Supplementary Appendix

This appendix has been provided by authors to give readers additional information about their work.

Supplement to: Vitamin D status in Mainland of China: a systematic review and meta-analysis.

Contents

Supplementary file 1: Search strategy

1. PubMed

Access Date: 4 Jun 2021

Search strategy:

("vitamin d"[MeSH Terms] OR "ergocalciferols"[MeSH Terms] OR "ergocalciferols"[MeSH Terms] OR "calcifediol"[MeSH Terms] OR "cholecalciferol"[MeSH Terms] OR "vitamin d deficiency"[MeSH Terms] OR "vitamin d"[Title/Abstract] OR "25 hydroxyvitamin d"[Title/Abstract] OR "calcifediol"[Title/Abstract] OR "ergocalciferols"[Title/Abstract] OR "cholecalciferol"[Title/Abstract] OR "vitamin d deficiency"[Title/Abstract]) AND ("china"[MeSH Terms] OR "china"[All Fields] OR "china s"[All Fields] OR "chinas"[All Fields] OR "china"[MeSH Terms] OR "asian continental ancestry group"[MeSH Terms] OR ("asian continental ancestry group"[MeSH Terms] OR ("asian"[All Fields] AND "continental"[All Fields] AND "ancestry"[All Fields] AND "group"[All Fields]) OR "asian continental ancestry group"[All Fields] OR "chinese"[All Fields] OR "chineses"[All Fields])) Search Results: 5197

2. Web of Science

Access Date: 4 Jun 2021

3. EMBASE

Access Date: 4 Jun 2021

Search strategy:

4. China National Knowledge Infrastructure (CNKI)

Access Date: 4 Jun 2021 Subject category: Medicine & Public Health Sub-database: Journal articles, Dissertations Search strategy: (SU="维生素 D") AND (SU="缺乏" + "水平" + "调查" + "流行" + "现状" + "现况") Search Results: 3783

5. WanFang

Access Date: 4 Jun 2021 Subject category: Medicine & Public Health Sub-database: Journal articles, Dissertations Search strategy: 题名或关键词:(("维生素D") and ("缺乏" or "水平" or "调查" or "流行" or "现状" or "现况")) Search Results:3594

6. VIP

Access Date: 4 Jun 2021 Subject category: Medicine & Public Health Search strategy: M=(("维生素 D") AND ("缺乏" or "水平" or "调查" or "流行" or "现状 " or "现况"))

Search Results:2002

Supplementary file 2: Hierarchical Bayesian model and the code from R software

1. The Hierarchical Bayesian model

Meta-analysis usually combines aggregated or individual results from several studies to create a pooled, more precise estimate of an effect. Due to the hierarchical structure (intra-study and between-study) of meta-analysis data, the hierarchical Bayesian approach is often used in meta-analysis. Meanwhile, the Bayesian approach allows us to account for uncertainty from the varying quality of data and borrow strength from non-missing data, and MCMC sampling allows for inference in a high-dimensional, constrained parameter space, while providing posterior estimation that allow straightforward inference on the wide variety of functionals of interest.

In our meta-analysis, the outcomes of interest were the prevalence of vitamin D (VitD) deficiency (<30 nmol/L, or < 12 ng/mL), VitD inadequacy (<50 nmol/L, or < 20 ng/mL), and mean serum 25(OH)D concentration (nmol/L).We use the Hierarchical Bayesian models to estimate the pooled prevalence of VitD deficiency, inadequacy and mean serum 25(OH)D concentration.

For the *i*th study which reported the dichotomous outcomes, the number of populations with VitD deficiency/ inadequacy in the *i*th study followed the binomial distribution:

$$
r_i \sim \text{binomial}(n_i, p_i) \tag{1}
$$

Where n_i was the total number of investigated population and p_i was the true prevalence of VitD deficiency/ inadequacy for the *i*th study.

The logit transformation of p_i followed a normal distribution among studies:

$$
\theta_i = logit(p_i) \sim normal(\mu, \sigma^2)
$$
 (2)

Where μ was the mean of logit(p_i) and σ^2 was the between-study variance. r_i and n_i were extracted from each study, θ_i , μ and σ^2 were parameters estimated from the model.

