

Cohort included

Bulbulyan, Russia, 1999	Included ^a	Not included
Coggiola, Italy, 2003	Included ^b	Included ^c
Fu, China, 1992	Included ^b	Not included
Honda, USA, 2002	Included ^a	Not included
Li, China, 1998	Included ^a	Not included
Mclean, multinational, 2006	Included ^a	Not included
Nie, China, 1992	Included ^b	Not included
Stern, USA, 2001	Included ^a	Not included
Selevan, USA, 1979	Included ^b	Included ^c
Straif, Germany, 2000	Included ^a	Not included
Thomas, USA, 1987	Included ^b	Not included
Wergeland, Norway, 1990	Included ^b	Included ^c
Wild, Austria, 2002	Included ^b	Included ^c
Wild, France, 2002	Included ^b	Included ^c
Summary estimates	Non-asbestiform talc: meta-SMR = 1.50 95% CI = 1.02-2.22 (Random effect)	Non-asbestiform talc: meta-SMR = 0.92 95% CI = 0.67-1.25 (Fixed effect)

- a. Talc with asbestiform fiber / asbestos; calculation of meta-SMR was separated from cohorts exposed to non-asbestiform talc
- b. Non-asbestiform talc
- c. Only talc millers were included

Description: The R script for the process of statistical analysis using the Meta and Metafor package in R 3.2.2 software. Additional information including the raw data are provided within the code.

Downloadable link: <https://goo.gl/wfDNzt>

```
# Talc Exposure and Risk of lung Cancer: A Meta-Analysis of Occupational Cohort Studies
```

```
# set-up:
```

```
rm(list=ls(all=TRUE))
```

```
ls()
```

```
# Load required packages: meta, metafor
```

```
if(require(meta)==FALSE){install.packages("meta");require(meta)}
```

```
if(require(metafor)==FALSE){install.packages("metafor");require(metafor)}
```

```
if(require(gsheet)==FALSE){install.packages("gsheet");require(gsheet)} # for reading online spreadsheet
```

```
# continuous data:
```

```
meta04lung <-
```

```
gsheet2tbl('https://docs.google.com/spreadsheets/d/1BYMCu3gKjjY5fYXPfIldufU8K0JSXWB1-EIVym_1j8/edit#gid=1782588271')
```

```
summary(meta04lung)
```

```
meta04lung$logsmr = log(meta04lung$obs / meta04lung$exp)
```

```
meta04lung$selogsmr = 1 / sqrt(meta04lung$obs)
```

```
meta04lung.gen = metagen(logsmr, selogsmr, study, sm="HR",data=meta04lung, comb.fixed = F)
```

```
meta04lung.gen
```

```
forest(meta04lung.gen, smlab = "SMR", leftlabs = c("Study", "logSMR", "SE"), rightlabs = c("SMR", "95%-CI", "Weights"))
```

```
funnel(meta04lung.gen)
```

```
# Egger's test for publication bias
```

```
metabias(meta04lung.gen, method.bias = "linreg", plotit = T)
```

```
# Sensitivity analysis: asbestos contamination
```

```
meta04lung.byvar = metagen(logsmr, selogsmr, study, sm="HR",data=meta04lung, byvar = contamination, comb.fixed = F)
```

```
meta04lung.byvar
```

```
forest(meta04lung.byvar, smlab = "SMR", leftlabs = c("Study", "logSMR", "SE"), rightlabs = c("SMR", "95%-CI", "Weights"))
```

```
# contamination = 0
```

```

# Sensitivity analysis: talc-producing vs. user industries
meta04lung$talcmine = c(0,1,1,1,0,0,0,1,0,0,1,1,1) # 1 = talc-producing, 0 = user
industries
meta04lung.byvar = metagen(logsmr, selogsmr, study, sm="HR",data=meta04lung, byvar
= talcmine, comb.fixed = F)
meta04lung.byvar
forest(meta04lung.byvar, smlab = "SMR", leftlabs = c("Study", "logSMR", "SE"),
rightlabs = c("SMR", "95%-CI", "Weights"))
# user industries
metagen(logsmr, selogsmr, study, sm="HR",data=subset(meta04lung, talcmine==0),
comb.fixed = F)
# talc-producing industry
metagen(logsmr, selogsmr, study, sm="HR",data=subset(meta04lung, talcmine==1),
comb.fixed = F)

