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Article

An Evolutionary Model for Ancient Origins of Polycystic Ovary Syndrome

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Abstract: Polycystic ovary syndrome (PCOS) is a common endocrinopathy of reproductive-aged women characterized by hyperandrogenism, oligo-anovulation and insulin resistance closely linked with preferential abdominal fat accumulation. As an ancestral primate trait, PCOS was likely further selected in humans when scarcity of food in hunter-gatherers of the late Pleistocene additionally programmed for enhanced fat storage to meet the metabolic demands of reproduction in later life. As an evolutionary model for PCOS, healthy normal-weight women with hyperandrogenic PCOS have subcutaneous (SC) abdominal adipose stem cells that favor fat storage through exaggerated lipid accumulation during development to adipocytes *in vitro*. In turn, fat storage is counterbalanced by reduced insulin sensitivity and preferential accumulation of highly-lipolytic intra-abdominal fat *in vivo*. This metabolic adaptation in PCOS balances energy storage with glucose availability and fatty acid oxidation for optimal energy use during reproduction; its accompanying oligo-anovulation allowed PCOS women from antiquity sufficient time and strength for childrearing of fewer offspring with a greater likelihood of childhood survival. Heritable PCOS characteristics are now affected by today's contemporary environment through epigenetic events that predispose to lipotoxicity with excess weight gain and pregnancy complications, calling for an emphasis on preventive healthcare to optimize the long-term, endocrine-metabolic health of PCOS women in today's obesogenic environment.

Keywords: polycystic ovary syndrome; hyperandrogenism; insulin resistance; adipocyte; adipose stem cells; evolution; body fat distribution; metabolic adaptation

1. Introduction

As the most common endocrinopathy of reproductive-aged women, polycystic ovary syndrome (PCOS) is characterized by hyperandrogenism, oligo-anovulation and insulin resistance closely linked with preferential abdominal fat accumulation [1]. Its clinical manifestations of hirsutism, menstrual irregularity, glucose intolerance and dyslipidemia worsen with obesity to increase the risks of developing subfertility, diabetes, metabolic syndrome and/or cardiovascular disease [2]. Almost one-half of women with PCOS in the United States have metabolic syndrome (i.e., increased abdominal [android] obesity, hyperglycemia, dyslipidemia and/or hypertension), with a prevalence higher than that of age-matched normal women in this country [1, 3] and of PCOS women in other countries where obesity is less common [4, 5].

Through an evolutionary perspective, the high worldwide prevalence of PCOS in today's environment should have disappeared over millennia unless a beneficial effect favored both survival and reproduction [6]. Perhaps not surprisingly, therefore, ancestral traits resembling PCOS have been reported throughout antiquity [7] and in a nonhuman primate (i.e., female rhesus macaques) [8-10], that shares a common ancestor with humans [11]. One explanation is that an ancient female primate trait resembling PCOS may have been favored originally in the cooling, increasingly arid and less

forested African environments of the Oligocene before ancestors of humans diverged from those of macaques [12,13], as the isolated continent of Africa contacted Euroasia [14], enabling inter-continental migration [15] (Figure 1). Such an ancestral trait may have been additionally favored in human hunter-gatherers of the late Pleistocene, or in more ancient human populations, when scarcity of food further selected for programming of enhanced fat storage to meet the metabolic demands of reproduction in later life (i.e., metabolic thrift) [7, 16-18]. Parallel evolution in macaques, particularly rhesus macaques living in semi-desert and high-altitude environments [13], may have emulated selection in humans for programming of enhanced fat storage (Figure 1). Such evolutionary metabolic adaptations in female primates, including women, would complement the ancient sympathoadrenal response to stress, whereby altered glucocorticoid and catecholamine activities mobilize hepatic glucose and FFAs from visceral fat to act in concert with insulin resistance and ensure sufficient energy during a “fight or flight” response for survival [19-21].

