

PREVENIRE LA CELIACHIA ?

CASERTA

19 MAGGIO 2012

luigi greco

Fattori Causali di una Patologia

Varianza Totale di una Malattia Multifattoriale

Genetica Ereditata
dai Genitori

Esperienza Ambientale
Condivisa

Esperienza non
condivisa

INFEZIONI

Genetica Ereditata dai
Genitori

Esperienza Ambientale
Condivisa

Esperienza non condivisa

MALATTIE GENETICHE

Genetica Ereditata dai Genitori

Esperienza
Ambientale
Condivisa

Esperienza
non condivisa



Gut. 2006 Jun;55(6):803-8.

**Concordance, disease progression,
and heritability of coeliac disease in
Italian twins.**

Nisticò L, Fagnani C., Coto I, Percopo S, Cotichini R, Limongelli
MG, Paparo F, D'Alfonso S, Giordano M, Sferlazzas C, Magazzu
G, Momigliano-Richiardi P, Greco L, Stazi MA

Table 2 Concordance by zygosity and sex in twin pairs

	Concordance (%)						
	Concordant	Discordant	Total	Probandwise	95% CI	Pairwise	95% CI
MZ male	5	1	6	90	70.6–100	81.8	49.7–100
MZ female	12	5	17	80.8	64.4–97.1	67.7	44.7–90.7
All MZ	17	6	23	83.3*	70.3–96.4	71.4†	52.3–90.6
DZ male	0	12	12	0		0	
DZ female	1	14	15	12.5	0–34.7	6.7	0–19.3
DZ opposite sex	4	19	23	26.9	5.2–48.7	15.6	1–30.1
All DZ	5	45	50	16.7*	3.6–29.8	9.1†	1.3–16.9
Total	22	51	73				

MZ, monozygotic, DZ, dizygotic; 95% CI, 95% confidence interval.

Test for difference between MZ and DZ twins: $*\chi^2 = 49.98, p = 1.55 \times 10^{-12}$; $\dagger\chi^2 = 40.77, p = 1.71 \times 10^{-10}$.

Geni + Esperienza Condivisa + Esperienza Individuale ?

(peso % di ciascun elemento)

CASI 'CLINICI' 1:1000

GENI 57%

Fattori comuni 42%

Fattori Individuali 1%

INCIDENZA 1:100

GENI 87%

Fattori comuni 12%

Fattori Individuali 1%

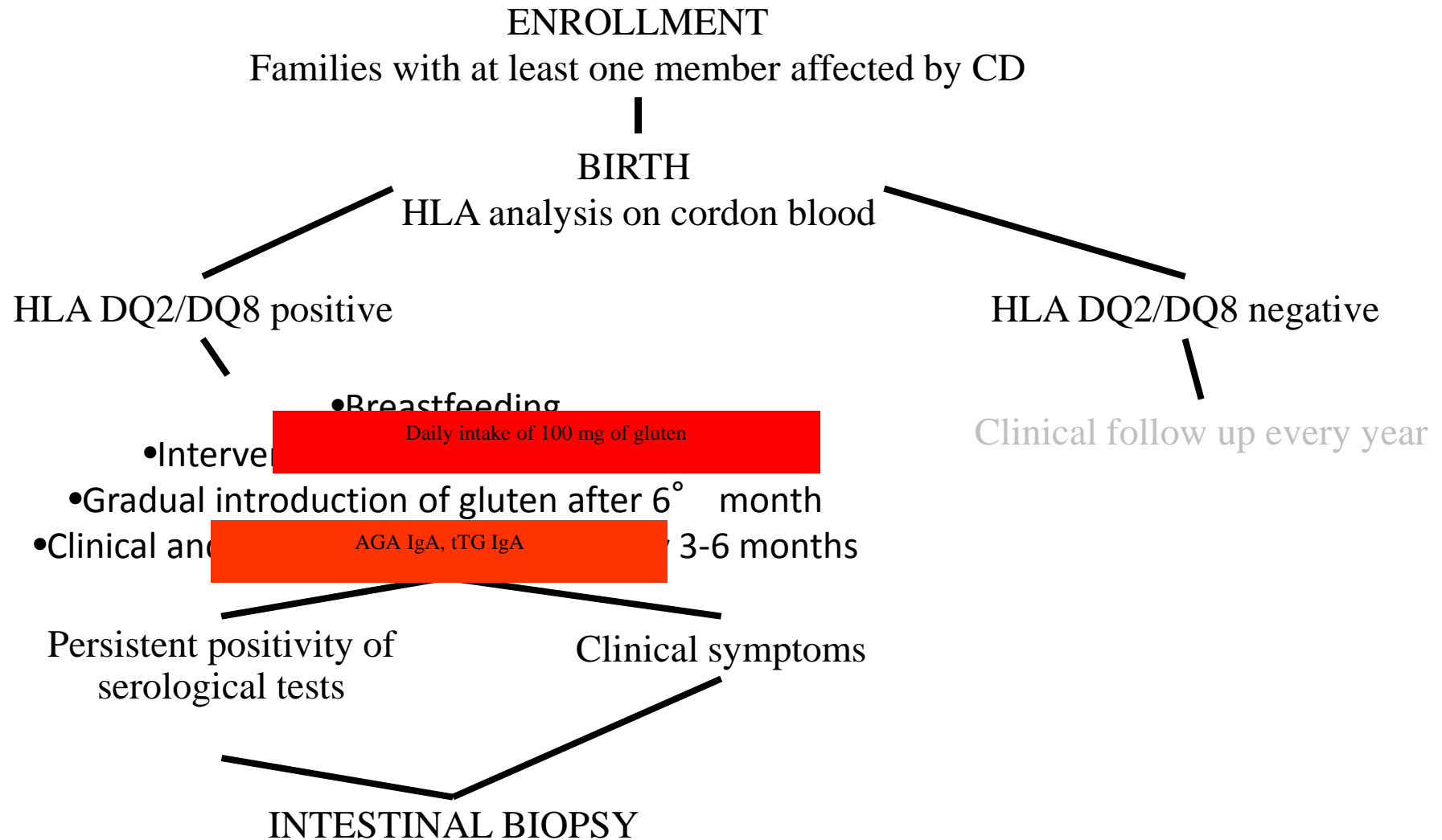
La finestra della prevenzione ?

