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# Bidirectional Mendelian randomization to explore the causal relationships between body mass index and polycystic ovary syndrome

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**STUDY QUESTION:** What are the causal relationships between polycystic ovary syndrome (PCOS) and body mass index (BMI)?

**SUMMARY ANSWER:** Bidirectional Mendelian randomization analyses suggest that increased BMI is causal for PCOS while the reverse is not the case.

**WHAT IS KNOWN ALREADY:** The contribution of obesity to the pathogenesis of PCOS is controversial. To date, published genetic studies addressing this question have generated conflicting results and have not utilized the full extent of known single nucleotide polymorphisms associated with body mass index (BMI).

**STUDY DESIGN, SIZE, DURATION:** This cross-sectional Mendelian randomization (MR) and genetic association study was conducted in 750 individuals of European origin and with PCOS and 1567 BMI-matched controls.

**PARTICIPANTS/MATERIALS, SETTING, METHODS:** Cases and controls were matched for BMI as well as for distribution of weight categories (normal weight, overweight, obese). Two-sample MR using inverse variance weighting (IVW) was conducted using a 92-SNP instrument variable for BMI with PCOS as the outcome, followed by two-sample MR with a 16-SNP instrument variable for PCOS with BMI as the outcome. Sensitivity analyses included MR-Egger and maximum likelihood methods. Secondary analyses assessed associations of genetic risk scores and individual SNPs with PCOS, BMI and quantitative androgen-related and glucose homeostasis-related traits.

**MAIN RESULTS AND THE ROLE OF CHANCE:** Each standard deviation genetically higher BMI was associated with a 4.89 (95% CI 1.46–16.32) higher odds of PCOS. Conversely, genetic risk of PCOS did not influence BMI. Sensitivity analyses yielded directionally consistent results. The genetic risk score of 92 BMI SNPs was associated with the diagnosis of PCOS (OR 1.043, 95% CI 1.009–1.078,  $P = 0.012$ ). Of the 92 BMI risk variants evaluated, none were associated individually with PCOS after considering multiple testing. The association of *FTO* SNP rs1421085 with BMI was stronger in women with PCOS ( $\beta = 0.071$ ,  $P = 0.0006$ ) than in controls ( $\beta = 0.046$ ,  $P = 0.065$ ).

**LIMITATIONS, REASONS FOR CAUTION:** The current sample size, while providing good power for MR and genetic risk score analyses, had limited power to demonstrate association of individual SNPs with PCOS. Cases and controls were not matched for age; however, this was mitigated by adjusting analyses for age. Dietary and lifestyle data, which could have been used to explore the greater association of the *FTO* SNP with BMI in women with PCOS, was not available.

<sup>†</sup>The authors consider that the first two authors should be regarded as joint First Authors.

**WIDER IMPLICATIONS OF THE FINDINGS:** Increasing BMI appears to be causal for PCOS but having PCOS does not appear to affect BMI. This study used the most comprehensive set of SNPs for BMI currently available. Prior studies using fewer SNPs had yielded conflicting results and may have been confounded because cases and controls were not matched for weight categories. The current results highlight the potential utility of weight management in the prevention and treatment of PCOS.

**STUDY FUNDING/COMPETING INTEREST(S):** National Institutes of Health Grants R01-HD29364 and K24-HD01346 (to R.A.), Grant R01-DK79888 (to M.O.G.), Grant U54-HD034449 (to R.S.L.), Grant U19-HL069757 (to R.M.K.). The funders had no influence on the data collection, analyses or conclusions of the study. No conflict of interests to declare.

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**Key words:** polycystic ovary syndrome / Mendelian randomization / genome wide association / genetic variants / single nucleotide polymorphism

## Introduction

Polycystic ovary syndrome (PCOS) affects 6–10% of reproductive aged women, making it the most common endocrinopathy in this age group (Goodarzi et al., 2011). Although PCOS is a heterogeneous disorder with multiple phenotypes, it is most classically characterized by hyperandrogenism and oligoovulation. Women with PCOS are at significantly increased risk for insulin resistance, dyslipidemia, impaired glucose tolerance and type 2 diabetes mellitus (Salley et al., 2007). Women with PCOS have a high prevalence (50–70%) of overweight and obesity, with obesity exacerbating the PCOS phenotype (Lim et al., 2013). Conversely, lifestyle modification and weight loss can improve features of PCOS (Nybacka et al., 2011).

Both PCOS and obesity are highly heritable traits (Stunkard et al., 1990; Vink et al., 2006). Studies evaluating the impact of obesity genes on the susceptibility for PCOS have yielded conflicting results. The fat mass and obesity associated gene (*FTO*), an important candidate gene for obesity identified in genome wide association studies (GWAS) (Loos, 2012), was associated with PCOS in some studies, whereas other studies did not find an association after controlling for BMI (Barber et al., 2008; Ewens et al., 2011; Li et al., 2013). A recent meta-analysis examining the relationship between *FTO* variants and PCOS found that the effect of the *FTO* variant on BMI is larger in women with PCOS compared to normal controls (Wojciechowski et al., 2012), suggesting that PCOS itself may modify the impact of *FTO* on BMI in women with PCOS.