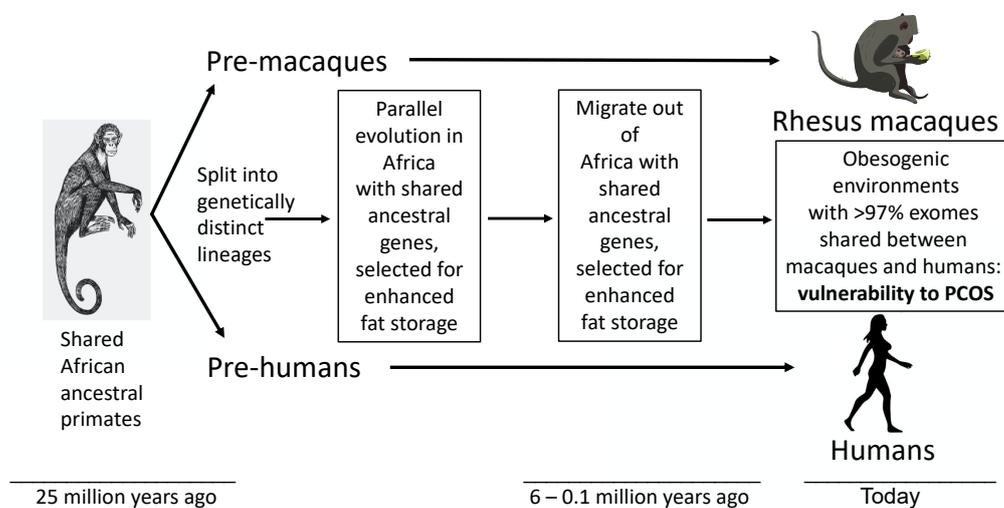


Figure 1. Polycystic ovary syndrome as an ancient metabolic-reproductive adaptation that originally enhanced fat storage for survival of humans during ancient times of food deprivation, and also favored fewer offspring with a greater likelihood of childhood survival, but now predisposes to endocrine-reproductive dysfunction in today’s obesogenic environment (16). Ancestral traits resembling PCOS also exist in female rhesus macaques [8-10] that share a common ancestor with humans through parallel evolution.

Through this evolutionary perspective, the present review examines PCOS as an ancient metabolic adaptation that underwent additional selection pressure for survival of humans during ancient times of food deprivation, but now predisposes to metabolic-endocrine-reproductive dysfunction in today’s obesogenic environment [17,18,22]. A parallel obesogenic environmental change experienced by female rhesus macaques in their natural habitat [13], as well as by macaques removed from their natural habitat decades ago and housed in United States National Primate Research Centers (NPRC) [23,24], may emulate the current obesogenic environmental challenge confronting humans (Figure 1). Consistent with this notion, approximately 15% of adult female rhesus macaques at the Wisconsin NPRC are naturally hyperandrogenic and exhibit PCOS-like traits [9,10]. Polycystic ovarian syndrome and PCOS-like phenotypes may thus form a continuum of ancient primate traits. Understanding trait-related molecular mechanisms, including genetic, epigenetic, protein and lipid interactions leading to optimal energy utilization, along with the perspective of providing benefits for survival and reproductive in both humans and rhesus macaques, offers novel insight into more effective clinical management for women with PCOS.

2. Genetics and epigenetics of PCOS

Heritability of PCOS has been established by family and twin studies [25-28]; the prevalence of PCOS in female first-degree relatives of affected women is 20-40% [25,27,29] with monozygotic versus dizygotic twin studies showing heritability of PCOS as high as 70% [26]. Large genome-wide association studies (GWAS) in cohorts of PCOS women and controls have identified several PCOS susceptible loci in candidate genes involving gonadotropin secretion/action, androgen biosynthesis/gonadal function, insulin action/metabolism and follicle development [1,30-38]. Several PCOS candidate genes are shared among women with differing PCOS phenotypes (i.e., Rotterdam, National Institutes of Health [NIH] criteria, or self-reported) [36]. Some, such as thyroid adenoma associated (*THADA*) and insulin receptor (*INSR*), are associated with metabolic disorders in PCOS and type 2 diabetes mellitus (T2DM) [39], others with high bioavailable (unbound) circulating T levels [40]. Genetic correlations between PCOS status and components of metabolic syndrome, including childhood obesity, T2DM, and fasting insulin, high-density lipoprotein-cholesterol (HDL-C) as well as triglyceride (TG) levels, further suggest shared genetic and biological origins between these parameters and PCOS [36,38]. That similar PCOS risk genes are expressed in women with PCOS from Chinese and European populations points to ancient human origins of PCOS [37,38], potentially dating back before the migration of humans out of sub-Saharan Africa 300,000-50,000 years ago or earlier [41,42].