And we could estimate the pooled prevalence of VitD deficiency/ inadequacy and the

corresponding 95% credible interval (CrI) through retransform the :

$$
prevalence = exp(\mu)/(1 + exp(\mu))
$$
 (3)

For the *i*th study which reported the mean of VitD concentration (*meani*), *meanⁱ* followed a normal distribution:

$$
mean_i \sim \text{normal}(\theta_i, S_i^2) \tag{4}
$$

Where θ_i was the true value of the VitD concentration in the *i*th study and S_i was standard error of the estimated *mean*i.

 θ_i followed a normal distribution among studies:

$$
\theta_i \sim \text{normal}(\mu, \sigma^2) \tag{5}
$$

Where μ was the pooled mean of the vitamin D concentration and σ^2 was the between-study variance.

The *mean*_i and *se_i* were extracted or calculated from each study, θ_i , μ and σ^2 were parameters estimated from the model.

The hierarchical model also called the random-effect model or mixed-effect model. In the above models, (1) and (4) were the within-study component of hierarchical model, (2) and (5) were between-study component, the study-specific and the pooled parameters can estimate from the hierarchical model.

2. The Hierarchical Bayesian meta-regression model

2.1 Study-level covariates

To assess the effects of sampling frame, latitude, urbanization, season, assays for serum 25(OH)D on the outcomes (prevalence of VitD inadequacy and mean concentration of VitD), we constructed the Hierarchical Bayesian meta-regression model for each studylevel covariate separately.

In the within-study level, the models were the same as formula (1) or (4).

In the between-study level, let *Xⁱ* stand for the vector of covariates of the *i*th study and *α* stand for the constant term. θ_i was the true value of logit transformation of prevalence of VitD inadequacy, or true value of the vitamin D concentration from the *i*th study, and $\alpha + X_i\beta$ predict the θ_i with residual variance, which followed a normal distribution:

$$
\theta_i = \alpha_i + \sum \beta_p X_{pi} \tag{6}
$$

$$
\alpha_i \sim \text{normal}(\mu, \sigma^2) \tag{7}
$$

The model included the random intercept and fix effect of the slope. From the model, we obtained the pooled prevalence of VitD inadequacy or mean concentration in each level of the specific covariate and the ratio or difference between two levels of the specific covariate.

For "sampling frame", we specified $x1=1$ as the study sampled with province or city level, x2=1 as the study sampled with county level, and the study sampled national wide as the reference (constant).

	Study (i) Sampling frame	xI_i	$x2_i$	n_i	r_i
1	National	$\overline{0}$	$\overline{0}$	\cdots	\cdots
$\overline{2}$	Province or	1	θ	\cdots	\cdots
	City				
3	County	θ		\cdots	\cdots
4	\cdots		$\overline{0}$	\cdots	\cdots
\ddotsc	\ddotsc		\cdots	\cdots	\cdots

Table A. Data structure of VitD inadequacy with the study-level covariate

When estimated the prevalence of VitD inadequacy, according to formulas (1), (6), (7), we obtained the pooled prevalence of VitD inadequacy when studies sampled from National, Province or City, County respectively:

$$
Prevalence (National) = exp(\mu)/(1 + exp(\mu))
$$
\n(8)

Prevalence (Province or City) = exp(
$$
\mu + \beta_1
$$
)/(1 + exp($\mu + \beta_1$)) (9)

$$
Prevalence (Country) = exp(\mu + \beta_2)/(1 + exp(\mu + \beta_2))
$$
\n(10)

And the Odds Ratio:

Odds Ratio (County vs. National) $= exp(\beta_2)$ (12)

Odds Ratio (Province or City vs. County) =
$$
exp(\beta_1 \cdot \beta_2)
$$
 (13)

When estimate the mean concentration, according to the formulas (4), (6), (7), we can obtain the pooled mean concentration of VitD inadequacy when studies sampled from National, Province or City, County respectively:

Mean concentration (Province or City)= $\mu + \beta_1$ (15)

Mean concentration (County)= $\mu + \beta_2$ (16)

And the difference of concentration (nmol/L):

Difference (County vs. National) $=\beta_2$ (18)

Difference (Province or City vs. County) $=\beta_1 \beta_2$ (19)

If the 95%CrI of the effect size (odds Ratio or difference) estimated from the HB meta-regression models included the null effect size of 1 or 0, then this covariate was not considered as the factor causing the heterogeneity of studies.