While there appears to be a relationship between PCOS and obesity, the direction and mechanism underlying this association are unknown. One approach to investigate parameters that are correlated, but not necessarily causally related, has been to determine whether genetic variations in a potential underlying trait are associated with the outcome of interest. In this approach, which ranges from simple association to formal instrumental variable (Mendelian randomization (MR)) analysis, an association between the genetic variants associated with the risk factor and the outcome of interest supports a causal relationship. Existing studies of genetic variants for obesity in PCOS have yielded conflicting results, with one study finding no association of a 12-single nucleotide polymorphism (SNP) BMI genetic risk score (GRS) with PCOS (Louwers et al., 2014) and another reporting positive results using 32 BMI SNPs in a Mendelian randomization analysis (Day et al., 2015). The aim of our study was to conduct the first bidirectional state-of-the-art two-sample MR analyses interrogating

causal relationships between BMI and PCOS. We also sought to determine whether the overall genetic burden for obesity, as well as individual BMI susceptibility alleles, predispose to PCOS. We pursued these aims using a comprehensive set of 92 SNPs for BMI, more than that used in prior studies (12 or 32 SNPs) (Louwers et al., 2014; Day et al., 2015). Another unique feature of this study, in contrast to prior studies, is that cases and controls were well-matched for BMI, avoiding any possible confounding effect of higher BMI in the women with PCOS.

## Materials and Methods

### Subjects

The cohort consisted of 750 subjects with PCOS and 1567 BMI-matched controls, all of European origin. All subjects with PCOS met the 1990 NIH criteria (Azziz et al., 2009) and thus had clinical hyperandrogenism (i.e. hirsutism) and/or hyperandrogenemia and chronic oligoovulation. Parameters for defining hirsutism, hyperandrogenemia, oligoovulation and exclusion of related disorders were previously reported (Jones et al., 2012). The majority (1469) of the control subjects were general community controls from either the Cholesterol and Atherosclerosis Pharmacogenetics (CAP) study (Simon et al., 2006) or the Multi-Ethnic Study of Atherosclerosis (MESA) (Bild et al., 2002), from which only European-origin individuals were selected. These included 287 and 1182 subjects, from 603 CAP and 2685 MESA subjects respectively, selected to match the BMI of the PCOS cases. Clinical characteristics of PCOS and control subjects are displayed in Table I. The cohort was matched not only for mean BMI, but also for distribution between BMI categories: normal weight (BMI < 25 kg/m<sup>2</sup>), overweight (BMI ≥ 25 kg/m<sup>2</sup> and < 30 kg/m<sup>2</sup>) and obese (BMI ≥ 30 kg/m<sup>2</sup>) (Table II).

The BMI-matched cohort described above was used for all analyses in this report, except the MR analysis in which PCOS was the exposure and BMI was the outcome, as described below.

### Ethical approval

The study was approved by the Institutional Review Boards of Cedars-Sinai Medical Center (CSMC) and all other recruiting centers. All participants gave written informed consent.

### Genotyping

Genotyping was previously performed at CSMC using Infinium II technology on the MetaboChip, following the manufacturer's protocol (Illumina, San Diego, CA). The MetaboChip is a high throughput genotyping platform that was designed to provide a method by which loci associated with a number of traits related to cardiac and metabolic diseases could be rapidly

**Table I** Baseline characteristics of PCOS and control subjects.

	PCOS (n = 750)	Controls (n = 1567)	P-value
Age (yr)	27 (23–31.9)	59.6 (51–68)	<0.0001
BMI (kg/m <sup>2</sup> )	31.7 (25.3–37.6)	30.6 (28.6–33.8)	0.59
Total Testosterone (nmol/L)	2.39 (1.77–3.08)	1.14 (0.88–1.72) <sup>a</sup>	<0.0001
DHEAS (μmol/L)	6.05 (4.17–8.53)	2.72 (1.84–4.48) <sup>a</sup>	<0.0001
Fasting insulin (pmol/L)	96.0 (54.6–156.0)	45.0 (27.0–73.2)	<0.0001
Fasting glucose (mmol/L)	4.77 (4.50–5.15)	5.00 (4.66–5.50)	<0.0001
HOMA2-IR	2.1 (1.4–3.3)	1.1 (0.77–1.79)	<0.0001
HOMA2-%B	176.2 (128.9–226.1)	97.2 (74.9–130.2)	<0.0001

Values presented as median (interquartile range). Transformed (log or square root) means were compared using unpaired t-tests. <sup>a</sup>Androgen levels were available from 98 deeply phenotyped controls.

**Table II** BMI distribution of PCOS and control subjects.

	PCOS (n = 750)	Controls (n = 1567)	Chi square P-value
Normal weight (BMI < 25 kg/m <sup>2</sup> )	23.1% (173)	23% (361)	0.9998
Overweight (BMI ≥25 and < 30 kg/m <sup>2</sup> )	20.4% (153)	20.4% (320)	
Obese (BMI ≥30 kg/m <sup>2</sup> )	56.5% (424)	56.5% (886)	

genotyped (Voight *et al.*, 2012). The genotyping and quality control details were previously described, which included a principal component analysis to correct for potential population stratification, allowing identification and removal of subjects with substantial non-Caucasian admixture (Jones *et al.*, 2012).

For this project, we initially focused on 97 SNPs associated with BMI in a large GWAS and MetaboChip analysis (Locke *et al.*, 2015). The genotypes for 93 of those 97 SNPs (or SNPs in linkage disequilibrium,  $r^2 > 0.8$ ) were extracted from our MetaboChip data. Four of the BMI-associated SNPs, or SNPs in linkage disequilibrium with these four, were not available on the MetaboChip and were not included in the analysis. One more SNP did not meet MR quality control, as described below, thus, 92 BMI SNPs were ultimately examined.