Importantly, women with NIH-defined PCOS have two distinct PCOS subtypes with different genetic heterogeneity: one defined as a “reproductive” group (23% of cases), characterized by higher luteinizing hormone (LH) and sex hormone binding globulin (SHBG) levels with relatively low body mass index (BMI) and insulin levels; the other defined as a “metabolic” group (37% of cases), characterized by higher BMI, glucose and insulin levels, with lower SHBG and LH levels [38,43]. These PCOS subtypes may differ in their developmental origins [43], with their heritability variably interacting with risk-increasing environmental factors to fully explain its prevalence.

Alternatively, rare variants in *DENND1A*; a gene encoding a 1009 amino acid protein with a clathrin-binding domain regulating endosome-mediated endocytosis, receptor cycling and calcium-dependent signaling cascades [44,45]; also have been associated with endocrine-metabolic traits in families of daughters with PCOS [46]. A posttranscription form of *DENND1A*, namely *DENND1A.v2*, is over-expressed in some PCOS women [47,48], with *DENND1A.v2* over-expression in human theca cells increasing androgen biosynthesis/release, potentially by PCOS-candidate gene *ZNF217* diminishing theca cell expression of microRNA miR-130b-3p, a noncoding microRNA transcriptional repressor [49].

Genetic variants of anti-mullerian hormone (AMH) and its type 2 receptor (AMHR2) also have been identified in about 7% of women with PCOS by NIH criteria, with 37 such variants having reduced *in vitro* bioactivity and diminished AMH inhibition of CYP17A1 as a risk factor for PCOS [50,51]. Both AMH and AMHR2 gene variants regulate intra-ovarian follicle development and hypothalamic GnRH function, and possibly ovarian androgen production [52], and may underlie elevated circulating AMH levels and ovarian hyperandrogenism in PCOS women [51].

Considered together, the current understanding of the genetics of PCOS suggests multiple contributing risk genes within which different variants can contribute to a PCOS phenotype. Given the heterogeneity of PCOS phenotypic expression, the high prevalence of PCOS, and its complex gene associations that account for some PCOS women, PCOS may have multiple molecular underpinnings that arise from common or varied developmental origins.

Epigenetic changes coexist with many of these PCOS candidate genes [53,54]. In SC abdominal adipose, over-expression of the LHCG receptor and under-expression of the insulin receptor in nonobese and obese PCOS women, respectively, accompany reciprocal DNA methylation patterns [55], while reciprocal changes of gene expression and DNA methylation also coexist in adipogenic pathways of overweight PCOS women [56]. In PCOS theca cells, moreover, decreased expression of miR-130b-3b (i.e., a noncoding microRNA transcriptional repressor) correlates with increased *DENND1A.V2* and CYP17A1 expression as well as with androgen

synthesis [49,57], while three PCOS-specific gene variants of AMHR2 occur in regions of higher methylation and acetylation activity [51]. PCOS susceptible loci alone, however, do not fully explain the majority of PCOS phenotypic expression [58], so that heritability of PCOS likely involves one or more PCOS candidate genes that have interacted with environmental factors throughout antiquity to modify target tissue phenotype through epigenetic events [5].

3. PCOS phenotypic expression

Most women with PCOS have systemic insulin resistance from perturbed insulin receptor/post receptor signaling, altered adipokine secretion and/or abnormal steroid metabolism [2] in combination with preferential abdominal fat accumulation worsened by obesity [1,59-61]. Most women with PCOS also have increased adiposity [62-64] that interacts with hyperandrogenism to worsen PCOS phenotypic expression [1-3,65-67] and insulin resistance [2,68,69]. Different PCOS phenotypes by Rotterdam criteria also vary in endocrine-metabolic dysfunction [70], with NIH-defined PCOS women (i.e., hyperandrogenism with oligo-anovulation) having the greatest risk of developing menstrual irregularity, anovulatory infertility, T2DM and metabolic syndrome [1]. Furthermore, women with PCOS from a referral population have a more severe phenotype than those from the general population [71,72].

