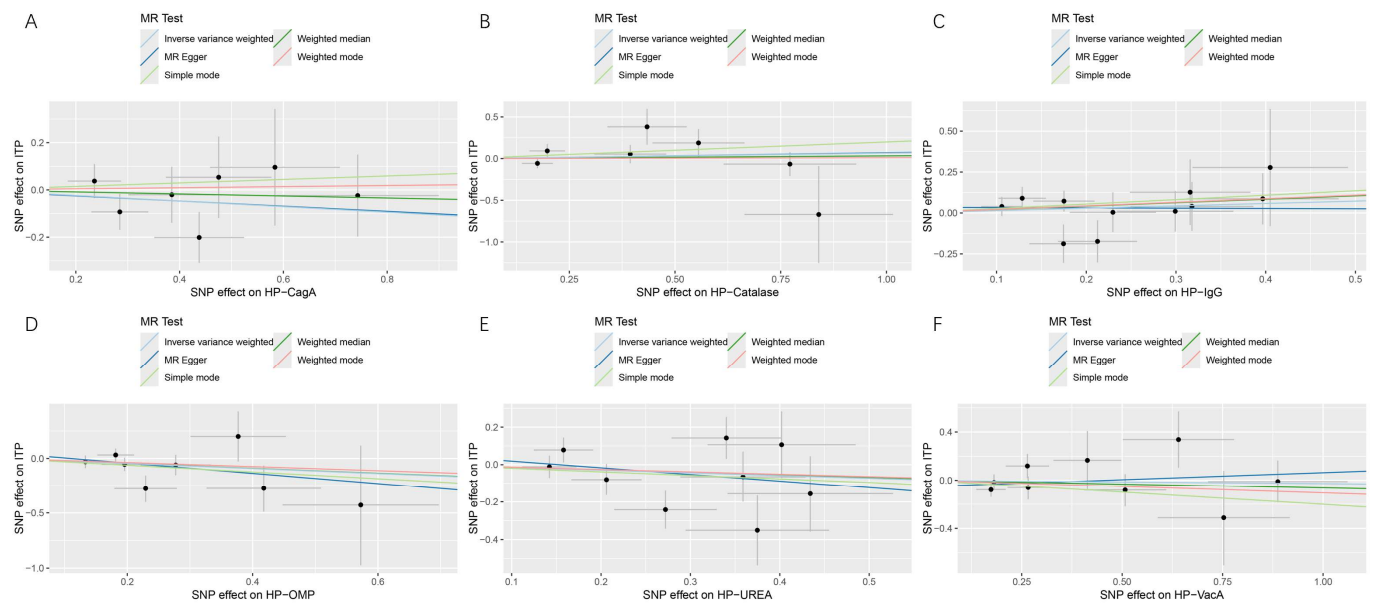


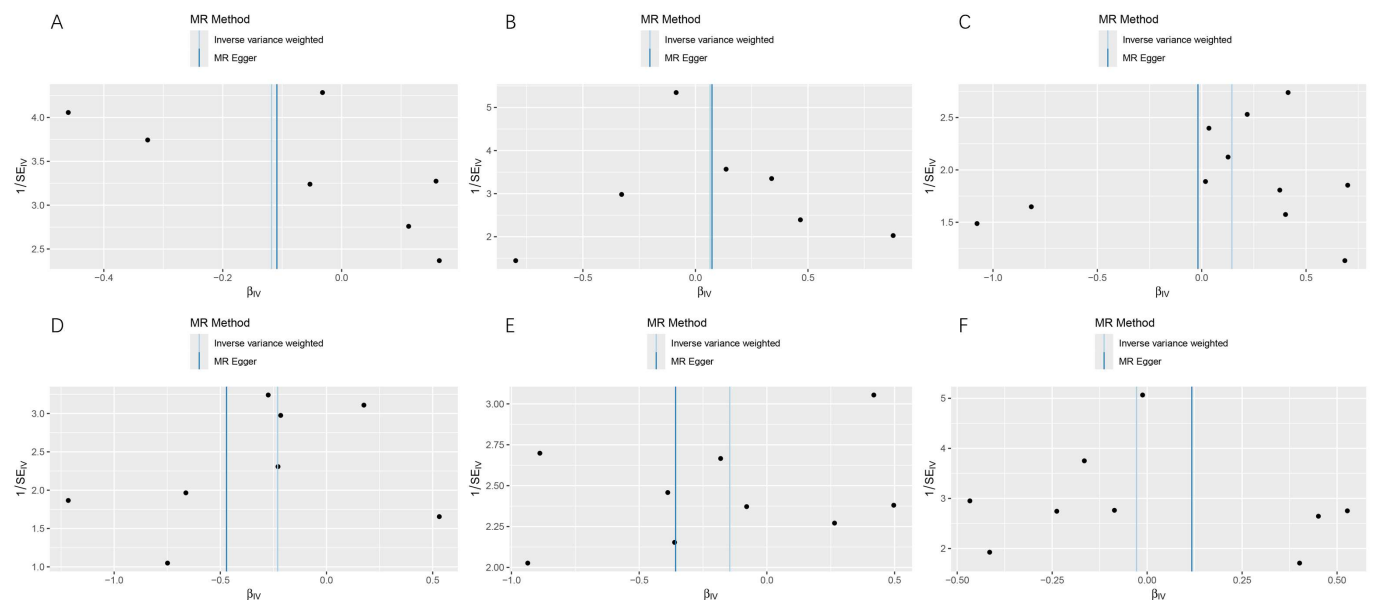
Original article

Causal Relationship between Helicobacter Pylori Antibodies and Immune Thrombocytopenia: A Mendelian Randomization Study

