term implications of reducing the prevalence of AIWG are numerous. Some of the more clinically relevant aspects pertain to improving patient care and quality of life. For one, this change could lead to significantly decreased rates of AP-induced metabolic and vascular conditions that are typically mediated through increased weight. It could also improve AP adherence, and consequently lower risk of illness relapse and hospitalization. This can have secondary effects on the healthcare system by reducing associated medical expenditures, as hospital costs are more than three times higher in AP non-compliant versus compliant schizophrenia patients⁴⁹⁶. Improved AIWG outcomes can also help minimize obesity stigmatization which has been associated with negative affect and various social disadvantages such as discriminatory hiring practices in employment settings⁴⁹⁷. In addition, clinically validated genetic biomarkers can be used to optimize and expedite drug design and development, respectively, with minimal associated costs. In particular, through a reduction in adverse events and the ability to select more genetically homogenous patient populations, molecular biomarkers can lower the attrition rate of APs during clinical trials, and thus, reduce the overall cost and time of drug development^{498,499}. However, before the IL-1β and BDNF polymorphisms identified in this study can be formally incorporated into genetic screening practices, they would need to receive further clinical validation and functional testing.

6.4. Future Directions

The results from the present study contribute to the existing literature by demonstrating the genetic involvement of inflammatory and neurotrophic factors in AIWG. Despite these findings, pharmacogenetic researchers have primarily studied AIWG by investigating the effects of various hypothalamic neurotransmitters and signalling factors. Consequently, there is a paucity of data on the role of inflammatory mediators within this association, with the predominance of available literature only focusing on the effects of TNF- α and leptin²¹⁻²³. To the

author's knowledge, there are no pharmacogenetic studies that have investigated the role of the interleukin family of cytokines in AIWG. Instead, studies of inflammatory involvement are often serologic, and thus, rooted in serum quantification of cytokine protein levels⁴⁴²⁻⁴⁴⁴.

Based on our study findings, it may be promising to investigate a broader collection of immune variants across genes regulating both inflammatory and anti-inflammatory mediators, and their relevant receptors and receptor antagonists. It may also be informative to examine epistatic interactions between immune markers and other neurotrophins beyond BDNF, such as nerve growth factor, based on their involvement in neuroimmune crosstalk. Similarly, with biological interactions occurring between immune markers and the HPA axis^{391,392}, investigating the interplay between cytokines and both prostaglandins and endocrine hormones like CRH may be useful. Additional relationships of interest include inter-cytokine interactions due to their observed ability to act synergistically³⁴⁸, in addition to cytokine interactions with hypothalamic signalling factors, neurotransmitters, and neuropeptides^{336,365,377,379,380}. In addition to immune factors, the type of weight gain information collected will affect the quality of research. At a minimum, studies investigating AIWG should collect information on weight (in kg), BMI, and waist circumference at baseline, at regular intervals throughout, and at the end of the study. If the study design permits, and if not too burdensome for patients, clinical information on blood pressure and fasting glucose levels should also be obtained. In the end, once significant SNPs have been identified, as in this study, functional investigations of allelic effects are warranted. There would also be significant clinical utility in determining the application of immunogenetic biomarkers within other AP-treated psychiatric disorders reporting AIWG like bipolar disorder⁵⁴, treatment-resistant MDD⁵⁵, mental retardation and autistic disorder⁵⁶, and Tourette's syndrome⁵⁷.

The relative success of immunogenetic research in AIWG will be highly dependent on the degree to which various research domains can be comprehensively integrated. Studies of genetic interaction effects are a cornerstone of these initiatives. However, in order to achieve large-scale scientific advances, biomarker data will need to be integrated across various research modalities, such as neuroimaging, proteomics, transcriptomics, clinical assessment, and in the case of our study, molecular genetics. All of these domains have yielded important findings – spanning from studies of brain morphology and activation patterns, PET quantification of TSPO, post-mortem investigations of S100B and astrogliosis, immunogenetics, c-*fos* patterns of neuronal activation, cytokine knockout models, quantification of cytokine mRNA and protein – that have contributed to characterizing the role of inflammation within psychiatric disease and metabolic disturbance. The inter-disciplinary study of biomarker research may assist in the discovery of consistently validated candidates that can provide promising insights into the biological basis of AIWG. This is similar to the goal behind the ongoing Canadian Biomarker Integration Network in Depression (CAN-BIND) study which aims to use this inter-modality approach to identify predictive candidates of treatment response in MDD⁵⁰⁰.