The same calculation process was applied for other covariates. And the specifications for other study-level covariates were as follow:

For "latitude", $x1=1$ indicated the study sampled from north areas only, $x2=1$ indicated the study sampled from both the south and north areas, and the study sampled from south areas only as the reference (constant). For "urbanization", $x1=1$ indicated the study sampled from rural areas only, $x2=1$ indicated the study sampled from both urban and rural areas, and the study sampled from urban areas only as the reference (constant). For "season", $x1=1$ indicated the VitD measured during summerautumn, x2=1 indicated the VitD measured covering at least a whole year, and the VitD measured during winter-spring as the reference (constant). For "assays", $x1=1$ indicated the VitD measured using the ELISA (Enzyme-linked immunosorbent assays), x2=1 indicated the VitD measured using the ECLIA

(Electrochemiluminescence immunoassay), x3=1 indicated the VitD measured using CLIA (Chemiluminescent assay) ,x4=1 indicated the VitD measured using the RIA (Radioimmunoassay) ,and the chemical assays including HPLC (High-performance liquid chromatography) and LC-MS/MS (Liquid chromatography coupled with mass spectrometry) as the reference (constant).

2.2 Sex difference and Age trend

We could extract the sex-specific or age-specific outcomes from most of the included studies, but few studies provided the sex- and age-specific outcomes. As a result, we constructed the Hierarchical Bayesian meta-regression model for sex-specific and agespecific outcomes separately.

Table B listed the data structure of the sex-specific VitD inadequacy. Each row indicated a study-sex group, and sex=0 indicated male and sex=1 indicated the female.

$Study-sex(ij)$	Study(j)	Sex_{ij}	n_{ij}	r_{ij}
1			\cdots	\cdots
2		θ	\cdots	\cdots
3	2		\cdots	\cdots
$\overline{4}$	2	θ	\cdots	\cdots
\cdots	\cdots	\cdots	\cdots	\cdots

Table B. Data structure of the sex-specific VitD inadequacy

In the *ij* study-sex group, *rij* followed the binomial distribution:

$$
r_{ij} \sim \text{binomial}(n_{ij}, p_{ij}) \tag{1}
$$

The logit transformation of p_{ij} , which was the θ_{ij} followed a normal distribution among studies. We constructed a linear relationship with sex:

$$
\theta_{ij} = \alpha_j + \beta_j S e x_{ij} \tag{20}
$$

$$
\alpha_j \sim \text{normal}(\mu_\alpha, \sigma_\alpha^2) \tag{21}
$$

$$
\beta_j \sim \text{normal}(\mu_\beta, \sigma_\beta^2) \tag{22}
$$

If we added the study-level covariate into the model above, the formula (21) was modified as:

$$
\alpha_j \sim \text{normal}(\mu_\alpha + \sum \beta_p X_{pj}, \sigma_\alpha^2) \tag{23}
$$

We obtained the pooled prevalence of VitD inadequacy for male and female respectively:

$$
Prevalence (Male) = exp(\mu_{\alpha})/(1 + exp(\mu_{\alpha}))
$$
\n(24)

Prevalence (Female)=
$$
exp(\mu_{\alpha}+\mu_{\beta})/(1+exp(\mu_{\alpha}+\mu_{\beta}))
$$
 (25)

And the Odds Ratio:

Odds Ratio (Female vs. Male)=
$$
exp(\mu_{\beta})
$$
 (26)

The age trend analysis was conducted only for children and adolescents (age≤18years), and older people(age ≥ 60 yeas) .Table C display the data structure of the age-specific VitD inadequacy. Each row indicated a study-age group, and the mid-point values of each age group were used as continuous variables to construct a linear trend HB model.

