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System and biological effects on quantitative milking speed phenotypes from inline milk meters

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NAAB

DRMS
DAIRY RECORDS MANAGEMENT SYSTEMS

EVALUATIONS FOR MILKING SPEED

- Interbull-participating countries (N = 14) include milking speed in their “workability” evaluations
  - Australia, Canada, Denmark/Sweden/Finland, France, Germany/Austria/Luxembourg, Great Britain, Italy, Japan, the Netherlands, New Zealand, Norway, Poland, Slovenia, and Switzerland
- Nearly all phenotypes collected during first parity only and sometimes from a single classification
- If milk flow rates were available, classification data were discarded

REGARDING QUANTITATIVE MS

- Heritabilities range from 0.02 – 0.42 depending on the trait definition
- Repeatabilities range from 0.40 – 0.54
- Conflicting evidence of variation in MS across lactations
- Favorable correlations between MS and milk yield
- Unclear relationship between udder health and MS

PROPOSED RESEARCH

DRMS
DAIRY RECORDS
MANAGEMENT SYSTEMS

Obj. 1: Assemble a **high-resolution dataset pertinent to MS** representing different dairy breeds, equipment manufacturers, parlor types, and milking management strategies

Obj. 2: Characterize MS for herds grouped by equipment manufacturer and parlor type and assess the impact of additional **system effects** on the phenotype

Obj. 3: Characterize any **biological effects** that impact MS, especially concerning udder health

Obj. 4: **Standardize** MS trait definition and estimate heritability to determine its suitability for selection

OBJ 1: ASSEMBLE DATA

DRMS DAIRY RECORDS MANAGEMENT SYSTEMS

Demographics

~300 herds
>230,000 cows
>300,000 lactations
>40 million observations

31 States
6+ Breeds
11 OEMs

DeLaval	80
GEA	75
Lely	47
Boumatic	46
AfiMilk	45
SCR	13
DairyMaster	10
AIC Waikato	5
AMS Galaxy	3
Jantec	2
Universal	2