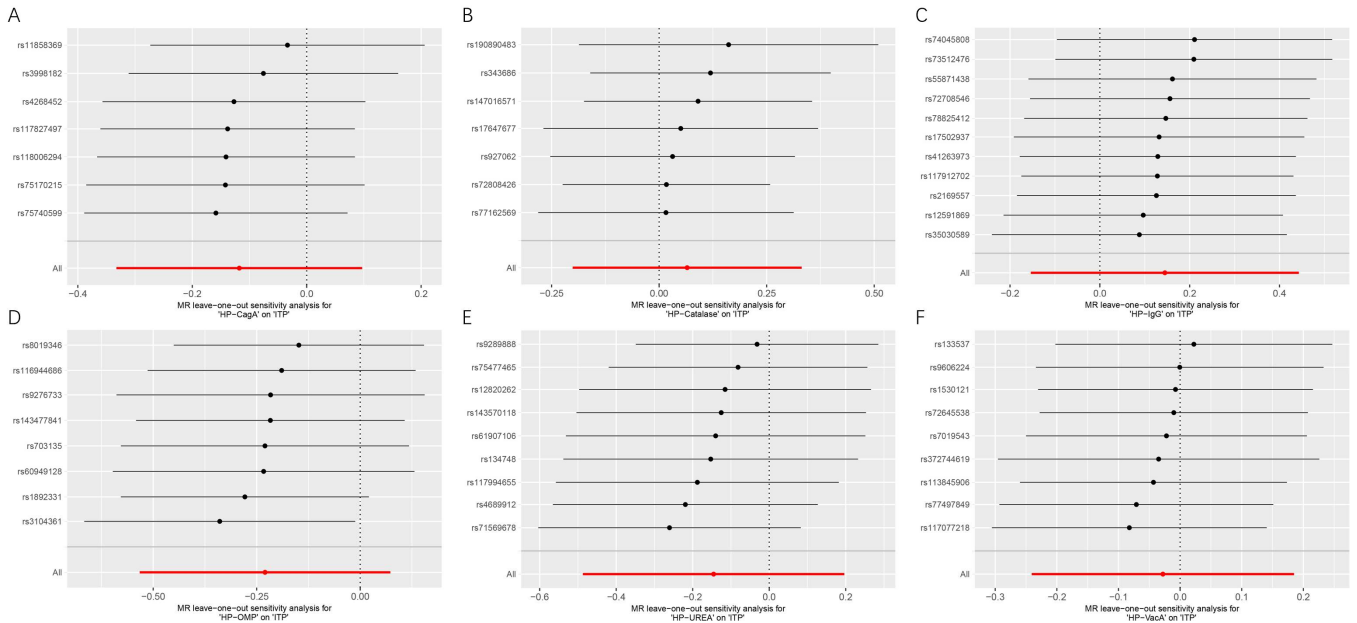
Supplementary Files



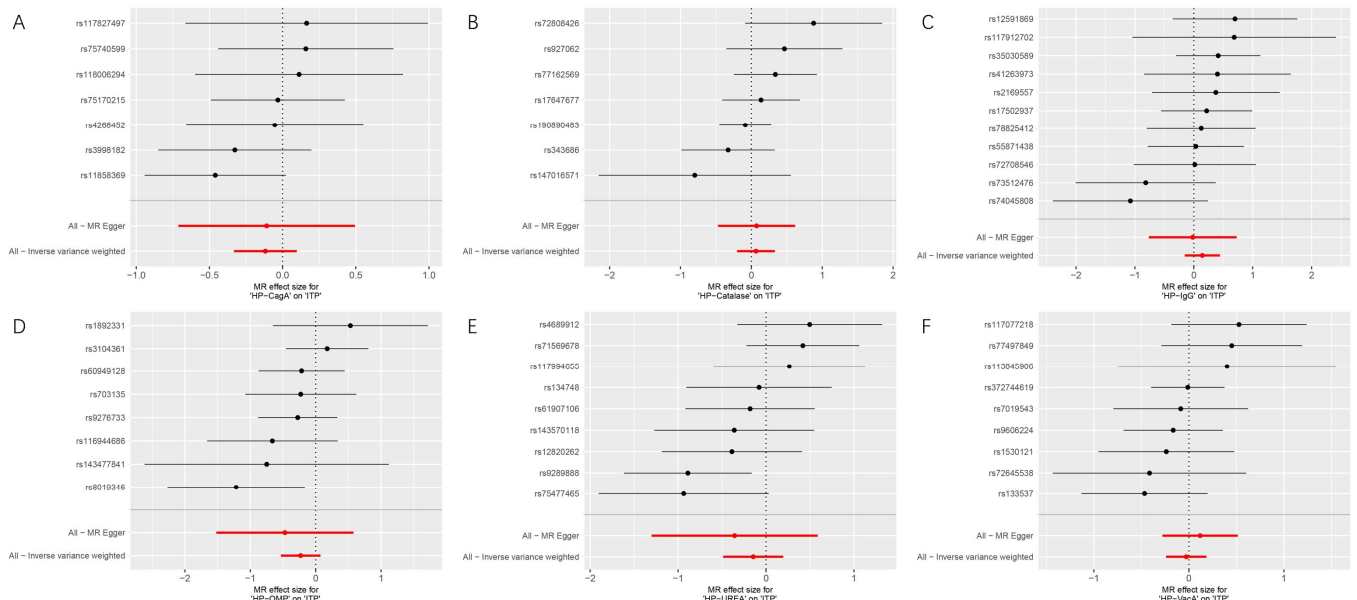
S1 Figure. Scatter plot. (A) HP-CagA and ITP; (B) HP-Catalase and ITP; (C) HP-IgG and ITP; (D) HP-OMP and ITP; (E) HP-UREA and ITP; (F) HP-VacA and ITP.



S2 Figure. Funnel plot. (A) HP-CagA and ITP; (B) HP-Catalase and ITP; (C) HP-IgG and ITP; (D) HP-OMP and ITP; (E) HP-UREA and ITP; (F) HP-VacA and ITP



S3 Figure. Leave-one-out sensitivity analysis. (A) HP-CagA and ITP; (B) HP-Catalase and ITP; (C) HP-IgG and ITP; (D) HP-OMP and ITP; (E) HP-UREA and ITP; (F) HP-VacA and ITP



S4 Figure. Forest plot. (A) HP-CagA and ITP; (B) HP-Catalase and ITP; (C) HP-IgG and ITP; (D) HP-OMP and ITP; (E) HP-UREA and ITP; (F) HP-VacA and ITP

S1 Table. Instrumental variables used in MR analysis of the association between HP antibody and ITP

