Effect of markers density on the accuracy of GEBV
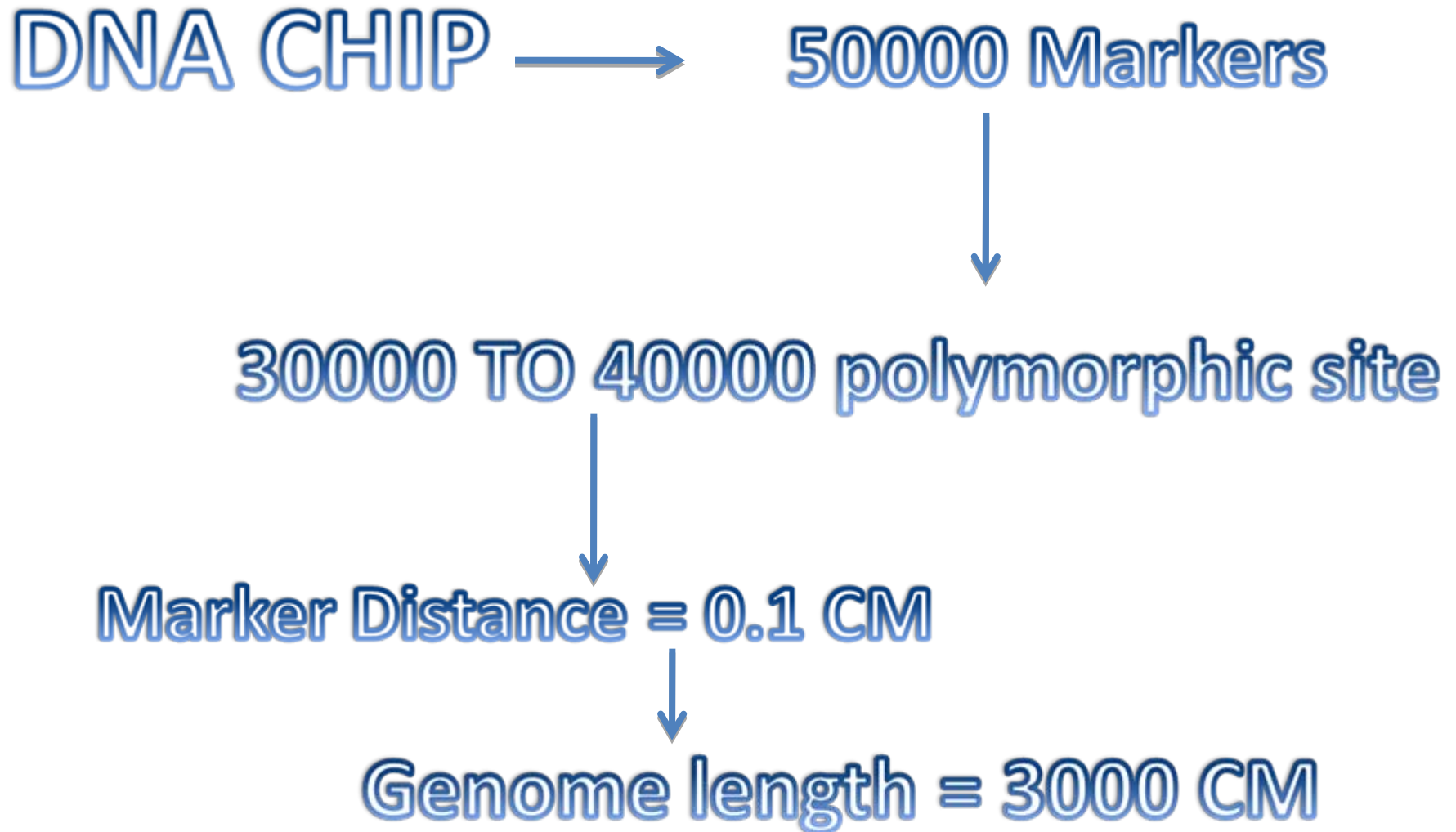
Presented By

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Introduction

DNA CHIP → 50000 Markers

↓

30000 TO 40000 polymorphic site

↓

Marker Distance = 0.1 CM

↓

Genome length = 3000 CM

Introduction

The previous studies

↓

The Impact of marker distance Between (0.1 to 1)