## Statistical analysis

All continuous parameters with a non-normal distribution were logarithmically or square root transformed. Clinical characteristics between cases and controls were compared using unpaired t-tests. The MR and association analyses described below were adjusted for age.

## Mendelian randomization

In the first set of two-sample MR analyses, we considered BMI as the exposure and PCOS as the outcome. Published summary results from the GWAS meta-analysis for BMI by Locke *et al.* were used to generate a genetic instrument for BMI, focusing on the 93 SNPs that were robustly associated with BMI. One SNP (rs2033529) was removed from the MR analysis due to allele harmonization issues between exposure and outcome data (Hartwig *et al.*, 2016). The remaining 92 SNPs were used to construct the genetic instrument for BMI. SNP to outcome estimates were obtained from our BMI-matched dataset. The primary MR analysis was conducted

using the inverse variance weighted (IVW) method, wherein the SNP to outcome estimate is regressed on the SNP to exposure estimate. We used fixed effects IVW given that we did not detect instrument variable assumption violations (neither heterogeneity nor pleiotropy were observed). The causal effect estimates, equivalent to beta coefficients, were calculated and then transformed to odds ratios.

Given that MR using conventional IVW may be affected by directional pleiotropy (in which exposure SNPs may act through alternative traits), we carried out sensitivity analyses wherein we conducted MR using additional techniques that are affected differently by genetic confounding. These included the maximum likelihood and MR-Egger methods (Pierce and Burgess, 2013; Bowden *et al.*, 2015). Since MR-Egger is robust against directional pleiotropy under the InSIDE (Instrument Strength Independent of Direct Effect) assumption, the intercept serves as an indicator of directional pleiotropy (Bowden *et al.*, 2015). All analyses were conducted in R 3.4.2 with the package ‘TwoSampleMR’ (Hemani *et al.*, 2018).

The second set of MR analyses handled PCOS as the exposure and BMI as the outcome. Summary results from a recent GWAS meta-analysis for PCOS in Europeans were used as the source of data to construct the instrument variable for PCOS (Day *et al.*, 2018). Of the 14 SNPs associated with PCOS at genome-wide significance therein, we included all except rs853854, which was excluded because it is an A/T SNP with an allele frequency close to 50%, thus avoiding ambiguity in analyzing such palindromic SNPs (Hartwig *et al.*, 2016). We also included three SNPs (rs13405728, rs2349415, rs2272046) originally identified in Chinese GWAS that were associated with PCOS in the European meta-analysis and were not in linkage disequilibrium with the 14 SNPs described above. Therefore, the instrument variable for PCOS consisted of 16 SNPs. SNP to outcome estimates were generated in the entire cohort of 2685 European subjects from MESA. Fixed effects IVW, MR-Egger and maximum likelihood MR analyses were conducted as described above.

## Genetic risk score and SNP analyses

To test for the combined effect of all BMI risk alleles, we generated an unweighted genetic risk score (GRS) for each subject. We used an unweighted score because effect sizes for BMI have been determined in individuals without PCOS and effect sizes for all SNPs for PCOS are unknown. Also, unweighted scores perform similarly to weighted scores when constituent SNP effect sizes are similar (Burgess and Thompson, 2013), as is the case for BMI SNPs (Loos, 2012). The GRS was the sum of alleles possessed by each individual that were previously associated with increased BMI. The 92 SNPs used in the MR analyses were included in the risk score (possible range 0–184). The association between the GRS and

PCOS was evaluated using logistic regression. Given that the cases and controls were matched for BMI, we did not adjust the regression for BMI.

We used linear regression to assess association of the GRS with BMI in the entire cohort as well as within cases and controls separately. Within the subjects with PCOS, we assessed the impact of the GRS on additional continuous quantitative traits (total testosterone, dehydroepiandrosterone sulfate (DHEAS), fasting glucose, fasting insulin and homeostasis model assessments of insulin resistance (HOMA2-IR) and beta-cell function (HOMA2-%B) (Levy et al., 1998)).

The individual association of the 92 SNPs (additive model) with PCOS was tested using logistic regression and with BMI using linear regression.

Significance was taken at a  $P$ -value of  $< 0.05$  for the GRS association analysis with PCOS. Analyses of the GRS against quantitative traits used a Bonferroni multiple testing corrected  $P$ -value of 0.007 (0.05/7) because seven quantitative traits were examined. For analyses of individual SNPs, we used a multiple testing corrected  $P$ -value of 0.00054 (0.05/92) based on 92 independent SNPs genotyped.

Generalized linear models were used to statistically compare the regression coefficients from the regression of BMI on the GRS between the PCOS cases and controls. A similar comparison was carried out comparing the association of the *FTO* SNP with BMI in cases and controls.

## Power analysis

For Mendelian randomization, the  $F$  statistic is an indicator of the strength of the instrument variable, with values over 10 reflecting strong instruments (Pierce et al., 2011). The 92-SNP instrument variable for BMI had an  $F$  statistic of 63.4, and the 16-SNP instrument variable for PCOS had an  $F$  statistic of 241.4. Thus, both instruments are well powered to estimate the causal effect of the exposure on the outcome.

