

# == Errata ==

## THE RUMINANT NUTRITION SYSTEM

### VOLUME II — TABLES OF EQUATIONS AND CODING

#### First Edition

June 6, 2024

The variable **rum.fd.bact.CHOB1.rate** was previously assigned two different meanings: (1) the daily yield of bacteria from CHO B1, and (2) the bacterial composition of CHO B1. To resolve this issue, **rum.fd.bact.CHOB1.rate** is now solely assigned to represent the daily yield of bacteria from CHO B1.

New variables have been introduced to account for the bacterial composition of CHO A and CHO B1, as detailed below. Depending on the diet, this adjustment significantly impacts the calculations of volatile fatty acids and ruminal pH.

\*.bact.NFC\_CHO.A.\* ==> \*.bact.NFC\_CHO\_A.\*

\*.bact.FC\_CHO.A.\* ==> \*.bact.FC\_CHO\_A.\*

\*.bact.CHOA.\* ==> \*.bact.CHO\_A.\*

\*.bact.NFC\_CHOB1.\* ==> \*.bact.NFC\_CHO\_B1.\*

\*.bact.FC\_CHOB1.\* ==> \*.bact.FC\_CHO\_B1.\*

#### List of Revised Equations

```
# ++++++
# Bacteria CHO and Protein Yield
# ++++++
# Bacterial carbohydrate A
rum.fd.bact.NFC_CHO_A.rate <- rum.fd.bact.NFC_CHO.rate * (Parm_rum.bact.CHOA/100)
rum.fd.bact.FC_CHO_A.rate <- rum.fd.bact.FC_CHO.rate * (Parm_rum.bact.CHOA/100)
rum.fd.bact.CHO_A.rate <- rum.fd.bact.NFC_CHO_A.rate + rum.fd.bact.FC_CHO_A.rate
rum.diet.bact.NFC_CHO_A.rate <- sum(rum.fd.bact.NFC_CHO_A.rate)
rum.diet.bact.FC_CHO_A.rate <- sum(rum.fd.bact.FC_CHO_A.rate)
rum.diet.bact.CHO_A.rate <- sum(rum.fd.bact.CHO_A.rate)
# Bacterial carbohydrate B1
rum.fd.bact.NFC_CHO_B1.rate <- rum.fd.bact.NFC_CHO.rate * (Parm_rum.bact.CHOB1/100)
rum.fd.bact.FC_CHO_B1.rate <- rum.fd.bact.FC_CHO.rate * (Parm_rum.bact.CHOB1/100)
rum.fd.bact.CHO_B1.rate <- rum.fd.bact.NFC_CHO_B1.rate + rum.fd.bact.FC_CHO_B1.rate
rum.diet.bact.NFC_CHO_B1.rate <- sum(rum.fd.bact.NFC_CHO_B1.rate)
rum.diet.bact.FC_CHO_B1.rate <- sum(rum.fd.bact.FC_CHO_B1.rate)
rum.diet.bact.CHO_B1.rate <- sum(rum.fd.bact.CHO_B1.rate)
```

