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IRISH CATTLE BREEDING FEDERATION

Inbreeding Trends in Pedigree Beef Cattle

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Wednesday & Thursday
5th & 6th December
Hodson Bay Hotel,
Athlone

Sheep Ireland
www.sheep.ie

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'Sustainable Farming – Progress through Genetics'

Department of
Agriculture,
Food and the Marine

An Roinn
Talmhaíochta,
Bia agus Mara

Inbreeding

What is it?

- Inbreeding is defined as the probability that two alleles are identical by descent and occurs when related individuals are mated to each other

Why is it a problem?

- Decline in performance of the resulting progeny
    - ➢ Inbreeding Depression

Traits affected:

- Post weaning gain
- Skeletal and Muscle traits
- Loin development
- Fertility traits
- Embryonic mortality
- Genetic defects

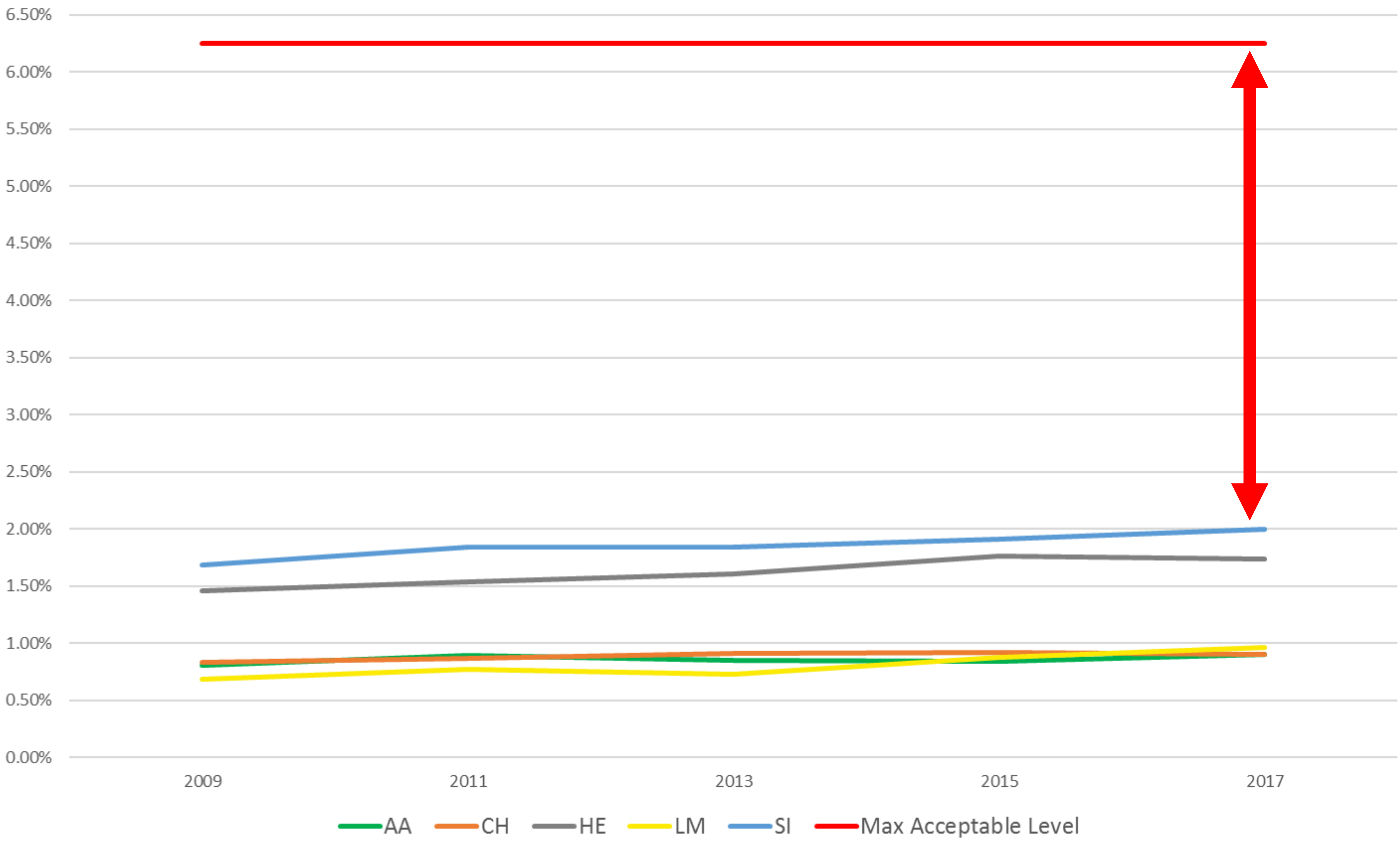
Inbreeding Level **(F)**

- Measurement of degree of inbreeding
- **6.25%** inbreeding is widely viewed as the maximum level acceptable for an individual
    - What does **6.25%** mean?

Inbreeding Coefficients for Various Matings

Relationship	Inbreeding Coefficient*
Female mated to its own sire	25%
Full Sibling mating (parents have common sire **AND** dam)	25%
Half Sibling mating (parents have common sire **OR** dam)	12.5%
Parents have a common grandparent	**6.25%**
Parents have a common great-grandparent	3.125%
***minimum value; will be higher if ancestors are themselves inbred**	

