EMMAX Software and EMMA Algorithm

EMMAX is a statistical test for large scale model association mapping accounting for the sample structure. In addition to the computational efficiency obtained by EMMA algorithm, EMMAX takes advantage of the fact that each loci explains only a small fraction of complex traits, which allows us to avoid repetitive variance component estimation procedure, resulting in a significant amount of increase in computational time of association mapping using mixed model.

EMMA, short for Efficient massive mapping algorithm, is an algorithm on efficiently mapping massive cDNA onto genomic sequences. The process of mapping massive cDNAs onto genomic sequences has been improved using more approximate mapping filtering based on an enhanced suffix array coupled with a pruned fast hash table, algorithms of block alignment extensions, and k-longest paths. When compared with the classical BLAT software in this field, the computing of EMMA ranges from two to forty-one times faster under similar prediction precisions.[19]

Table 1

One hundred and ninety-five cattle were utilized in the genetic analyses of the slick hair phenotype.

Breed code	Breed	Registered in breed[a]	SLICK haplotype[b]	Number of individuals[c]	Phenotype[d]	Notes
AN	Angus	Yes	No	10	Non-slick	
BS	Brown Swiss	Yes	No	10	Non-slick	
CR	Carora	?	No	10	Slick	
ZB	East African Zebu	No	No	10	Non-slick	
HO	Holstein	Yes	No	7	Non-slick	
ND	N'Dama	Yes	No	10	Non-slick	
ANRAN	RAN × Angus bull	No	Yes	1	Slick	
RP	Red Poll	Yes	Yes	10	Non-slick	
RAN	Romosinuano × Angus	No	Yes	11	Slick	
SE	Senepol	Yes	Yes	69	Slick	2 Individuals non-slick
SNG	Senepol × Angus	No	Yes	5	Slick	1 Individual non-slick
SHO	Senepol × Holstein	No	Yes	38	Slick/non-slick	40–97% HO
SNGSE	Senepol × SNG	No	Yes	2	Slick/non-slick	1 Individual non-slick
RS	Romosinuano	Yes	No	2	Slick	

This included three slick-haired Criollo composite breeds of Senepol, Carora, and Romosinuano and three cross-bred lineages utilizing Senepol and Romosinuano stock. Six ancestral breeds were included as non-slick control breeds for comparison and breed influence on the slick phenotype.

[a]Individuals used in the study were registered within their respective breed associations.
[b]Microsatellites DIK2416 (53 cM) and NRDIKM023 (54.4 cM) were genotyped or imputed for individuals.
[c]The total number of individuals available for analysis within a breed or cross-breed.
[d]The slick or non-slick phenotype characterized in individuals of each breed or cross-breed wthin the study.

In our research, researchers used Haploview software to identify significantly associated haplotype blocks with respective allele identification.[14] They said "Significance levels were generated using permutation testing within Haploview software using 100,000 permutations and a permutated p-value threshold of less than 0.001. Block designation and numeric ID were generated in Haploview with specific blocks referenced by their numeric ID hence forth. A Case/Control association test was used ignoring pairwise comparisons of markers when greater than 1000 kb apart."[14] Here, let's talk more about Haploview(check the picture above) and permutation test. Haploview is a bioinformatics software which is designed to analyze and visualize patterns of linkage disequilibrium (LD) for genetic data. It also have other functions, for example, it can also perform association studies, choosing tagSNPs and estimating haplotype frequencies.[20] Haploview is developed and maintained by Dr. Mark Daly's lab at the MIT/Harvard Broad Institute.[1] As for permutation test, it is a part of resampling in statistics. It is a statistical significance test. To learn more about it, check them online.