Supplementary Online Content

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This supplementary material has been provided by the authors to give readers additional information about their work.

eMethods 1. Search Strategies

MEDLINE (PubMed interface)

EMBASE (OVID interface)

Cochrane Central Register of Controlled Trials (CENTRAL, Wiley interface)

ClinicalTrials.gov

https://clinicaltrials.gov/ct2/results/refine?show_xprt=Y

(Prostatic Neoplasms) AND (Enzalutamide OR "MDV-3100" OR xtandi OR "915087-33-1" OR apalutamide OR "ARN-509" OR arn509 OR erleada OR "956104-40-8" OR abiraterone OR "CB-7598" OR CB7598 OR "154229-19-3" OR darolutamide OR "ORM-16497" OR "ORM-16555" OR "ODM-201" OR odm201 OR "bay 1841788" OR "bay1841788" OR "1297538-32-9" OR Docetaxel OR Docetaxol OR "Taxoltere Metro" OR "RP 56976" OR RP56976 OR Taxotere OR "NSC 628503" OR nsc628503 OR Daxotel OR dexotel OR docefrez OR "lit 976" OR "lit976" OR oncodocel OR taxespira OR taxoter OR texot OR "114977-28-5") AND (Hormone OR Castration OR androgen)

Filter with Study type "Interventional (Clinical Trial)" and Sex "Male"

EU Clinical Trials Register

<https://www.clinicaltrialsregister.eu/ctr-search/search>

(Prostatic Neoplasms) AND (Enzalutamide OR "MDV-3100" OR xtandi OR "915087-33-1" OR apalutamide OR "ARN-509" OR arn509 OR erleada OR "956104-40-8" OR abiraterone OR "CB-7598" OR CB7598 OR "154229-19-3" OR darolutamide OR "ORM-16497" OR "ORM-16555" OR "ODM-201" OR odm201 OR "bay 1841788" OR "bay1841788" OR "1297538-32-9" OR Docetaxel OR Docetaxol OR "Taxoltere Metro" OR "RP 56976" OR RP56976 OR Taxotere OR "NSC 628503" OR nsc628503 OR Daxotel OR dexotel OR docefrez OR "lit 976" OR "lit976" OR oncodocel OR taxespira OR taxoter OR texot OR "114977-28-5") AND (Hormone OR Castration OR androgen)

United States Food and Drug Administration (US FDA) and European Medicines Agency (EMA)

US FDA:<https://www.accessdata.fda.gov/scripts/cder/daf/>

EMA:<https://www.ema.europa.eu/en/medicines>

#1 Enzalutamide, #2 Apalutamide, #3 Abiraterone, #4 Darolutamide, #5 Docetaxel

eMethods 2. Models and WINBUGS code

The models and WINBUGS code used were adapted from Dias et al.¹

Models

1. Network meta-analysis models for survivals with contrast-based likelihood and for adverse events with armbased likelihood

1) For time-to-event outcomes, included trials reported contrast-based data: hazard ratio that is additive on log scale and assumed to be constant over time. Defining $y_{t_i,t_{ik}}$ as the log hazard ratio of the treatment in arm k of trial i, t_{i1} , relative to the treatment in arm 1 of trial i, t_{i1} , such that

$$
y_{t_{i1}t_{ik}} \sim Normal(\delta_{t_{i1}t_{ik}}, V_{t_{i1}t_{ik}})
$$

where $\delta_{t_{i1}t_{ik}}$ is the mean and $V_{t_{i1}t_{ik}}$ is the variance. For the multi-arm trial STAMPEDE, we accounted for the correlation between $y_{t_{i1}t_{ik}}$ of different arms because they share the arm 1.

$$
\begin{pmatrix} y_{t_{i1}t_{i2}} \\ \dots \\ y_{t_{i1}t_{i k}} \end{pmatrix} \sim Normal \begin{pmatrix} \delta_{t_{i1}t_{i2}} \\ \dots \\ \delta_{t_{i1}t_{i k}} \end{pmatrix}, \begin{bmatrix} V_{t_{i1}t_{i2}} & \dots & s e_{t_{i1}}^2 \\ \vdots & \ddots & \vdots \\ s e_{t_{i1}}^2 & \dots & V_{t_{i1}t_{i k}} \end{bmatrix}
$$