Finally, in considering that APs achieve partial treatment benefits through immunosuppressive action, it would be logical to examine the effects of cytokine gene variants on therapeutic drug response. In the present study, data on clinical response to APs were collected (but not currently analyzed) for all 188 chronic schizophrenia patients. Clinical response was assessed according to change in BPRS total scores (Δ BPRS) over the course of AP treatment. As a future direction of this project, we intend to examine Δ BPRS across genotypic groups for each SNP from our original panel. Similar to APs, antidepressants also show immunomodulatory properties^{195,501,502}. Therefore, examining immunogenetic biomarkers of antidepressant response may also be functionally predictive. Hence, we also intend to examine the relationship between our cytokine SNP panel and response to Duloxetine treatment in an MDD sample. Clinical response has been assessed using the Hamilton Rating Scale for Depression (HAMD) and Montgomery-Asberg Depression Scale (MADRS). It may also be promising to examine the role of cytokine variants in the disease phenotype of schizophrenia, and other psychiatric conditions characterized by up-regulated inflammatory signatures, such as MDD.

6.5. Conclusions

The aim of the present study was to investigate the role of genetic variants across IL-1 β , IL-2, IL-6 and BDNF in AIWG. The current literature provides evidence on cytokine and neurotrophin dysregulation within schizophrenia that, through modification by AP medication, can have secondary consequences that lead to hyperphagia and altered energy expenditure. Our data extend these observations by showing that IL-1 β SNPs rs4849127, rs16944, and rs1143634, in addition to BDNF Val66Met, were significantly involved in mediating the effects of FGA and

SGA treatment on AIWG in 188 patients with chronic schizophrenia. Additional analyses revealed that IL-1 β rs4849127*A, IL-6 rs1800795*G, and heterozygosity at IL-1 β rs16944 were associated with CSWG. Epistatic effects between BDNF Val66Met and cytokine SNPs IL-1 β rs13032029, IL-1 β rs16944, and IL-6 rs2069837 were also observed in patients treated with the high-risk drugs, clozapine and olanzapine. None of the primary replication SNPs, which included IL-1 β rs17042517, rs2723152, and rs1143634 and BDNF Val66Met, had their association with AIWG replicated using the CATIE data. Taken together, there is appreciable evidence to support the influence of cytokine genetic variation on AIWG. However, further studies are needed to confirm the predictive utility of these immunogenetic biomarkers and more clearly elucidate the underlying functional mechanisms that support a cytokine model of AIWG.

The scope of future immunogenetic analyses of AIWG should be extended to include additional genes regulating inflammatory and anti-inflammatory factors, and their relevant receptors. Functional gene variants identified from these studies may have promising applications in other AP-treated psychiatric populations, and in elucidating the role of inflammation within treatment response and the pathogenesis of psychiatric phenotypes. Overall, the discovery of clinically validated genetic biomarkers of AIWG may offer a potential platform for the design of predictive treatment algorithms that can personalize drug therapy to reduce the likelihood of adverse drug reactions. Future biomarker initiatives may benefit from the integration of clinically relevant data collected across various research modalities. Nevertheless, immunogenetic research is still in its infancy and requires further investigation.

