



# Evaluation of Evidence for Pathogenicity Demonstrates That *BLK*, *KLF11*, and *PAX4* Should Not Be Included in Diagnostic Testing for MODY

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**Maturity-onset diabetes of the young (MODY) is an autosomal dominant form of monogenic diabetes, reported to be caused by variants in 16 genes. Concern has been raised about whether variants in *BLK* (MODY11), *KLF11* (MODY7), and *PAX4* (MODY9) cause MODY. We examined variant-level genetic evidence (cosegregation with diabetes and frequency in population) for published putative pathogenic variants in these genes and used burden testing to test gene-level evidence in a MODY cohort ( $n = 1,227$ ) compared with a control population (UK Biobank [ $n = 185,898$ ]). For comparison we analyzed well-established causes of MODY, *HNF1A*, and *HNF4A*. The published variants in *BLK*, *KLF11*, and *PAX4* showed poor cosegregation with diabetes (combined logarithm of the odds [LOD] scores  $\leq 1.2$ ), compared with *HNF1A* and *HNF4A* (LOD scores  $> 9$ ), and are all too common to cause MODY (minor allele frequency  $> 4.95 \times 10^{-5}$ ). Ultra-rare missense and protein-truncating variants (PTV) were not enriched in a MODY cohort compared with the UK Biobank population (PTV  $P > 0.05$ , missense  $P > 0.1$  for all three genes) while *HNF1A* and *HNF4A* were enriched ( $P < 10^{-6}$ ). Findings of sensitivity analyses with different population cohorts supported our results. Variant and gene-level genetic evidence does not support *BLK*, *KLF11*, or *PAX4* as a cause of MODY. They should not be included in MODY diagnostic genetic testing.**

Maturity-onset diabetes of the young (MODY) is the most common subtype of monogenic diabetes. It is reported to be caused by heterozygous variants in 16 genes (1). MODY

accounts for  $\sim 3\%$  of all diabetes cases diagnosed before 30 years of age (2,3). The prevalence of MODY is estimated to be 108 cases per million (4). An accurate genetic diagnosis is important for patients with MODY, as it can determine the correct treatment (1,5) and provides an accurate assessment of the risk of diabetes for future offspring. The advent of next-generation sequencing has enabled a paradigm shift in genetic testing from focusing on single gene testing to gene panel tests for diseases (6). While this can boost diagnostic yield, it also has the potential to increase the risk of reporting variants in genes that are not a cause of MODY if genes are not carefully selected. This is likely to occur with next-generation sequencing, as it enables large numbers of genes to be tested more easily. An incorrect genetic diagnosis could result in stopping insulin in a patient with type 1 diabetes. It could lead to inappropriate testing of family members, causing increased anxiety in unaffected relatives and inflicting the psychological burden of having a genetic disease. Therefore, it is crucial that the gene panel only includes genes with robust aetiological evidence to prevent misdiagnosis of MODY.

*BLK*, *KLF11*, and *PAX4* are listed on Online Mendelian Inheritance in Man (OMIM) as MODY11, MODY7, and MODY9, but there is a need to reevaluate whether variants in these genes do cause MODY. Variants in *BLK* and *PAX4* have been reported to cause MODY via haploinsufficiency (7,8), while variants in *KLF11* were reported to cause the disease, potentially via a gain-of-function mechanism (9). These studies were conducted  $> 10$  years ago, before the availability of variant frequency in large population cohorts (7–9). *KLF11* and *PAX4* were identified

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based primarily on biological candidacy rather than the hypothesis-free genetic approach, which is now considered to be the most robust method for gene discovery studies. The only *BLK* coding variant (p.A71T) reported to cause MODY was later found to be very common in the population, raising doubt over the aetiological role of *BLK* (10). Rarity of a variant in a large control population as well as enrichment of variants in that gene in a disease cohort compared with a control population has become crucial evidence to support the gene-disease association alongside familial cosegregation (11,12).

Therefore, the aim of our study was to evaluate genetic evidence for variants in *BLK*, *KLF11*, and *PAX4* as a cause of MODY. We evaluated the existing evidence for these genes and assessed the gene-disease association using a large MODY cohort and population cohorts. We demonstrate that there is a lack of robust genetic evidence to support the aetiological role of variants in *BLK*, *KLF11*, and *PAX4* for MODY.