↓

On the accuracy of GEBV

Introduction

Introducing higher density DNA chip with more markers

Less distance between Markers in practice

THE OBJECTIVE OF THIS RESEARCH

The impact of higher marker density

↓

Marker distance less than 0.1 Cm
(0.05, 0.025, 0.0125 Cm)

↓

Accuracy of GEBV and its persistency over next generation

Sex limited traits   Ordinary traits

Low & Medium Heritability

Material &Methods

Methods &Material

Population structure and parameters used in simulation

Number of generation	1 to 58
Generation 1 to 50 create LD	50 male, 50 female
Generation 51 to 58	500 males, 500 females
Training set	Generations 51 to 52
Validation set	Generations 53 to 58
Heritability	0.1 and 0.5

Methods &Material

Simulated genome structure

(first and second trials)

Genome length	300 cM
Number of chromosomes	3
Number of markers per chromosome	100, 200, 1000, 2000
Marker distance (cM)	1, 0.5, 0.1, 0.05 cM
Number of QTLs	30
QTL effects	Normal distribution

Methods &Material

Simulated genome structure
(Third trials)

Genome length	100 cM
Number of chromosomes	1
Number of markers per chromosome	100, 200, 1000, 2000, 4000, 8000
Marker distance (cM)	1, 0.5, 0.1, 0.05, 0.025, 0.0125 cM

GENOMIC PREDICTION

$$\begin{bmatrix} \mathbf{X'X} & \mathbf{X'Z} \\ \mathbf{Z'X} & \mathbf{Z'Z+I}\alpha \end{bmatrix} \begin{bmatrix} \mathbf{b} \\ \mathbf{m} \end{bmatrix} = \begin{bmatrix} \mathbf{X'y} \\ \mathbf{Z'y} \end{bmatrix}$$

$$\alpha = \sigma^2_e / \sigma^2_m \qquad \sigma^2 m = \frac{\sigma^2 a}{n}$$
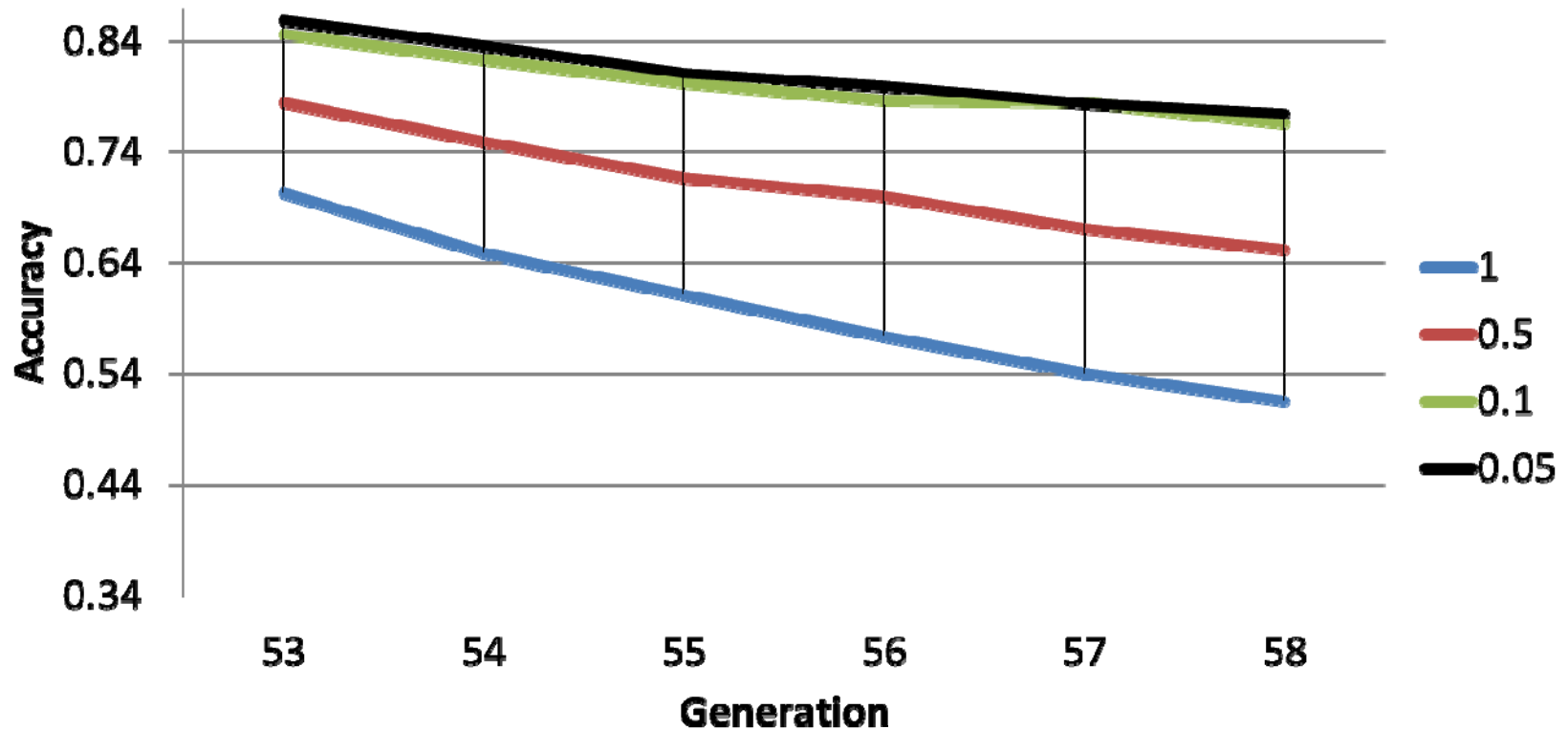
$$\text{GEBV}_i = \mathbf{Z}_i \hat{\mathbf{m}}_i$$