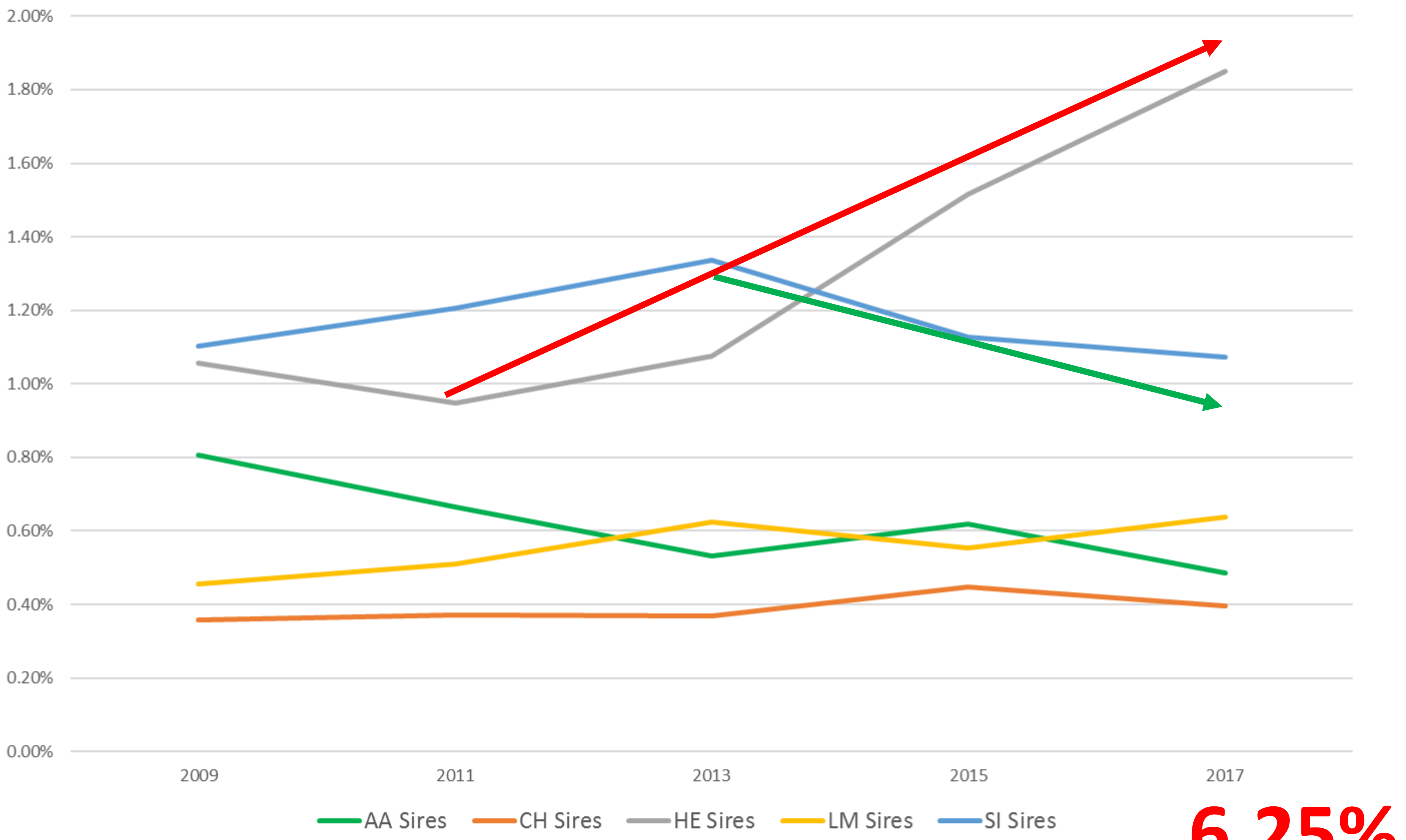
Inbreeding Level



AgTech – it's in our DNA