Risk of celiac disease autoimmunity and timing of gluten introduction in the diet of infants at increased risk of disease.

JAMA. 2005 May 18;293(19):2343-51.

<u><i>Glutine a mesi</i></u>	<u><i>Celiaci</i></u>	<u><i>Controlli</i></u>	<u><i>Odds Ratio CI</i></u>	<u><i>Estimate OR</i></u>
1-3 mesi	3 (6%)	40	0,83-10,4	2,9
4-6 mesi	12 (2%)	574	1	1
> 7 mesi	36 (4%)	895	0,92-3,42	1,78
	51	1509	Solo 25 casi	con biopsia

PREVENT-CD PROTOCOL



Basilio Malamisura

Centro Diagnosi Celiachia - Cava de' Tirreni



Incidence CD

Recruited: 1348

Randomised: 952

At 1 year 0.6%

At 2 years 4.6%

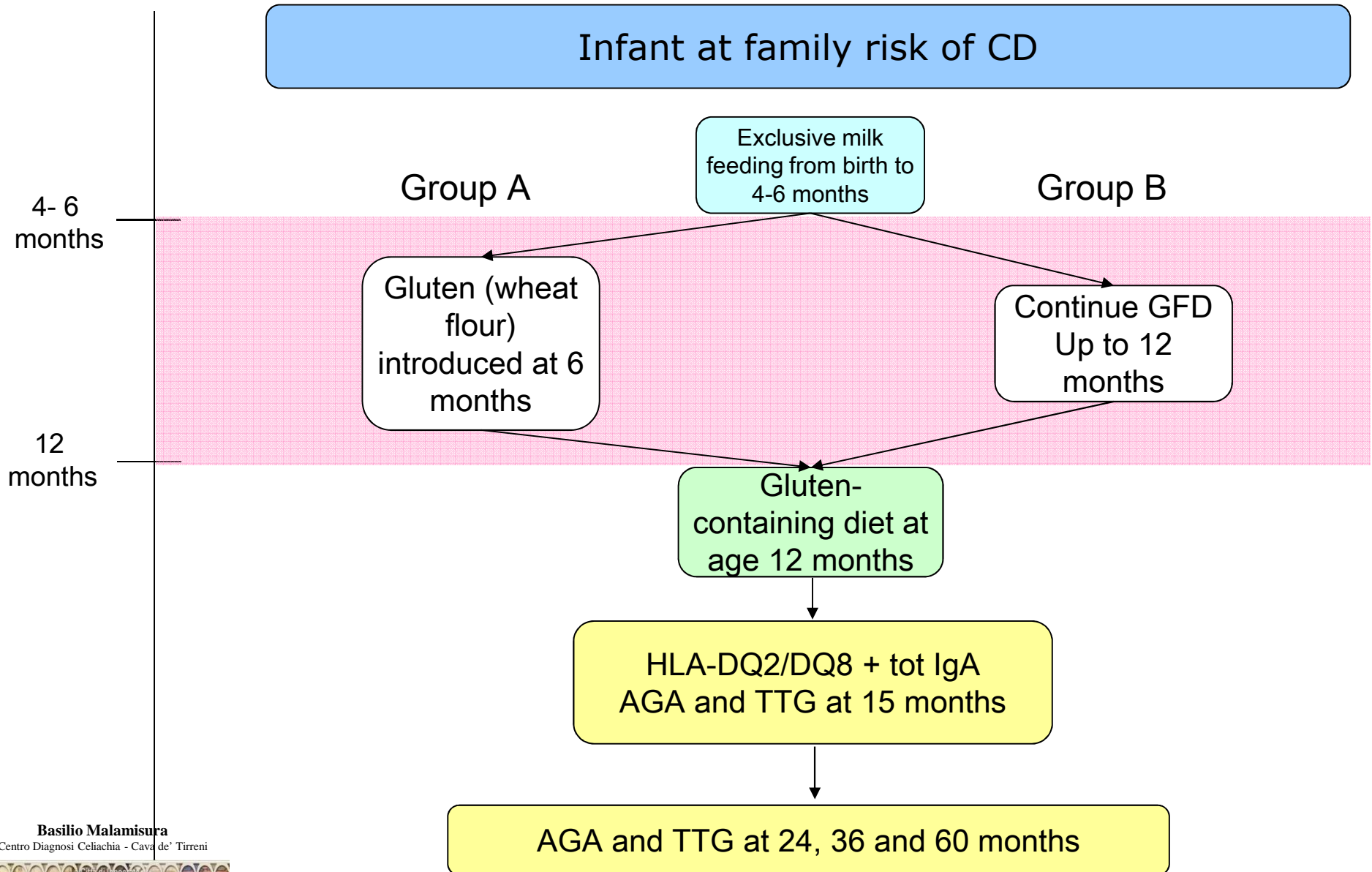
At 3 years 7.6%

Basilio Malamisura

Centro Diagnosi Celiachia - Cava de' Tirreni



Age at gluten introduction and risk of celiac disease (CD)



Biopsy-proven CD

Gruppo A

8

17

5

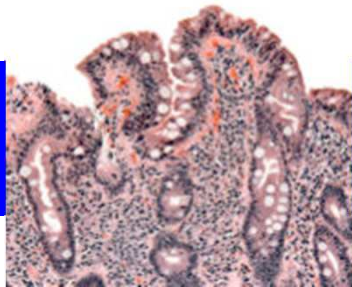
30

(group size)

(377)

(329)

(294)



15m

24m

36m

Tot

Gruppo B

1

6

10

17

(group size)

(345)

(325)

(283)