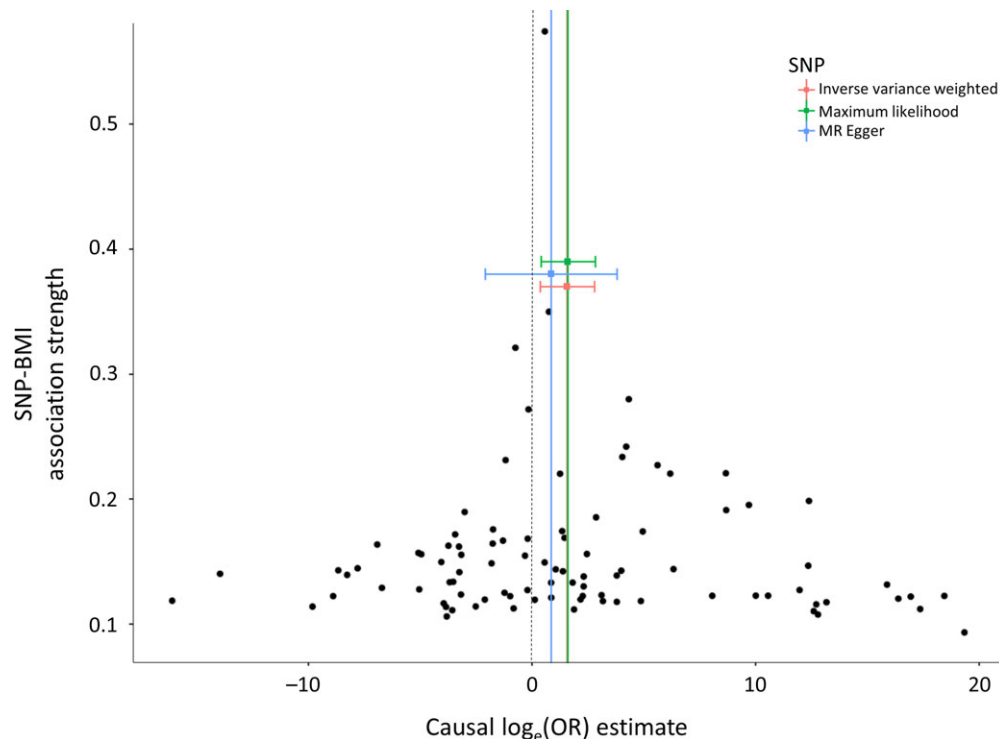
We used the PROC Power Procedure with LOGISTIC statement in SAS (SAS Institute, Cary, NC) to determine the power to detect association between the GRS and PCOS in our cohort. With a mean of 88.9 and standard deviation of 6.1 for the GRS in our cohort, the sample size of 750 cases and 1567 controls has excellent power ( $\geq 97\%$ ) to detect association with PCOS at odds ratio  $\geq 1.03$  and moderate power (72%) to detect association at odds ratio as low as 1.02.

## Results

The mean BMI was not significantly different between PCOS and control subjects in our BMI-matched cohort (Table I). In addition, controls

**Table III Mendelian randomization results for causality of BMI on PCOS**

IVW		MR-Egger				Maximum likelihood	
OR	95% CI	OR	95% CI	Intercept	P value for intercept	OR	95% CI
4.89	1.46–16.32	2.41	0.13–46.0	0.02	0.61	5.07	1.50–17.10



**Figure I Funnel plots showing the causal effect estimates of BMI on PCOS.** Black dots represent the causal effect estimates for each of the 92 SNPs. The three colored squares represent the causal effect estimates from the three MR methods, with corresponding horizontal lines displaying the 95% confidence intervals.

and PCOS subjects were evenly distributed between three BMI categories – normal weight, overweight and obese (Table II).

Causal effect estimates of BMI, as represented by the 92-SNP instrument, on PCOS are displayed in Table III. The primary MR analysis by IVW showed a significant causal effect, wherein each standard deviation genetically higher BMI was associated with a 4.89 (95% CI 1.46–16.32) higher odds of PCOS. The association of the 92-SNP instrument with PCOS was also evaluated using the maximum likelihood and MR-Egger techniques. As seen in Table III and Fig. 1, directionally consistent results were observed, suggesting that the findings are relatively unaffected by violation of MR assumptions. Scatterplots (Fig. 2) demonstrate that SNPs with greater effect on BMI have a greater effect on the risk of PCOS. The intercept of the MR-Egger regression was not significantly different from zero ( $P = 0.61$ ), suggesting that genetic pleiotropy is not driving the MR results.

MR analyses assessing causality in the opposite direction were also performed. None of the three MR methods found evidence of a causal effect of having PCOS on BMI (Table IV).

Consistent with the MR results, the GRS composed of BMI SNPs was associated with the diagnosis of PCOS (OR 1.043, 95% CI