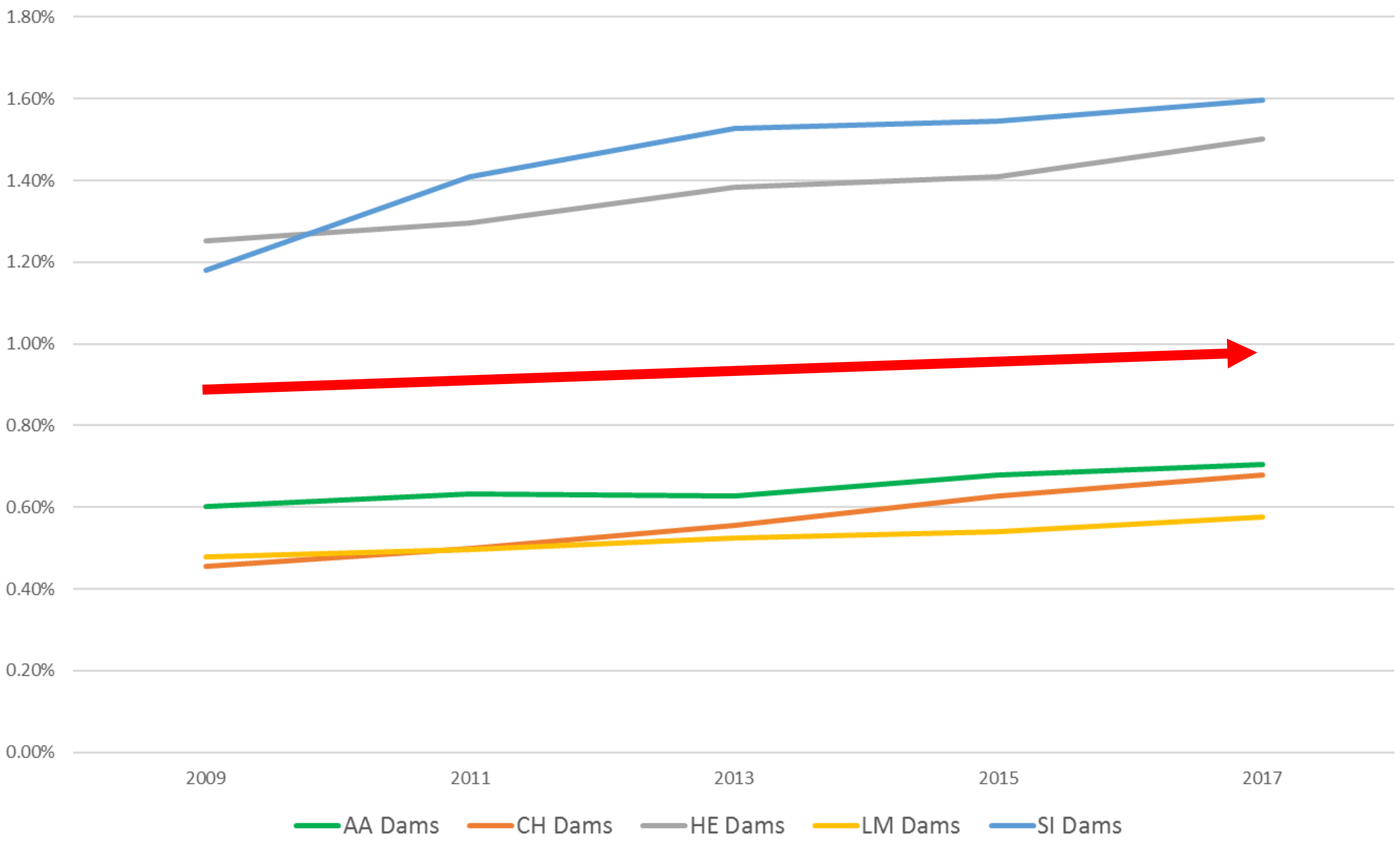
*Average level of inbreeding in pedigree calves born in a given year