Basilio Malamisura

Centro Diagnosi Celiachia - Cava de' Tirreni



Journal of Pediatric Gastroenterology and Nutrition

7:395-399 @ **1988** Raven Press, Ltd., New York

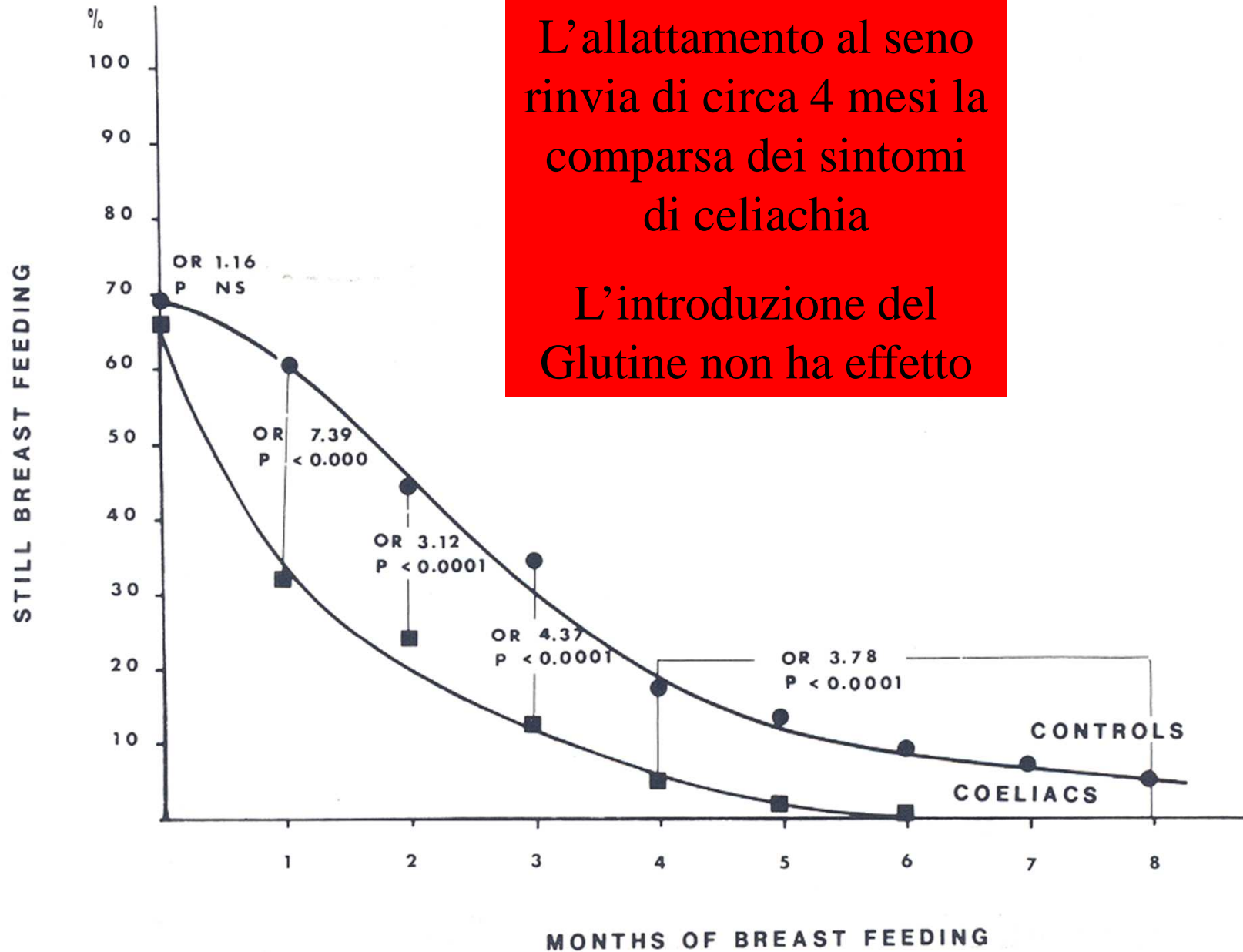
Case Control Study on Nutritional Risk Factors in Celiac Disease

L. Greco, S. Auricchio, M. Mayer, and M. Grimaldi

