A GRAPHICAL METHOD TO DETERMINE DOMINANT AND RECESSIVE GENE PERCENTS USING DIALLEL ANALYSIS IN COTTON

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INTRODUCTION

In diallel analysis widely used by plant breeders,
Wr vs Vr graph gives important knowledge about the parents.

In this graph, it’s possible to interpret distribution of dominant and recessive genes among the parents by investigating the relations
between $W*r=[Volo \times Vr]^{1/2}$ parabola and unit slope regression line.

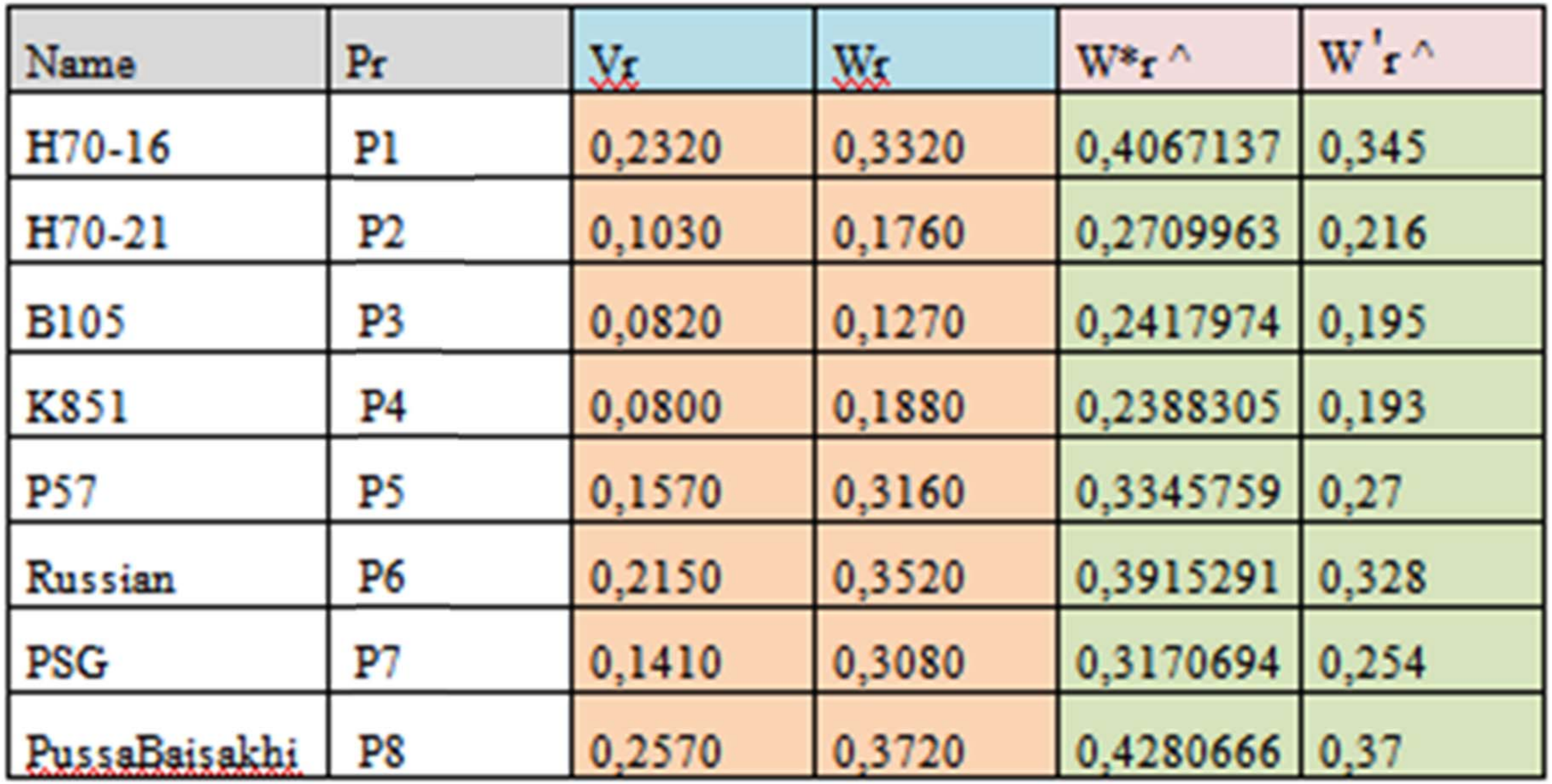
In this study,
finding intercept of unit slope line and
the values corresponding the two points where parabola is cut by this regression line
and
dividing the distance between those points into four equal parts and
finding exact recessive and dominant genes amount (as %)
are given with a numerical sample in cotton.

MATERIAL AND METHOD

In this study,
Singh (1980) example was used.
There are 8 parents and 3 replications.
Table 1 shows the array variances (Vr) and covariances (Wr).

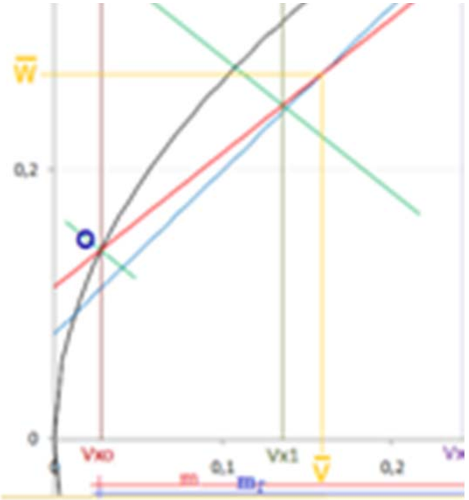
In addition, the study includes the necessary calculations
for plotting parabola (^W*r),
regression line (^Wr) for Vr and Wr and
unit slope regression line (^W’r)

Table 1. Numerical Sample from Singh (1980)



Name	Pr	Vr	Wr	W*r ^	W 'r ^
H70-16	P1	0,2320	0,3320	0,4067137	0,345
H70-21	P2	0,1030	0,1760	0,2709963	0,216
B105	P3	0,0820	0,1270	0,2417974	0,195
K851	P4	0,0800	0,1880	0,2388305	0,193
P57	P5	0,1570	0,3160	0,3345759	0,27
Russian	P6	0,2150	0,3520	0,3915291	0,328
PSG	P7	0,1410	0,3080	0,3170694	0,254
PussaBaisakhi	P8	0,2570	0,3720	0,4280666	0,37

Sequence variances (Vr) and covariances (Wr) are assumed to be independent and dependent, respectively.



VOLO value is the variance for the parents and was calculated as 0.713.

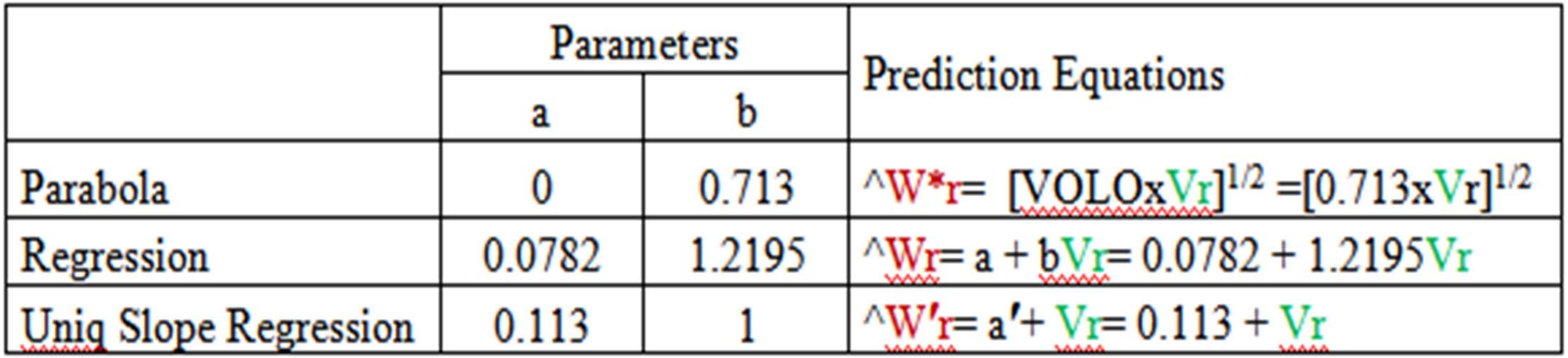
It is enough to find a′ value for the unit slope regression line.