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Appendix

APPENDIX A: Haplotype Analysis in Patients of European Ancestry on CLZ/OLZ

Tost Monkong	<u>Overall</u>	Hanlatyna	Fraguanav ^a	× ²	Haplotype
<u>Test Markers</u>	<u>P-Value</u> ^b	<u>maplotype</u>	rrequency	<u>x</u>	P-Value ^b
IL-1β rs1143643		C-A-G	28 (21.2%)	0.05	0.826
IL-1β rs1143634	0.615	C-G-A	46 (34.9%)	0.95	0.330
IL-1β rs3136558		T-G-A	58 (43.9%)	0.57	0.451
IL-1β rs1143634		A-G-G	28 (20.9%)	0.04	0.835
IL-1β rs3136558	0.479	G-A-A	37 (27.6%)	1.45	0.228
IL-1β rs16944		G-A-G	69 (51.5%)	0.83	0.363
IL-1β rs3136558		A-A-C	41 (30.1%)	0.86	0.355
IL-1β rs16944	0.640	A-G-T	68 (50.0%)	0.58	0.447
IL-1β rs13032029		G-G-C	27 (19.9%)	0.01	0.910
$II_{-1}B_{rs}16944$		A-C-A	12 (8.3%)	1.92	0.166
$H_{1B} = 13032020$	0.599	A-C-G	32 (22.2%)	0.01	0.909
$H_{10} = 10^{-10} \times $	0.566	G-C-G	30 (20.8%)	< 0.01	0.999
IL-1p 184649127		G-T-G	70 (48.6%)	0.45	0.502
II 2 $r_{\rm s}$ 2069776		C-T-A	17 (12.5%)	< 0.01	0.952
IL - 2 rs 2069770	0 794	C-T-G	15 (11.0%)	0.02	0.881
IL - 2 rs 2069772	0.794	T-C-G	44 (32.4%)	0.74	0.389
IL-2 132007778		T-T-G	60 (44.1%)	0.89	0.345
$II_{2} = 2 r_{0} 2060772$		C-G-A	43 (31.2%)	0.57	0.451
$H_{2} = 2 r_{s} 2069772$	0 796	T-A-A	18 (13.0%)	0.05	0.827
IL - 2 rs 2069778	0.790	T-G-A	33 (23.9%)	< 0.01	0.979
IL-2 132007702		T-G-C	44 (31.9%)	0.87	0.352
II 6 ro2060927		G-C-A	68 (47.9%)	0.25	0.618
IL-0.152009027 $IL-6 rs1800795$	0 701	G-C-G	11 (7.7%)	1.29	0.255
IL-0151000795	0.701	G-G-A	50 (35.2%)	0.03	0.874
112-0132007037		T-G-A	13 (9.2%)	0.01	0.943

II -6 rs1800795		C-A-G	56 (40.6%)	0.51	0.476
IL -6 rs2069837	0.641	C-A-T	9 (6.5%)	< 0.01	0.998
IL -6 rs2066992	0.041	C-G-G	11 (8.0%)	1.41	0.235
11-0132000772		G-A-G	62 (44.9%)	< 0.01	0.954
Ш. 6 то 2060927		A-G-C	83 (58.5%)	< 0.01	0.968
IL-0182009837	0.601	A-G-G	39 (27.5%)	0.34	0.562
IL-0.182000992	0.091	A-T-C	9 (6.3%)	0.01	0.941
IL-0182009840		G-G-C	11 (7.7%)	1.24	0.266
Ш. с. то 20ссоро2		G-C-C	75 (52.8%)	0.15	0.702
IL-0 IS2000992	0.046	G-C-T	19 (13.4%)	0.06	0.800
IL-0 182009840	0.940	G-G-C	39 (27.5%)	0.34	0.562
IL-0182009801		T-C-C	9 (6.3%)	0.01	0.941
		C-C-A	36 (24.1%)	0.08	0.777
IL-6 rs2069840		C-C-G	50 (34.0%)	0.01	0.913
IL-6 rs2069861		C-T-G	19 (12.8%)	0.03	0.869
IL-6 rs10242595	0.890	G-C-A	9 (6.3%)	0.58	0.447
		G-C-G	34 (22.8%)	0.51	0.475
1					

^aValues refer to frequency among haplotype options for the specified test markers; ^bUncorrected p-values; $IL-1\beta =$ interleukin 1 beta, IL-2 = interleukin 2, IL-6 = interleukin

