

Supplementary File S3: QUADAS Results

Domain 1: Patient Selection

Study	Recruitment	Enrolment consecutive /random?	Exclusions avoided?	Did selection introduce bias?	Criteria for genotyping	Risk of bias from patients matching review Q?
<b>Bancone_et_al_2015 (27)</b>	Purposive selection of known G6PD phenotype or genotype	no	yes	high	All participants	low
<b>Bancone_et_al_2016 (28)</b>	Exhaustive cross-sectional surveys	yes	yes	low	Phenotypically deficient males, all females	low
<b>Bancone_et_al_2017 (29)</b>	Health-facility based recruitment, pregnant women attending antenatal care	yes	yes	low	Genotyping for Mahidol was performed on all included women, while Chinese-4, Kaiping, Canton and Mediterranean variants were analysed only on women with either enzymatic activity below 80% of normal in Mahidol-wild type genotype or enzymatic activity below 30% and Mahidol-heterozygous genotype.	unclear
<b>Brito_et_al_2016 (30)</b>	Consecutive males, malaria patients from clinic, non-malaria from clinic and community	yes	no	high	Only genotyped those with G6PD <70%, 100% based on a mean of males, not median	low
<b>Deng_et_al_2017 (31)</b>	Unclear, 100 unrelated individuals fitting inclusion criteria were enrolled	no	unclear	high	All phenotypically deficient participants genotyped	low

<b>Johnson_et_al_2009 (32)</b>	random selection post census, only children 1-10 yrs, all participants genotyped, some standardized exclusion criteria	yes	no	low	110 randomly selected individuals tested for A-	low
<b>Kim_et_al_2011 (33)</b>	Cross sectional survey, two stage cluster sampling, 1 child / household	unclear	unclear	unclear	All phenotypically deficient participants genotyped (<4.5U/gHb)	low
<b>La_Rue_et_al_2014 (34)</b>	Blood samples from African-American blood donors	no	no	high	Genotyping selection not specified, but state it was biased towards lower G6PD activity	low
<b>Ley_et_al_2021 (35)</b>	Composite data from three studies: clinical trial of malaria patients, cross-sectional survey, case-control study	yes	yes	low	all individuals <70% AMM and a sample subsample above 70%	low
<b>Pal_et_al_2021 (36)</b>	Composite data from multiple studies: 3 diagnostic accuracy studies in USA, focusing on African-Americans in recruitment. 1 study in UK -requested testing already completed at Hammersmith Hospital Haematology laboratory	no	no	high	limited number', 'covering the critical G6PD activity dynamic range'	low
<b>Reading_et_al_2016 (37)</b>	Patients presenting with AHA + health controls, patients followed up 4+ months following AHA.	yes	yes	low	All AHA patients and all healthy controls	low

<b>Roca-Feltrer_et_al_2014 (38)</b>	Patients enrolled based on pre-defined eligibility criteria, how patients were identified is unclear	unclear	no	high	All individuals with <60% of AMM	low
<b>Roh_et_al_2016 (39)</b>	Cross sectional survey, two stage cluster sampling, 1 child / household	yes	no	low	625 / 631 genotyped	low
<b>Satyagraha_et_al_2015 (40)</b>	Cross-sectional surveys, villages in proximity to health centres, all residents invited to participate.	yes	yes	low	all G6PD deficient + convenience sample of G6PD normal. 80/104 agreed for genotyping.	low
<b>Satyagraha_et_al_2016 (41)</b>	Random selection of all residents of one village.	yes	yes	low	all G6PD deficient + those with low HB (<8g/dL)	low
<b>Satyagraha_et_al_2021 (42)</b>	Cross-sectional surveys, females >6yrs	unclear	yes	low	all individuals <80% normal activity	low
<b>Xia_et_al_2016 (43)</b>	Hospital-based sampling, method comparison study	unclear	yes	unclear	G6PD deficient by novel assay and/or G6PD/6PGD ratio + 80 randomly selected G6PD normal (40 each sex).	low

## Domain 2: Genotype

Study	How was genotyping done?	Was genotyping done without knowing spec results?	Could genotyping have introduced bias?
<b>Bancone_et_al_2015 (27)</b>	Sequencing	no	high
<b>Bancone_et_al_2016 (28)</b>	PCR-RFLP for Mahidol, Chinese-4, Canton, Viangchan	no	high
<b>Bancone_et_al_2017 (29)</b>	PCR-RFLP for Mahidol, Chinese-4, Kaiping, Mediterranean, Canton	no	high
<b>Brito_et_al_2016 (30)</b>	PCR-RFLP for A-, Chatham, Mediterranean, Aures	no	high
<b>Deng_et_al_2017 (31)</b>	SNaPshot assay	no	high
<b>Johnson_et_al_2009 (32)</b>	Genotyping for 3 A- variants	unclear	unclear
<b>Kim_et_al_2011 (33)</b>	Sequencing	no	high