*Department of Clinical Pediatrics, 2nd Faculty of Medicine,
University of Naples, Naples, Italy*

L'allattamento al seno
rinvia di circa 4 mesi la
comparsa dei sintomi
di celiachia

L'introduzione del
Glutine non ha effetto



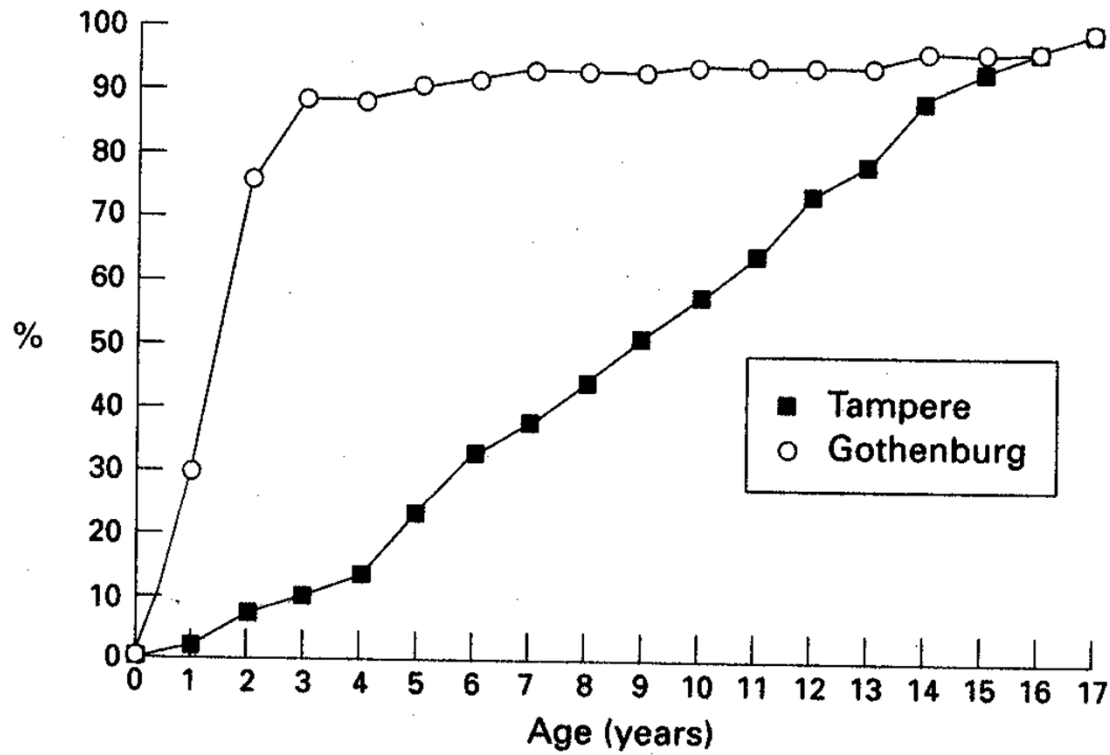
Abbiamo lavorato già 20 anni fa !