```

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# Sensitivity analysis: geography
meta04lung$geography01 = c(1,2,1,3,1,4,1,3,3,2,3,2,2) # 1=Asia, 2=Europe, 3=North
America, 4=multi-national
meta04lung.byvar = metagen(logsmr, selogsmr, study, sm="HR",data=meta04lung[-6,],
byvar = geography01, comb.fixed = F)
meta04lung.byvar
forest(meta04lung.byvar, smlab = "SMR", leftlabs = c("Study", "logSMR", "SE"),
rightlabs = c("SMR", "95%-CI", "Weights"))
# Asia (China + Russia)
metagen(logsmr, selogsmr, study, sm="HR",data=subset(meta04lung[-6,],
geography01==1), comb.fixed = F)
# Russian vs. Chinese studies
metagen(logsmr, selogsmr, study, sm="HR",data=subset(meta04lung[-6,],
geography01==1), byvar = language, comb.fixed = F)
# Europe
metagen(logsmr, selogsmr, study, sm="HR",data=subset(meta04lung[-6,],
geography01==2), comb.fixed = F)
# North America
metagen(logsmr, selogsmr, study, sm="HR",data=subset(meta04lung[-6,],
geography01==3), comb.fixed = F)

```

```

# Sensitivity analysis: duration of follow-up
meta04lung$duration = cut(meta04lung$duration_followed, c(0, 20, 40, 100), right = F,
labels = c("<20 years", "20-40 years", ">=40 years"))
summary(meta04lung$duration)
meta04lung.byvar = metagen(logsmr, selogsmr, study, sm="HR",data=meta04lung, byvar
= duration, comb.fixed = F)
meta04lung.byvar
forest(meta04lung.byvar, smlab = "SMR", leftlabs = c("Study", "logSMR", "SE"))

```

```

metagen(logsmr, selogsmr, study, sm="HR",data=subset(meta04lung, duration_followed
>= 20 & duration_followed < 40), comb.fixed = F)
# >=40 years
metagen(logsmr, selogsmr, study, sm="HR",data=subset(meta04lung, duration_followed
>= 40), comb.fixed = F)

# Sensitivity analysis: language
summary(meta04lung$language)
meta04lung.byvar = metagen(logsmr, selogsmr, study, sm="HR",data=meta04lung, byvar
= language, comb.fixed = F)
meta04lung.byvar
forest(meta04lung.byvar, smlab = "SMR", leftlabs = c("Study", "logSMR", "SE"),
rightlabs = c("SMR", "95%-CI", "Weights"))
# English
metagen(logsmr, selogsmr, study, sm="HR",data=subset(meta04lung, language ==
"English"), comb.fixed = F)
# Chinese
metagen(logsmr, selogsmr, study, sm="HR",data=subset(meta04lung, language ==
"Chinese"), comb.fixed = F)

# Sensitivity analysis: study quality (NOS score)
meta04lung$quality = cut(meta04lung$NOS_score, c(6, 8, 10), right = F, labels =
c("medium", "high"))
summary(meta04lung$quality)
meta04lung.byvar = metagen(logsmr, selogsmr, study, sm="HR",data=meta04lung, byvar
= quality, comb.fixed = F)
meta04lung.byvar
forest(meta04lung.byvar, smlab = "SMR", leftlabs = c("Study", "logSMR", "SE"),
rightlabs = c("SMR", "95%-CI", "Weights"))
# medium
metagen(logsmr, selogsmr, study, sm="HR",data=subset(meta04lung, quality ==
"medium"), comb.fixed = F)
# high
metagen(logsmr, selogsmr, study, sm="HR",data=subset(meta04lung, quality == "high"),
comb.fixed = F)

# Influence of excluding each individual cohort (leave-one-out method)
meta04lung.gen.inf = metainf(meta04lung.gen, pooled = "random")
meta04lung.gen.inf
forest(meta04lung.gen.inf, overall = F, smlab = "Meta-SMR", leftlabs = c(""), rightlabs =
c("Meta-SMR", "95%-CI"))

```

```
# Sensitivity analysis: gender
meta04lung_gender <-
gsheet2tbl('https://docs.google.com/spreadsheets/d/1BYMCu3gKjjY5fYXPfIlxdufU8K0JSX
WB1-EIVym_1j8/edit#gid=29647490')
summary(meta04lung_gender)
meta04lung_gender$logsmr = log(meta04lung_gender$obs / meta04lung_gender$exp)
meta04lung_gender$selogsmr = 1 / sqrt(meta04lung_gender$obs)
meta04lung_gender.byvar = metagen(logsmr, selogsmr, study,
sm="HR",data=meta04lung_gender[-9,], byvar = Gender, comb.fixed = F)
meta04lung_gender.byvar
forest(meta04lung_gender.byvar, smlab = "SMR", leftlabs = c("Study", "logSMR", "SE"),
rightlabs = c("SMR", "95%-CI", "Weights"))
# female
metagen(logsmr, selogsmr, study, sm="HR",data=subset(meta04lung_gender,
Gender=="female"), comb.fixed = F)
# male
metagen(logsmr, selogsmr, study, sm="HR",data=subset(meta04lung_gender,
Gender=="male"), comb.fixed = F)
```

Description: The EndNote file contains the original results of literature search, including the process of filtering and selection.

Downloadable link: <https://goo.gl/A5Yojg>