Special thanks to Robert Fourdraine & John Clay

OBJ 1: ASSEMBLE DATA

Data Cleaning

Summary stats on data

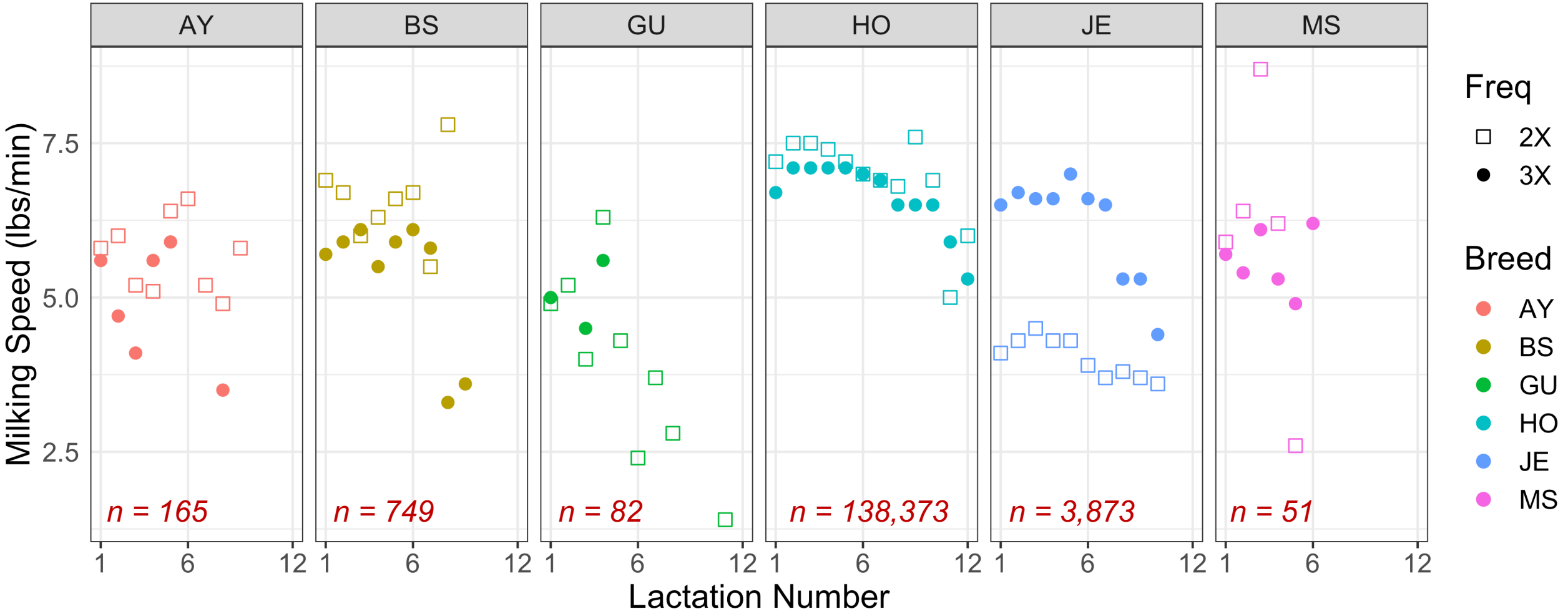
		N	Minimum	Q1	Median	Mean	Q3	Maximum	StDev		
Milking Duration										0 or missing	greater than 15
	M1time	38877488	0	3.6	4.4	5.425	5.4	1440	30.1	3254587	85677
	M2time	38611378	0	3.5	4.3	5.772	5.2	1440	39.791	3493311	89253
	M3time	29804057	-1435.5	3.5	4.2	6.17	5.1	-1435.5	46.83	12223012	61510