## RESEARCH DESIGN AND METHODS

### Study Populations

#### **MODY Cohort**

We included 1,227 unrelated probands from the U.K. who were referred for genetic testing for MODY from routine clinical care to the Exeter Genomics Laboratory at the Royal Devon and Exeter Hospital. Cohort characteristics can be found in Supplementary Table 1. None of these individuals were reported to have islet autoantibodies by the referring clinicians. Of patients, 84% were of self-reported European ancestry, and the overall rate of monogenic diabetes was 22.5%. Informed consent was obtained from the probands or their parents/guardians, and the study was approved by the North Wales ethics committee (17/WA/03).

#### **UK Biobank**

UK Biobank is a population-based cohort from the U.K. with deep phenotyping data and genetic data for ~500,000 individuals aged 40–70 years at recruitment (13,14). A subset of ~200,000 DNA samples from UK Biobank participants underwent exome sequencing; this data set was recently made available for research (15). Of individuals included, 94% were of self-reported White ethnicity. The UK Biobank resource was approved by the UK Biobank Research Ethics Committee, and all participants provided written informed consent to participate.

#### **gnomAD**

We used Genome Aggregation Database (gnomAD) v2.1.1 (141,456 individuals) and v3 (76,156 individuals) for alternative control populations in supplementary analyses. A detailed description of the cohort has previously been published (16). gnomAD v2.1.1 includes individuals with exome ( $n = 125,748$ ) and genome ( $n = 15,708$ ) data, whereas v3 includes individuals with genome data. Of

individuals in gnomAD v2.1.1, 46% are of non-Finnish European ancestry, while for v3 this is 45%.

### Genetic Testing

#### **MODY Cohort**

We undertook targeted next-generation sequencing of *BLK*, *PAX4*, and *KLF11* as well as *HNF1A* and *HNF4A* for probands suspected to have MODY, as previously described (6). Targets were covered at a mean read depth of 460X per base, and all bases had a mean coverage depth of at least 30 reads across the cohort. Variants were annotated against Genome Reference Consortium Human Build 37 (GRCh37) with Alamut Batch (Interactive Biosoftware, Rouen, France) using a RefSeq transcript: *BLK* NM\_001715.3, *KLF11* NM\_003597.4, *PAX4* NM\_001366110.1, *HNF1A* NM\_000545.6, and *HNF4A* NM\_175914.4.

#### **UK Biobank**

We included 185,898 unrelated individuals from all ethnicities with exome sequencing data (17). Detailed sequencing methodology for UK Biobank samples is provided by Szustakowski et al. (15) and is available from <https://biobank.ctsu.ox.ac.uk/showcase/label.cgi?id=170>. Variants were called against Genome Reference Consortium Human Build 38 (GRCh38). We lifted the variants over to GRCh37 (18) to ensure compatibility with the variants from our MODY cohort and then annotated variants using Alamut Batch with a RefSeq transcript: *BLK* NM\_001715.3, *KLF11* NM\_003597.4, *PAX4* NM\_001366110.1, *HNF1A* NM\_000545.6, and *HNF4A* NM\_175914.4.

#### **gnomAD**

The gnomAD consortium performed joint variant calling of the samples using a standardized BWA-Picard-GATK pipeline (16). GnomAD was quality controlled and analyzed with use of the Hail open-source framework for scalable genetic analysis (<https://gnomad.broadinstitute.org/about>). Variants in v2.1.1 were called against GRCh37 and in v3 against GRCh38. We lifted over v3 to GRCh37 and then annotated all gnomAD variants using Alamut Batch with use of a RefSeq transcript: *BLK* NM\_001715.3, *KLF11* NM\_003597.4, *PAX4* NM\_001366110.1, *HNF1A* NM\_000545.6, and *HNF4A* NM\_175914.4. As gnomAD is an agglomeration of different sequencing projects, some genomic regions have low coverage in some samples; therefore, to control for this, we removed the variants from both the MODY cohort and gnomAD cohorts if they were in a region of low coverage ( $\leq 10\times$  coverage in  $\leq 80\%$  of samples) in either cohort or flagged as low quality in gnomAD.

### Cosegregation Analysis of Putative Pathogenic Variants

We used author-provided LOD (logarithm of the odds) scores where available for the first published variants in *BLK*, *PAX4*, *KLF11*, *HNF1A*, and *HNF4A*, which suggested the causal role of those variants in MODY. This was only

available for *BLK* p.A71T (7). If the LOD score was not provided, we calculated it based on the Gene Clinical Validity Curation Process Standard Operating Procedure (19). We summed the LOD scores for multiple pedigrees where possible based on this guidance to calculate a combined LOD score. Using a binomial test we compared the observed proportion of family members with diabetes and a putative variant with the expected proportion of 0.5 if the variant was not associated with diabetes.