Changing pattern of childhood coeliac disease in Finland Acta Paediatr Scand. 1988 May;77(3):408-12

Long breast-feeding seemed to postpone the symptoms but the introduction of gluten was of no significance

We do not believe that coeliac disease has disappeared but that it will be found during the next decade

- **Different features of coeliac disease in two neighbouring countries** Arch Dis Child. 1993 Sep;69(3):375-80
- It is concluded that the intake of infant cereal protein might influence when and how clinical coeliac disease appears



Tampere	1	3	2	2	6	6	3	4	4	4	4	6	3	6	3	2	2	= 61
Gothenburg	25	40	11	0	2	1	1	0	0	1	0	0	0	2	0	0	3	= 86

Cumulative distribution of age at diagnosis in children with diagnosed coeliac disease by centre.

HLA ASSOCIATED RISK

			<i>DQ</i>	<i>Risk%</i>	
General population			Any	1%	
General population			DQ2/8+	2%	
General population			DQ2/8-	0%	
First Degree Relatives			Any	9%	
First Degree Relatives			DQ2/8-	0%	
First Degree Relatives			DQ2/8+	>15%	

Genotypic Relative Risk groups

DQ genotypes	DR genotype*	GR	Italy	France	Scandinavia
$\alpha_5 \beta_2 / \alpha_5 \beta_2$	DR3/DR3	G_1	1	1	1
$\alpha_5 \beta_2 / \alpha \beta_2$	DR3/DR7				
$\alpha_5 \beta / \alpha \beta_2$	DR5/DR7	G_2	0.68	0.28	0.23
$\alpha_5 \beta_2 / \alpha_5 \beta$	DR3/DRX	G_3	0.23	0.09	
$\alpha_5 \beta_2 / \alpha_3 \beta_3$					
$\alpha_5 \beta_2 / \alpha \beta$					
$\alpha \beta_2 / \alpha \beta_2$	DR7/DR7	G_4	0.27	0.10	0.08
$\alpha \beta_2 / \alpha_3 \beta_3$	DR7/DR4				
$\alpha_3 \beta_3 / \alpha_3 \beta_3$	DR4/DR4				
others	others	G_5	0.02	0.01	0.01