CND	Comotomo	<u>CSWG</u>	Non-CSWG	OD	050/ CI	2	D Value ^b
<u>SINP</u>	<u>Genotype</u>	$(n=35)^{a}$	<u>(n= 93)</u> ^a	<u>OK</u>	<u>95% CI</u>	χ	<u>P-value</u>
II -18 rs4849127	AA/GA	6 (17.1%)	11 (11.8%)	1 54	0.52 - 4.55		±0 559
112 1p 15+0+9127	GG	29 (82.9%)	82 (88.2%)	1.54	0.52 4.55		10.009
II -18 rs13032029	TT/CT	26 (78.8%)	69 (74.2%)	1 29	0 50 - 3 36	0.28	0 599
12 1p 1313032027	CC	7 (21.2%)	24 (25.8%)	1.27	0.50 5.50	0.20	0.077
II -18 rs16944	AA/GA	18 (51.4%)	42 (45.7%)	1.26	0.58 - 2.75	0.34	0 560
1L-10 1310944	GG	17 (48.6%)	50 (54.3%)	1.20	0.56 2.15	0.54	0.500
II_1B_rs3136558	GG/GA	16 (45.7%)	36 (38.7%)	1 33	0.61 – 2.92	0.52	0.472
IL-1p 185150558	AA	19 (54.3%)	57 (61.3%)	1.55			
II_1B_rs11/363/	AA/GA	16 (45.7%)	37 (39.8%)	1 28	0.58 - 2.79	0.37	0.544
1L-10 1311+3034	GG	19 (54.3%)	56 (60.2%)	1.20			
$II_{-1}B_{rs} = 11/36/3$	TT/CT	23 (67.6%)	66 (71.7%)	0.82	0.35 1.03	0.20	0.654
1L-10131145045	CC	11 (32.4%)	26 (28.3%)	0.02	0.55 1.75	0.20	
II -2 rs2069762	CC/CA	19 (54.3%)	55 (59.1%)	0.82	0 38 – 1 80	0.25	0.620
11-2 132007702	AA	16 (45.7%)	38 (40.9%)	0.02	0.50 1.00	0.25	0.020
II_2 rs2069778	AA/GA	9 (25.7%)	19 (21.1%)	1 29	0.52 - 3.22	0.31	0 579
11-2 132007770	GG	26 (74.3%)	71 (78.9%)	1.27	1.29 0.32 - 3.22	0.51	0.379
II -2 rs2069772	CC/CT	17 (50.0%)	47 (50.5%)	0 08	0.45 - 2.15	<0.01	0.957
11-2 132007772	TT	17 (50.0%)	46 (49.5%)	0.90	0.45 – 2.15	<0.01	0.757

APPENDIX B: Genetic Predictors of Antipsychotic-Induced CSWG in Europeans

II 2 rs2060776	CC/CT	16 (45.7%)	35 (38.5%)	1 35	0.61 2.96	0.55	0.458
IL-2 182009770	TT	19 (54.3%)	56 (61.5%)	1.55	0.01 - 2.90	0.55	0.458
II -6 rs2069827	TT/GT	7 (20.0%)	18 (19.4%)	1.04	0.39 - 2.76	<0.01	0.935
11-0132007027	GG	28 (80.0%)	75 (80.6%)	1.04	0.37 2.10	<0.01	0.755
II -6 rs1800795	GG/CG	21 (60.0%)	64 (70.3%)	0.63	0.28 - 1.43	1 23	0 268
	CC	14 (40.0%)	27 (29.7%)	0.05	0.20 1.13	1.20	0.200
II -6 rs2069837	GG/GA	6 (17.1%)	15 (16.1%)	1.08	0.38 - 3.04	0.02	0.890
12 0 132009037	AA	29 (82.9%)	78 (83.9%)	1.00	0.50 5.04	0.02	0.090
II 6 ro2066002	TT/GT	4 (11.4%)	9 (10.1%)	1 15	0.33 - 4.00		±1 000
112 0 132000772	GG	31 (88.6%)	80 (89.9%)	1.15			11.000
IL-6 rs2069840	GG/CG	17 (48.6%)	47 (50.5%)	0.92	0.43 - 2.01	0.04	0.843
	CC	18 (51.4%)	46 (49.5%)	0.72	0.12 2.01		01010
IL-6 rs2069861	TT/CT	6 (17.6%)	22 (23.7%)	0.69	0 25 - 1 89	0.52	0 470
	CC	28 (82.4%)	71 (76.3%)	0.07	0.20 1.09	0.02	0.170
II -6 rs10242595	AA/GA	18 (51.4%)	44 (47.8%)	1 16	0.53 - 2.52	0.13	0.717
12 0 15102 125 55	GG	17 (48.6%)	48 (52.2%)	1.10	0.00 2.02	0.15	0.717
BDNF Val66Met	Met/Met + Val/Met	7 (20.0%)	32 (35.2%)	0.46	0 18 – 1 17	2.72	0 099
	Val/Val	28 (80.0%)	59 (64.8%)	0.40	0.10 1.17		0.077

^aValues represent number (percent) or mean \pm standard deviation; ^bUncorrected p-values; [‡]Value calculated using Fisher Exact test; SNP = single nucleotide polymorphism, CSWG = clinically significant weight gain, \geq 7% weight change from baseline, OR = odds ratio, CI = confidence interval, IL-1 β = interleukin 1 beta, IL-2 = interleukin 2, IL-6 = interleukin 6, BDNF = brain-derived neurotrophic factor