### Statistical Analysis

For each analysis, variant frequency was defined in the MODY cohort plus the control cohort combined. We compared the frequency of ultra-rare (allele count = 1) protein-truncating variants (PTV) (essential splice site, stop-gain, and frameshift variants, excluding those in the last exon) and missense variants in each gene in the MODY cohort with that in the UK Biobank population cohort. We also provided the evidence of an association in terms of Bayesian false discovery probabilities (BFDP) as previously described (20). We replicated our analysis using two alternative control populations: gnomAD v2.1.1 (141,456 individuals) and gnomAD v3 (76,156 individuals) (16).

We used synonymous variants as a control to assess the difference in sequencing technologies and analysis pipeline. We also compared the frequency of rare variants (minor allele frequency [MAF] <0.0001) and the frequency of all PTV (no frequency filter) to test whether there was an undue influence of ultra-rare variants due to differences in capture platforms.

The most common *HNF1A* pathogenic variant is a frameshift variant (p.G292Rfs\*25) in exon 4 due to a duplication of a C nucleotide. This variant is difficult to detect robustly in exome/genome sequencing data due to its location in a repetitive poly-C tract and the presence of a common variant that adds an additional 5' C nucleotide to the tract (rs56348580 G>C, MAF = 0.26). Since we were unable to perform confirmatory Sanger sequencing in the UK Biobank or gnomAD cohorts, we excluded this variant from our analysis from all study cohorts.

We used Fisher exact test to assess variant enrichment in our MODY cohort and compute odds ratios (ORs) with 95% CIs. We used a threshold *P* value of 0.01 (0.05/5), as we tested five genes. We used Stata 16 (StataCorp, College Station, TX) for this analysis. BFDP was computed using a “gap” R package. We used a prior probability of association of 0.2. We calculated the variance of the prior log(OR), as described by Wakefield (20). We also explored different plausible priors as a sensitivity analysis.

### Data and Resource Availability

UK Biobank data are accessible via application: <https://www.ukbiobank.ac.uk/enable-your-research>. GnomAD data are publically available: <https://gnomad.broadinstitute.org/>. The MODY cohort data are not publically available due the limitations of the current ethics and to protect patient

confidentiality but are available from the corresponding authors on reasonable request. No applicable resources were generated or analyzed during the current study.

## RESULTS

### *BLK, KLF11, and PAX4* Variants Had Poor Cosegregation in the Published Pedigrees

Variants that are highly penetrant causes of MODY would be expected to show strong cosegregation with the disease. To evaluate the genetic evidence of cosegregation with disease, we reviewed published pedigrees for putative variants in *BLK*, *KLF11*, and *PAX4* causing MODY (Supplementary Table 2). We identified one *BLK*, three *KLF11*, and one *PAX4* pedigrees with more than three individuals with variants to calculate LOD scores (7–9). *KLF11* and *PAX4* variants showed poor cosegregation with diabetes in the families, with LOD scores of 1.2 and 0.6, respectively (Table 1). In line with low LOD scores, these variants were not associated with diabetes in family members in these pedigrees (*P* > 0.5) (Table 1). The *BLK* variant p.A71T also had a low LOD score of 1.16 and was modestly associated with diabetes in family members (*P* = 0.02). In contrast, the variants reported in the first articles for *HNF1A* (21) and *HNF4A* (22), which are well-established causes of MODY, showed strong cosegregation with diabetes, with combined LOD scores for the first reported variants of 9.63 and 15.05, respectively (Table 1).

### Putative Pathogenic Variants in *BLK, KLF11, and PAX4* Are Common in the Population

The frequency of a putative pathogenic variant should not exceed the expected prevalence of the commonest variant in the commonest genetic subtype of the disease. MODY is estimated to have a population frequency of 1.08 per 10,000 (4). We used the framework developed by Whiffin et al. (23,24) to calculate the maximum tolerated allele count in the population (gnomAD v2.1.1 [*n* = 141,456]) for a putative pathogenic variant causing MODY. We used *HNF1A*, the most common cause of MODY, as a model to calculate the maximum tolerated allele count in the population. *HNF1A* accounts for 52% of MODY cases (4), and the most common mutation (p.G292Rfs\*25) accounts for 19% of *HNF1A* cases (25). At 50% penetrance, the framework suggests that a pathogenic variant causing MODY should be present three or fewer times (frequency <2.1 × 10<sup>-5</sup>) in gnomAD v2.1.1 for *HNF1A*. As other genes will account for far fewer MODY cases, the putative pathogenic variants in *BLK*, *KLF11*, and *PAX4* should be even rarer.