The variance-covariance matrix has off-diagonal elements $se_{t_{i1}}^2$ which is the variance in the arm 1 estimated according to methods proposed by Dias et al.¹ To model the outcome, an identity link function $g(\gamma)$ was used.

$$
g(\gamma) = \delta_{t_{i1}t_{ik}}
$$

2) For serious adverse event (SAE), included trials reported arm-based data: the number of patients in each arm and the number who experienced SAE. Defining $n_{t_{ik}}$ as the of number of patients receiving the treatment in arm k of trial i, t_{i1} , and $r_{t_{ik}}$ as the number of patients among $n_{t_{ik}}$ who experienced SAE, such that

$$
r_{t_{ik}} \sim Binomial(p_{t_{ik}}, n_{t_{ik}})
$$

where $p_{t_{ik}}$ is the probability that a patient experienced SAE.As arm-based likelihood was used, no correlation adjustment is needed at likelihood level for multi-arm trials.¹ To model the outcome, a logit link function $g(y)$ will be used.

$$
g(\gamma) = logit(p_{t_{ik}}) = \mu_i + \delta_{t_{i1}t_{ik}}
$$

For trial i, μ_i is the log odds of SAE for the treatment in arm 1, and δ_{t_i,t_i} is the log odds ratio of the treatment in arm k relative to the treatment in arm 1.

For either outcome, the trial specific relative effect $\delta_{t_i,t_{ik}}$ is drawn from a common random effects distribution

$$
\delta_{t_{i1}t_{ik}} \sim Normal\big(d_{t_{i1}t_{ik}}, \sigma^2\big)
$$

where $d_{t_{i1}t_{ik}}$ is the mean and σ^2 is the common between-study variance. We accounted for the correlation between $\delta_{t_{i1}t_{ik}}$ of different arms within the multi-arm trial.

$$
\begin{pmatrix} \delta_{t_{i1}t_{i2}} \\ \dots \\ \delta_{t_{i1}t_{i2}} \end{pmatrix} \sim Normal \begin{pmatrix} d_{t_{i1}t_{i2}} \\ \dots \\ d_{t_{i1}t_{i k}} \end{pmatrix}, \Sigma (\sigma^2, 0.5) \}
$$

 $\Sigma(\sigma^2, 0.5)$ denotes a variance-covariance matrix with diagonal element σ^2 and off-diagonal elements 0.5 σ^2 . It implies that the correlation between any two-treatment-contrast within a multi-arm trial is 0.5.2 It follows that the fixed effects model is a special case, obtained by setting the σ^2 to zero, implying that $\delta_{t_i,t_{ik}} = d_{t_i,t_{ik}}$ for all *i*.

In our study, we label placebo/no treatment as the overall reference, i.e., treatment No.1. According to consistency equation3,4

$$
d_{t_{i1}t_{ik}} = d_{1t_{ik}} - d_{1t_{i1}}
$$

where $d_{1 t_{ik}}$ is the effect of the treatment in arm k of trial i relative to reference. And for any treatment s ($s > 1$), the effect relative to reference, d_{1s} , is the basic parameter of interest in a network meta-analysis through which all treatments are to be compared and ranked.