La_Rue_et_al_2014 (34)	Sequencing	no	high
Ley_et_al_2021 (35)	PCR-RFLP for Mahidol, Viangchan, Mediterranean, Orissa, Kalyan-Kerala	no	high
Pal_et_al_2021 (36)	Sequencing	no	high
Reading_et_al_2016 (37)	SNaPshot assay	yes	low
Roca-Feltrer_et_al_2014 (38)	Sequencing	no	high
Roh_et_al_2016 (39)	PCR-RFLP for A-	unclear	unclear
Satyagraha_et_al_2015 (40)	Sequencing	no	high
Satyagraha_et_al_2016 (41)	PCR-RFLP for Vanua Lava, Chatham, Viangchan and Kaiping	no	high
Satyagraha_et_al_2021 (42)	PCR-RFLP for Vanua Lava, Chatham, Viangchan, Coimbra, Kaiping + sequencing for indeterminate results	no	high
Xia_et_al_2016 (43)	Multicolour melting curve analysis	no	high

### Domain 3: Phenotype

Study	How was spec done?	Were replicate measures used?	Were control samples used regularly?	Was reaction temperature addressed?	Risk of bias due to spec. assay and/or procedures?	Was malaria status considered when defining deficiency?	Was spec done without knowing genotype?	Was '100% activity' defined based on study's own data?	Risk of bias due to spec methods and/or interpretation?
Bancone_et_al_2015 (27)	Duplicate testing using trinity, AMM from 26 normal males	yes	yes	yes	low	yes	yes	yes	low

<b>Bancone_et_al_2016 (28)</b>	Trinity, unclear if replicates used. Previously established AMM of 7.51 U/gHb used	yes	yes	yes	low	no	yes	yes	low
<b>Bancone_et_al_2017 (29)</b>	WHO method on WBC depleted samples done in triplicates. As only pregnant women, 'female population median' was used, 11.5U/g Hb	yes	yes	yes	low	no	yes	yes	high
<b>Brito_et_al_2016 (30)</b>	Pointe Scientific	yes	yes	yes	low	yes	yes	yes	low
<b>Deng_et_al_2017 (31)</b>	Single testing with Trinity, deficiency defined as <4.5U/gHb	no	yes	yes	high	no	yes	unclear	high
<b>Johnson_et_al_2009 (32)</b>	Single testing with Randox, time to testing not mentioned, deficiency defined from Randox recommendation	no	yes	yes	high	no	unclear	no	high
<b>Kim_et_al_2011 (33)</b>	Single testing with Trinity, deficiency defined as <4.5U/gHb, 100% is a mean, not an AMM	no	yes	yes	high	no	yes	yes	high
<b>La_Rue_et_al_2014 (34)</b>	Trinity, AMM of 7.18	yes	yes	yes	low		yes	yes	low
<b>Ley_et_al_2021 (35)</b>	Randox + Pointe Scientific	yes	yes	yes	low	yes	yes	yes	low

<b>Pal_et_al_2021 (36)</b>	Pointe Scientific	no	yes	yes	high		yes	unclear	unclear
<b>Reading_et_al_2016 (37)</b>	Randox	no	yes	yes	low	no	yes	no	low
<b>Roca-Feltrer_et_al_2014 (38)</b>	Single testing with Trinity, deficiency defined as <60%	no	yes	yes	high	no	yes	yes	high
<b>Roh_et_al_2016 (39)</b>	Single testing with Trinity done within 24 hours, deficiency defined as 60% of AMM	no	yes	yes	high	no	unclear	yes	high
<b>Satyagraha_et_al_2015 (40)</b>	Trinity	no	yes	yes	high	no	yes	no	high
<b>Satyagraha_et_al_2016 (41)</b>	Trinity, in triplicate	yes	yes	yes	low	no	yes	no	high
<b>Satyagraha_et_al_2021 (42)</b>	Trinity	no	yes	yes	high	yes	yes	no	high
<b>Xia_et_al_2016 (43)</b>	Zhongshan Biotech G6PD/6PGD ratio	unclear	yes	yes	unclear	no	yes	unclear	unclear

#### Domain 4: Flow and timing

<b>Study</b>	<b>Was spec done within 7d (sample at 4°C)?</b>	<b>Did all patients receive the same testing?</b>	<b>Were all patients included in analysis?</b>	<b>Could patient flow have introduced bias?</b>
<b>Bancone_et_al_2015 (27)</b>	yes	yes	yes	low
<b>Bancone_et_al_2016 (28)</b>	yes	yes	no	low

<b>Bancone_et_al_2017 (29)</b>	yes	yes	yes	low
<b>Brito_et_al_2016 (30)</b>	yes	yes	yes	high
<b>Deng_et_al_2017 (31)</b>	unclear	yes	no	high
<b>Johnson_et_al_2009 (32)</b>	unclear	yes	no	low
<b>Kim_et_al_2011 (33)</b>	yes	yes	no	high
<b>La_Rue_et_al_2014 (34)</b>	yes	yes	yes	low
<b>Ley_et_al_2021 (35)</b>	yes	no	yes	high
<b>Pal_et_al_2021 (36)</b>	yes	yes	yes	high
<b>Reading_et_al_2016 (37)</b>	unclear	no	no	high
<b>Roca-Feltrer_et_al_2014 (38)</b>	yes	yes	no	high
<b>Roh_et_al_2016 (39)</b>	yes	yes	no	low
<b>Satyagraha_et_al_2015 (40)</b>	yes	yes	no	high
<b>Satyagraha_et_al_2016 (41)</b>	yes	yes	no	high
<b>Satyagraha_et_al_2021 (42)</b>	yes	yes	no	high
<b>Xia_et_al_2016 (43)</b>	yes	yes	no	high