Both regression lines will cut at the point ($\overline{V}$, $\overline{W}$) (Figure 1). At this point, let:

$\hat{}$Wr= $\hat{}$W′r = $\overline{W} = a + b\overline{V} = a' + \overline{V}$

Then, $a' = \overline{W} - \overline{V} = 0.2714 - 0.1584 = 0.113$

Table 2. Parameters and equations of parabola, regression and unit slope regression

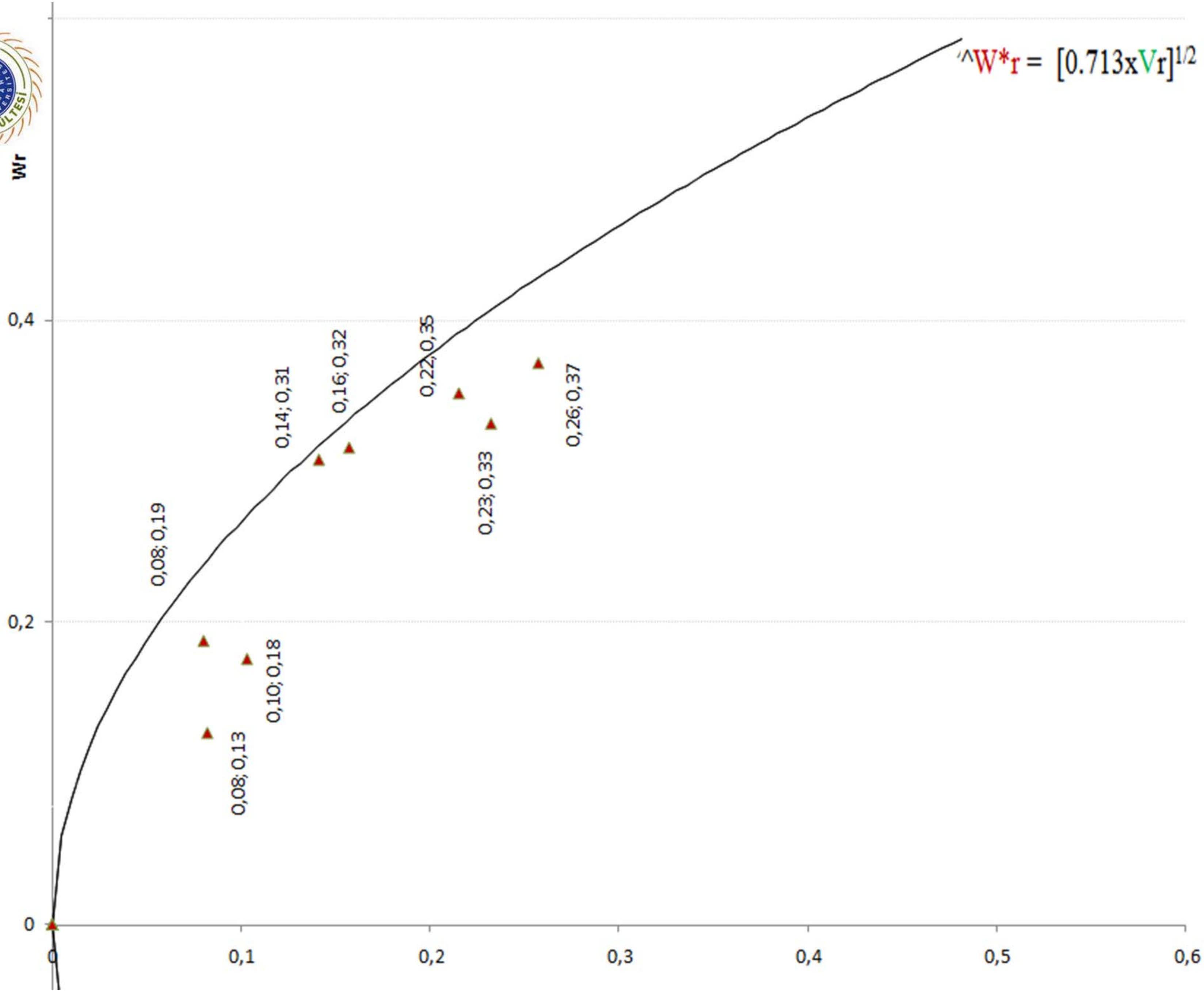


	Parameters		Prediction Equations
	a	b	
Parabola	0	0.713	^W*r= [VOLOxVr]$^{1/2}$ =[0.713xVr]$^{1/2}$
Regression	0.0782	1.2195	^Wr= a + bVr= 0.0782 + 1.2195Vr
Uniq Slope Regression	0.113	1	^W′r= a′+ Vr= 0.113 + Vr

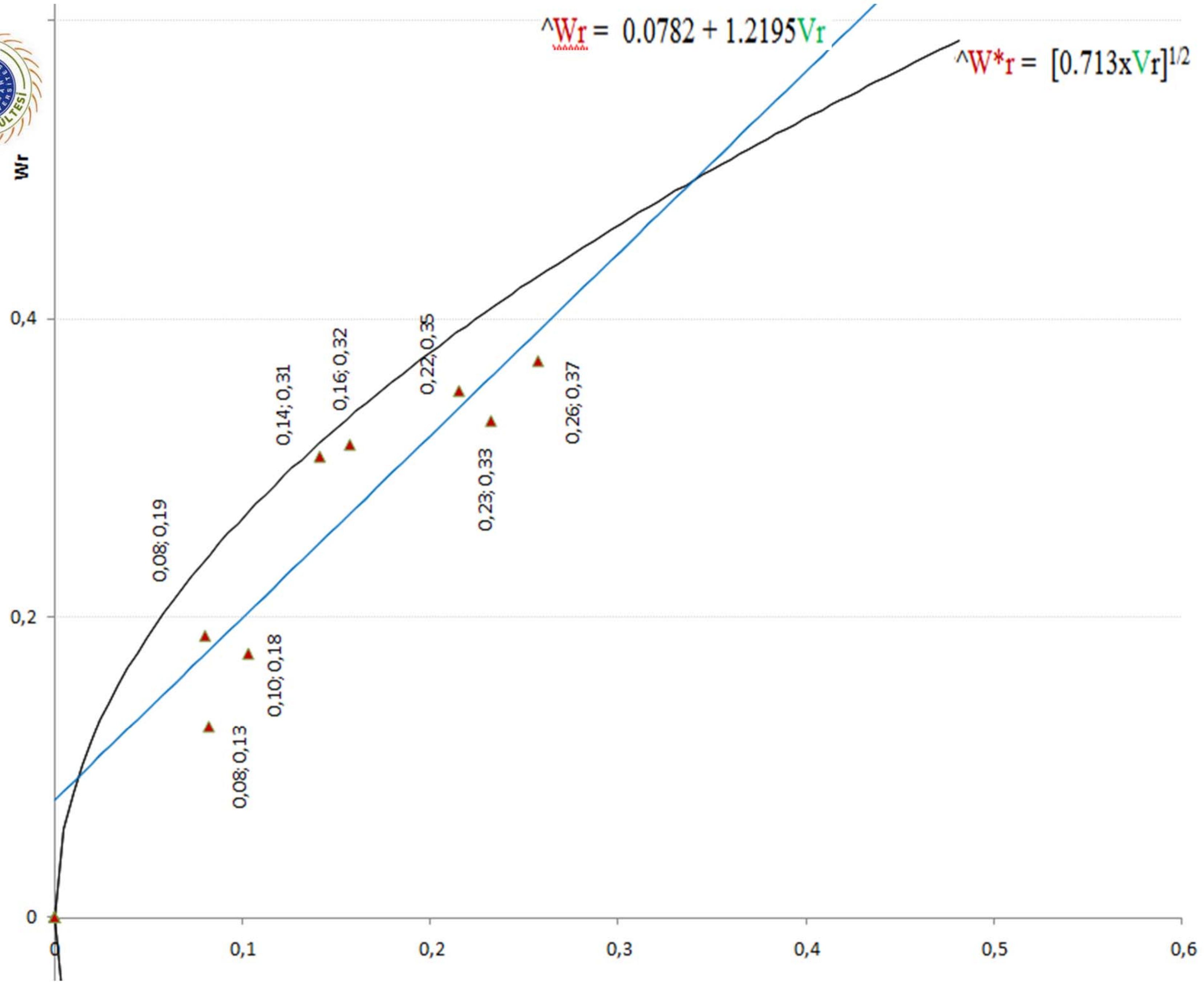
Parabola is drawn by using the value of ^W*r=[VOLOxVr]$^{1/2}$ corresponding to any one of the Vr values.