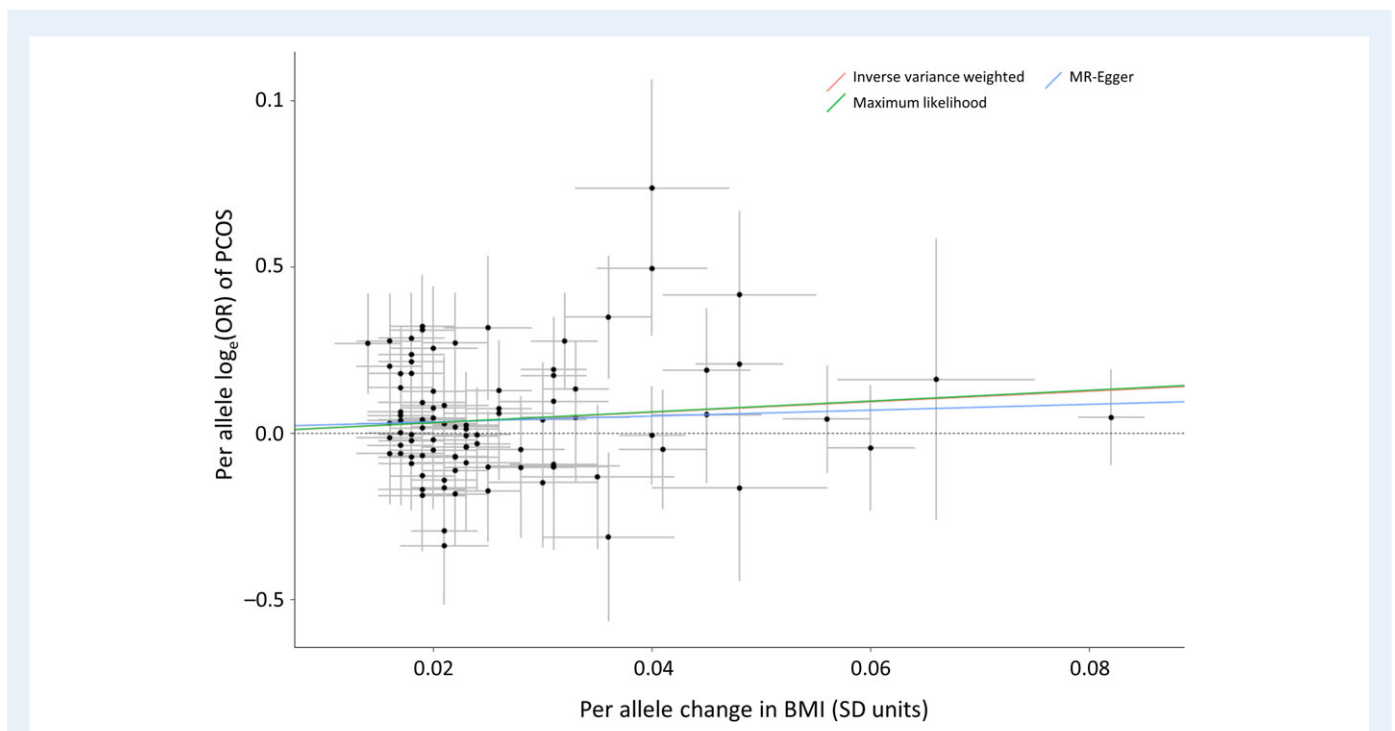
1.009–1.078,  $P = 0.012$ ) (Table V), indicating a 4.3% increase in odds of PCOS per increment in GRS. The mean GRS was 88.7 for controls and 89.4 for PCOS.

In the entire cohort, the GRS for the BMI risk alleles was positively associated with BMI ( $\beta = 0.080$ ,  $P = 0.0001$ ) with every unit increase in GRS resulting in a  $0.080 \text{ kg/m}^2$  increase in BMI. In women with PCOS and controls examined separately, the GRS association with BMI was similar, with no difference between the regression coefficients ( $P = 0.99$ ).

In the women with PCOS, no significant associations were observed between the GRS and any of the other quantitative traits assessed, including total testosterone ( $P = 0.51$ ), DHEAS ( $P = 0.09$ ), fasting glucose ( $P = 0.76$ ), fasting insulin ( $P = 0.20$ ), HOMA2-IR ( $P = 0.52$ ) and HOMA2-%B ( $P = 0.32$ ).

Of the 92 BMI risk variants evaluated, none were associated individually with PCOS after considering multiple testing (Table V).

*FTO* SNP rs1421085 ( $r^2 = 1$  with rs1558902 associated with BMI (Locke *et al.*, 2015)) was not associated with the diagnosis of PCOS (OR 1.05, 95% CI 0.79–1.39,  $P = 0.74$ ); however, it was associated with BMI in the entire cohort ( $\beta = 0.071$ ,  $P = 0.0006$ ) and within the



**Figure 2** Individual effects of 92 genetic variants on BMI and the odds of PCOS. The effect size in the entire cohort of each of the 92 SNPs on BMI (in standard deviation (SD) units) is on the X-axis. The  $\log_e$  odds ratio of each SNP for PCOS is on the Y-axis. The trend lines represent the results of the three MR analyses based on the 92 SNPs.

**Table IV** Mendelian randomization results for causality of PCOS on BMI.

IVW		MR-Egger				Maximum likelihood	
Beta	95% CI	Beta	95% CI	Intercept	P value for intercept	Beta	95% CI
0.003	-0.008–0.013	-0.13	-0.06–0.03	0.003	0.46	0.003	-0.008–0.013