We looked at the frequency of variants in *BLK*, *KLF11*, and *PAX4* that were reported to cause MODY before large-scale population data were made available publicly in 2016 (26) (Table 2). Publications on the variants since 2016 should have included the frequency of the variant in these databases as part of their screening process and thus would be expected to have only included rare variants

**Table 1—Cosegregation of *BLK*, *KLF11*, and *PAX4* published variants with diabetes**

Gene	No. pedigree used in analysis	Variants (reference no.)	Combined LOD score	No. of family members with diabetes and variant/total no. of family members with diabetes and genotype information	Proportion of family members with diabetes and variant (95% CI)	Binomial test <i>P</i> value (against expected proportion of 0.5)
<i>BLK</i>	1	p.A71T (7)	1.16	9/10	0.9 (0.55–1)	0.02
<i>KLF11</i>	3	p.A347S (9), p.T220M (9)†	1.2	2/4	0.5 (0.068–0.93)	1
<i>PAX4</i>	1	p.R164W (8)	—	2/2	1 (0.16–1)	0.5
<i>HNF1A</i>	7	p.G292Rfs*25 (21), p.P447L (21), p.V380Sfs*4 (21), p.E548Rfs*112 (21), p.R131Q (21), c.1768 + 1G>A (21), c.1108-2A>G (21)	9.63	38/39	0.97 (0.87–1)	$1.4 \times 10^{-10}$
<i>HNF4A</i>	2	p.Q255* (43), p.R141* (43)	15.05	49/50	0.98 (0.89–1)	$9 \times 10^{-14}$

Table shows the LOD scores and association of variants with diabetes in family members for variants where there were families with three or more people with the variant. We used author-provided LOD scores where available for the first published variants, which suggested the causal role of those variants in MODY. If the LOD score was not provided, we calculated it based on the Gene Clinical Validity Curation Process Standard Operating Procedure (19). We summed the LOD score for each pedigree to calculate the combined LOD score. †Two pedigrees with p.T220M were included in the combined LOD score calculation.

(see Supplementary Table 2 for full list of Human Gene Mutation Database [HGMD] variants in these genes).

All putative MODY-causing variants in *BLK*, *KLF11*, and *PAX4* with publication prior to 2016 were too common in the population to cause MODY. The allele count in gnomAD v2.1.1 was 4–8,608 times higher than the maximum tolerable allele count for the commonest cause of MODY (Table 2). The least common was *PAX4* p.R164W, which is seen 14 times in the whole of gnomAD v2.1.1 at a frequency of  $4.95 \times 10^{-5}$  but seen at higher frequency, of  $1.2 \times 10^{-4}$  (3 of 24,948), in the African/African American population. In contrast, the first reported variants in *HNF1A* and *HNF4A*, which were reported in the 1990s, are rare in the population, with the most common (p.P447L) present three times in gnomAD v2.1.1 ( $1.20 \times 10^{-5}$ ) (Table 2).

#### Rare Variants in *BLK*, *KLF11*, and *PAX4* Are Not Enriched in a MODY Cohort

Having conducted variant-level analyses on published variants in these genes, we then carried out a gene-level analysis to establish whether other rare variants in these genes are likely to be pathogenic for MODY. To assess this, we carried out a gene burden test comparing the frequency of ultra-rare coding variants in a cohort of 1,227 patients referred for MODY genetic testing with the frequency in the unrelated 185,898 exome-sequenced individuals from the UK Biobank population cohort (Table 3 and Fig. 1).

Ultra-rare (allele count = 1) PTV and missense variants in *BLK*, *KLF11*, and *PAX4* are not enriched in our MODY cohort compared with the UK Biobank (all *P*

values  $\geq 0.09$ ) (Table 3). The BFDP for ultra-rare PTV and missense variants was  $\geq 0.70$  for *BLK*, *KLF11*, and *PAX4* (Table 3). The results of BFDP remained  $\geq 0.37$  with use of other plausible priors (Supplementary Table 3). In contrast, variants in *HNF1A* and *HNF4A*, which are well-established causative genes for MODY, were greatly enriched in our MODY cohort (all *P* values  $\leq 2.79 \times 10^{-6}$ ) with a very low BFDP (all  $\leq 6.74 \times 10^{-5}$ ).