Then, **regression line** (^Wr = a + bVr) between Vr and Wr is drawn. This line is tested whether or not it is equal to 1.

If the hypothesis Ho: β=1 is accepted, the assumption becomes valid and **unit slope regression line** (^W’r = a’+ Vr) is drawn.

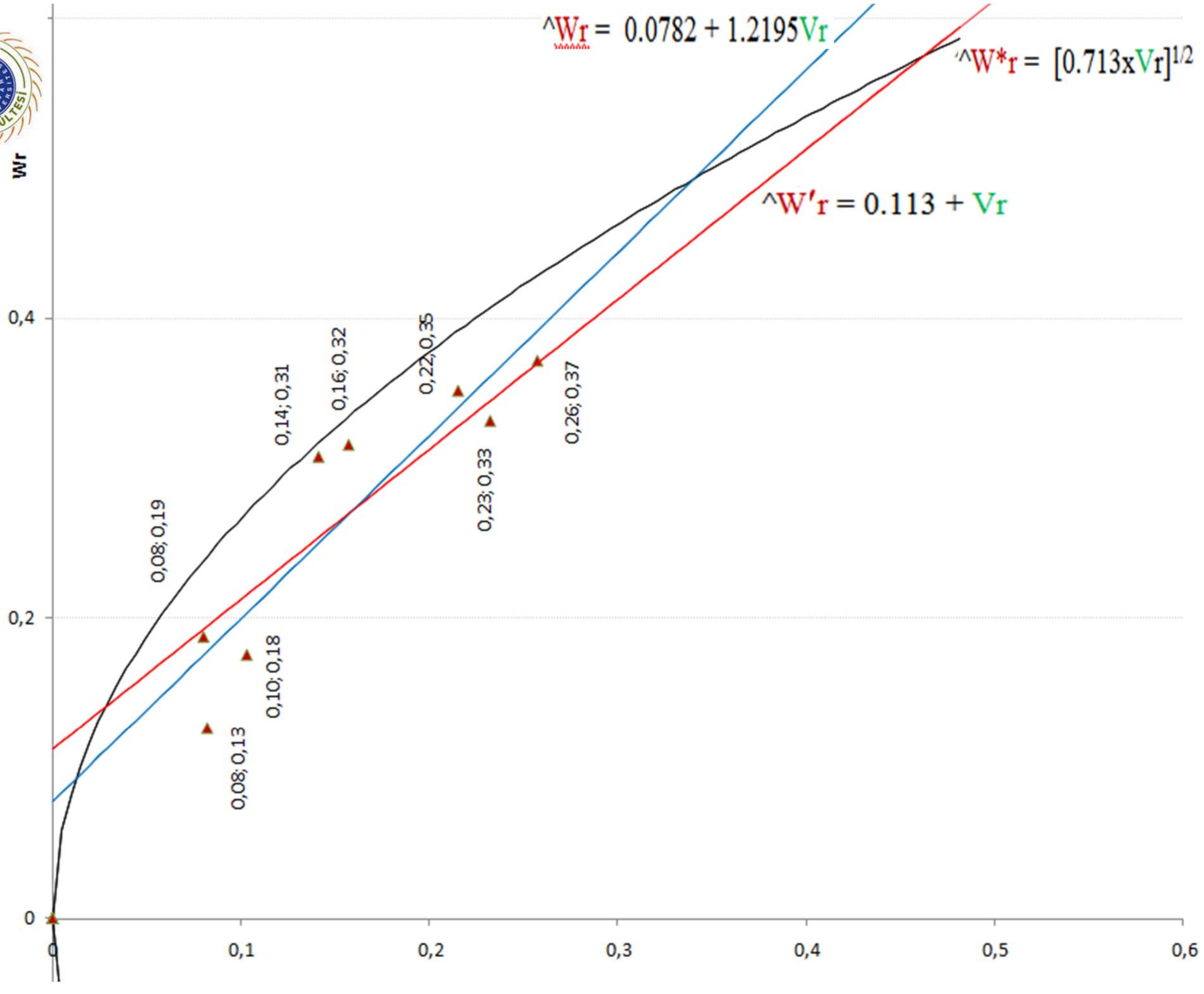


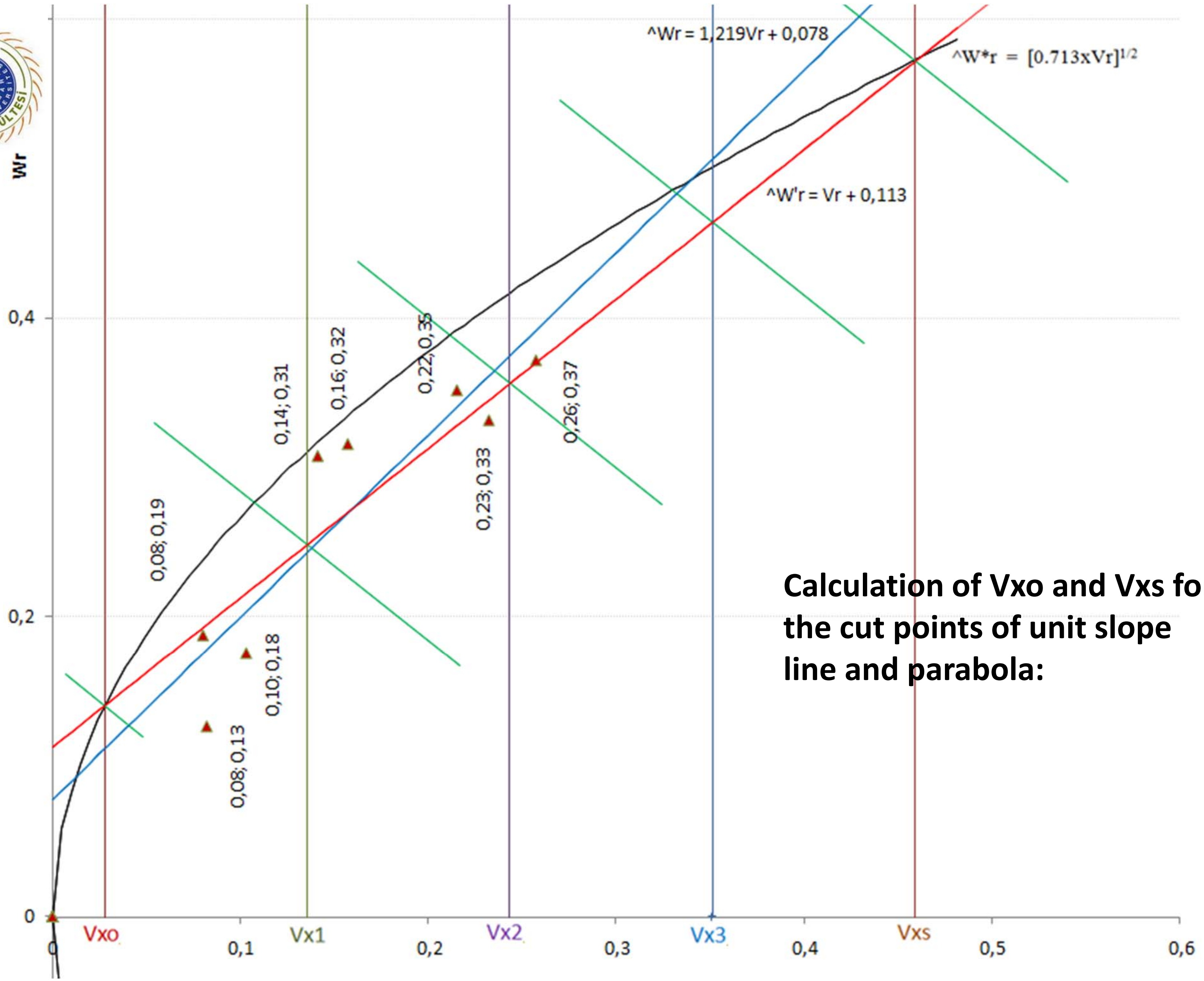
$\hat{}W^{*}r = [0.713xVr]^{1/2}$



$$\hat{}Wr = 0.0782 + 1.2195Vr$$

$$\hat{}W^*r = [0.713xVr]^{1/2}$$


^Wr = 0.0782 + 1.2195Vr
^W*r = [0.713xVr]^1/2
^W′r = 0.113 + Vr
Wr
0
0,2
0,4
0
0,1
0,2
0,3
0,4
0,5
0,6
0,08; 0,19
0,14; 0,31
0,16; 0,32
0,22; 0,35
0,26; 0,37
0,23; 0,33
0,10; 0,18
0,08; 0,13