Average Sire Inbreeding Level



6.25%

Average Dam Inbreeding Level

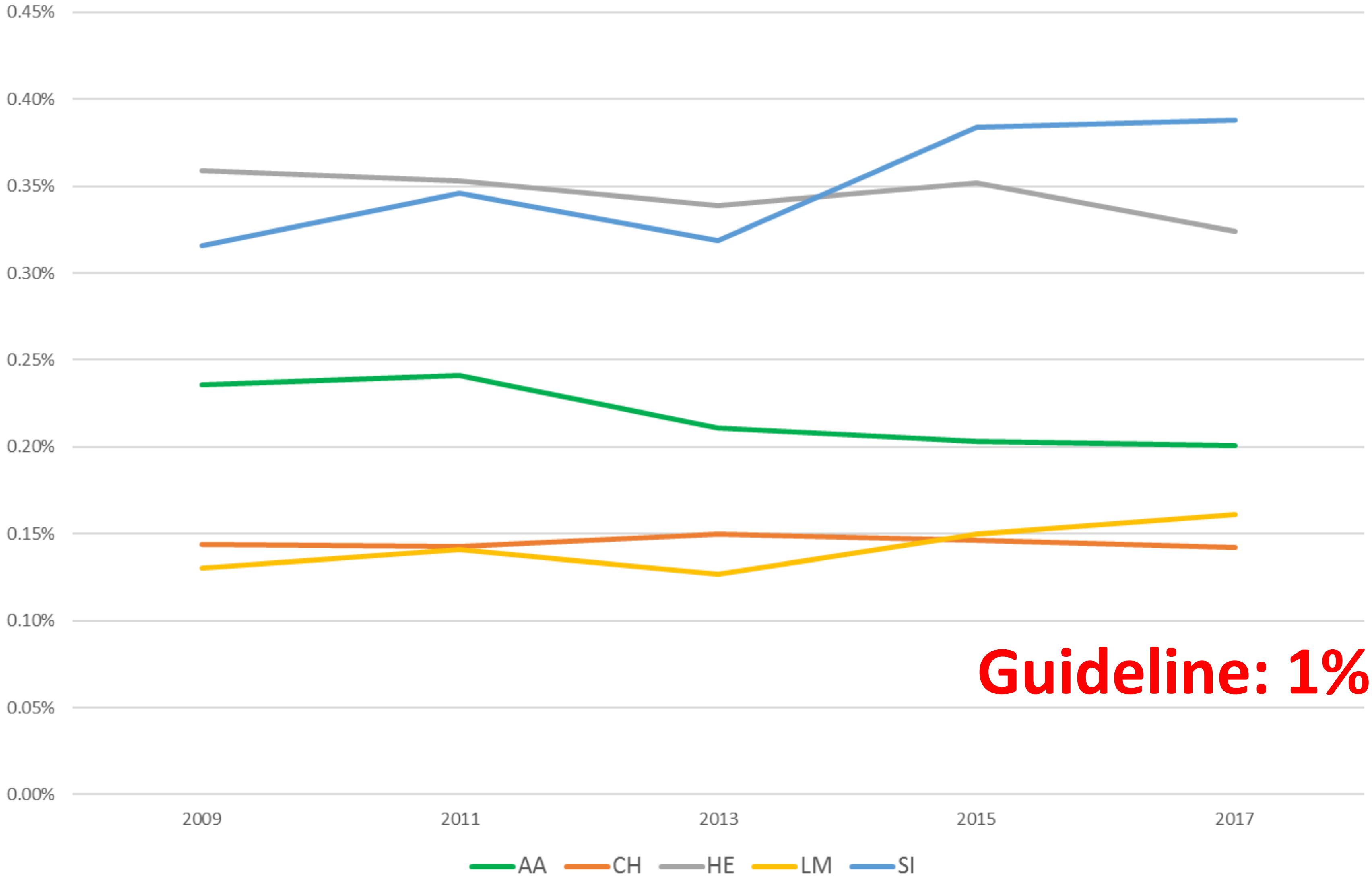


6.25%

Rate of Inbreeding **(ΔF)**

- Expresses the increase in average inbreeding level **(F)** from one generation to the next
- The maximum rate of inbreeding **(ΔF)** accepted is **1%**
- Guideline set by the Food and Agriculture Organisation of the United Nations **(FAO)**
- Above 1% - effective number of animals in the population falls below 50
    - 50 required to maintain levels of *genetic diversity*