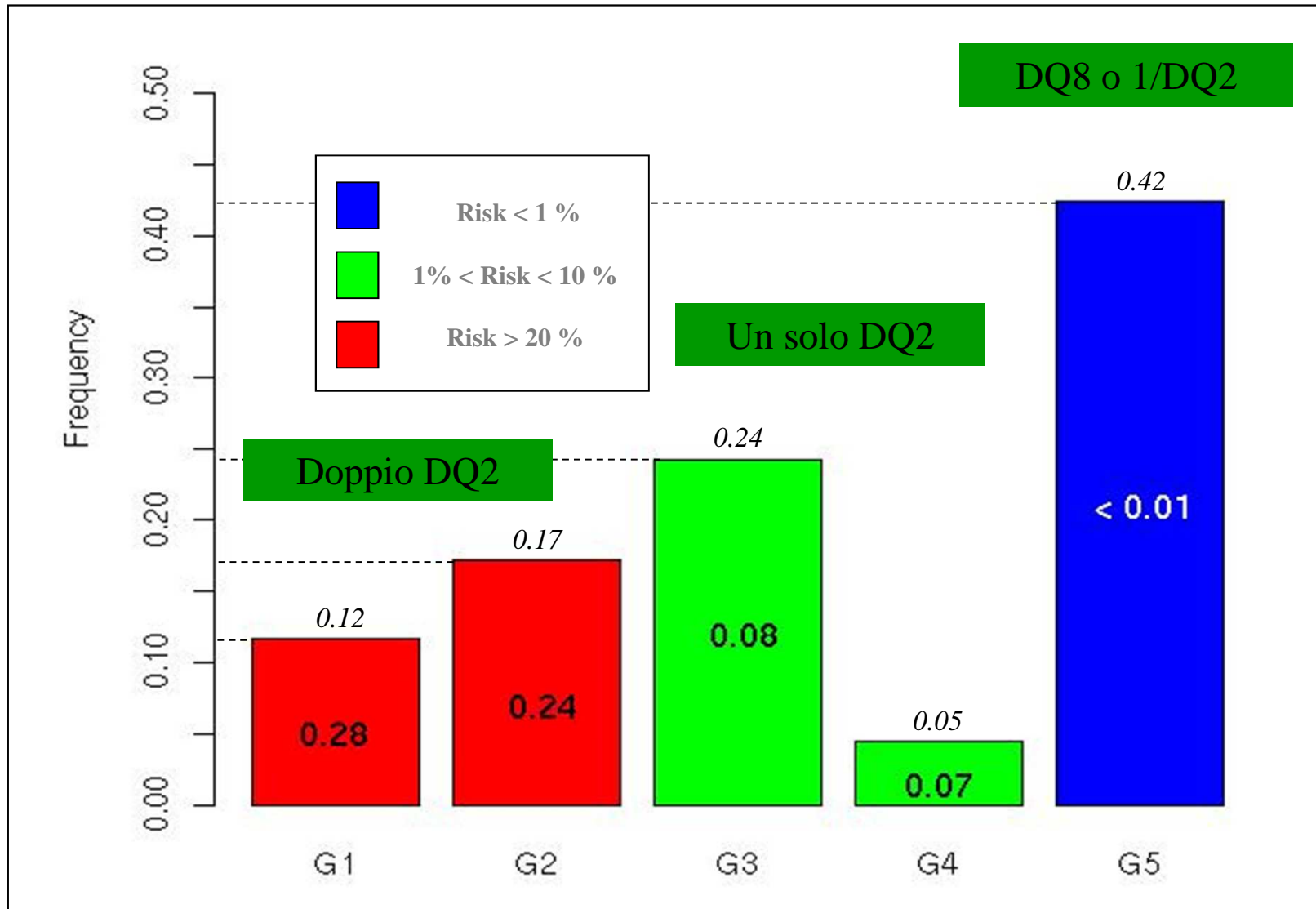
Rischio per un fratello di un probando in accordo al genotipo DQ dei genitori

	H1H1	H1H2	H1H3	H1H4	H1H5	H2H2	H2H3	H2H4	H2H5	H3H3	H3H4	H3H5	H4H4	H4H5	H5H5
H1H1			[8;29]	[8;29]	[8;29]		[8;29]	[8;29]	[8;29]						
H1H2		[7;29]	[8;29]	[7;29]	[1;29]	[7;29]	[7;29]	[7;29]	[1;29]	[8;24]	[7;24]	[1;24]			
H1H3			[1;29]	[1;29]	[1;29]		[1;29]	[1;29]	[1;29]						
H1H4				[7;29]	[1;29]	[7;29]	[1;29]	[7;29]	[1;29]						
H1H5					[1;29]	[1;29]	[1;29]	[1;29]	[1;29]						
H2H2							[7;24]				[7;24]	[1;24]			
H2H3							[1;24]	[1;24]	[1;24]	[1;24]	[1;24]	[1;24]			
H2H4										[1;24]	[1;24]	[1;24]			
H2H5										[1;24]	[1;24]	[1;24]			
H3H3															
H3H4															
H3H5															
H4H4															
H4H5															
H5H5															

Stima del rischio in base al genotipo dei genitori

- Rischio > 20%
- 15% < Rischio < 20%
- 10% < Rischio < 15%
- 1% < Rischio < 10%
- Rischio < 1%