#### Lack of Enrichment of Rare Variants in *BLK*, *KLF11*, and *PAX4* Is Not Due to Technical Artifacts

To ensure that our results are not due to differences in sequencing technologies or analysis pipelines between case and control subjects, we performed a series of sensitivity analyses. Firstly, we analyzed synonymous variant frequency in our MODY cohort and control population and showed that the frequency of synonymous variants in all five genes was similar in our MODY cohort and the UK Biobank population (all *P* > 0.05) (Supplementary Table 4).

Secondly, we replicated our gene burden analysis using gnomAD v2.1.1 and v3 as two alternative population cohorts with sequencing on different platforms (exome vs. genome, respectively) and with a different analysis pipeline versus the UK Biobank. Despite these differences, we found similar results, with no enrichment in PTV or missense variants in *BLK*, *KLF11*, or *PAX4* (Supplementary Tables 5 and 6).

Finally, to remove any undue influence of ultra-rare variants caused by differences in capture platforms, we performed a gene burden analysis for rare PTV and missense

**Table 2—Population frequency of variants in *BLK*, *KLF11*, and *PAX4* published as MODY causing**

Gene	Variant	Allele count/total alleles in gnomAD v2.1.1	Allele frequency in gnomAD v2.1.1	Allele count in ancestry with maximum frequency/total alleles in the ancestry	Maximum allele frequency in a single ancestry in gnomAD v2.1.1 (ancestry)	Reference no. for variants
<i>BLK</i>	p.A71T	3,281/282,812	0.012	420/10,368	0.041 (Ashkenazi Jewish)	7
<i>KLF11</i>	p.Q62R	25,823/282,778	0.091	1,497/10,370	0.144 (Ashkenazi Jewish)	9
	p.T220M	1,207/282,762	$4.27 \times 10^{-3}$	1,098/24,958	0.044 (African/African American)	9
	p.A347S	36/282,304	$1.28 \times 10^{-4}$	17/35,410	$4.80 \times 10^{-4}$ (Latino/Admixed American)	9
<i>PAX4</i>	p.R31L	105/250,972	$4.18 \times 10^{-4}$	102/30,616	0.003 (South Asian)	44
	p.R164W	14/282,800	$4.95 \times 10^{-5}$	3/24,948	$1.2 \times 10^{-4}$ (African/African American)	8
	p.R192H	2,214/282,856	$7.83 \times 10^{-3}$	2,182/19,946	0.109 (East Asian)	8
<i>HNF1A</i>	p.P447L	3/249,186	$1.20 \times 10^{-5}$	1/20,812	$4.81 \times 10^{-5}$ (Finnish European)	21
	p.V380Sfs*4	0	0	0	0	21
	p.E548Rfs*112	0	0	0	0	21
	p.R131Q	1/251,390	$3.98 \times 10^{-6}$	1/113,698	$8.80 \times 10^{-6}$ (non-Finnish European)	21
	c.1768 + 1G>A	0	0	0	0	21
	c.1108-2A>G	0	0	0	0	21
<i>HNF4A</i>	p.Q255*	0	0	0	0	42
	p.R141*	0	0	0	0	43

Allele frequency taken from gnomAD v2.1.1. The table provides coding variants reported before 2016 that are reported to cause MODY, as the release of ExAC (26) that year meant for variants published since then investigators have had access to a large control population as part of their screening process. The *HNF1A* and *HNF4A* variants included here for comparison are those from the original articles used in the LOD score calculations in Table 1.

variants (MAF <0.0001). We also compared the frequency of all PTV in our MODY cohort and control population, as all PTV in these genes are considered to be pathogenic. These analyses showed results similar to those of our main analysis: rare PTV and missense variants, and all PTV, in *BLK*, *KLF11*, and *PAX4* were not enriched in our MODY cohort, whereas all of these variant subsets in *HNF1A* and *HNF4A* showed great enrichment in our MODY cohort. (Supplementary Tables 7 and 8).