To understand the origins of PCOS, the above variables underlying endocrine-metabolic dysfunction in PCOS need to be eliminated when comparing the clinical characteristics of healthy, normal-weight PCOS women by NIH criteria with age/BMI-balanced controls [68,69,71,73,74]. In doing so, healthy normal-weight PCOS women by NIH criteria show low-normal insulin sensitivity (Si) by frequently sampled intravenous glucose tolerance testing (FSIVGTT) in combination with preferential abdominal fat accumulation (i.e., android fat) by total body dual-energy x-ray absorptiometry (DXA) [59,75,76]. Compared to age- and BMI-matched controls, normal-weight PCOS women by NIH criteria also exhibit adipose insulin resistance (adipose-IR; defined by the product of fasting circulating free fatty acid [FFA] and insulin levels) [73,76,77].

4. Total abdominal (android) fat mass

Abdominal fat mass comprises two major adipose depots: subcutaneous (SC) and intra-abdominal adipose. In humans, SC abdominal adipose normally stores lipid as protection against insulin resistance, while intra-abdominal adipose has the opposite effect [78]. Total body dual-energy x-ray absorptiometry studies confirm that android fat mass and the percent android fat relative to total body fat are greater in normal-weight PCOS women than age- and BMI-matched controls [59,75]. In all women combined, android fat mass positively correlates with circulating levels of total testosterone (T), free T, androstenedione (A4), and fasting insulin, as does the percent android fat mass relative to total body fat with circulating levels of total T, free T, A4, and fasting insulin [59,76]. Android fat mass in these individuals also negatively correlates with circulating cortisol levels, demonstrating an opposing system interplay of testosterone with cortisol in the control of android fat mass in women with PCOS [76].

Adjusting for fasting insulin levels, android fat mass remains positively correlated with circulating total T levels, as does the percent android fat mass relative to total body fat with circulating levels of total T, free T, and A4 [59]. In these normal-weight PCOS women, moreover, androgen receptor blockade by low-dose flutamide simultaneously decreases percent android fat and increases fasting glucose levels, supporting the role of androgen excess in the metabolic adaptation of PCOS through body fat distribution [16,79].

4.1. Intra-abdominal adipose

Intra-abdominal (visceral) adipose in humans is normally highly lipolytic and resists androgen inhibition of catecholamine-induced lipolysis (lipid breakdown) despite expressing androgen receptors [80]. Intra-abdominal fat mass in normal-weight NIH-defined PCOS women is increased in proportion to circulating androgen concentrations, and fasting levels of insulin, TG and non-high-

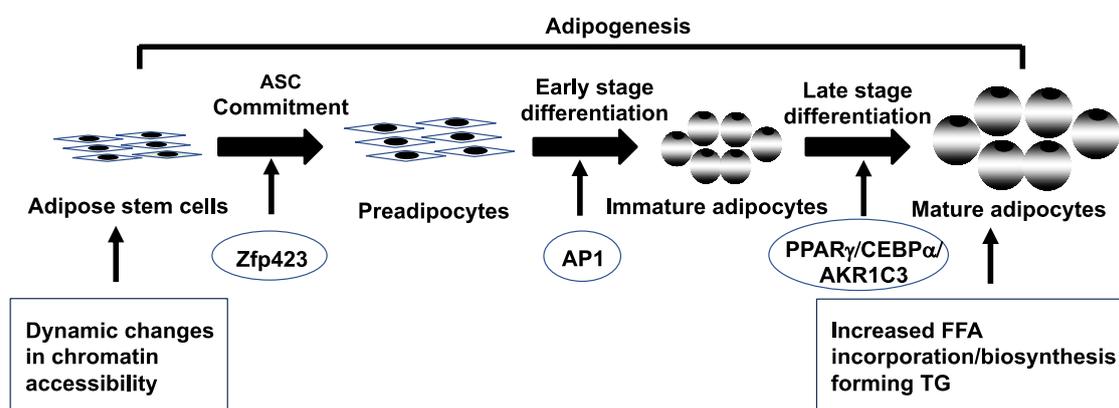
density lipoprotein (non-HDL) cholesterol [59]; it also exhibits exaggerated catecholamine-induced lipolysis in nonobese PCOS women [81,82]. These intra-abdominal fat characteristics favor enhanced FFA availability for hepatic lipid storage and utilization [83]. They also promote insulin resistance with obesity, however, when increased FFA availability exceeds the capacity of target tissues to oxidize fat or convert diacylglycerols to triacylglycerols [81,82,84].