PROBABILITA' PER UN FRATELLO DI UN PROBANDO DI APPARTENERE A Gi E RISCHIO CORRISPONDENTE

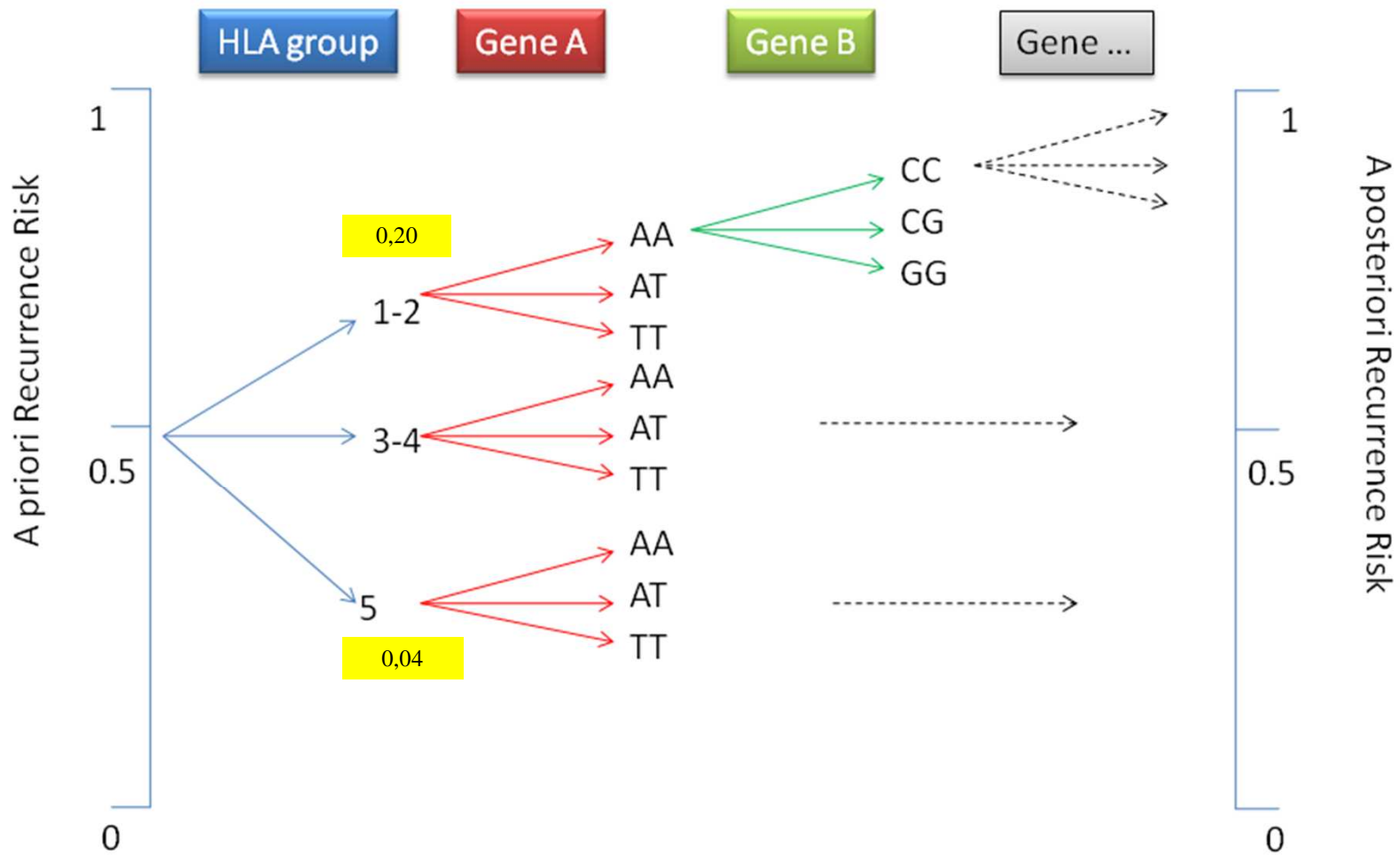


Che dobbiamo fare ?



Scoraggiare un matrimonio ?

Bayesian Approach



Case-control association analyses at the single SNP level

Subunit of NF-kB

Regulator of G-protein signalling

Chr	SNP	Locus	A1	A2	CD cases, Controls	MAF CD	MAF Controls	χ^2	p-value	OR (95% CI)
1	rs2816316	RGS1	A	C	102,1169:253	0.14	0.18	6.10	0.0135	1.299 (1.055-1.598)
2	rs917997	IL18RAP		A	965:309, 1092:330	0.24	0.23	0.408	0.5231	0.9438 (0.7901-1.127)
2	rs842647	REL	A	G	967:307, 1080:342	0.24	0.24	0.001	0.9774	0.9974 (0.8357-1.190)
3	rs64111	CCR3	G	A	741:533, 906:516	0.41	0.36	8.707	0.0032	0.7918 (0.6780-0.9247)
3	rs17810546	SCHIP1	A	G	1158:116, 1312:110	0.09	0.07	1.641	0.2002	0.8370 (0.6373-1.099)
3	rs1464510	LPP	C	A	646:628, 844:578	0.49	0.40	20.32	6.5E-06	0.7045 (0.6048-0.8206)
4	rs13119723	KIAA1109	A	G	1135:139, 1220:196	0.11	0.14	5.285	0.0215	1.312 (1.040-1.654)
4	rs1315111	KIAA1109	A	G	1139:135, 1225:195	0.10	0.14	6.143	0.0132	1.343 (1.063-1.697)
6	rs2271332	OLIG3	A	G	1008:248, 1162:256	0.19	0.23	1.246	0.2643	0.8955 (0.7376-1.087)
6	rs1738074	TAGAP	G	A	681:593, 816:604	0.46	0.42	4.376	0.0365	0.8500 (0.7299-0.9899)
19	rs3760746	TNFSF10	T	C	1276, 461:375	0.42	0.41	0.362	0.5473	0.9372 (0.7588-1.158)