**Table V Association analysis for BMI-increasing GWAS risk alleles with the diagnosis of PCOS.**

Chr	Position	SNP	Nearest gene(s)	Risk increasing allele	Risk allele frequency	OR	95% CI	P value
-	-	Genetic risk score	-	-	-	1.043	1.01–1.08	0.012
1	47457264	rs977747	TALI	T	0.392	0.96	0.73–1.28	0.80
1	49210592	rs3127553 <sup>a</sup>	AGBL4	G	0.372	0.96	0.73–1.26	0.77
1	50332407	rs11583200	ELAVL4	C	0.386	1.00	0.76–1.32	0.98
1	72523773	rs3101336	NEGR1	C	0.642	1.14	0.87–1.51	0.34
1	74764232	rs1514175 <sup>a</sup>	FPGT, TNNI3K	T	0.435	1.00	0.75–1.32	0.97
1	78219349	rs12401738	FUBP1	A	0.327	0.85	0.64–1.13	0.26
1	96696685	rs11165643	PTBP2	T	0.573	0.93	0.71–1.23	0.62
1	109956211	rs17024393	GNAT2	C	0.028	1.18	0.53–2.76	0.70
1	176156103	rs543874	SEC16B	G	0.192	1.23	0.88–1.73	0.22
1	200050910	rs2820292	NAVI	C	0.539	1.14	0.86–1.49	0.36
2	622348	rs13021737	TMEM18	G	0.804	0.96	0.66–1.38	0.81
2	25003800	rs10182181	ADCY3	G	0.478	1.19	0.91–1.56	0.20
2	26782315	rs11126666	KCNK3	A	0.261	0.87	0.63–1.20	0.39
2	59159129	rs1016287	LINC01122	T	0.289	1.02	0.75–1.40	0.88
2	62906552	rs11688816	EHBP1	G	0.511	1.03	0.79–1.37	0.78
2	142759755	rs2121279	LRP1B	T	0.121	1.37	0.90–2.11	0.14
2	164275935	rs1460676	FIGN	C	0.167	1.29	0.90–1.87	0.17
2	181259207	rs1528435	UBE2E3	T	0.623	1.20	0.90–1.60	0.22
2	207963763	rs17203016	CREB1	G	0.178	0.71	0.50–1.01	0.057
2	213121476	rs7599312	ERBB4	G	0.736	0.83	0.61–1.13	0.26
2	219057996	rs492400	USP37	C	0.427	1.03	0.78–1.37	0.83
2	226824609	rs2972143 <sup>a</sup>	LOC646736	A	0.35	1.31	0.98–1.76	0.069
3	25081441	rs6804842	RARB	G	0.583	0.94	0.71–1.24	0.64
3	61211502	rs2365389	FHIT	C	0.598	1.05	0.79–1.39	0.75
3	85912107	rs7622475 <sup>a</sup>	CADM2	C	0.224	1.04	0.74–1.46	0.81
3	142788703	rs2035935 <sup>a</sup>	RASA2	C	0.066	0.84	0.49–1.48	0.56
3	187301576	rs4234589 <sup>a</sup>	ETV5	A	0.863	1.05	0.71–1.58	0.78
4	44877284	rs10938397	GNPDA2	G	0.424	0.99	0.75–1.33	0.97
4	77315142	rs17001561 <sup>a</sup>	SCARB2	A	0.166	0.90	0.62–1.32	0.60
4	103407732	rs13107325	SLC39A8	T	0.083	1.52	0.93–2.50	0.093
4	145878514	rs11727676	HHIP	T	0.902	0.73	0.45–1.19	0.21
5	75050998	rs2112347	POC5	T	0.632	1.14	0.85–1.53	0.39
5	153518086	rs7715256	GALNT10	G	0.431	0.94	0.70–1.27	0.69
6	34671142	rs205262	C6orf106	G	0.291	0.93	0.69–1.26	0.65
6	50944238	rs734597 <sup>a</sup>	TFAP2B	A	0.168	1.21	0.84–1.75	0.30
6	109084356	rs9400239	FOXO3	C	0.713	1.37	1.00–1.86	0.048
6	120227364	rs9374842	LOC285762	T	0.758	0.83	0.60–1.15	0.26
6	137717234	rs13201877	IFNGR1	G	0.128	0.92	0.62–1.36	0.67
6	162953340	rs13191362	PARK2	A	0.889	0.90	0.60–1.36	0.62
7	75001105	rs1167827	HIP1	G	0.572	1.07	0.81–1.43	0.60
7	95007450	rs6465468	ASB4	T	0.296	0.94	0.70–1.27	0.69
8	76969139	rs17405819	HNF4G	T	0.7	1.31	0.98–1.76	0.070
8	81538012	rs16907751	ZBTB10	C	0.888	0.88	0.57–1.33	0.54
8	85242264	rs2033732	RALYL	C	0.749	1.10	0.80–1.50	0.56
9	15624326	rs4740619	C9orf93	T	0.544	1.77	1.03–3.04	0.036
9	28404339	rs10968576	LINGO2	G	0.31	0.84	0.62–1.13	0.26
9	110972163	rs6477694	EPB41L4B	C	0.341	1.06	0.80–1.40	0.71