Accuracies were calculated as the correlation between simulated and estimated breeding values
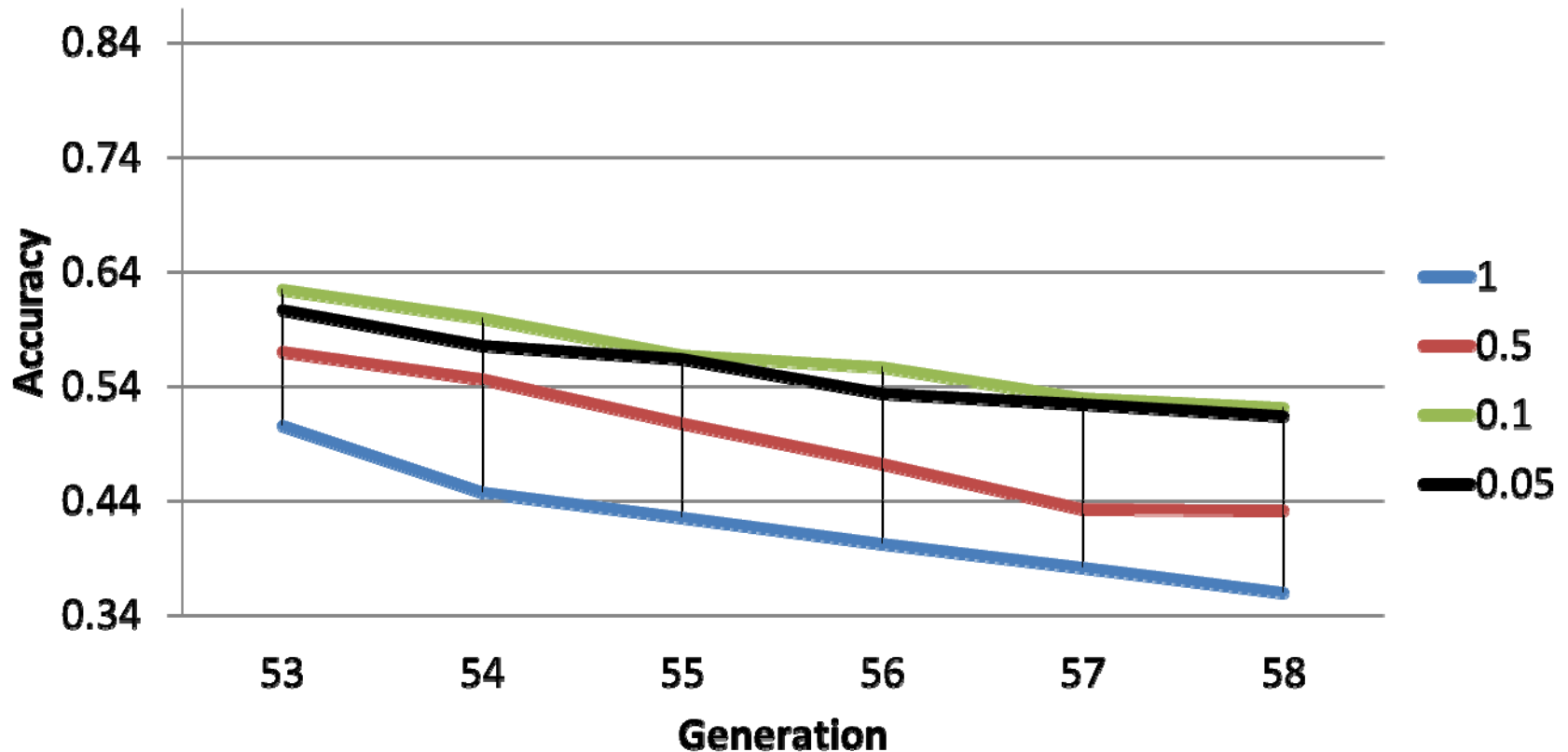
Results &Discussion