Calculation of Vxo and Vxs for the cut points of unit slope line and parabola:

Where the unite slope regression line (^W'r = a'+ Vr) cuts with parabola (^W*r = $[VOLOxVr]^{1/2}$), both equations gives the same Wr value (Figure).

Then the expression below can be written:
^W'r =^W*r = a'+ Vr =. $[VOLOxVr]^{1/2}$

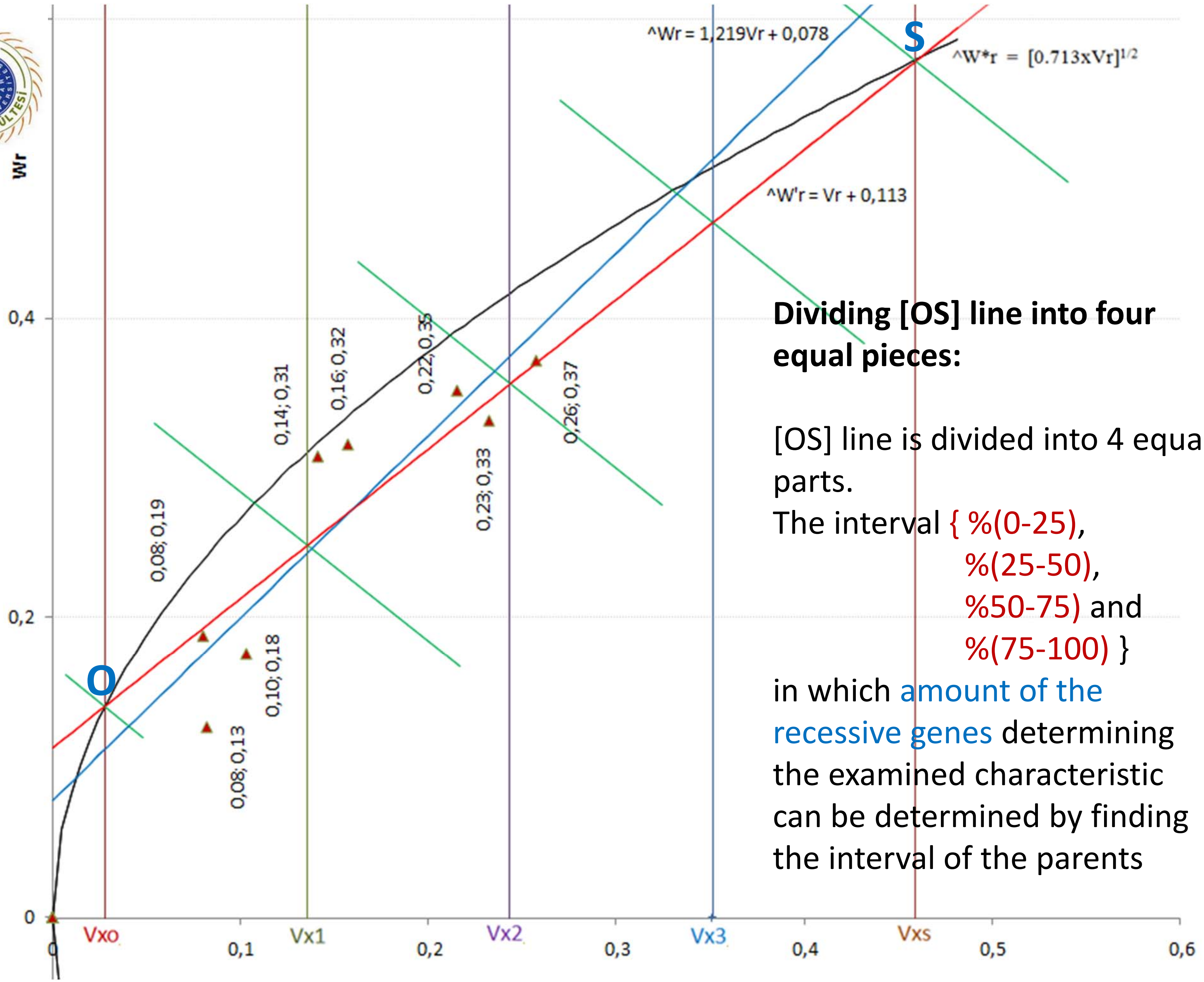
After several mathematical calculations it becomes a second degree equation with two unknowns as shown below;

$AV^2r+BVr+ C = 0$

Here, A=1, B=(2 a' - VOLO) ve C= a'^2. When the equation solved, cut points, Vxo and Vxs will be;

$Vxo = (1/2)\{ VOLO \mathbf{-} [VOLO(VOLO - 4a')]^{1/2} \}- a'$
Vxo $= (1/2)\{ 0.713 \mathbf{-} [0.713(0.713 - 4(0.113))]^{1/2} \}- 0.113 =$ **0.0278**

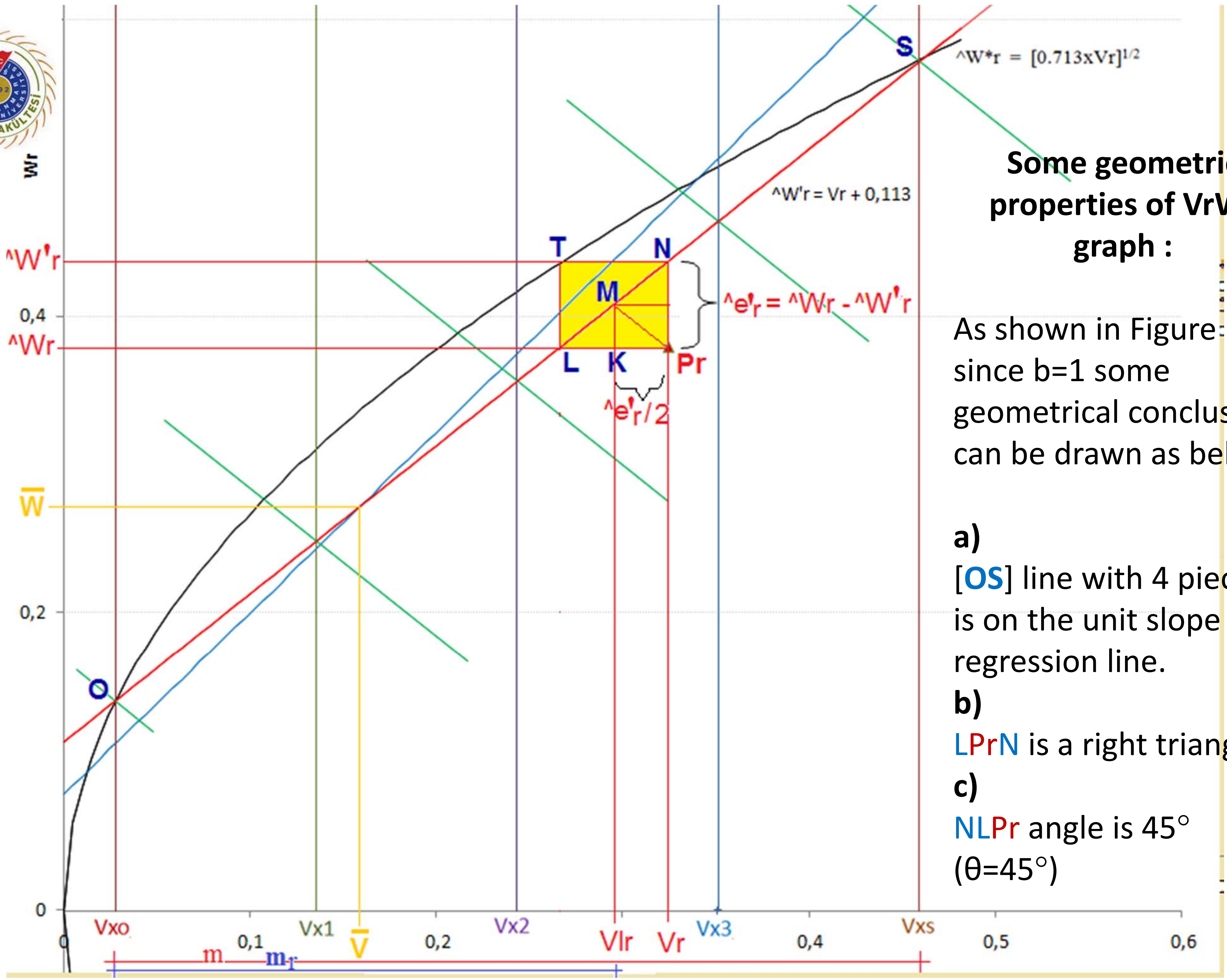
Similarly, for the other cut point;
$Vxs = (1/2)\{ VOLO \mathbf{+} [VOLO(VOLO - 4a')]^{1/2} \}- a'$
Vxs $= (1/2)\{ 0.713 \mathbf{+} [0.713(0.713 - 4(0.113))]^{1/2} \}- 0.113 =$ **0.4592**