Table C. Data structure of the age-specific VitD inadequacy(children)

Study-age (ij)	Study(j)	Age_{ij}	n_{ij}	r_{ij}
		3	\cdots	\cdots
$\overline{2}$		4	\cdots	\cdots
3		5	\cdots	\cdots
$\overline{4}$	2	4	\cdots	\cdots
\cdots	\cdots	\cdots	\cdots	\cdots

The regression model for age was similar as for sex.

In the *ij* study-age group, *rij* followed the binomial distribution:

$$
r_{ij} \sim \text{binomial}(n_{ij}, p_{ij}) \tag{1}
$$

The logit transformation of p_{ij} , which was the θ_{ij} followed a normal distribution among studies, and we constructed a linear relationship with age:

$$
\theta_{ij} = \alpha_j + \beta_j A g e_{ij} \tag{27}
$$

$$
\alpha_j \sim \text{normal}(\mu_\alpha, \sigma_\alpha^2) \tag{21}
$$

$$
\beta_j \sim \text{normal}(\mu_\beta, \sigma_\beta^2) \tag{22}
$$

Then we used the estimated prevalence of VitD inadequacy of ages from 1 to 18, or 60 to 90 to draw the age trend plot.

$$
Prevalence (Age_k) = exp(\mu_\alpha + \mu_\beta Age_k)/(1 + exp(\mu_\alpha + \mu_\beta Age_k))
$$
 (28)

Where *k*= 1 to 18 for children and adolescents, and *k*=60 to 90 for older people. If we added the study-level covariate into the above model, the formula (21) was modified as:

$$
\alpha_j \sim \text{normal}(\mu_\alpha + \sum \beta_p X_{pj}, \sigma_\alpha^2) \tag{23}
$$

And then we could draw the age trend of VitD inadequacy for each level of the covariate respectively.

For the mean concentration of VitD, the sex or age HB regression models were similar with the regression of prevalence of VitD inadequacy, except for the within study-sex or study-age group distribution:

$$
mean_{ij} \sim \text{normal}(\theta_{ij}, \sigma_{ij}^2) \tag{4}
$$

3. Parameter Estimation

All HB models were fitted with the Markov chain Monte Carlo (MCMC) algorithm and Gibbs sampling to estimate the posterior distribution of the outcomes. Non-informative prior was specified for all the parameters. The uncertainty intervals (or CrI) represent the 2.5-97.5 percentiles of the posterior distribution of the estimation. Inferences were based on 5000 iterations, and the first 2500 of which were used as burn-in. All the hierarchical Bayesian analyses were performed using the "R2jags" package of R software (version 4.0.3). In the BUGS model, normal distribution was written as mean and precision $\tau^2 = \frac{1}{\sigma^2}$ which was not the variance σ^2 .

4. Code of "R2jags" package from R software

The codes from R in our study were displayed below for the analysis of prevalence of vitamin D deficiency, inadequacy, and sufficiency, the codes for the analysis of VitD concentration were omit.

4.1 Prevalence of VitD deficiency/inadequacy/sufficiency without covariates

```
# write bugs model in R as a function
bayesmodel.1<-function(){
  for (i \text{ in } 1:N) \{ # N, the number of studies
    r[i] \sim \text{dbinom (p[i], n[i])} # data model
    logit(p[i]) < -y[i] # the logit transformation for p
  }
   for (i in 1:N}
    y[i] \sim \text{donorm} (mu, tau) # hierarchical model for y
   }
   tau \lt- pow(sigma, -2) \qquad \qquad # \tan = 1/\text{sigma}^2mu \sim \text{dnorm}(0.0, 1.0E-6) # noninformative prior on mu
   sigma \sim dunif (0, 1000) # noninformative prior on sigma
   prevalence\leq -\exp(\text{mu})/(1+\exp(\text{mu})) # the pooled prevalence
  sigma2<-sigma*sigma
}
jags.params.1 <-c("mu","sigma2","p","prevalence")
set.seed(123)
jags.1 <- jags(data=list(N=length(data$Studyid),r=data$count,n=data$n), 
inits=NULL, jags.params.1, n.iter=5000, model.file=bayesmodel.1)
```
#Where *data* was the dataframe of each outcome for children or adults, *studyid* was the study identification for each study, *count* was the number of populations with vitamin D deficiency/ inadequacy, *n* was the corresponding total number of investigated populations.