...

```
if (genRPT)
{
  rptREBactComp_DMI <- fds["FeedName.x"]
}
```

```

names(rptREBactComp_DMI) <- "FeedName"
rptREBactComp_DMI["NFC CP"] <- rum.fd.bact.NFC_CP.rate
rptREBactComp_DMI["FC CP"] <- rum.fd.bact.FC_CP.rate
rptREBactComp_DMI["NFC TP"] <- rum.fd.bact.NFC_TP.rate
rptREBactComp_DMI["FC TP"] <- rum.fd.bact.FC_TP.rate
rptREBactComp_DMI["NFC NA"] <- rum.fd.bact.NFC_NA.rate
rptREBactComp_DMI["FC NA"] <- rum.fd.bact.FC_NA.rate
rptREBactComp_DMI["NFC CW"] <- rum.fd.bact.NFC_CW.rate
rptREBactComp_DMI["FC CW"] <- rum.fd.bact.FC_CW.rate
rptREBactComp_DMI["NFC CHO"] <- rum.fd.bact.NFC_CHO.rate
rptREBactComp_DMI["FC CHO"] <- rum.fd.bact.FC_CHO.rate
rptREBactComp_DMI["NFC CHOA"] <- rum.fd.bact.NFC_CHO_A.rate
rptREBactComp_DMI["FC CHOA"] <- rum.fd.bact.FC_CHO_A.rate
rptREBactComp_DMI["NFC CHOB1"] <- rum.fd.bact.NFC_CHO_B1.rate
rptREBactComp_DMI["FC CHOB1"] <- rum.fd.bact.FC_CHO_B1.rate
rptREBactComp_DMI["NFC Fat"] <- rum.fd.bact.NFC_Fat.rate
rptREBactComp_DMI["FC Fat"] <- rum.fd.bact.FC_Fat.rate
rptREBactComp_DMI["NFC Ash"] <- rum.fd.bact.NFC_Ash.rate
rptREBactComp_DMI["FC Ash"] <- rum.fd.bact.FC_Ash.rate

...

# Carbohydrate - Bacteria
duo.fd.bact.NFC_CHO.rate <- rum.fd.bact.NFC_CHO.rate
duo.fd.bact.FC_CHO.rate <- rum.fd.bact.FC_CHO.rate
duo.fd.bact.CHO.rate <- rum.fd.bact.CHO.rate
duo.fd.bact.NFC_CHO_A.rate <- rum.fd.bact.NFC_CHO_A.rate
duo.fd.bact.FC_CHO_A.rate <- rum.fd.bact.FC_CHO_A.rate
duo.fd.bact.CHO_A.rate <- rum.fd.bact.CHO_A.rate
duo.fd.bact.NFC_CHO_B1.rate <- rum.fd.bact.NFC_CHO_B1.rate
duo.fd.bact.FC_CHO_B1.rate <- rum.fd.bact.FC_CHO_B1.rate
duo.fd.bact.CHO_B1.rate <- rum.fd.bact.CHO_B1.rate
duo.diet.bact.NFC_CHO.rate <- rum.diet.bact.NFC_CHO.rate
duo.diet.bact.FC_CHO.rate <- rum.diet.bact.FC_CHO.rate
duo.diet.bact.CHO.rate <- rum.diet.bact.CHO.rate
duo.diet.bact.NFC_CHO_A.rate <- rum.diet.bact.NFC_CHO_A.rate
duo.diet.bact.FC_CHO_A.rate <- rum.diet.bact.FC_CHO_A.rate
duo.diet.bact.CHO_A.rate <- rum.diet.bact.CHO_A.rate
duo.diet.bact.NFC_CHO_B1.rate <- rum.diet.bact.NFC_CHO_B1.rate
duo.diet.bact.FC_CHO_B1.rate <- rum.diet.bact.FC_CHO_B1.rate
duo.diet.bact.CHO_B1.rate <- rum.diet.bact.CHO_B1.rate
if (genRPT)
{
  rptDuoCHO_DMI <- fds["FeedName.x"]
  names(rptDuoCHO_DMI) <- "FeedName"
  rptDuoCHO_DMI["CHOA"] <- duo.fd.bact.CHO_A.rate
  rptDuoCHO_DMI["CHOB1"] <- duo.fd.bact.CHO_B1.rate
  report(rptDuoCHO_DMI, "\nDuodenal Bacterial Carbohydrate, g/d", "", "", 3, 3, 1000, 8, TRUE,
FALSE, TRUE, FALSE, TRUE, FALSE, TRUE)
}

...

# Digested Carbohydrate - Bacteria
si.fd.bact.GCHOA.rate <- (Parm_rum.bact.IDCHOA/100) * duo.fd.bact.NFC_CHO_A.rate +
(Parm_rum.bact.IDCHOA/100) * duo.fd.bact.FC_CHO_A.rate
si.fd.bact.GCHOB1.rate <- (Parm_rum.bact.IDCHOB1/100) * duo.fd.bact.NFC_CHO_B1.rate +
(Parm_rum.bact.IDCHOB1/100) * duo.fd.bact.FC_CHO_B1.rate
si.fd.bact.GCHO.rate <- si.fd.bact.GCHOA.rate + si.fd.bact.GCHOB1.rate
si.diet.bact.GCHOA.rate <- sum(si.fd.bact.GCHOA.rate)
si.diet.bact.GCHOB1.rate <- sum(si.fd.bact.GCHOB1.rate)
si.diet.bact.GCHO.rate <- sum(si.fd.bact.GCHO.rate)
si.GCHO.rate <- si.fd.GCHO.rate + si.diet.bact.GCHO.rate

...

if (flag_fecal == 0)
{
  # Fox et al., (2004; Anim. Feed Sci. Technol. 112:29-78) Endogenous
  fc.fd.Endogenous.fat.rate <- (1.19/100) * anim.fd.DMI.rate
  fc.fd.Endogenous.ash.rate <- (1.7/100) * anim.fd.DMI.rate