## DISCUSSION

Variant- and gene-level genetic evidence presented in this study suggests that variants in *BLK*, *KLF11*, and *PAX4* do not cause MODY. The lack of cosegregation of published MODY-causing variants, presence in the population at high frequency, and lack of enrichment of rare variants in a MODY cohort are consistent with these genes not causing MODY. The robustness of our approach is demonstrated by the results supporting the well-established causality of *HNF1A* and *HNF4A* variants.

Variants in *BLK*, *KLF11*, and *PAX4* were reported to cause MODY >10 years ago, before large-scale variant population frequency became available (7–9). Only small numbers of control subjects were available for ruling out variants being present in the population.

*BLK* was first described in 2009 (7) through follow-up of linkage to the 8p23 region (27) in six MODY families and identification of variants in *BLK* in three of the families.

The frequency of the *BLK* variants was tested in 336 White control individuals and, for one variant, an additional 577 African American control individuals. *BLK* was identified via a linkage approach; it is possible that another candidate gene within the region of linkage is responsible for the disease in those families. Bonnefond et al. (10) found that the only nonsynonymous variant in *BLK* reported to cause MODY was common in normoglycemic individuals. This is the variant (p.A71T) that has a positive LOD score in the published pedigree; however, as *BLK* was identified by linkage, the LOD score would necessarily be positive regardless of the pathogenicity of the variant and, as also demonstrated by its frequency in gnomAD, the variant is clearly too common to cause MODY. No large MODY pedigrees with cosegregation have been described for *BLK* since the initial report. Noncoding variants in *BLK* were also reported to cause MODY (7); however, as our main cohorts consisted of targeted and exome sequencing data, we were unable to investigate noncoding variants. It is unlikely that noncoding variants would be pathogenic given the lack of evidence for coding variants in *BLK* as a cause of MODY and that both coding and noncoding variants were proposed to cause the disease via loss of function.

*KLF11* was proposed as a cause of MODY, with a candidate gene approach, in 2005 (9). The frequency of the reported *KLF11* variants was judged in only 313 normoglycemic individuals and 313 patients with type 2 diabetes. In functional studies with use of Gal4 reporter assays,

**Table 3—Results of gene burden tests comparing the frequency of variants in *BLK*, *KLF11*, and *PAX4* in a disease cohort with that in a population cohort**

Variant type	Gene	Allele count in MODY cohort	Allele frequency in MODY cohort	Allele count in population cohort (UK Biobank)	Allele frequency in population cohort (UK Biobank)	OR (95% CI)	P	Prior probability	BFDP
Ultra-rare PTV	<i>BLK</i>	1	$4.10 \times 10^{-4}$	14	$3.77 \times 10^{-5}$	10 (0.26–71)	0.09	0.2	0.71
	<i>KLF11</i>	0	0	15	$4.03 \times 10^{-5}$	0 (0–39)	1	0.2	0.8
	<i>PAX4</i>	0	0	6	$1.61 \times 10^{-5}$	0 (0–97)	1	0.2	0.8
	<i>HNF1A</i>	15	$6.11 \times 10^{-3}$	3	$8.07 \times 10^{-6}$	762 (215–4,108)	$1.37 \times 10^{-30}$	0.2	$1.20 \times 10^{-9}$
	<i>HNF4A</i>	3	$1.22 \times 10^{-3}$	2	$5.38 \times 10^{-6}$	228 (26–2,724)	$2.79 \times 10^{-6}$	0.2	0.03
	Ultra-rare missense variants	<i>BLK</i>	1	$4.10 \times 10^{-4}$	141	$3.79 \times 10^{-4}$	1 (0.03–6.00)	0.6	0.2
<i>KLF11</i>		2	$8.10 \times 10^{-4}$	122	$3.28 \times 10^{-4}$	2.5 (0.3–9.0)	0.2	0.2	0.78
<i>PAX4</i>		2	$8.10 \times 10^{-4}$	84	$2.26 \times 10^{-4}$	3.6 (0.43–13.00)	0.1	0.2	0.70
<i>HNF1A</i>		21	$8.56 \times 10^{-3}$	102	$2.74 \times 10^{-4}$	31 (19–51)	$1.70 \times 10^{-23}$	0.2	$5.80 \times 10^{-38}$
<i>HNF4A</i>		14	$5.70 \times 10^{-3}$	83	$2.23 \times 10^{-4}$	26 (13–46)	$4.41 \times 10^{-15}$	0.2	$1.20 \times 10^{-25}$