#The forest plot was draw from the observational prevalence of each study and the pooled prevalence of deficiency/inadequacy from the above model.

4.2 Prevalence of VitD inadequacy with study-level covariates

```
# write bugs model in R as a function
bayesmodel.2<-function(){
  for (i \text{ in } 1:N) \{ # N, the number of studies
    r[i] \sim \text{dbinom (p[i], n[i])} # data model
    logit(p[i]] \le -y[i] # the logit transformation for p
   } 
  for (i in 1:N}
```

```
y[i] < -beta[1] + \beta_1 * x1[i] + \beta_2 * x2[i]beta[<b>i</b>] ~< dnorm (mu, tau) # hierarchical model for y
```

```
tau \langle - pow(sigma, -2) \qquad # tau = 1/\text{sigma}^2sigma \sim dunif (0, 1000) \# noninformative prior on sigma
mu \sim dnorm (0.0, 1.0E-6) \# noninformative prior on mu
beta1~ dnorm (0.0, 1.0E-6) # noninformative prior on beta1
beta2\sim dnorm (0.0, 1.0E-6) \# noninformative prior on beta2
```

```
P.0 \leq \exp(\theta \cdot \tan(1 + \exp(\theta \cdot \tan))) # the prevalence if x1 = -0 \& x2 = -0P.1 \langle-exp(beta0+beta1)/(1+exp(beta0+beta1)) # the prevalence if x1=1P.2 < -exp(beta0+beta2)/(1+exp(beta0+beta2)) # the prevalence if x2=1OR.1 <-exp(beta1) \# the OR in x1=1 vs. x1==0&x2==0
OR.2 <-exp(beta2) \# the OR in x2=1 vs. x1==0&x2==0
OR.2_1 <-exp(beta2-beta1) \# the OR in x2=1 vs. x1==1
sigma2<-sigma*sigma
```

```
}
```
}

```
jags.params.2 <-c("mu","beta1","beta2","sigma2","p","P.0","P.1","P.2","OR.1", 
"OR.2", "OR.2_1")
set.seed(123)
jags.2<- jags(data=list(N=length(data$Studyid),r=data$count,n=data$n,
x1=data$x1, x2=data$x2), inits=NULL, jags.params.2, n.iter=5000,
model.file=bayesmodel.2)
```
#The meta-regression with study-level covariates were applied in vitamin D inadequacy only because of the limited number of studies for vitamin D deficiency. #Where *data* was the dataframe of vitamin D inadequacy for children or adults, *studyid* was the study identification for each study , *count* was the number of population with vitamin D inadequacy, *n* was the total number of investigated population, and x1,x2 were the indicator variables of the study-level covariate.