```

```

# Bacteria
fc.fd.bact.CHO.rate <- (duo.fd.bact.CHO_A.rate + duo.fd.bact.CHO_B1.rate) -
(si.fd.bact.GCHOA.rate + si.fd.bact.GCHOB1.rate)
fc.fd.bact.CP.rate <- duo.fd.bact.CP.rate - si.fd.bact.GProt.rate
fc.fd.bact.EE.rate <- duo.fd.bact.fat.rate - si.fd.bact.GFat.rate
fc.fd.bact.ash.rate <- duo.fd.bact.ash.rate - si.fd.bact.GAsh.rate
fc.fd.bact.rate <- fc.fd.bact.CP.rate + fc.fd.bact.CHO.rate + fc.fd.bact.EE.rate +
fc.fd.bact.ash.rate
fc.CHO.rate <- fc.fd.CHO.rate + fc.fd.bact.CHO.rate
fc.CP.rate <- fc.fd.CP.rate + fc.fd.bact.CP.rate
fc.EE.rate <- fc.fd.EE.rate + fc.fd.bact.EE.rate + fc.fd.Endogenous.fat.rate
fc.ash.rate <- fc.fd.ash.rate + fc.fd.bact.ash.rate + fc.fd.Endogenous.ash.rate
fc.fd.IDM.rate <- (fc.CP.rate + fc.CHO.rate + fc.EE.rate + fc.ash.rate)/0.91
fc.fd.IOM.rate <- fc.fd.IDM.rate - fc.ash.rate
fc.fd.Endogenous.CP.rate <- fc.fd.IDM.rate * 0.09
fc.CP.rate <- fc.fd.CP.rate + fc.fd.bact.CP.rate + fc.fd.Endogenous.CP.rate # Add the
endogenous contribution
}
if (flag_fecal == 1)
{
# Cannas et al. (2004; J. Anim. Sci. 82:149-169) Endogenous and bacterial CP, EE, and Ash
contributions are computed together
fc.fd.Endogenous.CP.rate <- 0
fc.fd.Endogenous.fat.rate <- 0
fc.fd.Endogenous.ash.rate <- 0
# Bacteria + Endogenous
fc.fd.bact.CHO.rate <- (duo.fd.bact.CHO_A.rate + duo.fd.bact.CHO_B1.rate) -
(si.fd.bact.GCHOA.rate + si.fd.bact.GCHOB1.rate)
fc.fd.bact.CP.rate <- (30/1000) * anim.fd.DMI.rate
fc.fd.bact.EE.rate <- (11.9/1000) * anim.fd.DMI.rate
fc.fd.bact.ash.rate <- (17/1000) * anim.fd.DMI.rate
fc.fd.bact.rate <- fc.fd.bact.CP.rate + fc.fd.bact.CHO.rate + fc.fd.bact.EE.rate +
fc.fd.bact.ash.rate
fc.CHO.rate <- fc.fd.CHO.rate + fc.fd.bact.CHO.rate
fc.CP.rate <- fc.fd.CP.rate + fc.fd.bact.CP.rate + fc.fd.Endogenous.CP.rate
fc.EE.rate <- fc.fd.EE.rate + fc.fd.bact.EE.rate + fc.fd.Endogenous.fat.rate
fc.ash.rate <- fc.fd.ash.rate + fc.fd.bact.ash.rate + fc.fd.Endogenous.ash.rate
fc.fd.IDM.rate <- fc.CP.rate + fc.CHO.rate + fc.EE.rate + fc.ash.rate
fc.fd.IOM.rate <- fc.CP.rate + fc.CHO.rate + fc.EE.rate
}
if (flag_fecal == 2)
{
# Tedeschi et al. (2010; Small Ruminant Res. 89:174-184) Endogenous: assumes that only 15%
was from endogenous origin
fc.fd.Endogenous.CP.rate <- 0.15 * (30/1000) * anim.fd.DMI.rate
fc.fd.Endogenous.fat.rate <- (11.9/1000) * anim.fd.DMI.rate
fc.fd.Endogenous.ash.rate <- (17/1000) * anim.fd.DMI.rate
# Bacteria
fc.fd.bact.CHO.rate <- (duo.fd.bact.CHO_A.rate + duo.fd.bact.CHO_B1.rate) -
(si.fd.bact.GCHOA.rate + si.fd.bact.GCHOB1.rate)
fc.fd.bact.CP.rate <- duo.fd.bact.CP.rate - si.fd.bact.GProt.rate
fc.fd.bact.EE.rate <- duo.fd.bact.fat.rate - si.fd.bact.GFat.rate
fc.fd.bact.ash.rate <- duo.fd.bact.ash.rate - si.fd.bact.GAsh.rate
fc.fd.bact.rate <- fc.fd.bact.CP.rate + fc.fd.bact.CHO.rate + fc.fd.bact.EE.rate +
fc.fd.bact.ash.rate
fc.CHO.rate <- fc.fd.CHO.rate + fc.fd.bact.CHO.rate
fc.CP.rate <- fc.fd.CP.rate + fc.fd.bact.CP.rate + fc.fd.Endogenous.CP.rate
fc.EE.rate <- fc.fd.EE.rate + fc.fd.bact.EE.rate + fc.fd.Endogenous.fat.rate
fc.ash.rate <- fc.fd.ash.rate + fc.fd.bact.ash.rate + fc.fd.Endogenous.ash.rate
fc.fd.IDM.rate <- fc.CP.rate + fc.CHO.rate + fc.EE.rate + fc.ash.rate
fc.fd.IOM.rate <- fc.CP.rate + fc.CHO.rate + fc.EE.rate
}
}

```