Exposure	SNP	effect_allele	other_allele	Exposure			Outcome			F. statistic	
				Beta	SE	pval	Beta	SE	pval		
HP-GroEL	rs3104037	T	C	0.134	0.028	1.90E-06	0.091	0.060	1.30E-01	22.69	
	rs61680606	C	A	0.152	0.032	2.38E-06	N/A	N/A	N/A	22.26	
	rs7099832	C	G	-0.134	0.028	1.31E-06	N/A	N/A	N/A	23.40	
	rs117341694	A	G	0.543	0.116	2.73E-06	0.329	0.219	1.33E-01	22.00	
	rs1367344	C	T	-0.155	0.033	2.68E-06	-0.074	0.069	2.84E-01	22.04	
HP-IgG	rs41263973	G	A	0.316	0.067	2.74E-06	0.127	0.201	5.27E-01	22.06	
	rs2169557	C	T	-0.106	0.023	4.55E-06	-0.040	0.059	4.99E-01	21.08	
	rs77516628	A	T	0.188	0.040	2.94E-06	N/A	N/A	N/A	21.92	
	rs72708546	G	A	-0.230	0.048	1.90E-06	-0.004	0.122	9.72E-01	22.77	
	rs35030589	G	A	-0.175	0.034	3.40E-07	-0.073	0.064	2.57E-01	26.10	
	rs117912702	G	A	0.405	0.087	3.02E-06	0.278	0.357	4.37E-01	21.87	
	rs73512476	G	T	0.213	0.044	1.47E-06	-0.174	0.129	1.79E-01	23.26	
	rs17502937	G	T	-0.397	0.085	2.89E-06	-0.087	0.157	5.81E-01	21.96	
	rs74045808	C	T	-0.175	0.038	4.49E-06	0.188	0.117	1.09E-01	21.11	
	rs55871438	T	C	0.299	0.065	4.02E-06	0.010	0.125	9.34E-01	21.32	
	rs78825412	C	A	0.318	0.069	3.64E-06	0.040	0.150	7.88E-01	21.51	
	rs12591869	C	A	-0.129	0.027	1.29E-06	-0.090	0.069	1.95E-01	23.52	
	HP-VacA	rs113063793	T	A	0.373	0.076	7.97E-07	N/A	N/A	N/A	24.36
		rs72645538	G	A	0.753	0.164	4.66E-06	-0.312	0.391	4.25E-01	20.97
rs113845906		A	G	0.413	0.085	9.97E-07	0.166	0.242	4.93E-01	23.93	
rs1530121		C	T	-0.266	0.051	1.96E-07	0.063	0.097	5.14E-01	27.08	
rs372744619		G	A	0.887	0.174	3.29E-07	-0.011	0.175	9.52E-01	26.07	
rs77497849		G	A	0.264	0.054	9.13E-07	0.119	0.100	2.33E-01	24.10	
rs10246445		C	A	-0.488	0.107	4.92E-06	N/A	N/A	N/A	20.87	
rs7019543		T	G	0.181	0.038	2.01E-06	-0.016	0.066	8.12E-01	22.59	
rs59104649		T	A	0.683	0.147	3.44E-06	N/A	N/A	N/A	21.56	
rs117077218		T	C	0.640	0.139	3.95E-06	0.337	0.233	1.47E-01	21.29	
rs148556020		A	T	0.631	0.137	4.44E-06	N/A	N/A	N/A	21.06	
rs11044935		T	A	0.428	0.091	2.22E-06	N/A	N/A	N/A	22.39	
rs73500239		C	G	0.236	0.050	2.38E-06	N/A	N/A	N/A	22.26	
rs9606224		T	C	0.507	0.102	6.91E-07	-0.084	0.135	5.35E-01	24.64	
rs133537		C	T	-0.174	0.037	2.25E-06	0.081	0.059	1.68E-01	22.37	
HP-UREA		rs9289888	T	C	0.272	0.057	2.12E-06	-0.242	0.101	1.65E-02	22.48
		rs4689912	C	T	-0.158	0.033	1.90E-06	-0.078	0.066	2.37E-01	22.70
		rs71569678	C	A	0.340	0.061	2.99E-08	0.142	0.111	2.01E-01	30.71
	rs75477465	A	G	0.375	0.080	3.03E-06	-0.351	0.185	5.78E-02	21.80	
	rs61907106	A	G	-0.359	0.070	3.27E-07	0.065	0.135	6.29E-01	26.09	
	rs12820262	A	G	0.206	0.039	1.59E-07	-0.080	0.084	3.40E-01	27.47	
	rs60386004	T	A	0.192	0.041	2.49E-06	N/A	N/A	N/A	22.17	
	rs143570118	T	C	0.434	0.093	2.76E-06	-0.157	0.202	4.36E-01	21.98	
	rs117994655	A	G	0.402	0.083	1.21E-06	0.106	0.177	5.48E-01	23.55	
	rs134748	T	G	-0.142	0.031	3.50E-06	0.011	0.060	8.51E-01	21.52	
HP-OMP	rs703135	A	G	-0.133	0.028	2.09E-06	0.030	0.058	5.98E-01	22.51	
	rs1156822	T	A	-0.128	0.028	4.36E-06	N/A	N/A	N/A	21.10	
	rs55862931	C	G	-0.146	0.032	3.82E-06	N/A	N/A	N/A	21.35	
	rs143477841	A	G	-0.573	0.125	4.37E-06	0.429	0.546	4.32E-01	21.09	
	rs9276733	G	A	0.196	0.036	8.14E-08	-0.054	0.060	3.74E-01	28.77	
	rs3104361	C	T	0.181	0.029	6.48E-10	0.032	0.058	5.84E-01	38.17	
	rs79155431*	A	C	-0.277	0.056	8.53E-07	0.060	0.093	0.521	24.24	