C	<u>CSWG</u>	Non-CSWG	OD	050/ 01	2	D V /a ha a b
Genotype	$(n=24)^{a}$	<u>(n= 26)</u> ^a	<u>OK</u>	<u>95% CI</u>	χ	<u>P-value</u>
AA/GA	13 (54.2%)	12 (46.2%)	1 38	0.45 - 4.20	0 321	0.571
GG	11 (45.8%)	14 (53.8%)	1.50	0.45 4.20	0.521	0.071
TT/CT	11 (45.8%)	12 (46.2%)	0.99	0.32 - 3.01	<0.01	0.092
CC	13 (54.2%)	14 (53.8%)	0.77	0.52 5.01	<0.01	0.902
AA/GA	19 (79.2%)	19 (73.1%)	1 40	0 38 - 5 20	0.25	0.614
GG	5 (20.8%)	7 (26.9%)	1.40	0.58 - 5.20	0.23	0.014
GG/GA	5 (20.8%)	8 (30.8%)	0.59	9 0.16 - 2.15	0.64	0.424
AA	19 (79.2%)	18 (69.2%)	0.39			
AA/GA	11 (45.8%)	7 (26.9%)	2 30	0.71 – 7.49	1 94	0.164
GG	13 (54.2%)	19 (73.1%)	2.30		1.94	
TT/CT	8 (33.3%)	10 (38.5%)	0.80	0.25 2.55	0.14	0.706
CC	16 (66.7%)	16 (61.5%)	0.00	0.25 - 2.55	0.14	
CC/CA	4 (17.4%)	4 (15.4%)	1 16	0.25 5.27		±1.000
AA	19 (82.6%)	22 (84.6%)	1.10	0.23 - 5.27		11.000
AA/GA	1 (4.2%)	3 (11.5%)	0.33	0.03 - 3.45		±0.611
GG	23 (95.8%)	23 (88.5%)	0.55	0.55 0.05 - 5.45		10.011
CC/CT	5 (21.7%)	3 (11.5%)	2 13	0.45 - 10.12		±0.448
TT	18 (78.3%)	23 (88.5%)	2.13	0.45 - 10.12		10.440
	GenotypeAA/GAGGTT/CTCCAA/GAGG/GAAA/GAGGGC/CAAA/GAGGCC/CAAA/GAGGCC/CAAA/GAGGCC/CTTT	Genotype $CSWG$ (n= 24)aAA/GA13 (54.2%)GG11 (45.8%)TT/CT11 (45.8%)CC13 (54.2%)AA/GA19 (79.2%)GG5 (20.8%)GG/GA5 (20.8%)GG/GA11 (45.8%)GG13 (54.2%)AA/GA11 (45.8%)GG13 (54.2%)TT/CT8 (33.3%)CC16 (66.7%)CC/CA4 (17.4%)AA/GA1 (4.2%)GG23 (95.8%)CC/CT5 (21.7%)TT18 (78.3%)	GenotypeCSWG (n=24)aNon-CSWG (n=26)aAA/GA13 (54.2%)12 (46.2%)GG11 (45.8%)14 (53.8%)TT/CT11 (45.8%)12 (46.2%)CC13 (54.2%)14 (53.8%)AA/GA19 (79.2%)19 (73.1%)GG/GA5 (20.8%)7 (26.9%)GG/GA5 (20.8%)8 (30.8%)AA/GA11 (45.8%)7 (26.9%)GG/GA5 (20.8%)8 (30.8%)AA/GA11 (45.8%)7 (26.9%)GG/GA5 (20.8%)18 (69.2%)AA/GA11 (45.8%)7 (26.9%)GG13 (54.2%)19 (73.1%)TT/CT8 (33.3%)10 (38.5%)CC16 (66.7%)16 (61.5%)CC/CA4 (17.4%)4 (15.4%)AA/GA19 (82.6%)22 (84.6%)AA/GA1 (4.2%)3 (11.5%)GG23 (95.8%)23 (88.5%)CC/CT5 (21.7%)3 (11.5%)TT18 (78.3%)23 (88.5%)	$\begin{array}{ c c c c c c c c c c c c c c c c c c c$	$\begin{array}{ c c c c c c c c c c c c c c c c c c c$	$\begin{array}{ c c c c c c c c c c c c c c c c c c c$