Dividing [OS] line into four equal pieces:

[OS] line is divided into 4 equal parts.

The interval { %(0-25),
%(25-50),
%50-75) and
%(75-100) }
in which amount of the recessive genes determining the examined characteristic can be determined by finding the interval of the parents



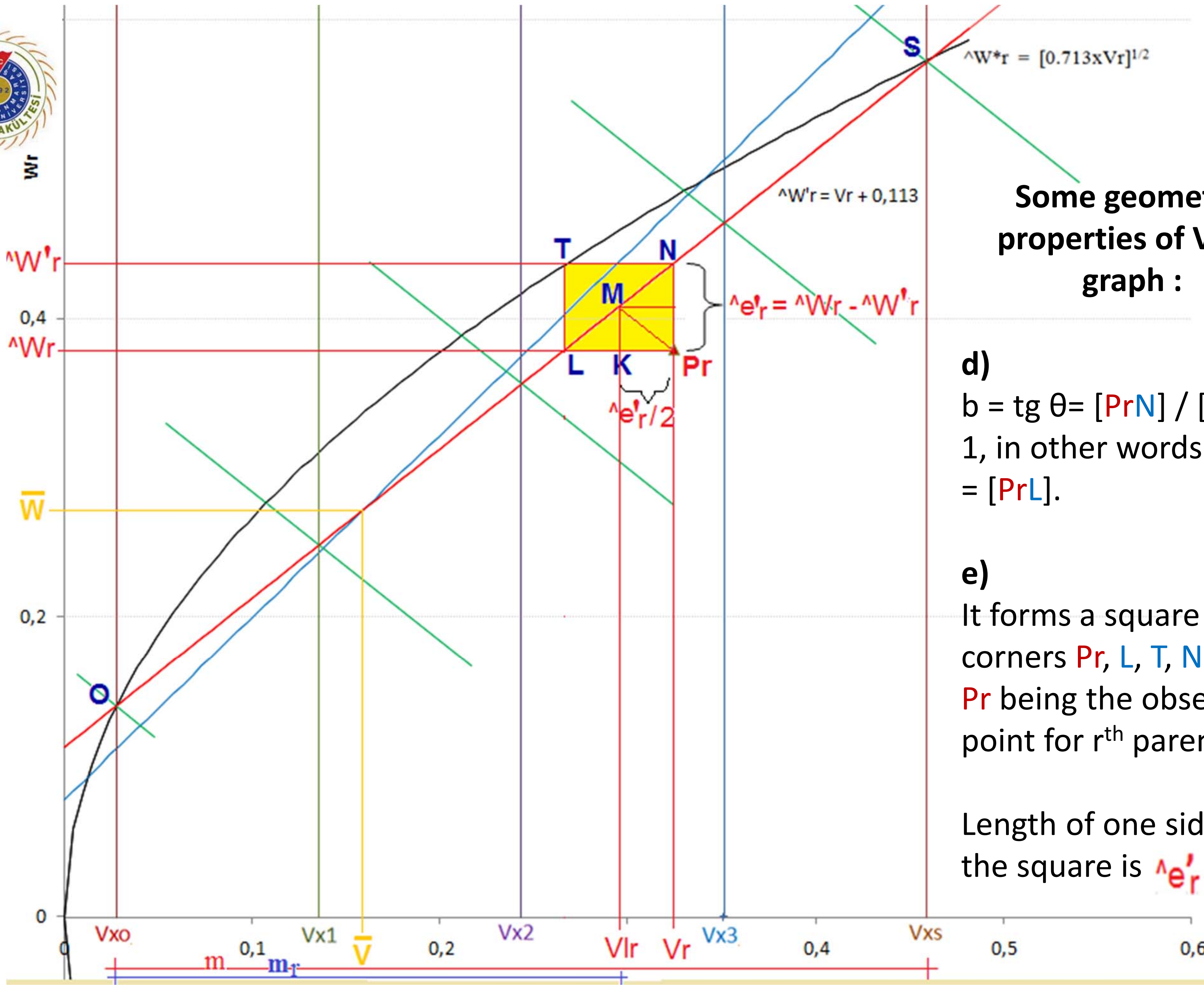
Some geometric properties of VrWr graph :

As shown in Figure 1, since b=1 some geometrical conclusions can be drawn as below:

a)
[**OS**] line with 4 pieces is on the unit slope regression line.

b)
LPrN is a right triangle.

c)
NLPr angle is 45°
(θ=45°)



Some geometric properties of VrWr graph :

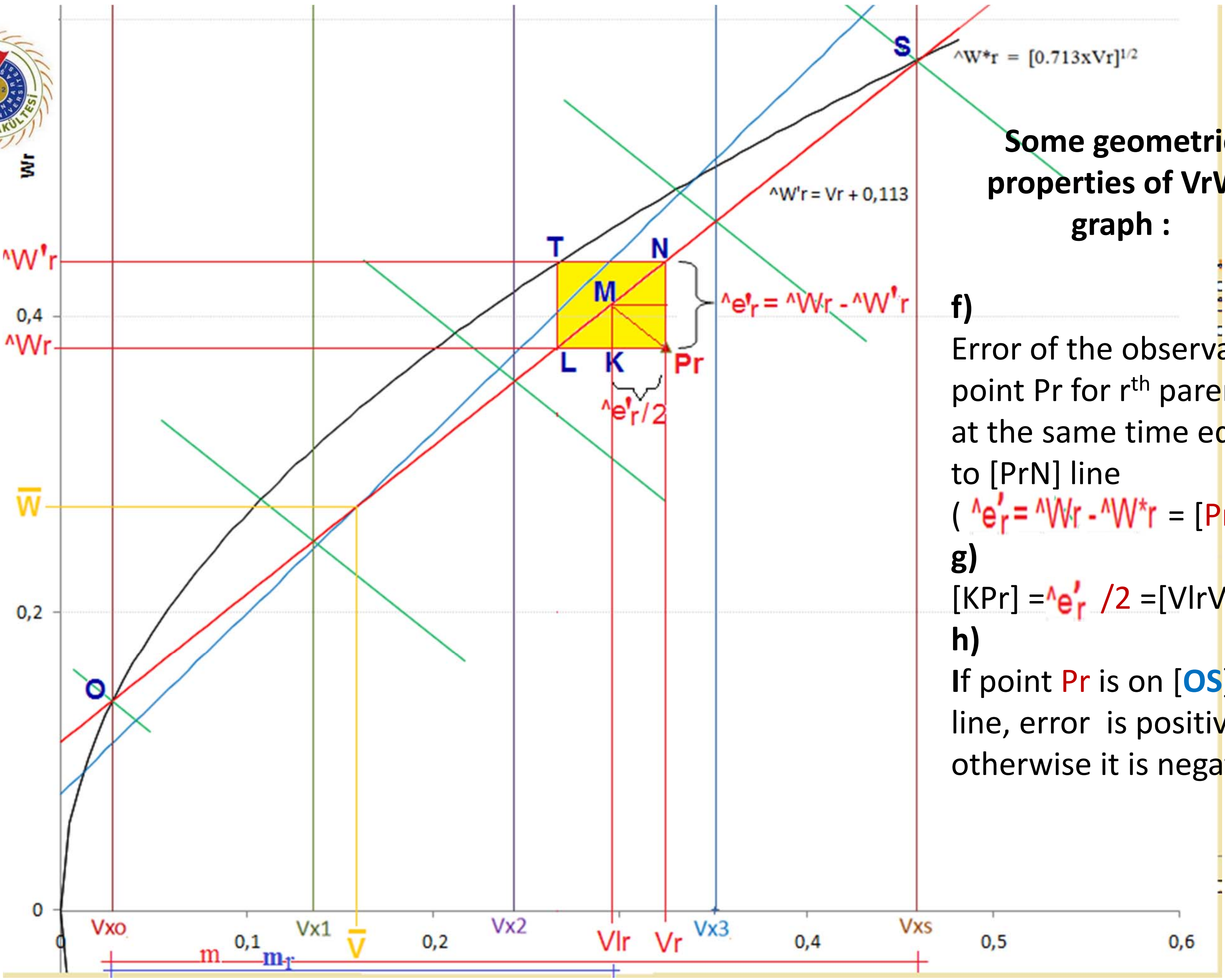
d)