Continued



**Table V** *Continued*

Chr	Position	SNP	Nearest gene(s)	Risk increasing allele	Risk allele frequency	OR	95%_CI	P value
9	119418304	rs1928295	<i>TLR4</i>	T	0.548	1.02	0.77–1.35	0.91
9	128500735	rs10733682	<i>LMX1B</i>	A	0.49	1.00	0.76–1.33	0.99
10	87400884	rs7899106	<i>GRID1</i>	G	0.052	2.09	1.11–3.99	0.022
10	102385430	rs17094222	<i>HIF1AN</i>	C	0.216	0.90	0.65–1.26	0.55
10	104859028	rs11191560	<i>NT5C2</i>	C	0.091	1.10	0.68–1.81	0.70
10	114748339	rs7903146	<i>TCF7L2</i>	C	0.704	1.01	0.75–1.37	0.93
11	8644592	rs7113874 <sup>a</sup>	<i>TRIM66</i>	C	0.638	1.03	0.77–1.37	0.84
11	27656701	rs7103411 <sup>a</sup>	<i>BDNF</i>	T	0.782	0.95	0.67–1.35	0.79
11	43820854	rs2176598	<i>HSD17B12</i>	T	0.264	0.98	0.71–1.35	0.91
11	47607569	rs3817334	<i>MTCH2</i>	T	0.409	1.08	0.82–1.42	0.59
11	114527614	rs12286929	<i>CADM1</i>	G	0.54	0.89	0.68–1.18	0.43
12	48533735	rs7138803	<i>BCDIN3D</i>	A	0.388	1.32	1.00–1.76	0.054
12	121347850	rs11057405	<i>CLIP1</i>	G	0.921	0.91	0.55–1.47	0.69
13	26908262	rs1885988 <sup>a</sup>	<i>MTIF3</i>	G	0.17	0.86	0.59–1.26	0.44
13	53000207	rs12429545	<i>OLFM4</i>	A	0.132	1.05	0.72–1.54	0.80
13	65103705	rs9540493	<i>MIR548X2</i>	A	0.424	1.15	0.87–1.51	0.32
13	78478920	rs1441264	<i>MIR548A2</i>	A	0.625	0.91	0.69–1.20	0.52
14	24998019	rs10132280	<i>STXBP6</i>	C	0.687	0.99	0.74–1.33	0.96
14	28806589	rs12885454	<i>PRKD1</i>	C	0.666	0.75	0.56–1.00	0.049
14	78969207	rs7141420	<i>NRXN3</i>	T	0.519	0.97	0.73–1.29	0.83
15	49535902	rs3736485	<i>DMXL2</i>	A	0.467	1.24	0.94–1.64	0.13
15	65869870	rs2241420 <sup>a</sup>	<i>MAP2K5</i>	G	0.754	0.91	0.66–1.25	0.57
15	70881044	rs7164727	<i>LOC100287559</i>	T	0.684	1.27	0.94–1.71	0.12
16	3567359	rs758747	<i>NLRC3</i>	T	0.288	0.96	0.71–1.30	0.79
16	19842890	rs12446632	<i>GPRC5B</i>	G	0.855	1.64	1.10–2.43	0.014
16	28240912	rs2650492	<i>SBK1</i>	A	0.293	1.09	0.82–1.45	0.57
16	28796987	rs3888190	<i>ATP2A1</i>	A	0.377	1.21	0.92–1.60	0.17
16	29922838	rs4787491	<i>INO80E</i>	G	0.541	0.99	0.75–1.30	0.93
16	31037396	rs9925964	<i>KAT8</i>	A	0.619	1.03	0.78–1.37	0.81
16	47620091	rs2080454	<i>CBLN1</i>	C	0.356	1.07	0.80–1.42	0.65
16	52358455	rs1421085 <sup>a</sup>	<i>FTO</i>	C	0.43	1.05	0.79–1.39	0.74
17	1951886	rs9914578	<i>SMG6</i>	G	0.196	0.95	0.68–1.34	0.78
17	5223976	rs1000940	<i>RABEP1</i>	G	0.305	1.38	1.02–1.88	0.037
17	76230166	rs12940622	<i>RPTOR</i>	G	0.582	0.98	0.74–1.30	0.88
18	19358886	rs1808579	<i>C18orf8</i>	C	0.545	1.20	0.92–1.57	0.19
18	38401669	rs7239883	<i>LOC284260</i>	G	0.385	1.22	0.92–1.63	0.16
18	55034299	rs7243357	<i>GRP</i>	T	0.818	1.02	0.71–1.45	0.92
18	55980115	rs6567160	<i>MC4R</i>	C	0.235	1.04	0.76–1.43	0.79
19	18315825	rs17724992	<i>PGPEP1</i>	A	0.736	1.04	0.76–1.42	0.79
19	39001372	rs29941	<i>KCTD15</i>	G	0.701	0.93	0.69–1.26	0.65
19	50087459	rs2075650	<i>TOMM40</i>	A	0.861	1.06	0.72–1.57	0.76
19	50894012	rs2287019	<i>QPCTL</i>	C	0.805	1.42	0.99–2.03	0.059
19	52281735	rs2303108 <sup>a</sup>	<i>ZC3H4</i>	G	0.695	0.95	0.70–1.30	0.77
20	50521269	rs6091540	<i>ZFP64</i>	C	0.723	0.84	0.62–1.14	0.28
21	39213610	rs2836754	<i>ETS2</i>	C	0.621	1.32	1.00–1.75	0.051

<sup>a</sup>SNPs rs3127553, rs1514175, rs2972143, rs7622475, rs2035935, rs4234589, rs17001561, rs734597, rs7113874, rs7103411, rs1885988, rs2241420, rs1421085, rs2303108 are in linkage disequilibrium ( $r^2 > 0.8$ ) with published (Locke et al., 2015) SNPs, rs657452, rs12566985, rs2176040, rs13078960, rs16851483, rs1516725, rs17001654, rs2207139, rs4256980, rs11030104, rs12016871, rs16951275, rs1558902, rs3810291, respectively. Gene names are those given in the publication that identified these SNPs (Locke et al., 2015). Association analyses are adjusted for age.



women with PCOS ( $\beta = 0.11$ ,  $P = 0.0019$ ). In the controls, rs1421085 did not quite attain a significant association with BMI ( $\beta = 0.046$ ,  $P = 0.065$ ). The association between *FTO* SNP rs1421085 and BMI was significantly different between PCOS subjects and controls ( $P = 0.033$ ).

## Discussion

This is the first study to conduct bidirectional MR between BMI and PCOS. Our MR results indicate that increased BMI is causal for PCOS, while having PCOS does not have a causal impact on BMI. In line with these results, we found that a genetic risk score based on BMI-increasing alleles was associated with PCOS. We also report detailed results centered on the *FTO* SNP, which is of considerable interest to PCOS researchers.