TRIAL NUMBER 1

Discussion &Results

Chart1-The accuracy of GEBV for the individuals of validation set in different marker density for trait with heritability equal to 0.5
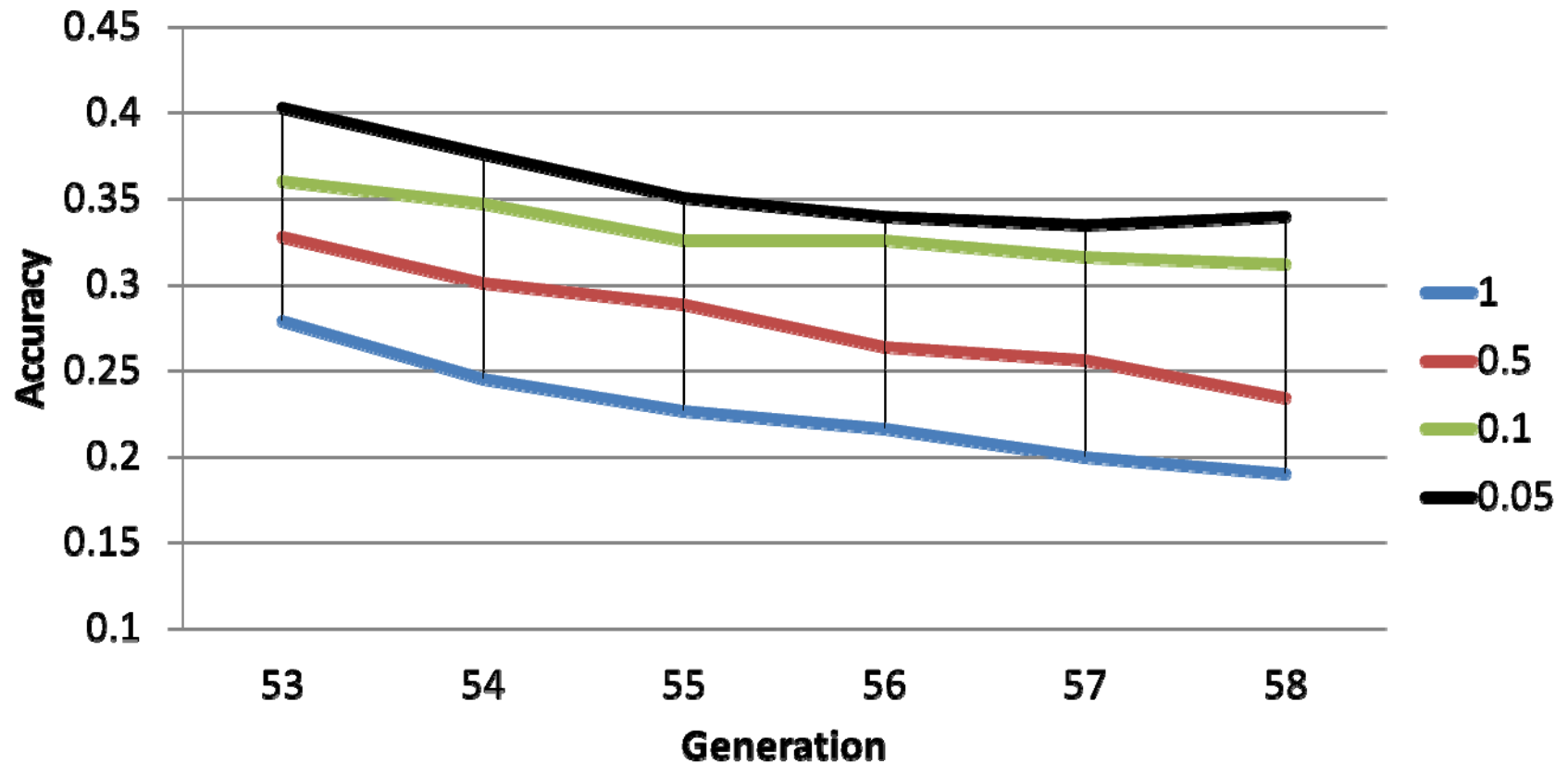
Discussion &Results