OBJ 1: ASSEMBLE DATA

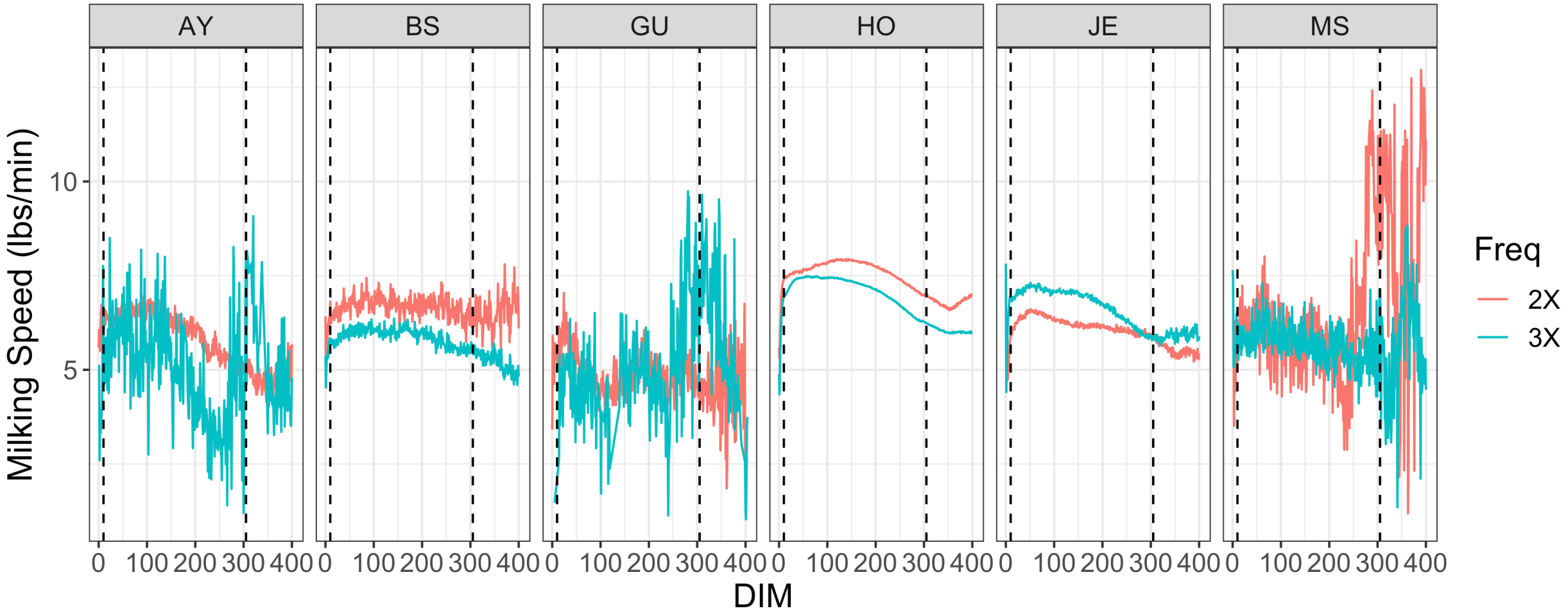
Data Cleaning

	AY		BS		GU		HO		JE		MS	
	2X	3X	2X	3X	2X	3X	2X	3X	2X	3X	2X	3X
Initial Records	28,412	1,632	67,850	93,193	20,233	495	6,154,246	21,772,400	633,289	599,840	2,119	5,334
After 1/1/2022	28,412	1,597	62,282	92,829	17,604	495	5,852,454	21,224,965	527,501	521,253	2,119	5,334
0 < duration < 15	25,374	994	45,509	57,621	12,130	398	5,138,997	15,803,428	475,668	392,451	1,354	3,661
0 < milk < 60	25,223	993	45,177	57,349	12,126	398	4,778,714	15,665,401	474,852	392,130	1,348	3,659
1 < MSPD < 15	24,646	956	39,324	56,806	10,972	389	4,611,960	15,422,775	463,138	378,765	1,333	3,613
>10 obs per cow	24,621	953	39,193	56,603	10,939	389	4,606,970	15,407,922	461,910	377,735	1,333	3,585
% reduction in data	**13.3%**	**41.6%**	**42.2%**	**39.3%**	**45.9%**	**21.4%**	**25.1%**	**29.2%**	**27.1%**	**37.0%**	**37.1%**	**32.8%**