APPENDIX C: Genetic Predictors of Antipsychotic-Induced CSWG in Africans

II -2 rs2069776	CC/CT	7 (29.2%)	6 (24.0%)	1 30	0 37 – 4 65	0.17	0.682
12 2 152007770	TT	17 (70.8%)	19 (76.0%)	1.50	0.57 1.05	0.17	0.002
II -6 rs2069827	TT/GT	1 (4.2%)	1 (3.8%)	1.09	0.06 - 18.40		±1 000
12 0 132009027	GG	23 (95.8%)	25 (96.2%)	1.09	0.00 10.40		11.000
II -6 rs1800795	GG/CG	4 (16.7%)	4 (16.0%)	1.05	0.23 - 4.78		±1 000
	CC	20 (83.3%)	21 (84.0%)	1.05	0.23 1.70		11.000
II -6 rs2069837	GG/GA	7 (30.4%)	5 (19.2%)	1 84	0 49 - 6 87	0.83	0 363
12 0 132009037	AA	16 (69.6%)	21 (80.8%)	1.04	0.49 0.07	0.05	0.505
II 6 m 2066002	TT/GT	3 (13.0%)	5 (19.2%)	0.63	0 13 - 2 99		±0.706
112 0 132000772	GG	20 (87.0%)	21 (80.8%)	0.05	0.15 2.99		10.700
II -6 rs2069840	GG/CG	8 (33.3%)	8 (30.8%)	1 13	0.34 - 3.70	0.04	0 846
	CC	16 (66.7%)	18 (69.2%)	1.15	0.51 5.70	0.01	0.010
II -6 rs2069861	TT/CT	2 (8.3%)	1 (3.8%)	2 27	0 19 - 26 81		±0.602
11 0 152007001	CC	22 (91.7%)	25 (96.2%)	2.27	0.17 20.01		10.002
II -6 rs10242595	GG/GA	16 (66.7%)	19 (73.1%)	0.74	0.22 - 2.48	0.24	0.621
11-01810242393	AA	8 (33.3%)	7 (26.9%)	0.71	0.22 2.10	0.21	0.021
BDNF Val66Met	Met/Met + Val/Met	3 (13.0%)	2 (7.7%)	1 80	0 27 – 11 86		±0.655
	Val/Val	20 (87.0%)	24 (92.3%)	1.00	0.27 - 11.80		10.000

^aValues represent number (percent) or mean \pm standard deviation; ^bUncorrected p-values; [‡]Value calculated using Fisher Exact test; SNP = single nucleotide polymorphism, CSWG = clinically significant weight gain, \geq 7% weight change from baseline, OR = odds ratio, CI = confidence interval, IL-1 β =interleukin 1 beta, IL-2 = interleukin 2, IL-6 = interleukin 6, BDNF = brain-derived neurotrophic factor

CND	Construes	<u>CSWG</u>	Non-CSWG	OD	050/ CI	2	D Value ^b
<u>SINP</u>	<u>Genotype</u>	$(n=23)^{a}$	<u>(n= 51)</u> ^a	<u>OK</u>	<u>95% CI</u>	χ	<u>P-value</u>
II -18 rs4849127	AA/GA	5 (21.7%)	7 (13.7%)	1 75	0 49 - 6 23	9 - 6 23	±0 498
12 1p 15+0+9127	GG	18 (78.3%)	44 (86.3%)	1.75	0.47 0.23		10.190
II -18 rs13032029	TT/CT	16 (76.2%)	35 (68.6%)	1 46	0.46 - 4.69	0.41	0.521
12 1p 1313032027	CC	5 (23.8%)	16 (31.4%)	1.40	0.40 4.07	0.41	0.521
II1B_rs16944	AA/GA	14 (60.9%)	25 (49.0%)	1.62	0.59 - 4.40	0.89	0 345
IL-10 1310744	GG	9 (39.1%)	26 (51.0%)	1.02	0.39 - 4.40	0.89	0.345
II_1B_rs3136558	GG/GA	9 (39.1%)	20 (39.2%)	1.00	0 0.36 - 2.73	36 - 2.73 < 0.01	0.994
IL-1p rs3136558	AA	14 (60.9%)	31 (60.8%)	1.00		<0.01	
II 18 r_{s} 11/13/63/	AA/GA	10 (43.5%)	21 (41.2%)	1 10	0.41 - 2.97	0.04	0.853
IL-10 181145054	GG	13 (56.5%)	30 (58.8%)	1.10			
$II_{-1}\beta_{rs} = 11/36/3$	TT/CT	14 (60.9%)	32 (64.0%)	0.88	0.32 2.42	0.07	0.797
1L-10 1311+30+3	CC	9 (39.1%)	18 (36.0%)	0.00	0.52 2.72	0.07	
II -2 rs2069762	CC/CA	15 (65.2%)	25 (49.0%)	1 95	0.70 - 5.40	1 68	0 196
11-2 132007702	AA	8 (34.8%)	26 (51.0%)	1.75	0.70 5.40	1.00	0.170
II_2 rs2069778	AA/GA	6 (26.1%)	13 (26.5%)	0.98	0.32 - 3.01	~0.01	0.968
112-2 132007770	GG	17 (73.9%)	36 (73.5%)	0.76	0.90 0.52 - 5.01	<0.01	0.700
II -2 rs2069772	CC/CT	11 (50.0%)	28 (54.9%)	0.82	0.30 - 2.24	0.15	0.700
112-2 182007772	TT	11 (50.0%)	23 (45.1%)	0.82	0.30 - 2.24	0.15	0.700