Chart 2- The accuracy of GEBV for the individuals of validation set in different marker density for trait with heritability equal to 0.1
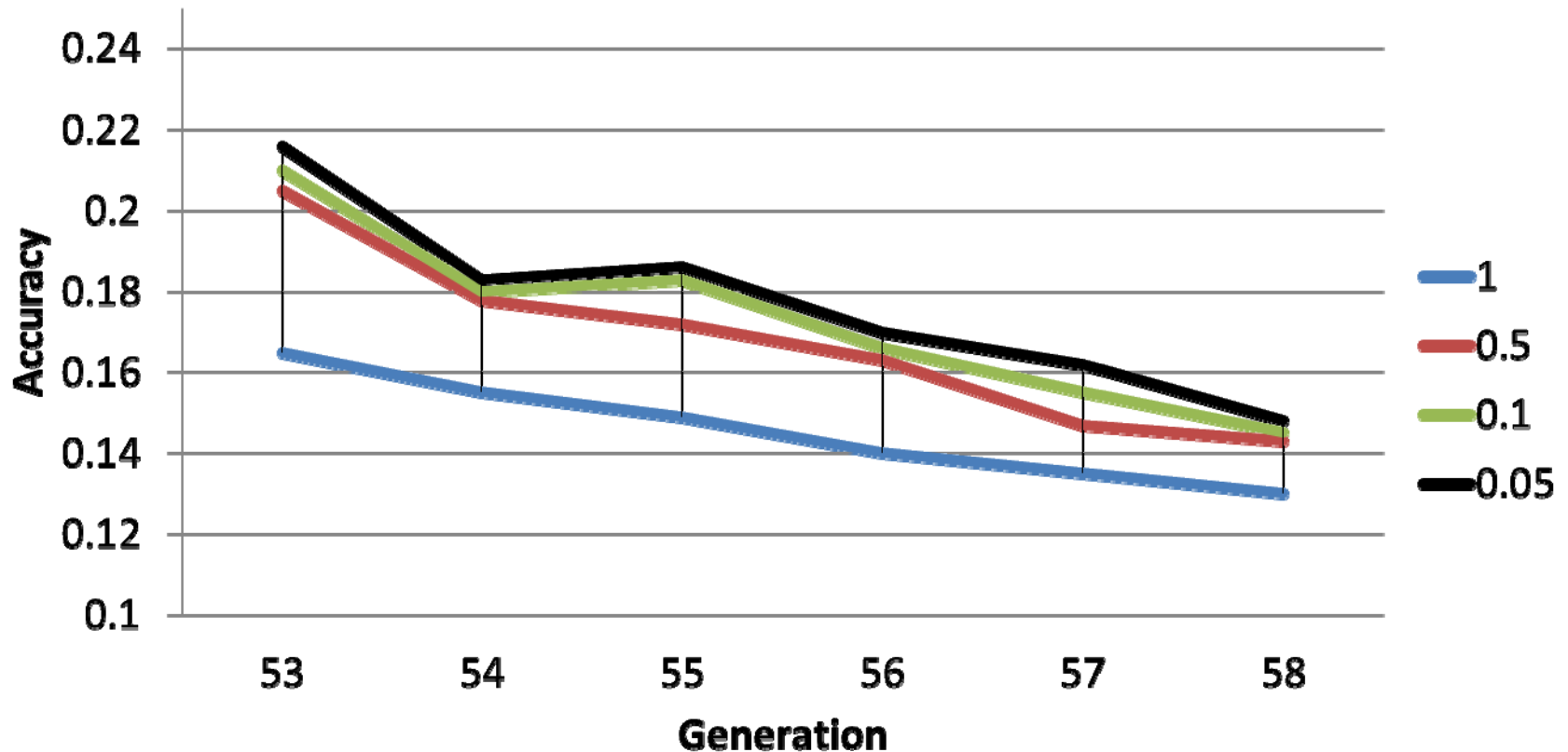
TRIAL NUMBER 2