b = tg θ= [PrN] / [PrL] = 1, in other words [PrN] = [PrL].

e)

It forms a square with corners Pr, L, T, N;
Pr being the observed point for r^{th} parent.

Length of one side of the square is $^\wedge e'_r$



Some geometric properties of VrWr graph :

f)

Error of the observation point Pr for r^th parent is at the same time equal to [PrN] line

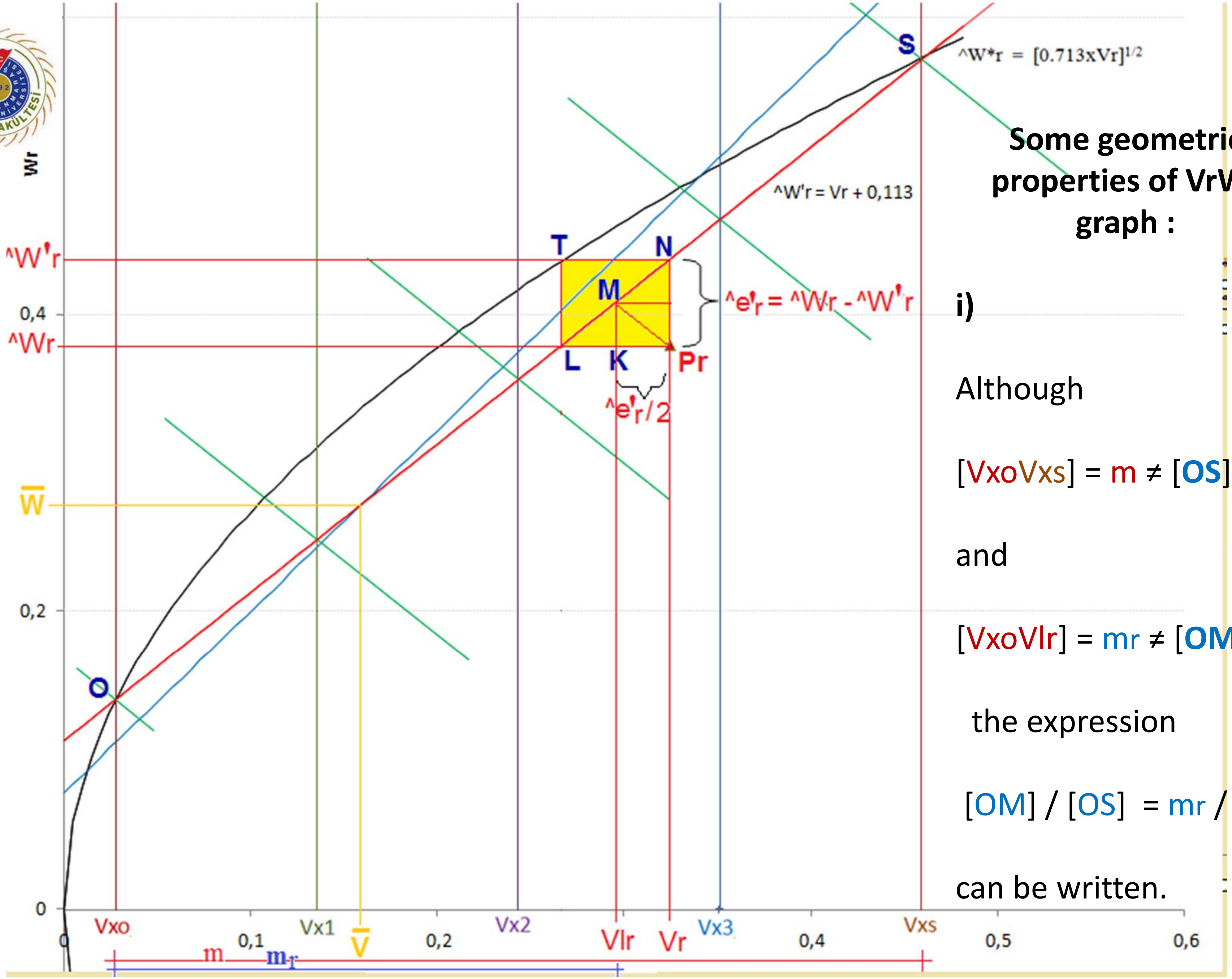
($^\wedge e'_r = {}^\wedge Wr - {}^\wedge W^*r$ = [PrN])

g)

[KPr] = $^\wedge e'_r$ /2 = [VlrVr]

h)

If point Pr is on [**OS**] line, error is positive, otherwise it is negative.



Some geometric properties of VrWr graph :

i)

Although

[VxoVxs] = m ≠ [**OS**]