4.3 Sex-specific prevalence of VitD inadequacy

```
bayesmodel.3 <-function(){
  for (i \text{ in } 1:N) \{ # N, the number of study-sex groups
    r[i] \sim \text{dbinom (p[i], n[i])} # data model
    logit(p[i]) \le -y[i] # the logit transformation for p
    y[i] < -alpha[Study[i]]+beta[Study[i]]*sex[i] # hierarchical model for y
   }
  for (i \text{ in } 1:J) \{ # J, the number of study
    alpha[i] \sim \text{dnorm}(mu.a, tau.a)beta[i] \sim \text{dnorm}(mu.b, tau.b) } 
  tau.a <- pow(sigma.a,-2) \# \tan.a = 1/\text{sigma.a}^2tau.b <- pow(sigma.b,-2) \# tau.b = 1/\text{sigma.b}\text{-}2sigma.a \sim dunif (0, 1000) # noninformative prior on sigma.a
  sigma.b \sim dunif (0, 1000) # noninformative prior on sigma.b
  mu.a \sim dnorm (0.0, 1.0E-6) \# noninformative prior on mu.a
  mu.b \sim dnorm (0.0, 1.0E-6) \qquad # noninformative prior on mu.b
  P.male \langle -\exp(\mu u \cdot a)/(1+\exp(\mu u \cdot a)) # the prevalence for male
  P.female \langle -exp(mu.a+mu.b)/(1+exp(mu.a+mu.b)) # the prevalence for female
  OR \leq -\exp(\text{mu.b}) # the OR for female vs. male
 sigma.a2<-sigma.a*sigma.a
```

```
}
```

```
jags.params.3<-c("mu.a","mu.b","sigma.a2","sigma.b","p","P.male","P.female","OR")
set.seed(123)
jags.sex <-jags(data=list(N=length(data$Studyid),J=length(unique(data$Studyid)), 
r=data$count,n=data$n,Study=data$Studyid,sex=data$sex), inits=NULL, 
jags.params.3, n.iter=5000,model.file=bayesmodel.3)
```
#Where *data* was the dataframe of sex-specific vitamin D inadequacy for children or adults, *studyid* was the study identification for each study , *count* was the sex-specific number of population with vitamin D inadequacy in each study, *n* was the corresponding number of investigated population, and sex=1 indicate female and sex=0 indicate male.

4.4 Age-specific prevalence of VitD inadequacy

```
bayesmodel.4<-function(){
  for (i \text{ in } 1:N) \{ # N, the number of study-age groups
    r[i] \sim \text{dbinom (p[i], n[i])} # data model
    logit(p[i]) \le -y[i] # the logit transformation for p
    y[i] < -alpha[Study[i]]+beta[Study[i]]*age[i] # hierarchical model for y
   }
  for (i \text{ in } 1:J) \uparrow # J, the number of study
    alpha[i] \sim \text{dnorm}(mu.a, tau.a)beta[i] \sim \text{dnorm}(mu.b, tau.b) }
  tau.a <- pow(sigma.a,-2) \# \tan a = 1/\text{sigma}.a^2tau.b <- pow(sigma.b.-2) \qquad \qquad # \tan.b = 1/\text{sigma}.b^2sigma.a \sim dunif (0, 1000) # noninformative prior on sigma.a
  sigma.b \sim dunif (0, 1000) # noninformative prior on sigma.b
  mu.a \sim dnorm (0.0, 1.0E-6) \qquad # noninformative prior on mu.a
  mu.b \sim dnorm (0.0, 1.0E-6) \# noninformative prior on mu.b
  OR < \text{exp}(mu.b) # the OR every one year increased in age
 sigma.a2<-sigma.a*sigma.a
```

```
}
```

```
jags.params.4 < -c("mu.a", "mu.b", "sigma.a2", "sigma.b", "p", "OR")set.seed(123)
jags.age<-jags(data=list(N=length(data$Studyid),J=length(unique(data$Studyid)), 
r=data$count,n=data$n,Study=data$Studyid,age= data $age), inits=NULL, 
jags.params.4, n.iter=5000, model.file=bayesmodel.4)
```
#Where *data* was the dataframe of age-specific vitamin D inadequacy for children or adults, *studyid* was the study identification for each study , *count* was the number of population with vitamin D inadequacy in each age group, *n* was the corresponding total number of investigated population, and age was the midpoint of age group from each study.

Supplementary tables

Table S1. Characteristics of the included studies

F: Female, M: Male. North and south were divided based on the Qinling Mountains-Huaihe River line boundary.

ELISA: Enzyme-linked immunosorbent assays; ECLIA: Electrochemiluminescence immunoassay; CLIA: Chemiluminescent assay; RIA: Radioimmunoassay;

HPLC: High-performance liquid chromatography; LC-MS/MS: Liquid chromatography coupled with mass spectrometry

+ : The investigation site in this study was above Qinling Mountains-Huaihe River line boundary in Jiangsu province.

Table S2. Risk of bias assessment of the included studies^a

^a: The risk of bias of the included studies were evaluated by a tool by Hoy.