BREED, FREQUENCY, & PARITY

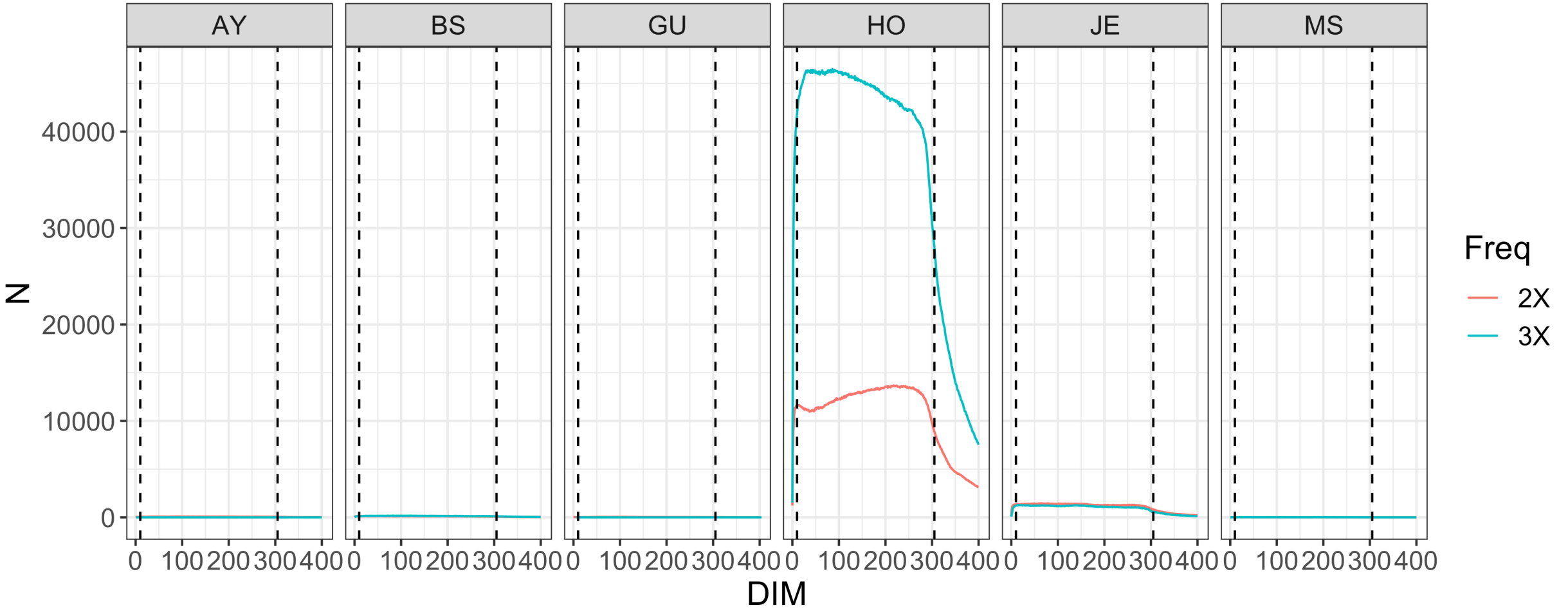


BREED, FREQUENCY, & DIM



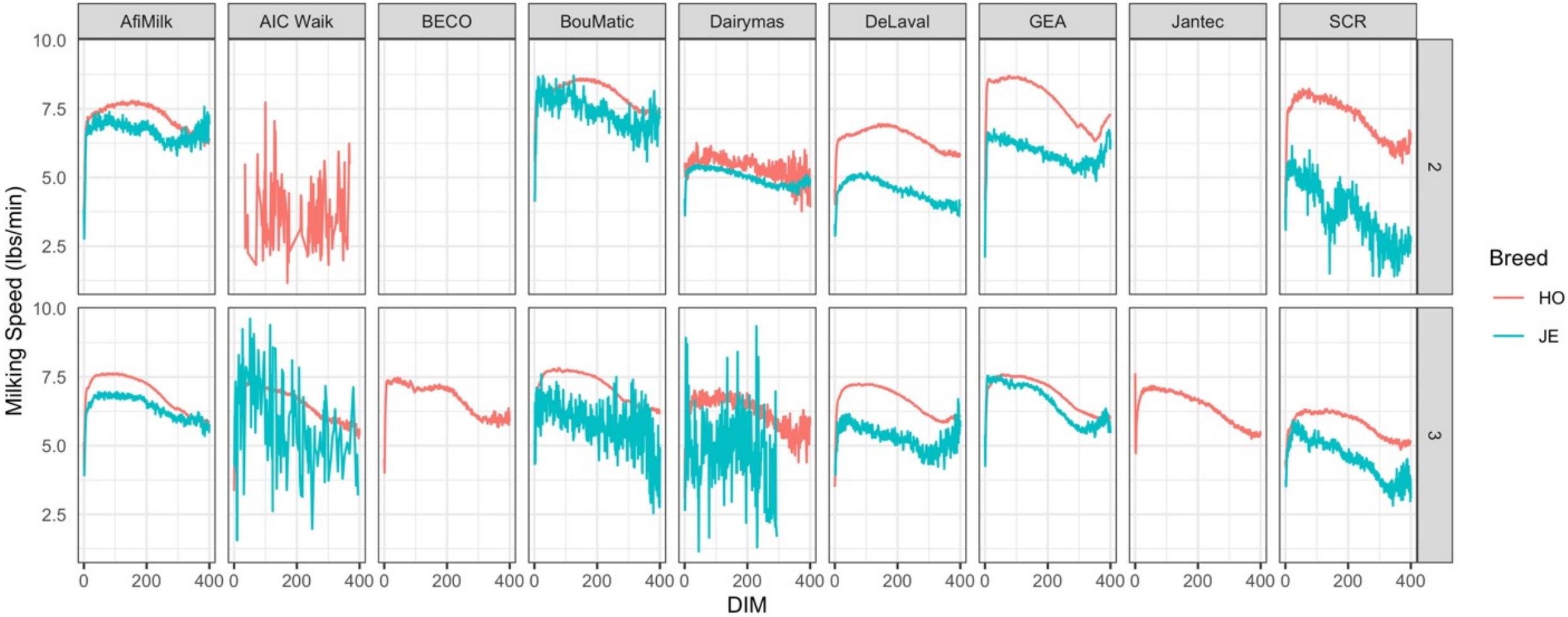
BREED, FREQUENCY, & DIM

Sparsity is a challenge

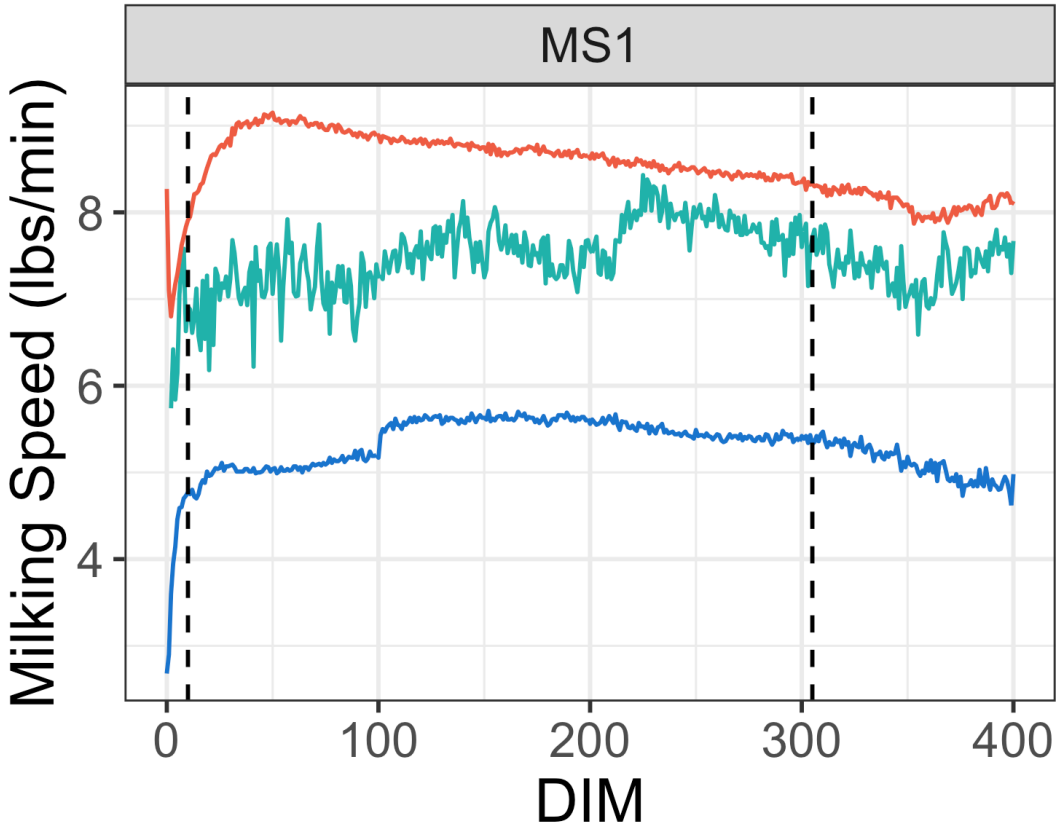


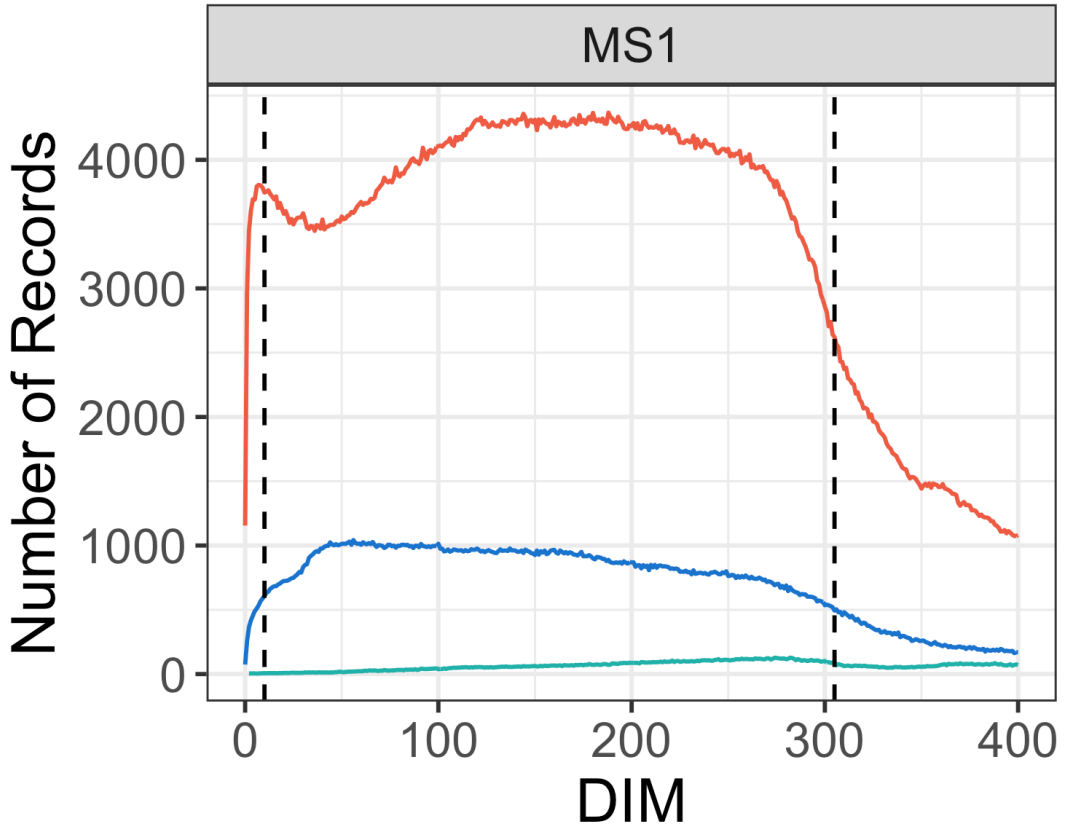
OEM, BREED, FREQUENCY, & DIM

HO & JE ONLY



AMS & OEM, HOLSTEIN ONLY





WHAT ELSE DO WE KNOW?

- AMS cows appear to milk faster than conventional cows; this may be an artifact of OEM
- MS is slightly faster for milkings earlier in the day
- Milking interval is not strongly correlated with milking speed in conventional or AMS herds (R^2 ~ 0.01 – 0.10)

WHAT'S NEXT?

- Untangle relationship of MS to SCS and clinical mastitis
- Consider alternate phenotypes (e.g., milking duration)
  - Milking speed (lbs/min) creates a ratio problem
- Generate preliminary PTAs and heritability estimates

Surveys indicate high producer enthusiasm for MS evaluations

Key Messages

- MS is actively used by both conventional and AMS herds
- MS evaluations could be of significant economic value
- We need to first understand system & biological effects on MS to standardize a phenotype definition and determine its suitability for selection

THANK YOU

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