Appendix: A – Details of Search Strategy

Databases searches were run in PubMed, EMBASE and the Cochrane Central Register of Controlled Trials within the Cochrane Library using a combination of MESH terms, EMTREE terms, and key words that describe ERCP. We used the Cochrane Highly Sensitive Search Strategy and the RCT filter for EMBASE as recommended by the Cochrane Handbook 6.4.11 for identifying RCTs. (Lefebvre C, Manheimer E, Glanville J. Chapter 6: Searching for studies. In: Higgins JPT, Green S (editors). Cochrane Handbook for Systematic Reviews of Interventions Version 5.1.0 (updated March 2011). The Cochrane Collaboration, 2011.)

**PubMed search**

(“cholangiopancreatography, endoscopic retrograde”[MeSH Terms] OR (“cholangiopancreatography”[All Fields] AND "endoscopic"[All Fields] AND "retrograde"[All Fields]) OR "endoscopic retrograde cholangiopancreatography”[All Fields] OR "ercp”[All Fields]) AND (((randomized controlled trial[pt]) OR (controlled clinical trial[pt]) OR (randomized[tiab]) OR (PLACEBO) OR (clinical trials as topic[mesh:noexp]) OR (randomly[tiab]) OR (trial[ti])) NOT (animals[mh] NOT humans[mh]))

**EMBASE search**

(cholangiopancreatographies OR 'cholangiopancreatography'/exp OR 'cholangiopancreatography' OR cholangiopancreatography/exp OR cholangiopancreatography OR 'ercp'/exp OR 'ercp' OR ercp/exp OR ercp OR 'sphincterotomy'/exp OR 'sphincterotomy' OR sphincterotomy/exp OR sphincterotomy OR sphincterotomies OR 'papillotomy'/exp OR 'papillotomy' OR papillotomy/exp OR papillotomy OR papillotomies)

AND

('phase 1 clinical trial'/exp OR 'phase 1 clinical trial' OR 'phase 2 clinical trial'/exp OR 'phase 2 clinical trial' OR 'phase 3 clinical trial'/exp OR 'phase 3 clinical trial' OR 'phase 4 clinical trial'/exp OR 'phase 4 clinical trial')
clinical trial' OR 'randomized controlled trials'/exp OR 'randomized controlled trials' OR 'randomised controlled trials' OR 'rcts' OR 'ccts' OR 'clinical trials'/exp OR 'clinical trials' OR 'clinical trials'/exp OR 'clinical trials' OR 'randomised controlled trial'/exp OR 'randomised controlled trial' OR 'randomized control trial' OR 'controlled clinical trials'/exp OR 'controlled clinical trials' OR 'phase one' OR 'phase 1' OR 'phase i' OR 'phase two' OR 'phase 2' OR 'phase ii' OR 'phase three' OR 'phase 3' OR 'phase iii' OR 'phase four' OR 'phase 4' OR 'phase iv' OR 'randomized controlled clinical trial' OR 'randomised controlled clinical trial' OR 'randomized controlled clinical trials' OR 'randomised controlled clinical trials' OR 'randomized clinical trial' OR 'randomised clinical trial' OR 'randomized clinical trials' OR 'randomised clinical trials' OR 'rct' OR 'cct' OR 'multicenter study'/exp OR 'multicenter study' OR 'multicentre study' OR 'multicenter studies'/exp OR 'multicenter studies' OR 'multicentre studies' OR 'randomized controlled trial'/exp OR 'randomized controlled trial' OR 'controlled clinical trial'/exp OR 'controlled clinical trial' OR 'randomized' OR 'placebo'/exp OR 'placebo' OR 'drug therapy'/exp OR 'drug therapy' OR 'randomly' OR 'trial')

Cochrane Library search

"("cholangiopancreatography,QUOTESPACEendoscopicQUOTESPACEendoscopic"[MeSH Terms] OR "cholangiopancreatography"[All Fields] AND "endoscopic"[AllFields] AND "retrograde"[All Fields])OR "endoscopic"[All Fields] AND "retrograde"[All Fields] AND "cholangiopancreatography"[All Fields] OR "ercp"[All Fields] ) in Cochrane Central Register of Controlled Trials"
Appendix: B

Code for Bayesian multivariate meta-regression model in WinBUGS to evaluate heterogeneity and consistency

```r
model {  
  for(i in 1:S) {  
    eff.study[i, b[offset[i]], b[offset[i]]] <- 0  
    for(k in (offset[i] + 1):(offset[i + 1]-1)) {  
      eff.study[i,t[k],b[k]] <- eff.des[d[k],t[k]] + RE[i,t[k]] - RE[i,b[k]]  
    }  
  }  
  # Heterogeneity  
  for(i in 1:S) {  
    RE[i,1] <- 0  
    RE[i,2:T] ~ dmnorm(zero[], Prec[])  
  }  
  # Prec is the inverse of the structured heterogeneity matrix  
  for(i in 1:1{T-1}) {  
    for(j in 1:1{T-1}){  
      Prec[i,j] <- 2*(equals(i,j)-1/T)/(tau*tau)  
    }  
  }  
  for(i in 1:A) {  
    logit(p[i]) <- mu[study[i]] + eff.study[study[i],t[i],b[i]]  
    r[i] ~ dbin(p[i],n[i])  
  }  
  # For computing DIC  
  for(i in 1:A) {  
    rhat[i] <- p[i] * n[i]  
    dev[i] <- 2 * (r[i] * (log(r[i])-log(rhat[i])) + (n[i]-r[i]) * (log(n[i]-r[i]) - log(n[i]-rhat[i])))  
  }  
  devs <- sum(dev[])  
  # Priors  
  for(i in 1:S) {  
    mu[i] ~ dnorm(0,0.05)  
  }  
  tau ~ dunif(0,2)  
  # Initialize eff.des for studies 1 through 22 (all contain trt 1 or A)  
  for(i in 1:22) {  
    for(k in (offset.design[i] + 1):(offset.design[i] + num.ests[i])) {  
      eff.des[i,t[k]] ~ dnorm(0,0.01)  
    }  
  }  
  # Initialize eff.des for studies 23 through 23 (no trt 1 or A)  
  for(i in 23:D) {  
    for(k in (offset.design[i]):(offset.design[i] + num.ests[i]-1)) {  
      eff.des[i,t[k]] ~ dnorm(0,0.01)  
    }  
  }  
  for(i in 1:8) {  
    for(j in 1:8){  
      wxw[i,j]<-w[i]*w[j]  
    }  
  }  
  # Define inconsistency parameters  
```

Raw data in the WINBUGS format, used in the primary network meta-analysis.

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