and

[VxoVlr] = mr ≠ [**OM**],

the expression

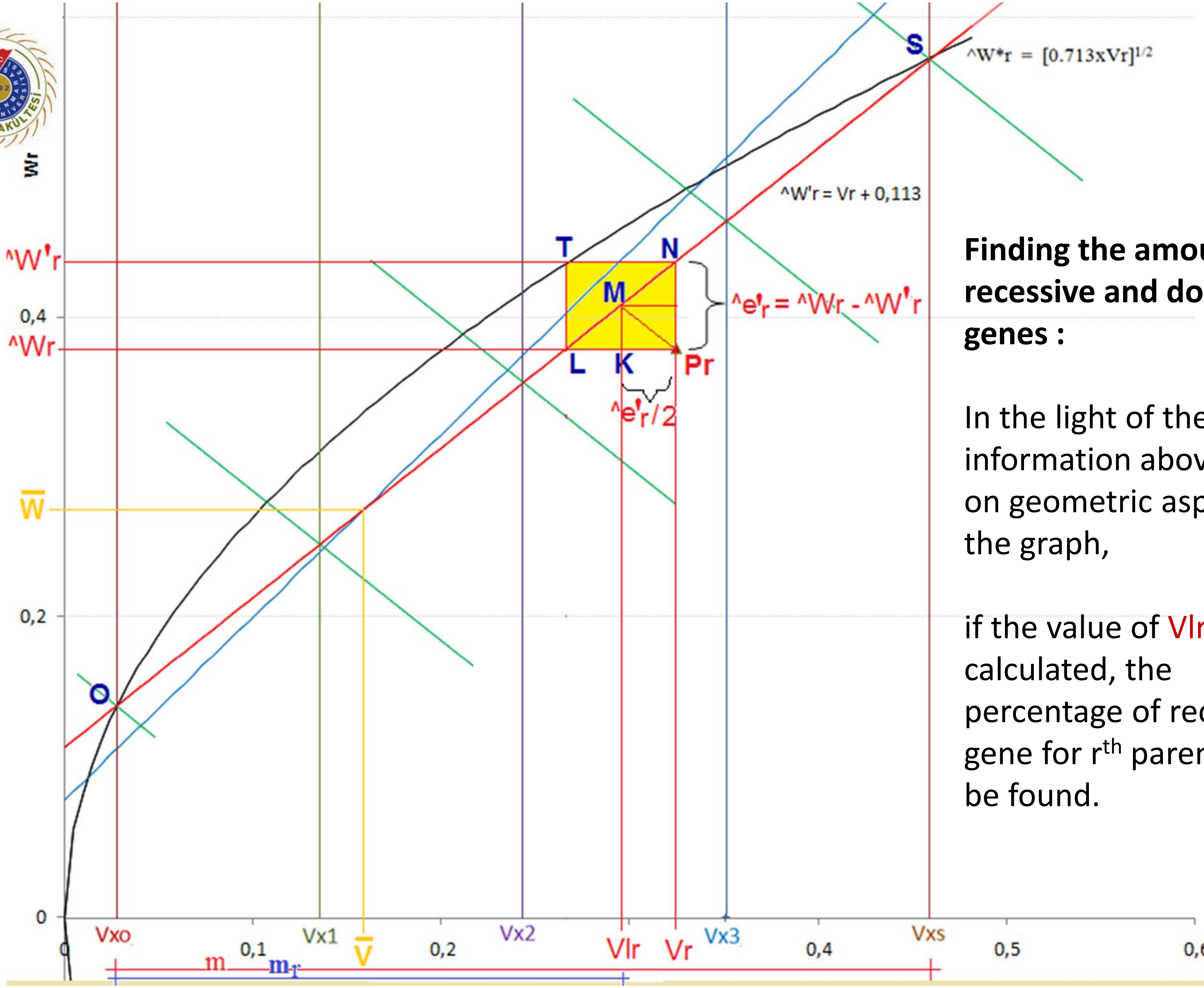
[OM] / [OS] = mr / m

can be written.

In this study, formulas which divide the [**OS**] line or [VxoVxs] line on the horizontal V axis into 4 equal pieces are constructed.
This way, the recessive gene interval including Pr observation point for any parent can be determined by using the projection of point M intercepting (cut) [**OS**] line vertically onto the V axis.
m = Vxs –Vxo = 0.4592 – 0.0278 = 0.4314.
Values of Vx1, Vx2 ve Vx3 which divide this interval into four pieces are as shown below, along with the numerical examples:
Vx1 = Vxo + (1)m/4 = 0.0278 + (1)(0.4314)/4 = 0.1361
Vx2 = Vxo + (2)m/4 = 0.0278 + (2)(0.4314)/4 = 0.2435
Vx3 = Vxo + (3)m/4 = 0.0278 + (3)(0.4314)/4 = 0.3514

Inputting these values in the unit slope regression equation, Wx1, Wx2 and Wx3 can be estimated:
^W’**x**1 = a’+ Vx1 = 0.113 + 0.1361 = 0.2491
^W’**x**2 = a’+ Vx2 = 0.113 + 0.2435 = 0.3565
^W’**x**3 = a’+ Vx3 = 0.113 + 0.3514 = 0.4644

So, points dividing [**OS**] line into four equal pieces are (0.1361; 0.2491), (0.2435; 0.3565) and (0.3514; 0.4644).



Finding the amount of recessive and dominant genes :

In the light of the information above,
on geometric aspects of the graph,

if the value of Vlr is calculated, the percentage of recessive gene for rth parent can be found.

Since [KPr] = ^e'r /2, then Vlr = Vr + ^e'r/2. (Mark that ^e'is negative).

So the recessive gene percentage for rth parent is %Rr;

%Rr = [(Vlr – Vxo) / (Vxs – Vxo]*100 = (mr – m)*100

And dominant gene percentage %Dr is;

%Dr = 100 – %Rr

In the numerical example, recessive and dominant gene percentages for r^{th} parent when r=1 are;

a' = 0.113, Vxo= 0.0278, Vxs= 0.4592

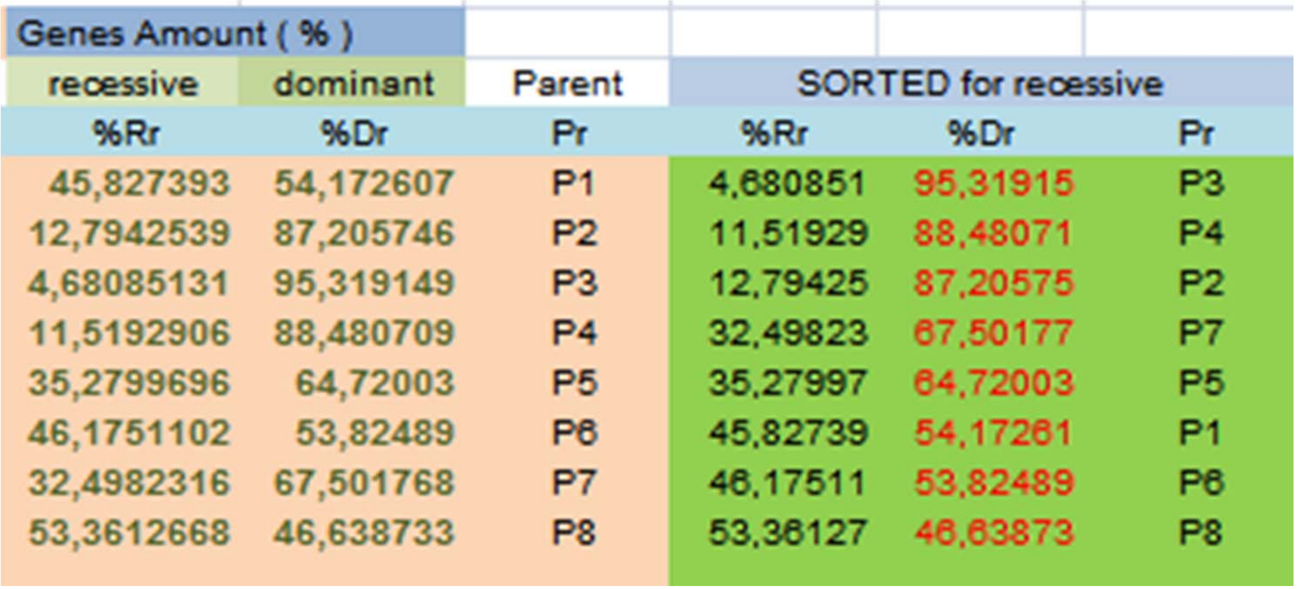
^W'1 = a'+ V1 = 0.113 + 0.232 = 0.345
^ e'1 = W1 – ^W'1= 0.332 – 0.345 = – 0.013
Vl1 = V1 – ^ e'1 /2 = 0.232 – 0.013/2 = 0.2255
m1 = Vl1 – Vxo = 0.2255 – 0.0278 = 0.1977
m = Vxs – Vxo = 0.4592 – 0.0278 = 0.4314