Rate of Inbreeding **(ΔF)**



Guideline: 1%

Contribution vs Relationship

- **Marginal Contribution**
  - Not necessarily the bulls with the largest number of progeny
  - How many times they appear in the pedigrees of the reference population
- **Relationship to Population**
  - How related a bull is to the reference population
  - If a bull has relationship of 3% to the reference population
    - Inbreeding percentage of a mating between the bull and the average dam results in a progeny with an inbreeding level (**F**) of 1.5%

Reference population is all pedigree females, still alive, older than one year and born after the year 2000

Relationship to Population

Breed	AI Code	Name	Relatedness
AA	BJP	BOHEY JASPER	4.87%
	SUB	SUNSET ACRES BANG	4.35%
	CYI	CONEYISLAND LEGEND	4.24%
CH	CF52	DOONALLY NEW	7.26%
	PTE	PIRATE	5.89%
	KIB	LIMKILN BOSCO	5.48%
HE	BHG	BISHOPHILL GENERAL	8.72%
	SAD	STANDARD LAD 93J IMP CAN	7.68%
	F179	GAGEBORO EUGENIC	6.48%
LM	MBP	MILBROOK DARTANGAN ET	3.58%
	KJB	BROOKLANDS F0959	3.42%
	NEU	NEWTOWN BUNTY 1 (ET)	3.40%
SI	HCC	HILLCREST CHAMPION	6.62%
	CQA	CURAHEEN VIO (ET)	6.15%
	TSO	CURAHEEN TYSON (ET)	5.78%

Marginal Contribution to Population

Breed	AI Code	Name	Marginal Contribution
AA	**SUB**	SUNSET ACRES BANG	**4.42%**
	F195	TIVANAGH BARON	**3.14%**
	LWF	LAWSONS FORD BAGATELLE Z094	**3.05%**
CH	**CF52**	DOONALLY NEW	**6.29%**
	PTE	PIRATE	**4.26%**
	IDU	INDURAIN	**3.62%**
HE	**SAD**	STANDARD LAD 93J IMP CAN	**7.66%**
	CKVX	CH 3223 VISA ET 57X	**6.15%**
	CUV	CHURCHILL STORM V583	**5.51%**
LM	**MUC**	MAS DU CLO	**4.15%**
	SYP	SYMPA	**3.79%**
	DAU	DAUPHIN	**2.66%**
SI	**AS26**	SIEGFRIED	**4.15%**
	GHS	GRETNA HOUSE SUPERSONIC	**3.78%**
	REV	RACEVIEW KING	**2.65%**

10.6%

Genomic Inbreeding

- Measures the relationship between two animals by assessing the level of homozygosity in their genes
  - More accurate measure of inbreeding
  - To calculate, the population needs to be genotyped
- On average progeny receive 50% of their DNA from each parent.
- Full siblings may share more or less than 50% of their genetics (average)
- Identify the percentage of genes sibling animals have in **common**
- Identifies animals that share the same genes, **not related** through pedigree

Genomic Inbreeding

- Critical information when creating breeding strategies
    - Avoid the mating of animals that are carriers for undesirable traits
- Identify animals with overlap in the pedigree but have no genes in common
    - Increases the number of potential sires for planned matings
- Through genotyping, more animals are being parentage verified
    - Identify incorrect sires and correct them
    - Fewer accidental cases of inbreeding

➢ **Population MUST be genotyped**

Conclusion

- Inbreeding cannot be completely avoided in small populations
  - ➢ Trace back far enough - all animals are related
- Positive trends – some breeds need to exercise caution
- Opportunity to identify outcross bulls
  - Based off relatedness/contribution
- Going forward – Genomic Inbreeding

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