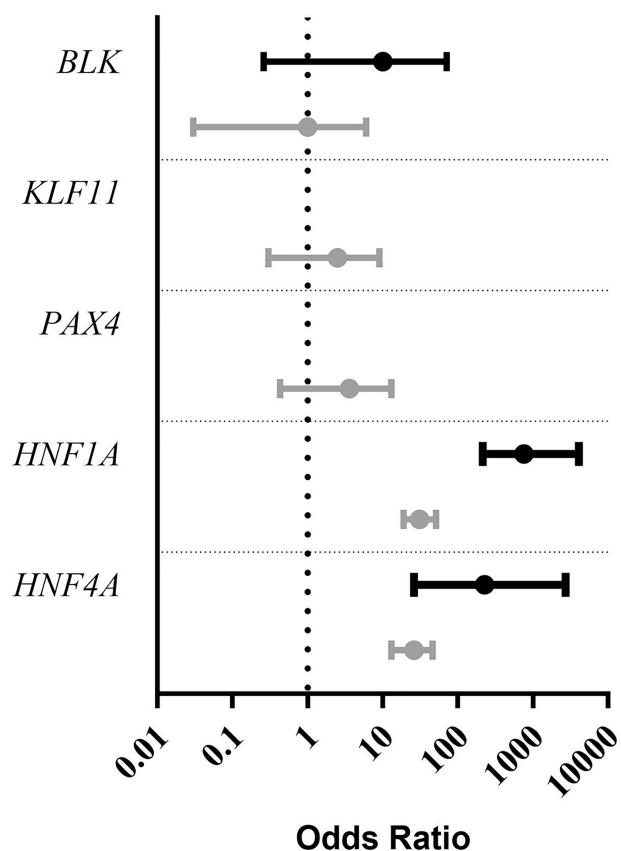
The frequency of ultra-rare (allele count = 1) PTV and missense variants in a MODY cohort ( $n = 1,227$ ) was compared with the frequency in the UK Biobank population cohort ( $n = 185,898$ ).

a possible mechanism of action was suggested for the variants via gain of function causing increased *KLF11* repression activity. If pathogenic variants in *KLF11* act via gain of function then we would not expect to see enrichment of PTV in a MODY cohort but we might expect to see enrichment of missense variants. We did not see enrichment of either type of variant, and the previously identified *KLF11* variants are too common in the population to be disease causing.

*PAX4* was associated with MODY in patients from Thailand (8). The variants were screened in a maximum of 344 individuals without diabetes. While the control subjects of this study were from the same population as the case subjects, in using data from gnomAD we now know that p.R192H is common in East Asians and both this variant and p.R164W are too common to cause MODY (p.R192H seen 2,214 times in gnomAD v2.1.1 and p.R164W seen 14 times). Plengvidhya et al. (8) used luciferase reporter assays to show that p.R164W impairs the repressor activity of *PAX4* on the insulin and glucagon promoters. However, they stated that the impairment was relatively small; thus, it is possible that the reduction may be insufficient to result in a clinical phenotype. No large MODY pedigrees with cosegregation for a variant in *PAX4* have been described since the initial report.

In our study we had a large cohort of MODY cases and took advantage of the availability of large population cohorts. The lack of enrichment for *BLK*, *KLF11*, and *PAX4* PTV and missense variants in a MODY cohort compared with a population cohort is consistent with these genes not causing MODY. However, alternative explanations may be that the mechanism of action for these genes is not loss of function (as has been suggested for *KLF11* [9]) or they are an extremely rare cause of MODY. However, we did not see enrichment in missense variants (at either allele count = 1 or MAF <0.0001), suggesting that this is unlikely. In line with our results, gnomAD pLI (probability of being loss of function intolerant) and missense constraint scores for these genes are low, suggesting that these genes are not under strong negative selection—in contrast to *HNF1A* and *HNF4A*, which have high constraint scores. These data suggest that variants in these genes do not cause a rare monogenic disorder.