%R1 = (m1/m)100 = (0.1977 / 0.4314)100 = %45.83

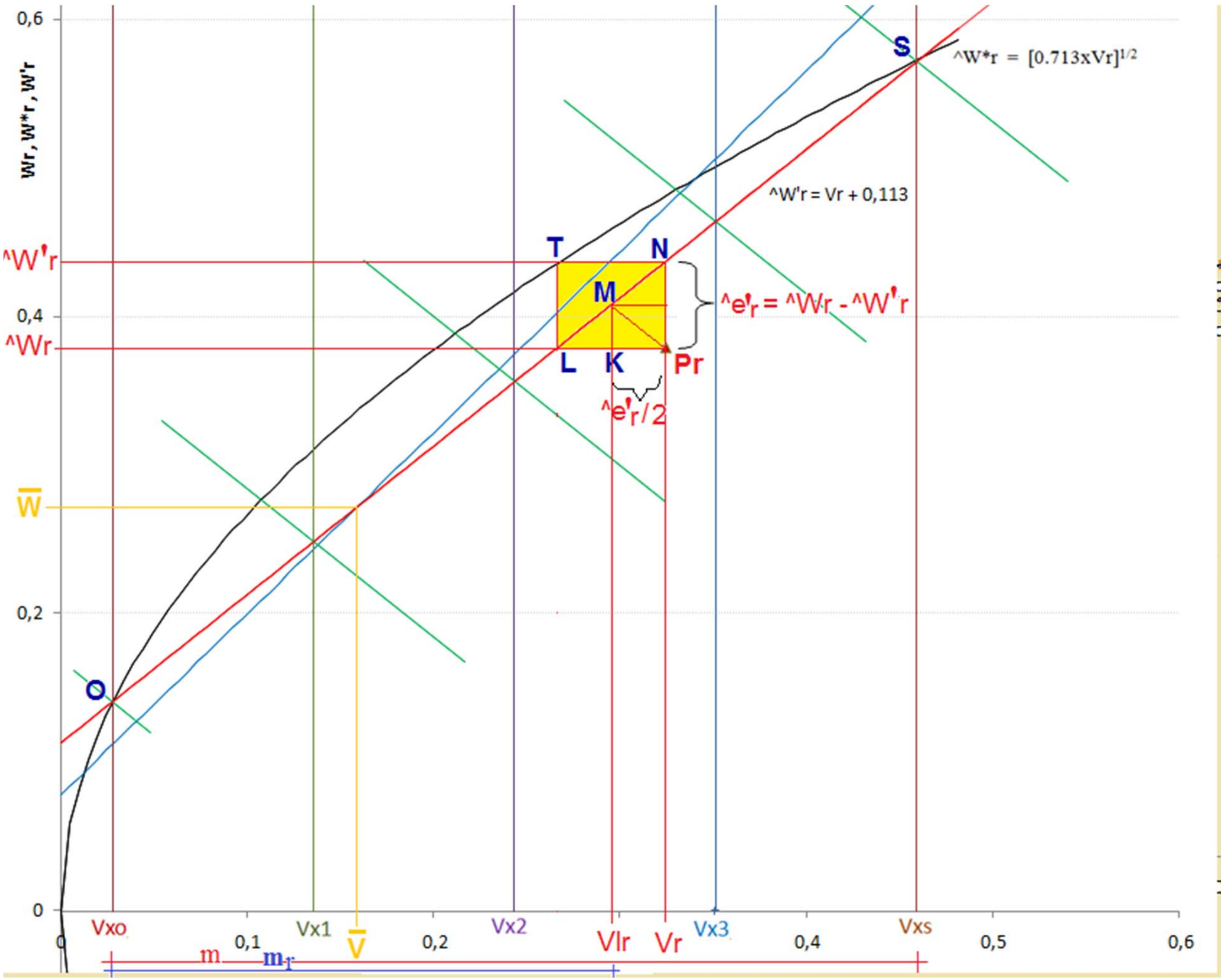
%D1 = 100 – 45.83 = %54.17

Recessive and dominant gene percentages for all parents calculated by this method are given in Table 3 respectively:

Tablo 3. Recessive and dominant gene percentages



Genes Amount (%)					
recessive	dominant	Parent	SORTED for recessive		
%Rr	%Dr	Pr	%Rr	%Dr	Pr
45,827393	54,172607	P1	4,680851	95,31915	P3
12,7942539	87,205746	P2	11,51929	88,48071	P4
4,68085131	95,319149	P3	12,79425	87,20575	P2
11,5192906	88,480709	P4	32,49823	67,50177	P7
35,2799696	64,72003	P5	35,27997	64,72003	P5
46,1751102	53,82489	P6	45,82739	54,17261	P1
32,4982316	67,501768	P7	46,17511	53,82489	P6
53,3612668	46,638733	P8	53,36127	46,63873	P8


Wr, W*r, W'r
0,6
0,4
0,2
0
^W'r
^Wr
W̄
S
^W*r = [0.713xVr]$^{1/2}$
^W'r = Vr + 0,113
T
N
M
L
K
Pr
^e'r = ^Wr - ^W'r
^e'r/2
O
Vxo
Vx1
V̄
Vx2
Vlr
Vr
Vx3
Vxs
0
0,1
0,2
0,4
0,5
0,6
m
mr

CONCLUSION

In this study,
finding the two cut points of unit slope regression line and the parabola is shown.

It is also shown that the [OS] line between these two points is divided into four equal pieces.

Additionally, point estimations of percentages of recessive and dominant genes for parents' observed Pr points is given.

Some geometric properties of VrWr graph are used for these calculations.

Now it is possible for the researchers to find the amount of recessive and dominant genes more precisely as point estimation (for example 45.83%), instead of an interval estimation (25 – 50%), graphically.

THANKS. . .

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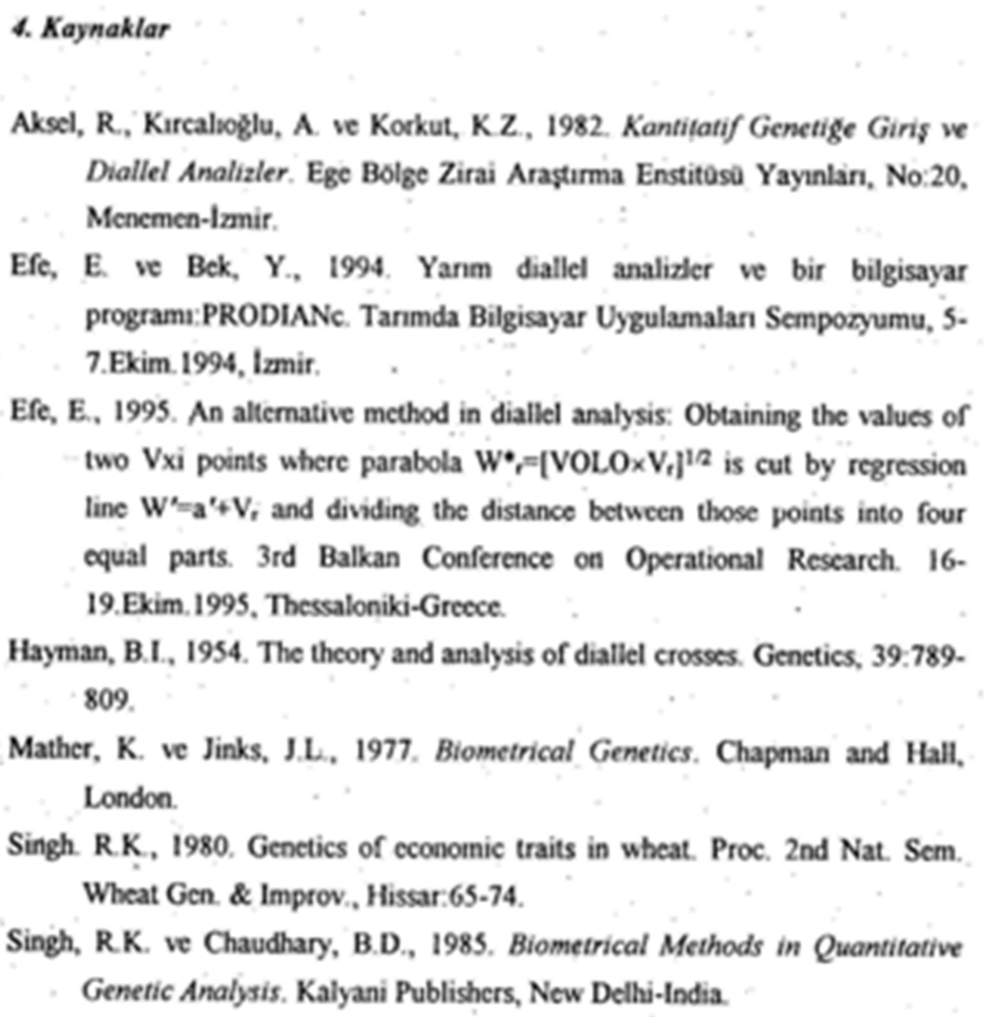

4. Kaynaklar

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