A previous study by Louwers et al., which did not include formal MR analysis, did not find an association between BMI risk alleles and PCOS independent of BMI (Louwers et al., 2014). This study also used a genetic risk score, but the score was constructed from only 12 SNPs. We similarly did not find an association between the genetic risk score and the diagnosis of PCOS when we used only the same 12 SNPs for the risk score (data not shown). In addition, compared to the NIH criteria used to diagnose PCOS in our cohort, the Rotterdam criteria used in the previous study may result in reduced power due to greater heterogeneity of cases and a higher proportion of undiagnosed cases within population based controls (up to 20%) (Yildiz et al., 2012).

In turn, a GWAS for PCOS by Day et al. (2015) in European individuals found in Mendelian randomization analysis that a GRS based on 32 BMI-raising alleles (Speliotes et al., 2010) was strongly associated with PCOS in a large sample size. In our cohort, a sub-analysis using a GRS based on the 24 available SNPs of these 32 was also associated with PCOS (OR 1.054, 95% CI 1.024–1.084,  $P = 0.0003$ ), providing confirmation of the results of Day et al. in an independent cohort (no overlap in subjects).

Our study, conducting MR and GRS analysis using 92 SNPs, is the most comprehensive to date. This work is the first to conduct two-sample MR in the PCOS genetics field. Two-sample MR, in which the instrument-exposure and instrument-outcome associations are calculated in non-overlapping samples, has emerged as the preferred method for conducting MR, avoiding biases that may arise when the associations are assessed in a single sample (Hartwig et al., 2016). The large number of SNPs increased the power of the GRS, allowing us to detect association with BMI despite having a modest sample size by GWAS standards.

Another feature distinguishing our study is that we conducted sensitivity analyses with multiple MR methods, an increasingly common practice in high-quality MR studies (Wang et al., 2017; Au Yeung et al., 2018). IVW is usually employed as the primary MR method because it has the greatest power to detect effects. Though less powerful, MR-Egger is included among the sensitivity analyses because it is resistant to pleiotropy and provides a test to detect pleiotropy (intercept versus zero) (Burgess and Thompson, 2017). The finding of directionally consistent results from multiple MR methods increases the robustness of our results.

Another advantage of our study was that our cases and controls were matched for BMI, avoiding the common scenario (as seen in the

GWAS (Day et al., 2015)) where cases are more obese than controls, which could confound MR and GRS or SNP association with BMI variants. In the earlier study of 12 SNPs, cases and controls were matched for mean BMI; however, unlike our study, cases and controls differed in distribution across weight groups (normal, overweight, obese) (Louwers et al., 2014).

The *FTO* SNP rs1421085 did not attain independent significant association with PCOS in our sample, but it was associated with obesity in the entire cohort and within the PCOS subjects. Furthermore, we found the effect size of *FTO* on BMI was stronger in PCOS subjects than in controls. This is consistent with prior evidence from a meta-analysis demonstrating that *FTO* plays a greater role in BMI in PCOS than in the general population (Wojciechowski et al., 2012). PCOS may modify the influence of *FTO* on BMI. This might also reflect lifestyle patterns in PCOS, as adverse diets have been found to strengthen the association of *FTO* variation with BMI (Qi et al., 2014). Indeed, the balance of evidence suggests greater energy consumption in women with PCOS than in unaffected women (Lin and Lujan, 2014). Whether this explains the differential association of *FTO* variation with BMI deserves investigation.

Recent studies suggest that the magnitude of association with BMI of genetic variants (GRS and select individual SNPs including *FTO*) for BMI may be stronger in younger individuals, possibly related to the environment becoming more obesogenic in recent decades (Rosenquist et al., 2015; Winkler et al., 2015; Walter et al., 2016). As the women with PCOS were younger than the controls, this could artifactually increase the magnitude of the association of genetic variants with BMI in the women with PCOS. While we did not observe this with the GRS, it is a concern for the *FTO* variant. This concern is mitigated by the fact that our results are similar with and without adjustment for age. Similarly, in the meta-analysis cited above, after age adjustment the effect of *FTO* variation on BMI remained greater in PCOS than in general cohorts (Wojciechowski et al., 2012). Large-scale studies of longitudinal cohorts of women with PCOS would be needed to fully answer whether age drives the stronger association of the *FTO* SNP with BMI in PCOS.

In summary, we report the first two-sample, bidirectional MR analysis examining the relationship between PCOS and BMI in cases and controls well-matched for BMI to avoid any confounding effects of higher BMI in the women with PCOS. The MR results, backed by the GRS results and the observations of others (Day et al., 2015), suggests that obesity influences the development of PCOS. On the other hand, having PCOS appears not to increase the risk of obesity. These results have significant implications for patient counseling and suggest that anti-obesity measures should be tested for their ability to prevent or treat PCOS.

## Authors' roles

M.A.B. and M.O.G. conceived and designed the study. Y.H., M.A.B., M.R.J. and X.G. contributed to analysis of the data. Y.I.C., J.I.R., R.M.K., R.S.L., and R.A. acquired the data. M.A.B. and M.O.G. drafted the article. Y.H., M.R.J., X.G., Y.I.C., J.I.R., R.M.K., R.S.L., and R.A. critically revised the article. All authors gave final approval of the version to be published.

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## Conflict of interest

The funders had no influence on the data collection, analyses or conclusions of the study. There are no conflict of interests to declare.

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