^b: Yes: The study was a national survey. No: The study was province or county level.

c : Yes: The response rate for the study was ≥75%,or an analysis was performed that showed no significant difference in relevant demographic characteristics between responders and non-responders;

No: The response rate was <75%, or if any analysis comparing responders and non-responders was done, it showed a significant difference in relevant demographic characteristics between responders and non-responders, or haven't reported the response rate.

Table S3. Parameters from HB meta-regression models for Vitamin D inadequacy (< 50 nmol/L)

N: Number of studies for each levels of the covariates. For sex or age, N is the number of study-sex or study-age groups.

* : Categories with less than 3 studies and the "Unknown" category of season were not included in the HB meta-regression model.

+ : For adults, populations with age > 60 years old groups were included in the age trend model.

	Children and Adolescents		Adults		
Covariates	N	Between-study variance (σ^2)	N	Between-study variance (σ^2)	
Sampling frame					
National	$\overline{4}$		$\overline{4}$		
Province or City	17	275.4(169.9, 451.7)	24	185.2(108.4, 305.3)	
County	15		6		
Latitude					
South	16		13		
North	14	280.4(170.8, 454.7)	16	181.1(108.1, 304.9)	
Both	6		5		
Urbanization					
Urban	10		15		
Rural	18	242.9(147.1, 398.8)	1^*	180.8(106.7, 301.8)	
Both	8		18		
Season					
Summer	15		9		
Winter	11	230.1(130.7, 394.3)	9	153.1(80.6, 280.5)	
Both	5		8		
Unknown [*]	5		8		
Assays					
LC-MS/MS or HPLC	19		$\overline{3}$		
ELISA	$\overline{4}$		13		
ECLIA	5		5		
CLIA	3	225.3(131.0, 386.6)	6	196.0(112.5, 336.3)	
RIA	$\overline{4}$		6		
EIA^*	$\overline{0}$		$\mathbf{1}$		
$CPBA^*$	$\mathbf{1}$		$\overline{0}$		
Sex					
Study-sex group	57	325.1(181.7, 571.1)	47	178.0(102.3, 309.4)	
Age (years)					
Study-age group ⁺	81	236.2(117.8, 444.5)	19	351.3(117.7, 940.9)	

Table S4. Parameters from HB meta-regression models for Vitamin D concentration (nmol/L)

N: Number of studies for each levels of the covariates. For sex or age, N is the number of study-sex or study-age groups.

* : Categories with less than 3 studies and the "Unknown" category of season were not included in the HB meta-regression analysis.

 \pm : For adults, populations with age \geq 60 years old groups were included in the age trend model.

Supplementary figures

Figure S1. Forest plot for overall mean 25(OH)D concentrations of adults in Mainland of China

The forest plot was drawn from the observational mean concentration with 95%CI of each study and the pooled mean concentration with 95%CrI estimated from Hierarchical Bayesian model. N is the total number of participants in the study. Thirty-five individual studies were included in this model. The between-study variance (σ^2) estimated from the model was 175.3(104.6, 288.9).

Figure S2. Forest plot for overall mean 25(OH)D concentrations of children and

adolescents in Mainland of China

N is the total number of participants in the study. The forest plot was drawn from the observational mean concentration with 95%CI of each study and the pooled mean concentration with 95%CrI estimated from Hierarchical Bayesian models. Thirty-five individual studies were included in this model. The between-study variance (σ^2) estimated from the model was 273.2(167.9, 449.3).

Figure S3. Pooled prevalence of Vitamin D inadequacy (A) and overall mean 25(OH)D concentrations (B) of adults in Mainland of China based on sex

Figure S4. Forest plot for mean 25(OH)D concentrations of adults in Mainland of

China based on sex

The forest plot was drawn from the observational mean concentration with 95%CI of each study. The pooled mean concentration with 95%CrI was estimated from Hierarchical Bayesian models.

Figure S5. Forest plot for Vitamin D inadequacy of adults in Mainland of China

based on sex

The forest plot was drawn based on the observational prevalence with 95%CI of each study. The pooled prevalence with 95%CrI was estimated using Hierarchical Bayesian models.

Figure S6. Estimated mean 25(OH)D concentrations of children and adolescents in Mainland of China based on sex

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