

APPENDIX I - Format File300-EBV and File700-GEVB

Col	Name	Start	Format	Description	Example
1	rec type	1	a3	Record type ¹	300
2	brd_eval	5	a3	Breed of evaluation ²	HOL
3	pop	9	a3	Population code ³	USA
4	trt	13	a3	Trait of evaluation ⁴	mil
5	brd_anim	17	a3	Breed of animal	HOL
6	cou_orig	20	a3	Country of first registration	USA
7	sex	23	a1	Sex of animal	M
8	id_no	24	a12	Animal identification number	003000336289
9	typ_prf	37	i2	Type of proof ⁵	11
10	off_pub	40	a1	Official publication of proof ⁶	Y
11	status	42	i2	Animal status ⁷	10
12	ndau	44	i8	Number of daughters ⁸	115
13	nhrd	52	i8	Number of herds ⁹	75
14	edc	60	i8	Number of effective daughter contributions ¹⁰	133
15	rel	69	f7.4	Repeatability/Reliability ¹¹	82
16	ebv	76	f10.	National predicted genetic merit ¹²	2.780

IMPORTANT NOTE !!!!!

In the old fileformat 01x-020 and 115, the national proofs were multiplied by a factor: (prod=100; conf=100; udder=1000; long=1000; calv=1000; fert=1000; fert=1000; work=1000). This multiplication will no longer be needed.

¹Valid record types:

300 for EBV
700 for GEBV

²Breed codes accepted:

BSW=Brown Swiss type; GUE=Guernsey type; HOL=Holstein-Friesian (Black & White) type; JER=Jersey type; RDC=Red Dairy Cattle type ; SIM=Simmental type.

³Valid population codes: ARG AUS BEL CAN CHE ^aCHR CZE ^bDEA DEU ^cDFS

^dDNR ESP EST FIN FRA ^eFRM ^fFRR GBR HUN IRL ISR ITA JPN LTU LVA

NLD NZL POL PRT SVN SVK SWE USA URY ZAF

where: ^aSwiss Red Holstein; ^b Austria+Germany; ^cDenmark + Finland + Sweden; ^dDenmark Red Holstein ^e France Montbeliarde; ^fFrench Pie Rouge

⁴Accepted traits abbreviations:

Production ==> mil = milk;fat =fat; pro = protein;

Conformation ==> sta = stature;cwi = chest width;bde = body depth;ang = angularity;ran = rump angle;rwi = rump width;rls = rear-leg set;rlr = rear-leg rear view;fan = foot angle;hde = heel depth/hoof height; fua = fore udder attachment; ruh = rear udder height; ruw = rear udder width; usu = udder support;ude = udder depth;ftp = front teat placement;fll = (front) teat length;rtp = rear teat placement;ous = overall udder score; ofl = overall feet&legs score; ocs = overall conformation score; bcs = body condition score; loc = locomotion;

Udder ==>scs = somatic cell; mas = mastitis

Longevity ==> dlo = direct longevity;

Calving ==> dce = direct calving ease;mce = maternal calving ease;dsb= direct stillbirth;msb = maternal stillbirth

Female fertility ==>hco = heifer conception;crc = cow recycling;cc1 = lactating cow's ability to conceive (1);cc2 = lactating cow's ability to conceive (2);int= interval traits

Workability ==> msp = milking speed;tem = temperament

⁵Accepted codes:

00 (unknown);

11 (based on first crop sampling daughters);

12 (based on first and second crop daughters);

13 (based on parent average and genomic information only);

21(based on imported semen of proven bull, second crop daughters only);

22 (based on mostly, more than 50%, imported daughters or daughters born from imported embryos.)

⁶Accepted abbreviations:

Y (if bull proof meets national standards for official publication in the country sending information.);

P (if bull is part of a simultaneous progeny-testing program, but the proof does not yet meet national standards for official publication);

N (otherwise).

⁷Valid codes for status of bulls:

00(unknown);

10(bull randomly sampled through an official AI scheme);

15 (young bull, genomically selected);

20(other bull. Records with “20” in this file will be excluded from the international evaluation, unless type of proof is “21”).

⁸Field for number of daughters should be positive. For missing value put 0.

⁹Field for number of herds should be positive. For missing value put 0.

¹⁰ *Production, conformation, udder health, fertility and workability traits:*

Weighting factor used for these traits is “the effective daughter contribution (EDC)”, which is described In the Interbull document Code of practice, Appendix IV, “Weighting factor for international genetic evaluation”, updated April 27, 2004. EDC values should be rounded to the nearest integer value.

Calving: The weighting factors used for calving traits it the total number of calvings for the direct effects and number of daughters with calving for maternal effect

Longevity: The weighting factor used for longevity traits depends on the national genetic evaluation model. For linear models the weighting factor is the same as described above for conformation, fertility, production, udder health and workability traits. For survival models number of culled daughters is used as the weighting factor.

¹¹Reliability values are nationally calculated reliability values expressed in percents with 4 decimals. For missing value put 0.

¹²National predicted genetic merit values published domestically. For threshold models the submitted values are from the underlying scale. For missing values put 9999999999. Please note! In the old fileformat 01x-020 and 115, the national proofs were multiplied by a factor: (prod=100; conf=100;udder=1000;long=1000;calv=1000;fert=1000; fert=1000;work=1000). This multiplication will no longer be needed.

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