4.2. Subcutaneous abdominal adipose

Subcutaneous abdominal adipose normally protects against insulin resistance by balancing lipogenesis (lipid formation) with lipolysis (lipid breakdown) in mature adipocytes in combination with adipogenesis (whereby adipose stem cells [ASCs] initially commit to preadipocytes and then differentiate into newly-formed adipocytes) (Figure 2) [85-87]. In this manner, SC adipose can increase its fat storage through enlargement of mature adipocytes (i.e., hypertrophy) and development of new adipocytes (i.e., hyperplasia) to buffer fatty acid influx as energy intake exceeds its expenditure [88,89].

Within SC adipose, androgen normally diminishes insulin-stimulated glucose uptake and impairs catecholamine-stimulated lipolysis through reduced β_2 -adrenergic receptor and hormone-sensitive lipase (HSL) protein expression [80,81,90]. Women with PCOS have similar SC abdominal adipose characteristics of diminished insulin-mediated glucose uptake, reduced glucose transporter type 4 (GLUT-4) expression [91] and catecholamine lipolytic resistance [92,93]. Importantly, catecholamine lipolytic resistance in normal-weight PCOS women [92,93] can be counterbalanced by impaired insulin suppression of lipolysis in overweight PCOS women [94].

Within SC adipose, an aldo-ketoreductase enzyme, namely aldo-ketoreductase type 1C3 (AKR1C3) generates local T from A4 [95,96]. AKR1C3 gene expression and activity are greater in SC gluteal than omental fat, with SC gluteal fat favoring androgen activation (i.e., AKR1C3), and omental cells favoring androgen inactivation (i.e., aldo-ketoreductase type 1C2 [AKR1C2]) [96]. In PCOS women, increased AKR1C3-mediated androgen activation enhances lipid storage through increased lipogenesis and decreased lipolysis [97,98], promoting fat accretion [75,98, 99] despite diminished



immature/mature adipocytes [95-97]. Dynamic changes in chromatin accessibility of SC abdominal ASCs during adipogenesis activates different transcriptional factors/genes (zinc-finger protein 423 [Zfp423], activator protein-1 [AP-1], peroxisome proliferator-activated receptor γ [PPAR γ], CCAAT enhancer binding protein α [CEBP α] and aldo-ketoreductase type 1C3 [AKR1C3]), leading to increased free fatty acid (FFA) incorporation/biosynthesis, thus forming triglycerides (TG) in newly-formed mature adipocytes [79,97,98,99,100].

4.3. Subcutaneous abdominal stem cells and cellular reprogramming

Subcutaneous abdominal ASCs from normal-weight PCOS women exhibit altered dynamic chromatin accessibility during adipogenesis compared to control ASCs, and are characterized by limited chromatin accessibility in undifferentiated ASCs (quiescent stage) followed by exaggerated availability (active stage) in newly-formed adipocytes [100]. These chromatin remodeling patterns of PCOS stem cells accompany enrichment of binding motifs for transcription factors (TFs) of the activator protein-1 (AP-1) subfamily during early cell differentiation, with altered gene expression of adipogenic/angiogenic functions involving androgen-insulin interactions through transforming growth factor (TGF)- β 1 signaling [77].

In these SC abdominal ASCs of normal-weight PCOS women, an exaggerated commitment to preadipocytes via zinc-finger protein 423 (*ZFP423*) overexpression negatively correlates with fasting circulating glucose levels [99], and accompanies a greater proportion of small SC abdominal adipocytes [59,77], presumably to buffer against fatty acid influx [89,101]. Similar small SC abdominal adipocytes occur in other individuals [101-103], in whom they protect against insulin resistance through stem cell *ZFP423* upregulation from epigenetic modifications [104].