Discussion &Results

Chart3 -The accuracy of GEBV for the individuals of validation set in different marker density for sex-limited traits with heritability equal to 0.5

Discussion &Results

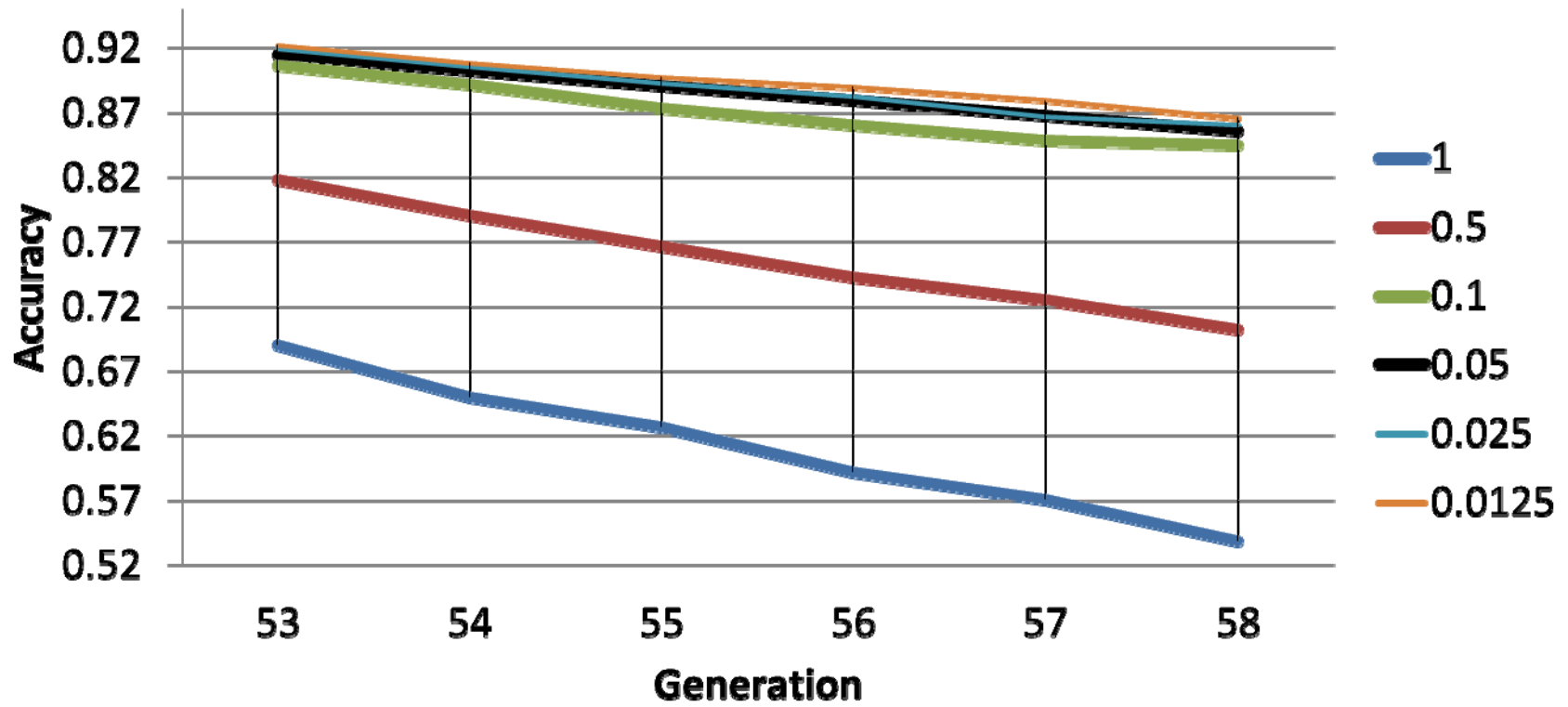Chart4-The accuracy of GEBV for the individuals of validation set in different marker density for sex limited traits with heritability equal to 0.1
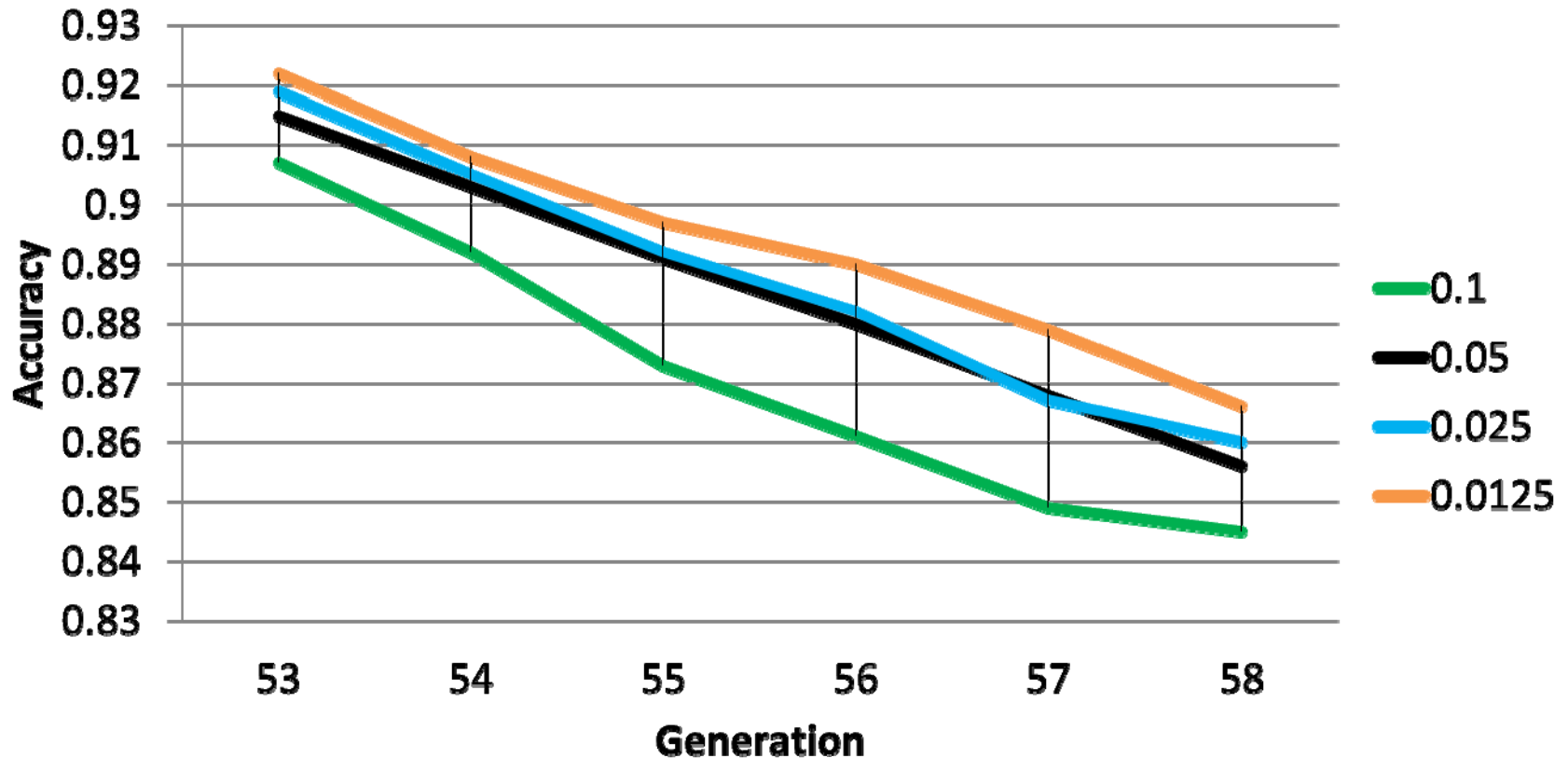
TRIAL NUMBER 3