	rs116944686	A	G	0.418	0.091	4.78E-06	-0.277	0.213	1.93E-01	20.92
	rs8019346	A	G	0.229	0.050	4.24E-06	-0.279	0.123	2.33E-02	21.15
	rs1892331	G	A	0.377	0.076	7.40E-07	0.200	0.228	3.79E-01	24.51
HP-Catalase	rs190890483	A	G	-0.772	0.157	8.63E-07	0.066	0.144	6.47E-01	24.21
	rs72808426	T	C	-0.434	0.094	3.79E-06	-0.381	0.214	7.49E-02	21.37
	rs58679787	T	C	0.777	0.168	3.84E-06	N/A	N/A	N/A	21.34
	rs343686	C	A	-0.175	0.037	1.75E-06	0.057	0.059	3.28E-01	22.85
	rs6456714	G	C	0.171	0.036	2.18E-06	N/A	N/A	N/A	22.43
	rs77162569	T	C	-0.556	0.109	3.27E-07	-0.188	0.166	2.57E-01	26.08
	rs17647677	C	T	-0.394	0.085	3.65E-06	-0.054	0.110	6.27E-01	21.44
	rs927062	G	A	-0.198	0.042	2.60E-06	-0.092	0.083	2.64E-01	22.09
	rs147016571	G	A	-0.840	0.176	1.76E-06	0.671	0.581	2.49E-01	22.84
HP-CagA	rs116421363	C	A	-0.223	0.048	2.68E-06	N/A	N/A	N/A	22.03
	rs75170215	C	T	0.743	0.156	2.02E-06	-0.024	0.173	8.90E-01	22.58
	rs75740599	A	G	0.236	0.051	4.27E-06	0.037	0.072	6.03E-01	21.14
	rs3998182	C	T	0.285	0.055	2.04E-07	-0.093	0.076	2.22E-01	27.00
	rs571061419	A	G	-0.392	0.085	4.21E-06	N/A	N/A	N/A	21.17
	rs6530847	A	T	-0.210	0.045	3.41E-06	N/A	N/A	N/A	21.57
	rs4268452	T	C	-0.385	0.084	4.62E-06	0.021	0.119	8.63E-01	20.99
	rs117827497	G	A	-0.584	0.125	3.10E-06	-0.096	0.247	6.97E-01	21.76
	rs138363822	G	A	0.218	0.048	4.30E-06	N/A	N/A	N/A	21.12
	rs117537486	C	G	0.597	0.130	4.22E-06	N/A	N/A	N/A	21.16
	rs149747348	C	G	-0.895	0.194	3.92E-06	N/A	N/A	N/A	21.30
	rs56264437	A	G	0.234	0.049	1.99E-06	N/A	N/A	N/A	22.60
	rs11858369	G	A	0.438	0.086	4.18E-07	-0.201	0.108	6.21E-02	25.61
	rs553266653	C	A	-0.732	0.159	4.04E-06	N/A	N/A	N/A	21.24
	rs118006294	C	T	-0.475	0.102	3.04E-06	-0.054	0.172	7.56E-01	21.79

SNP, single nucleotide polymorphism; SE, standard error

N/A: The SNP could not be found in the outcome database or were palindromic.

* This is a proxy SNP.