

Quantitative trait loci study in Baluchi sheep

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➤ **Conclusion:** The present study contributes to the understanding of chromosomal regions that explain part of the variability of wool quality in Baluchi sheep.

✓ objective:

To study of QTL affecting sheep wool traits in Baluchi sheep.

➤ Materials & methods:

□ Animal and phenotypes

❖ 503 individuals from 2 flocks

- ✓ 13 paternal half-sib families
- ✓ average family size 38 (16 – 59)
- ✓ records from two years (2009 and 2010)

❖ Wool traits

- ✓ staple length (SL; cm)
- ✓ greasy and clean fleece weight (GFW and CFW; g)
- ✓ clean wool yield (YLD, %)
- ✓ average fiber diameter (AFD; μm)
- ✓ coefficient of variation of AFD (CVAFD; %)
- ✓ kemp and continuous medullated fibers (KEMP; %)
- ✓ discontinuous medullated fibers (HET; %)
- ✓ true wool (TRUE, %)
- ✓ and partition of fiber diameter to 5 group (FD20, FD30, FD40, FD50 and FDup50; %)

□ Genotyping

- ✓ 15 microsatellite markers
- ✓ OVAR1(8 markers; from 80.8 to 230.8cM)
- ✓ OVAR5 (4 markers; from 12.8 to 95.7cM)
- ✓ OVAR25 (3 markers; from 0 to 52.6cM)

□ QTL analysis

- ✓ Single trait
- ✓ multi-marker regression
- ✓ GridQTL software

➤ Results:

- **OVAR1** : 7 putative QTL for CFW, GFW, CVAFD, SL, TRUE, KEMP and HET (Figure 1A, 1B and 1C).
- **OVAR5** : 2 putative QTL was related to HET and CFW
- **OVAR25** : 4 putative QTL for HET, KEMP, TRUE and GFW traits (Figure 2A and 2B)