Following exaggerated commitment to preadipocytes, these same abdominal ASCs from normal-weight PCOS exhibit accelerated lipid accumulation in newly-formed adipocytes *in vitro* that predicts reduced serum FFA levels and improved systemic insulin sensitivity *in vivo* [99,75]. These differentiating PCOS stem cells can overexpress the genes, peroxisome proliferator-activated receptor γ (*PPAR γ*) and CCAAT enhancer binding protein *a* (*CEBPa*), in combination with increased *AKR1C3* gene expression during adipocyte maturation *in vitro* (Figure 2) [79,98,100].

From a causal perspective, administration of flutamide (an androgen receptor blocker) to healthy normal-weight PCOS women attenuates accelerated lipid accumulation within these newly-formed adipocytes *in vitro* and increases fasting circulating glucose levels (but within the normal range) [79]. In addition to intrinsic changes in PCOS stem cell characteristics, therefore, local androgen excess in PCOS appears to enhance lipid storage in SC abdominal adipocytes [79,98,99] and favor insulin sensitivity [75,105,106].

5. Lipotoxicity

Lipotoxicity refers to the ectopic lipid accumulation in non-adipose tissue, where it induces oxidative/endoplasmic reticulum stress linked with insulin resistance and inflammation [107]. Overweight/obese PCOS women; with greater preferential abdominal fat accumulation, hyperandrogenism, and insulin resistance [2]; are at particular risk of developing lipotoxicity due to excess FFA uptake into non-adipose cells, in part from increased highly-lipolytic intra-abdominal fat with impaired insulin suppression of lipolysis [81,82,94, 108-110]. In these individuals, excess fatty acid influx in skeletal muscle and liver promotes diacylglycerol-induced insulin resistance, impairs insulin signaling via increased insulin receptor serine phosphorylation, and disrupts mitochondrial oxidative phosphorylation [84, 111]. Enlarged SC abdominal mature adipocytes in overweight compared to normal-weight PCOS women also fosters a pro-inflammatory lipid depot environment [59,94].

Within today's contemporary lifestyle, NIH-defined PCOS women have a 2- to 3-fold higher prevalence of metabolic syndrome (33-47%) than that of age-matched normal women [3, 112-114], which is reduced by diminished abdominal fat accumulation [114]. Beginning in adolescence, an increased risk for developing metabolic syndrome [115] is evident in hyperandrogenic women [116] who preferentially increase abdominal adiposity with weight gain [61].

Increased abdominal fat in PCOS women also increases the risk of developing nonalcoholic fatty liver disease (NAFLD) [117-119], with non-alcoholic hepatic steatosis varying in inflammation and fibrosis [120]. Obesity in PCOS women is an important risk factor for hepatic steatosis [117], as is androgen excess *per se*, since the probability of hepatic steatosis (37%) and elevated serum aminotransferase levels are greater in hyperandrogenic women with PCOS than age- and weight-matched controls [121-122]. Magnetic resonance spectroscopy further confirms greater liver fat content in women with hyperandrogenic PCOS than non-hyperandrogenic PCOS [123].

6. Parallel evolution of PCOS-like traits in naturally hyperandrogenic female rhesus macaques

Ancestors of macaques migrated out of Africa before humans (Figure 1), about 5-6 million years ago [12,15]. Second only to humans, contemporary rhesus macaques occupy the largest habitat range of any primate, somewhat emulating humans in their diversity of habitats, including obesogenic urban environments [13]. Such close evolutionary history to humans bestows considerable similarities in genomic, developmental, physiological, anatomical, neurological, behavioral and aging characteristics, as well as comparable breadth of natural disease susceptibility [10], including female hyperandrogenism, PCOS [8,9] and obesity [124]. Obesity in rhesus macaques is heritable [125], emulates that in humans [126-128], and may associate with human obesity risk genes [125], increased risk of T2DM [127,129], dyslipidemia [12,126,128, 130] and cardiometabolic disease [131,132]. In female rhesus macaques, as in women, hyperandrogenism enhances obesity outcomes [128,130,133]. Examining the etiology for female rhesus macaque hyperandrogenism and accompanying PCOS-like traits, including metabolic dysfunction, may thus provide supportive evidence for parallel evolution of these traits to humans and for a shared vulnerability to PCOS (Figure 1). In addition, female rhesus macaques and humans share menstrual cycle traits, including a relatively lengthy follicular or preovulatory phase, exposing selection of a single preovulatory follicle to hyperandrogenic anovulatory consequences of prolonged LH hypersecretion, FSH hyposecretion [134], as well as hyperinsulinemia [10].