Variants in these genes could still be acting as polygenic risk factors for diabetes. *PAX4* has been reported in the literature as a type 2 diabetes risk factor in East Asian populations (28,29). Fuchsberger et al. (30), in a study of 6,504 type 2 diabetes case and 6,436 control subjects, found a lack of exome-wide enrichment of PTV and deleterious missense variants for *BLK* ( $P \approx 0.001$ ), *KLF11* ( $P > 0.05$ ), and *PAX4* ( $P > 0.05$ ). However, the *PAX4* p.R192H variant (a proposed MODY variant) showed association with type 2 diabetes in East Asian case subjects (OR 1.79) but not with age of diabetes diagnosis ( $P = 0.64$ ), suggesting that this variant influences risk of type 2 diabetes rather than early-onset MODY. Similar to



**Figure 1**—Graph showing the ORs for ultra-rare (allele count = 1) PTV (black lines) and missense variants (gray lines) in a MODY cohort ( $n = 1,227$ ) compared with the population cohort UK Biobank ( $n = 185,898$ ). Dotted line shows an OR of 1. Bar not shown for *KLF11* and *PAX4* PTV, as OR is 0, which cannot be plotted on a log axis.

this, in a recent large type 2 diabetes case-control study of 20,791 case and 24,440 control subjects investigators did not find an exome wide-significant association in these genes, except for the *PAX4* p.R192H variant, which was associated with type 2 diabetes in East Asians (31). However, the lack of exome-wide significance may reflect the relatively small size of these studies.

A limitation of our study is that by virtue of using publicly available control populations there were cross-platform differences between case and control individuals. This issue was mitigated by removal of genomic positions with low coverage in one cohort from the other and in our sensitivity analyses with use of synonymous variants as a negative control and testing alternative population control cohorts. Despite using a large MODY cohort, we still had a relatively limited sample size of cases, which could trend our gene burden tests of ultra-rare variants toward negative results. To ensure a lack of power was not determining the results we also used sensitivity analyses with  $MAF < 0.001$ , and these did not suggest there was an association between *BLK*, *KLF11*, or *PAX4* and MODY. One other caveat to our

burden testing results is the fact that both our MODY cohort and the UK Biobank are predominantly European ancestry. We cannot rule out that an enrichment might be seen in MODY cohorts from other ancestries, particularly for *PAX4*, which was originally reported in East Asian ancestry. It must be acknowledged that the power of cosegregation analysis was limited, particularly for *BLK* and *PAX4*, as they are only based on one family each. However, in detailed review of all the published articles on putative pathogenic variants we did not identify additional large published pedigrees for cosegregation analysis.

Our study results have important implications for genetic diagnostic laboratories worldwide who offer testing for MODY. Based on our results, we recommend that *BLK*, *KLF11*, and *PAX4* should not be included in the gene panels for genetic testing for MODY and should not be reported as a cause of MODY. Studies are still reporting variants in these genes as a cause of MODY, and they are routinely tested in clinical practice (32–36). In our systematic review of the National Center for Biotechnology Information Genetic Testing Registry we found that 19 of 25 panels offered by diagnostic genetic laboratories still have at least one of these genes on their panel. The results of our study remove the ambiguity of the etiological role of these genes for MODY and provide the clearest results to date that refute their role as causative genes for MODY. Excluding these genes from diagnostic panels will prevent misdiagnosis of MODY and reduce workload for laboratories. The results from our study provide much needed evidence to gene curation efforts such as Clinical Genome Resource (ClinGen) and the Gene Curation Coalition (GenCC) to support the removal of these three genes from MODY genetic panels (37,38). The ClinGen curation panel also came to a similar conclusion using their own scoring system (12) independently of our study. They classified *BLK* and *PAX4* as “Refuted” genes (<https://search.clinicalgenome.org/kb/genes/HGNC:1057>; <https://search.clinicalgenome.org/kb/genes/HGNC:8618>) and *KLF11* as a “Disputed” gene (<https://search.clinicalgenome.org/kb/genes/HGNC:11811>). However, it is important to note that in addition to their own approach, they used our current work as previously published as a conference abstract to reach their conclusion. We also strongly recommend that variants in *BLK*, *KLF11*, and *PAX4* should be removed as a cause of MODY on databases such as HGMD (39), OMIM (40), ClinVar, and PanelApp (41) that are widely used by diagnostic laboratories and geneticists worldwide.

In conclusion, we present evidence from reanalysis of published variants in *BLK*, *KLF11*, and *PAX4* that they are too common to cause MODY and have poor cosegregation with diabetes in those families and, since their initial description, no large MODY families with cosegregation of a variant have been published. We have shown a lack of enrichment of rare variants in these genes in a MODY cohort compared with a population cohort, providing evidence that rare variants in these genes do not cause

MODY. Overall, the evidence does not support *BLK*, *KLF11*, or *PAX4* as causes of MODY, and they should not be included in diagnostic genetic testing.

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