APPENDIX D: Genetic Predictors of Antipsychotic-Induced CSWG in Europeans on CLZ/OLZ

II -2 rs2069776	CC/CT	11 (47.8%)	21 (42.9%)	1 22	0.45 - 3.31	0.16	0.692
IL-2 132007770	TT	12 (52.2%)	28 (57.1%)	1.22	0.45 5.51	0.10	0.072
II -6 rs2069827	TT/GT	5 (21.7%)	8 (15.7%)	1 49	0 43 - 5 19		±0.526
12 0 132009027	GG	18 (78.3%)	43 (84.3%)	1.49	0.+5 5.17		10.520
IL -6 rs1800795	GG/CG	17 (73.9%)	34 (69.4%)	1 25	0.41 - 3.80	0.16	0 694
	CC	6 (26.1%)	15 (30.6%)	1.23	0.11 5.00	0.10	0.091
II -6 rs2069837	GG/GA	1 (4.3%)	10 (19.6%)	0.19	0.02 - 1.55		±0.156
12 0 132007057	AA	22 (95.7%)	41 (80.4%)	0.17	0.02 1.55		10.100
II 6 ro2066002	TT/GT	3 (13.0%)	6 (12.5%)	1.05	0.24 - 4.63		±1 000
112 0 132000772	GG	20 (87.0%)	42 (87.5%)	1.05	0.24 4.03		
IL-6 rs2069840	GG/CG	11 (47.8%)	26 (51.0%)	0.88	0.88 0.33 - 2.36	0.06	0.802
	CC	12 (52.2%)	25 (49.0%)	0.00	0.00 2.00	0.00	0.002
IL-6 rs2069861	TT/CT	6 (26.1%)	12 (23.5%)	1 15	0 37 – 3 56	0.06	0.812
	CC	17 (73.9%)	39 (76.5%)	1110	0.07 0.00	0.00	0.012
IL-6 rs10242595	AA/GA	10 (43.5%)	27 (52.9%)	0.68	0.25 - 1.84	0.57	0.451
	GG	13 (56.5%)	24 (47.1%)	0.00	0.20 1.01	0.07	01101
BDNF Val66Met	Met/Met + Val/Met	4 (17.4%)	18 (36.7%)	0.36	0.11 – 1.23	2.76	0.097
	Val/Val	19 (82.6%)	31 (63.3%)	0.50	0.11 1.23	2.70	0.097

^aValues represent number (percent) or mean \pm standard deviation; ^bUncorrected p-values; [‡]Value calculated using Fisher Exact test; SNP = single nucleotide polymorphism, CSWG = clinically significant weight gain, \geq 7% weight change from baseline, OR = odds ratio, CI = confidence interval, IL-1 β = interleukin 1 beta, IL-2 = interleukin 2, IL-6 = interleukin 6, BDNF = brain-derived neurotrophic factor