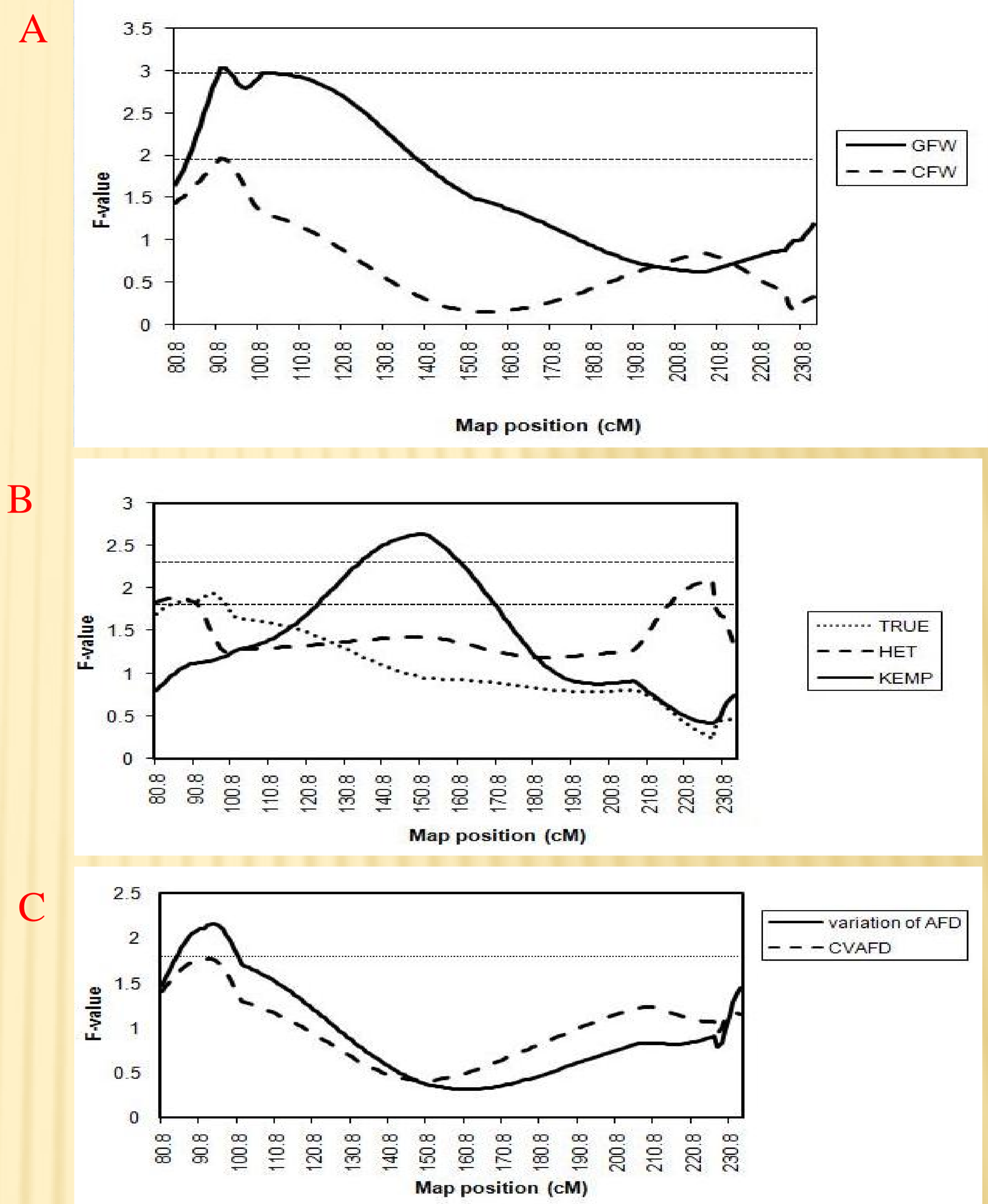


Figure 1. The F-value profile obtained from across family analysis for different wool traits on OVAR1.

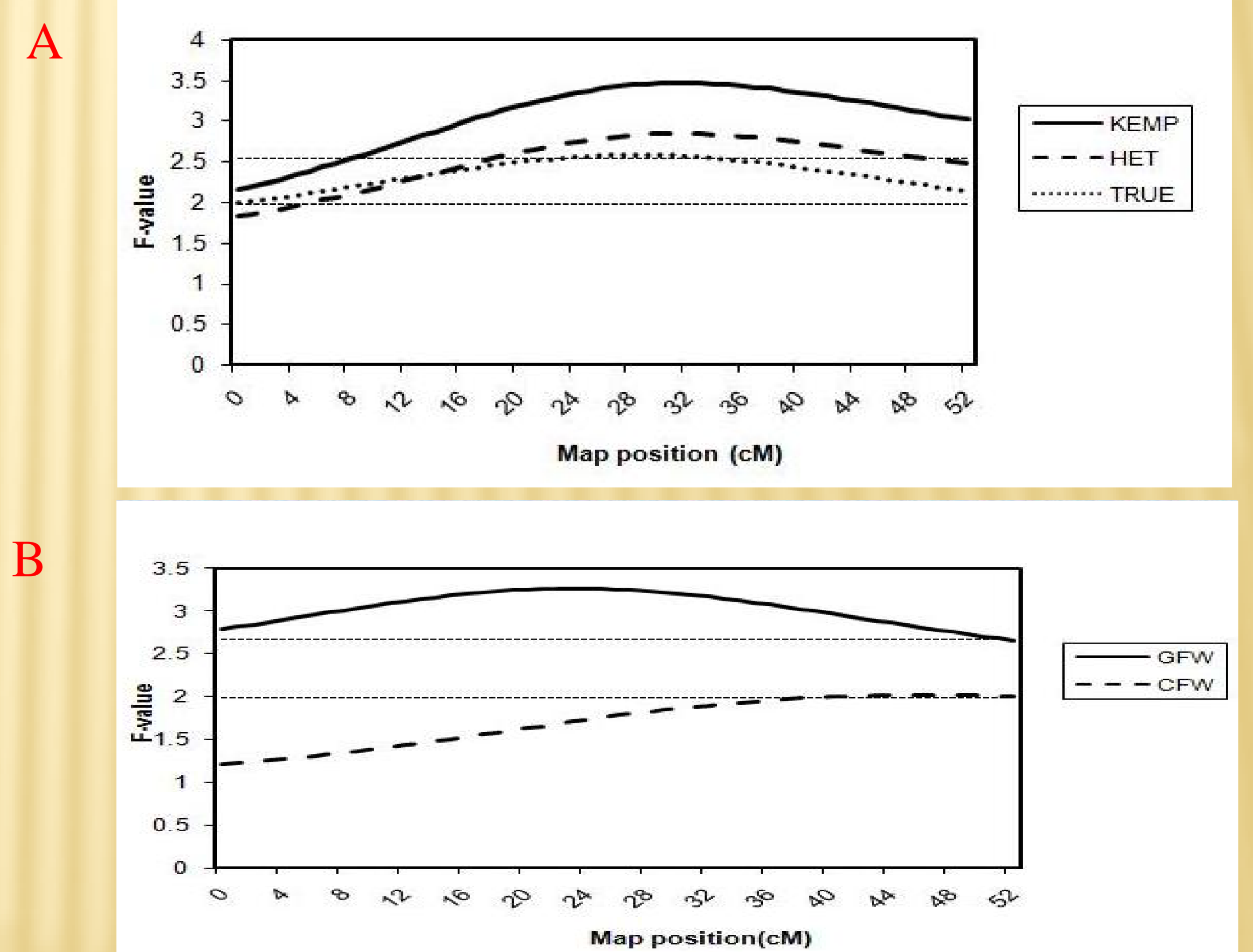


Figure 2. The F-value profile obtained from across family analysis for wool quality traits on OVAR25.

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