Hyperandrogenic female rhesus monkeys with increased adiposity also emulate metabolic dysfunction as seen in women with PCOS. They exhibit increased abdominal subcutaneous and visceral adiposity [128,133, 135], adipose insulin resistance and impaired insulin secretion [136], along with an increased incidence of T2DM [137]. Their SC abdominal adipocytes demonstrate an altered ability to store fat relative to BMI [128,135, 138,130], with impaired preadipocyte differentiation into adipocytes accompanying decrease in C/EBP α mRNA. An associated enhancement of SC abdominal ASC commitment to preadipocytes through increased ZFP423 mRNA expression may indicate a compensatory mechanism for impaired preadipocyte differentiation [138]. Those with the highest testosterone values demonstrate increased BMI, central adiposity and insulin resistance [8,128].

Hyperandrogenism in female rhesus monkeys may have developmental origins, emulating PCOS in women. A positive correlation of adult anogenital distance with circulating testosterone levels in hyperandrogenic adult female rhesus monkeys suggests mid-gestational hyperandrogenic origins [9]. Increased anogenital distance has also been reported for girls born to women with PCOS [139] and in women with PCOS [140]. Elevated maternal circulating levels of anti-mullerian hormone from polycystic ovaries may enhance maternal hyperandrogenism and amplify epigenetic transgenerational transmission of hyperandrogenic phenotype in female offspring [141]. Consistent with these findings, gestational hyperandrogenism in rhesus monkeys induces maternal hyperinsulinemia and hyperglycemia, and reliably generates 75% of female offspring with heterogenous PCOS-like phenotypes [142], with gestational hyperinsulinemia inducing ectopic pericardial and perirenal fetal lipid accumulation [143]. Given these findings implicating hyperandrogenic developmental origins in the etiology of preferential fat storage, female rhesus monkeys may provide unique insight into proximate mechanisms amplifying outcomes from inheritance of PCOS risk genes, calling for gene editing studies of monkey embryos/cells to express female phenotypes generated by specific PCOS risk genes in individuals of known genetic backgrounds [10,144].

7. Conclusions

Polycystic ovary syndrome has persisted from antiquity to become the most common endocrine-metabolic disorder of reproductive-aged women. While its ancestral traits once favored abdominal fat deposition and increased energy availability through hyperandrogenism and insulin resistance for reproduction within hostile environments of food deprivation, these same traits now underlie different PCOS phenotypes with various risks for endocrine-metabolic dysfunction that are worsened by obesity. Healthy normal-weight women with NIH-defined PCOS have SC abdominal

adipose characteristics that favor lipid storage in combination with low-normal insulin sensitivity accompanied by increased highly-lipolytic intra-abdominal fat deposition. As an ancestral trait programmed by genetic inheritance and epigenetic amplification during gestation, such an evolutionary metabolic adaptation in normal-weight PCOS women balances enhanced SC adipose storage with increased circulating glucose availability and free fatty acid oxidation as energy substrate for brain, muscle and other crucial target tissues. This metabolic adaptation in hyperandrogenic PCOS women also favors oligo-ovulation, which allowed women from antiquity sufficient time for childrearing of fewer offspring who in turn had a greater likelihood of childhood survival [6].

8. Future Directions

These heritable PCOS characteristics are now adversely affected by today's contemporary environment through epigenetic events that predispose to lipotoxicity with excess weight gain and pregnancy complications. Understanding the evolutionary origins of PCOS emphasizes the need for a greater focus on preventive healthcare with early and appropriate lifestyle as well as therapeutic choices to optimize the long-term, endocrine-metabolic health of PCOS women in today's obesogenic environment.

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Informed Consent statement: Informed consent was obtained from all subjects involved in the study. Written informed consent was obtained from the patient(s) to publish this paper.

Data Availability statement: not applicable

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