CND	Constant of	<u>CSWG</u>	Non-CSWG	OD	050/ CI	2	D V /a ha a b
<u>SINP</u>	<u>Genotype</u>	$(n=20)^{a}$	<u>(n= 17)</u> ^a	<u>OR</u>	<u>95% CI</u>	χ	<u>P-value</u>
II -18 rs4849127	AA/GA	12 (60.0%)	8 (47.1%)	1 69	0.46 - 6.23	0.62	0.431
1L-10134049127	GG	8 (40.0%)	9 (52.9%)	1.07	0.40 0.23	0.02	0.451
$II_{-1}\beta_{rs} = 13032029$	TT/CT	10 (50.0%)	7 (41.2%)	1 /3	0 39 - 5 26	0.20	0 591
IL-10 1313032027	CC	10 (50.0%)	10 (58.8%)	1.+5	0.37 5.20	0.27	0.571
II 18 r_{s} 169/4	AA/GA	17 (85.0%)	13 (76.5%)	1 74	0.33 0.10		±0.680
IL-10 1810944	GG	3 (15.0%)	4 (23.5%)	1.74	0.33 - 9.19		+0.080
IL-1β rs3136558	GG/GA	3 (15.0%)	5 (29.4%)	0.42	0.09 - 2.12		ŧ0.428
	AA	17 (85.0%)	12 (70.6%)	0.42			
$II_{1}B_{re1}1/363/$	AA/GA	8 (40.0%)	6 (35.3%)	1 22	0.32 – 4.66	0.09	0.769
IL-10 181145054	GG	12 (60.0%)	11 (64.7%)	1.22		0.09	
II 18 rs11/36/3	TT/CT	7 (35.0%)	6 (35.3%)	0 00	0.26 2.82	<0.01	0.985
IL-10 181145045	CC	13 (65.0%)	11 (64.7%)	0.77	0.20 - 5.62		
II -2 rs2069762	CC/CA	3 (15.8%)	2 (11.8%)	1.41	0.21 - 9.62		±1 000
112-2 132009702	AA	16 (84.2%)	15 (88.2%)	1.41	0.21 9.02		11.000
II -2 rs2069778	AA/GA		1 (5.9%)				
112-2 132007770	GG	20 (100%)	16 (94.1%)				
II -2 rs2069772	CC/CT	5 (26.3%)	1 (5.9%)	5 71	0 59 - 54 96		±0.182
12 2 132007772	TT	14 (73.7%)	16 (94.1%)	5.71	0.39 - 34.96		10.102

APPENDIX E: Genetic Predictors of Antipsychotic-Induced CSWG in Africans on CLZ/OLZ

IL-2 rs2069776	CC/CT	6 (30.0%)	3 (18.8%)	1.86	0.38 - 9.00		ŧ0 700
	TT	14 (70.0%)	13 (81.2%)	1.00			
IL-6 rs2069827	TT/GT						
	GG	20 (100%)	17 (100%)				
IL-6 rs1800795	GG/CG	2 (10.0%)	1 (6.2%)	1 67	0.14 - 20.23		±1 000
	CC	18 (90.0%)	15 (93.8%)	1.07	0111 20125		11.000
II -6 rs2069837	GG/GA	5 (26.3%)	3 (17.6%)	1.67	0 33 - 8 35		±0.695
12 0 132009037	AA	14 (73.7%)	14 (82.4%)	1.07	0.55 0.55		10.095
II 6 ro2066002	TT/GT	2 (10.5%)	3 (17.6%)	0.55	0.08 - 3.76		±0.650
112 0 132000772	GG	17 (89.5%)	14 (82.4%)		0.00 5.70		10.050
II -6 rs2069840	GG/CG	5 (25.0%)	5 (29.4%)	0.80	0 19 - 3 42		±1 000
12 0 132009040	CC	15 (75.0%)	12 (70.6%)	0.00	0.17 5.42		
II -6 rs2069861	TT/CT	1 (5.0%)	1 (5.9%)	0.84	0.05 - 14.57		±1 000
12 0 132009001	CC	19 (95.0%)	16 (94.1%)	0.04	0.05 14.57		11.000
II -6 rs10242595	GG/GA	12 (60.0%)	13 (76.5%)	0.46	0 11 – 1 94	1 14	0.286
1L-01810242393	AA	8 (40.0%)	4 (23.5%)	0.40	0.11 1.94	1.17	0.200
BDNE Val66Met	Met/Met + Val/Met		1 (5.9%)				
	Val/Val	19 (100%)	16 (94.1%)				

^aValues represent number (percent) or mean \pm standard deviation; ^bUncorrected p-values; [‡]Value calculated using Fisher Exact test; SNP = single nucleotide polymorphism, CSWG = clinically significant weight gain, \geq 7% weight change from baseline, OR = odds ratio, CI = confidence interval, IL-1 β = interleukin 1 beta, IL-2 = interleukin 2, IL-6 = interleukin 6, BDNF = brain-derived neurotrophic factor