2. Parametric survival meta-analysis models

We reconstructed time-to-event data from published Kaplan Meier curves using methods described in the statistical analysis section of the main paper. We fit a series of first-order fractional polynomial models with power parameter p={-2,- 1,-0.5,0.5,1,2,3}, which include common parametric distributions for survival times such as Weibull (p=0) and Gompertz $(p=1)$.⁵ Deviance information criterion (DIC) was used to compare models and assess goodness of fit.⁶

Survival curves can be divided into J consecutive intervals over the follow-up period: $[t_1, t_2]$, $(t_2, t_3]$, ..., $[t_1, t_{1+1}]$, with t_1 =0. For each time interval $j = 1, 2, 3, ..., J$,

$$
r_{t_{ikj}} \sim Binomial\left(p_{t_{ikj}}, n_{t_{ikj}}\right)
$$

where $r_{t_{ik}}$ is the number of events derived from the reconstructed time-to-event data in the jth interval [t_i , t_{i+1}] for treatment in arm k of trial i, $r_{t_{ikj}}$ is the number of participants at risk at the start of the jth interval, and $p_{t_{ikj}}$ is the event probability for the *j*th interval. When the time intervals are relatively short, the hazard $h_{t_{ik}}$ is assumed to be constant within the time interval, such that

$$
p_{t_{ikj}} = 1 - \exp(-h_{t_{ikj}} * du)
$$

where du is the length of the interval. To model the outcome, a link function $g(y)$ will be used.

$$
g(\gamma) = \log (h_{t_{ikj}}) = \alpha_{0,t_{ik}} + \alpha_{0,t_{ik}} * u_j^p
$$

$$
\begin{pmatrix} \alpha_{0,t_{ik}} \\ \alpha_{1,t_{ik}} \end{pmatrix} = \begin{pmatrix} \mu_{0,i} \\ \mu_{1,i} \end{pmatrix} + \begin{pmatrix} \delta_{0,t_{i1}t_{ik}} \\ d_{1,1t_{ik}} - d_{1,1t_{i1}} \end{pmatrix}
$$

where $p = \{-2, -1, -0.5, 0, 0.5, 1, 2, 3\}$ and $u^0 = \ln(u)$. As mentioned in the main paper, this covers common parametric survival distributions such as Weibull ($p = 0$) and Gompertz ($p = 1$). And $\alpha_{0,t_{ik}}$ is the scale parameter and $\alpha_{1,t_{ik}}$ is the shape parameter.

 δ_{0,t_i,t_i} is the trial specific relative effect on scale parameter, drawn from a common random effects distribution $\delta_{0,t_1,t_2} \sim Normal(0, \sigma^2)$

where σ^2 is the common between-study variance. We accounted for the correlation between $\delta_{0,t_{i1}t_{ik}}$ of different arms within the multi-arm trial with the above mentioned method. It follows that the fixed effects model is a special case, obtained by setting the σ^2 to zero, implying that $\delta_{0,t_{i1}t_{ik}} = d_{0,1}t_{ik} - d_{0,1}t_{i1}$ for all i.

 $d_{1,1 t_{ik}}-d_{1,1 t_{i1}}$ is the fixed treatment effect on shape parameter, which along with $u_j{}^p$ describes the change of log hazad ratio over time. In special cases where $d_{1,1 t_{ik}} - d_{1,1 t_{i1}}$ equals to zero, $\delta_{0,t_{i1} t_{ik}}$ is the trial specific hazard ratio.

For Bayesian inference, diffuse priors were ascribed to allow the observed trial data to be the main, overwhelming, influence on effect estimates.7 Note that for network meta-analysis of randomized control trial data, pooling occurs at the relative effect level, i.e., we pool trial-specific relative effect $\delta_{t_i,t_{ik}}$ to estimate the d_{1s} , whereas μ_i is regarded as a nuisance parameter.