Discussion &Results

Chart 5 -The accuracy of GEBV for the individuals of validation set in different marker density for trait with **heritability equal to 0.5**

Discussion &Results

Chart 6 -The accuracy of GEBV for the individuals of validation set in very dense markers for trait with heritability equal to 0.5

Discussion &Results

Chart 7 -The accuracy of GEBV for the individuals of validation set in different marker density for trait with heritability equal to 0.1
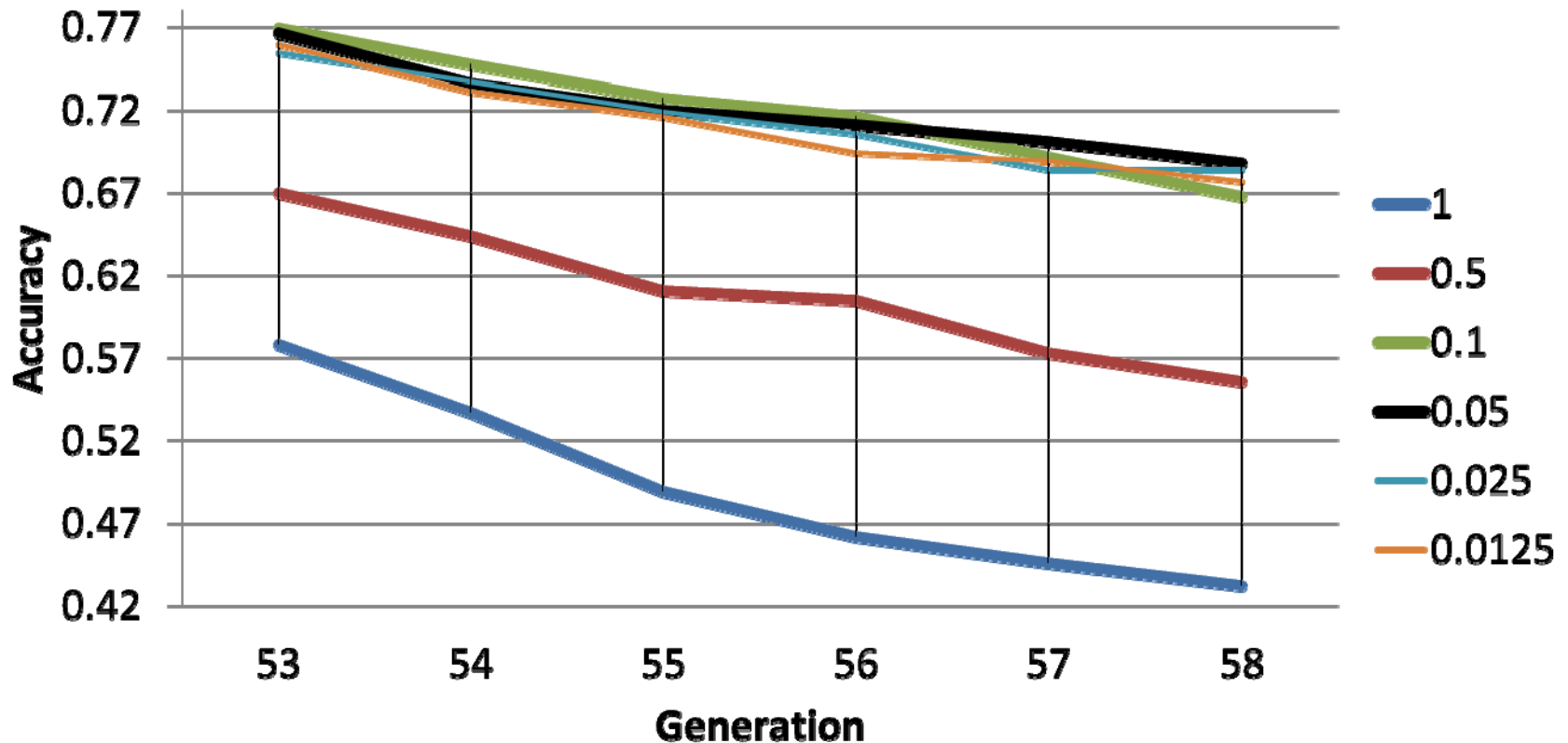
Short Massage of this presentation

The accuracy of GEBV

Direct relationship with marker density

Due to higher linkage disequilibrium in more dense markers

(Calus et al., 2008; Muir, 2007; Solberg et al., 2006)

Short Massage of this presentation

Heritability   **Marker Density**

More important

The accuracy of GEBV

(Goddard, 2009; Saatchi et al., 2010).

Short Massage of this presentation

Higher amount of information

leads to

Better estimation of marker effects

(Calus and Veerkamp, 2007; Muir, 2007; Saatchi et al., 2010)

Short Massage of this presentation

The accuracy of GEBV decrease over generations

Recombination and Change in LD

Weaker relationship

(Habier et al,2007

Short Massage of this presentation

More persistency of accuracy of GEBV

More marker density

More LD

(Habier et al,2007

Thanks for your consideration