WINBUG code

1. Fixed effects model

model{ # *** PROGRAM STARTS for (j in 1:N){ # LOOP THROUGH EVENTS # time in months transformed according to power P timen[j]<-(time[j]) timen1[j]<-(equals(P,0)*log(timen[j])+(1-equals(P,0))*pow(timen[j],P)) r[j]~dbin(p[j], z[j]) # likelihood p[j]<-1-exp(-h[j]*dt[j]) # hazard over time log(h[j])<-Alpha[s[j],a[j],1]+Alpha[s[j],a[j],2]*timen1[j] } for (i in 1:ns){ # LOOP THROUGH STUDIES for (k in 1:na[i]){ # LOOP THROUGH ARMS

```
 Alpha[i,k,1]<-mu[i,1]+d[t[i,k],1]-d[t[i,1],1] # model for linear predictor of alpha_0 
   Alpha[i,k,2]<-mu[i,2]+d[t[i,k],2]-d[t[i,1],2] # model for linear predictor of alpha_1
  }
}
# priors
for (i in 1:ns){ # LOOP THROUGH STUDIES
 mu[i,1:2] ~ dmnorm(mean[1:2],prec[,]) \qquad \qquad # vague priors for all trial baselines
}
d[1,1]<-0 # alpha_0 treatment effect is zero for reference treatment
d[1,2]<-0 # alpha_1 treatment effect is zero for reference treatment
for (k in 2:nt){ # LOOP THROUGH TREATMENTS
 d[k,1:2] \sim dmnorm(mean[1:2],prec[,]) \qquad \qquad # vague priors for treatment effects
}
# output
for (m in 1:maxt){ # create time points for output; maxt reflects maximum time point
 time1[m]<-(equals(P,0)*log(m) + (1-equals(P,0))*pow(m,P) )
}
# hazard ratios over time for all possible contrasts
for (c in 1:(nt-1)){
 for (k in (c+1):nt)\{ for (m in 1:maxt){
    log(HR[c,k,m])<-(d[k,1]-d[c,1])+(d[k,2]-d[c,2])*time1[m] 
   }
  }
}
# provide estimates of survival probabilities over time by treatment 
for (k \text{ in } 1 \text{ :} nt) alpha0[k]<-mu[7,1]+d[k,1] # alpha_0 by treatment using baseline from study 7 (STAMPEDE trial)
  alpha1[k]<-mu[7,2]+d[k,2] # alpha_1 by treatment using baseline from study 7 (STAMPEDE trial)
  for (m in 1:maxt){
  log(HAZARD[k,m])<-alpha0[k]+alpha1[k]*time1[m] # hazard over time by treatment
  CUM_H[k,m]<-sum(HAZARD[k,1:m]) # cumulative hazard over time by treatment T[k,m]<-1-exp(-CUM_H[k,m]) # mortality over time by treatment
                                        # mortality over time by treatment
         S[k,m]<-1-T[k,m] # survival over time by treatment
        rk[k,m] \leq rank(T[,m],k) # rank over time by treatment
  }
\left.\begin{array}{c} \end{array}\right\}# *** PROGRAM ENDS
model{ # *** PROGRAM STARTS
for (j in 1:N){ # LOOP THROUGH EVENTS
2. Random effects model
model{ # *** PROGRAM STARTS
for (j in 1:N){ # LOOP THROUGH EVENTS
# time in months transformed according to power P
  timen[j]<-(time[j]) 
  timen1[j]<-(equals(P,0)*log(timen[j])+(1-equals(P,0))*pow(timen[j],P) ) 
 r[i]~\simdbin(p[j], z[j]) # likelihood
  p[j]<-1-exp(-h[j]*dt[j]) # hazard in each interval
```

```
# hazard over time
 log(h[j])<-Alpha[s[j],a[j],1]+Alpha[s[j],a[j],2]*timen1[j] 
}
for (i in 1:ns){ # LOOP THROUGH STUDIES
 w[i,1]<-0 # adjustment for multi-arm trials is zero for control arm
  delta[i,1]<-0 # treatment effect is zero for control arm
  for (k in 1:na[i]){ # LOOP THROUGH ARMS
  Alpha[i,k,1]<-mu[i,1]+delta[i,k] # model for linear predictor of alpha_0
   Alpha[i,k,2]<-mu[i,2]+d[t[i,k],2]-d[t[i,1],2] # model for linear predictor of alpha_1
  }
  for (k in 2:na[i]){ # LOOP THROUGH ARMS
   # trial-specific random effects distributions for alpha_0 treatment effects 
   delta[i,k]~dnorm(md[i,k],taud[i,k]) 
   # mean of distributions (with multi-arm trial correction)
   md[i,k]<-d[t[i,k],1]-d[t[i,1],1] +sw[i,k]
  w[i,k] < \text{delta}[i,k] - d[t[i,k],1] + d[t[i,1],1] # adjustment for multi-arm trials
  sw[i,k] < -sum(w[i,1:k-1])/(k-1) # cumulative adjustment for multi-arm trials
   # precision of distributions (with multi-arm trial correction)
   taud[i,k] <- tau *2*(k-1)/k 
  }
}
# priors
for (i in 1:ns){ # LOOP THROUGH STUDIES
 mu[i,1:2] ~ dmnorm(mean[1:2],prec[,]) \qquad \qquad # vague priors for all trial baselines
}
d[1,1]<-0 # alpha_0 treatment effect is zero for reference treatment
d[1,2]<-0 # alpha_1 treatment effect is zero for reference treatment
for (k in 2:nt){ # LOOP THROUGH TREATMENTS
  d[k,1:2] ~ dmnorm(mean[1:2],prec[,]) # vague priors for treatment effects 
}
sd^{\sim}dunif(0,2) # vague prior for between-trial SD
tau<-1/(sd*sd) # between-trial precision = (1/between-trial variance)
# output
for (m \in \{m\} \land ... \land m) # create time points for output
time1[m]<-(equals(P,0)*log(m) + (1-equals(P,0))*pow(m,P) )
}
# hazard ratios over time for all possible contrasts
for (c in 1:(nt-1)){
 for (k in (c+1):nt){
   for (m in 1:maxt){
    log(HR[c,k,m])<-(d[k,1]-d[c,1])+(d[k,2]-d[c,2])*time1[m] 
   }
  }
}
```

```
# provide estimates of survival probabilities over time by treatment 
for (k in 1:nt){
 alpha0[k]<-mu[7,1]+d[k,1] # alpha_0 by treatment using baseline from study 8
 alpha1[k]<-mu[7,2]+d[k,2] \qquad # alpha_1 by treatment using baseline from study 8
  for (m in 1:maxt){
        log(HAZARD[k,m])<-alpha0[k]+alpha1[k]*time1[m] # hazard over time by treatment
         CUM_H[k,m]<-sum(HAZARD[k,1:m]) # cumulative hazard over time by treatment
   T[k,m]<-1-exp(-CUM_H[k,m]) # mortality over time by treatment
        S[k,m] < -1 - T[k,m] # survival over time by treatment<br>
rk[k,m] < -rank(T[,m],k) # fank over time by treatmen
                                          #rank over time by treatment
  }
}
} # *** PROGRAM ENDS
```
eTable 1. Data Items Extracted

Definitions of outcomes:

- Radiographic progression-free survival: time from randomization to radiographic progression based on Prostate Cancer Working Group 2 criteria for bone lesions and the Response Evaluation Criteria in Solid Tumors, version 1.1, for soft-tissue lesions, or death from any cause, whichever occurred first.
- Overall survival: time from randomization to death from any cause.
- Serious adverse event: an untoward medical occurrence associated with the use of a drug and results in any of the following outcomes: death, a life-threatening adverse event, inpatient hospitalization or prolongation of existing hospitalization, a persistent or significant incapacity or substantial disruption of the ability to conduct normal life functions, or a congenital anomaly/birth defect.⁸

eTable 2. Outcomes Assessed in Included Trials

Abbreviation: BFI-SF, Brief Pain Inventory—Short Form; EORTC QLQ, European Organization for the Research and Treatment of Cancer Quality of Life Questionnaire; FACT-P, Functional Assessment of Cancer Therapy-Prostate; PCWG, Prostate Cancer Working Group; PSA, prostate-specific antigen; QoL, quality of life; RECIST, Response Evaluation Criteria in Solid Tumors;

eTable 3. Results of Included Trials for Overall Survival, Radiographic Progression Free Survival, and Serious Adverse Events

Abbreviation: ADT, androgen deprivation therapy; CI, confidence interval; HR, hazard ratio; OS, overall survival; rPFS, radiographic progression-free survival (including progression-free survival in STAMPEDE, time to clinical progression in CHAARTED, and clinical progression-free in ENZAMET); SAE, serious adverse events, SNA, Standard non-steroid antiandrogen (bicalutamide, nilutamide, or flutamide).

a STAMPEDE trial did not report SAE or AE that let to treatment discontinuation for metastatic castration-sensitive prostate cancer patients.

b LATITUDE trial allowed cross-over after the first interim analysis. Adjusted overall survival estimates for treatment switching was used.

^c STAMPEDE trial is a multi-arm multi-stage platform design where different active treatments were tested at different time periods but shared the same control arm that enrolled patients continuously.

eTable 4. Relative Effect Estimates for All Possible Pairwise Treatment Comparisons

Overall survival, hazard ratio (95% CI)

Radiographic progression-free survival, hazard ratio (95% CI)

Serious adverse events, odds ratio (95% CI)

Abbreviation: CI, credible interval; Standard non-steroid antiandrogen (bicalutamide, nilutamide, or flutamide).

eFigure 1. Flowchart of Study Selection Process

Bibliographic databases

Trial registries

Regulatory documents

eFigure 2. Treatment Ranking Probabilities for Overall Survival, Radiographic Progression-Free Survival, and Serious Adverse Events

Overall survival

Radiographic progression free survival

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Serious Adverse events

eFigure 3. Network Meta-analysis Results for Subgroups Based on Disease Volume

Radiographic progression-free survival, high disease volume

Radiographic progression-free survival, low disease volume

High volume disease was defined as presence of visceral metastases or four or more bone metastases, with at least one outside the vertebral column or pelvis the CHAARTED trial criteria.9

eFigure 4. Treatment ranking over time derived from parametric survival network metaanalysis

Overall survival

Radiographic progression free survival

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eFigure 5. Hazard Ratios over time derived from parametric survival network meta-analysis Overall survival

Radiographic progression free survival

Abbreviation: rPFS, radiographic progression free survival.

eReferences

- 1. Sofia Dias AEA NJW, Jeroen P. Jansen, Alexander J. Sutton. *Network Meta-Analysis for Decision-Making (Statistics in Practice).* Wiley; 2018.
- 2. Dias S, Sutton AJ, Ades AE, Welton NJ. Evidence synthesis for decision making 2: a generalized linear modeling framework for pairwise and network meta-analysis of randomized controlled trials. *Medical decision making : an international journal of the Society for Medical Decision Making.* 2013;33(5):607-617.
- 3. Lu G, Ades A. Modeling between-trial variance structure in mixed treatment comparisons. *Biostatistics.* 2009;10(4):792-805.
- 4. Lu GA. Assessing evidence consistency in mixed treatment comparisons. *Journal of the American Statistical Association.* 2006;101:447-459.
- 5. Jansen JP. Network meta-analysis of survival data with fractional polynomials. *BMC Med Res Methodol.* 2011;11:61.
- 6. Spiegelhalter DJ, Best NG, Carlin BP, Van Der Linde A. Bayesian measures of model complexity and fit. *Journal of the Royal Statistical Society: Series B (Statistical Methodology).* 2002;64(4):583-639.
- 7. Sofia Dias AEA, Nicky J. Welton, Jeroen P. Jansen, Alexander J. Sutton. *Network Meta-Analysis for Decision-Making (Statistics in Practice).* Wiley; 2018.
- 8. CFR Code of Federal Regulations Title 21. <https://www.accessdata.fda.gov/scripts/cdrh/cfdocs/cfcfr/CFRSearch.cfm?fr=312.32> Published 2018. Updated April 1, 2018. Accessed.
- 9. Sweeney CJ, Chen YH, Carducci M, et al. Chemohormonal Therapy in Metastatic Hormone-Sensitive Prostate Cancer. *The New England journal of medicine.* 2015;373(8):737-746.