Chemokine receptor

Structural role in maintaining cell shape and motility; it may be involved in signal trasduction and activation of gene transcription

Rho GTPase activatin protein

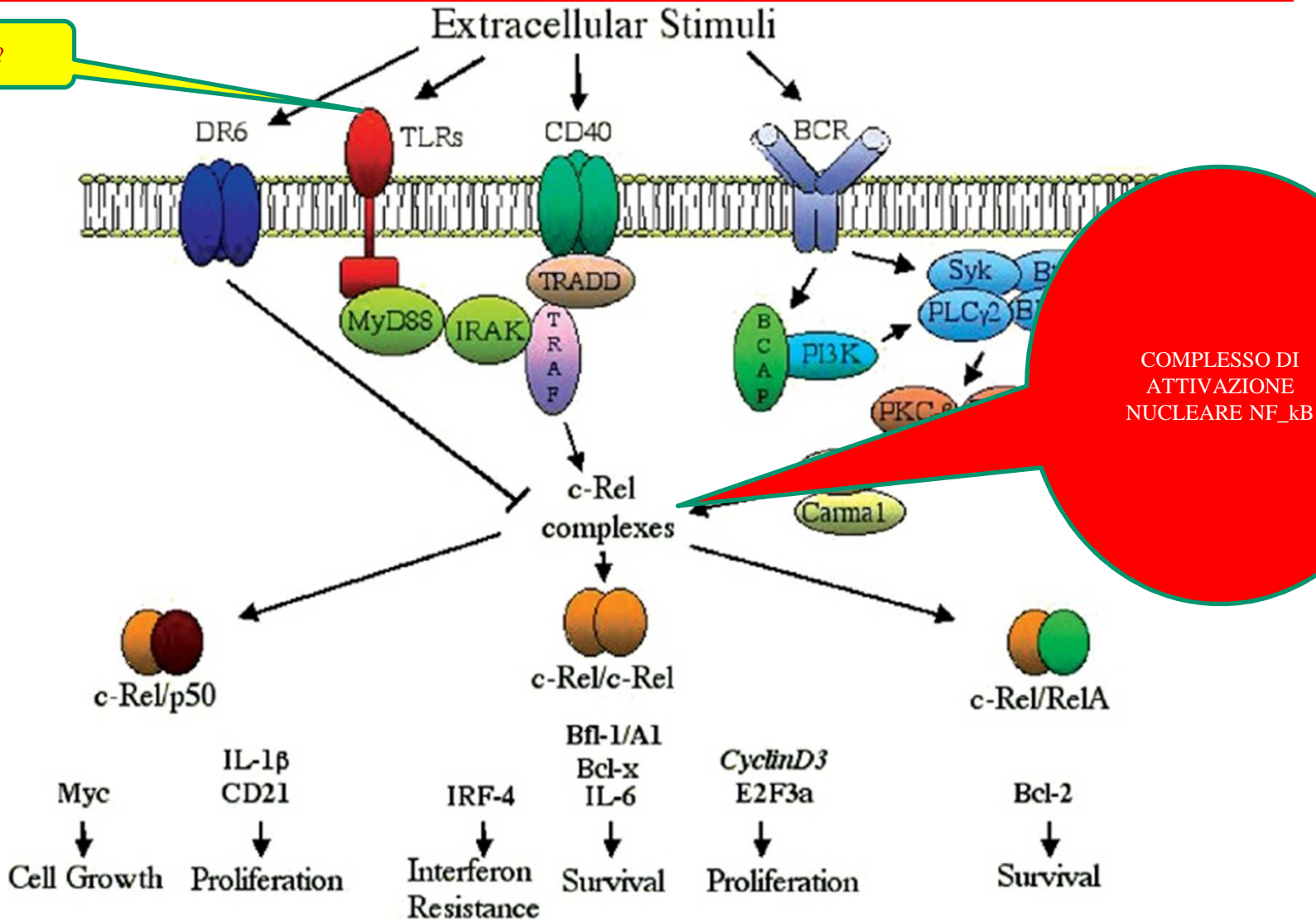
Endopeptidase

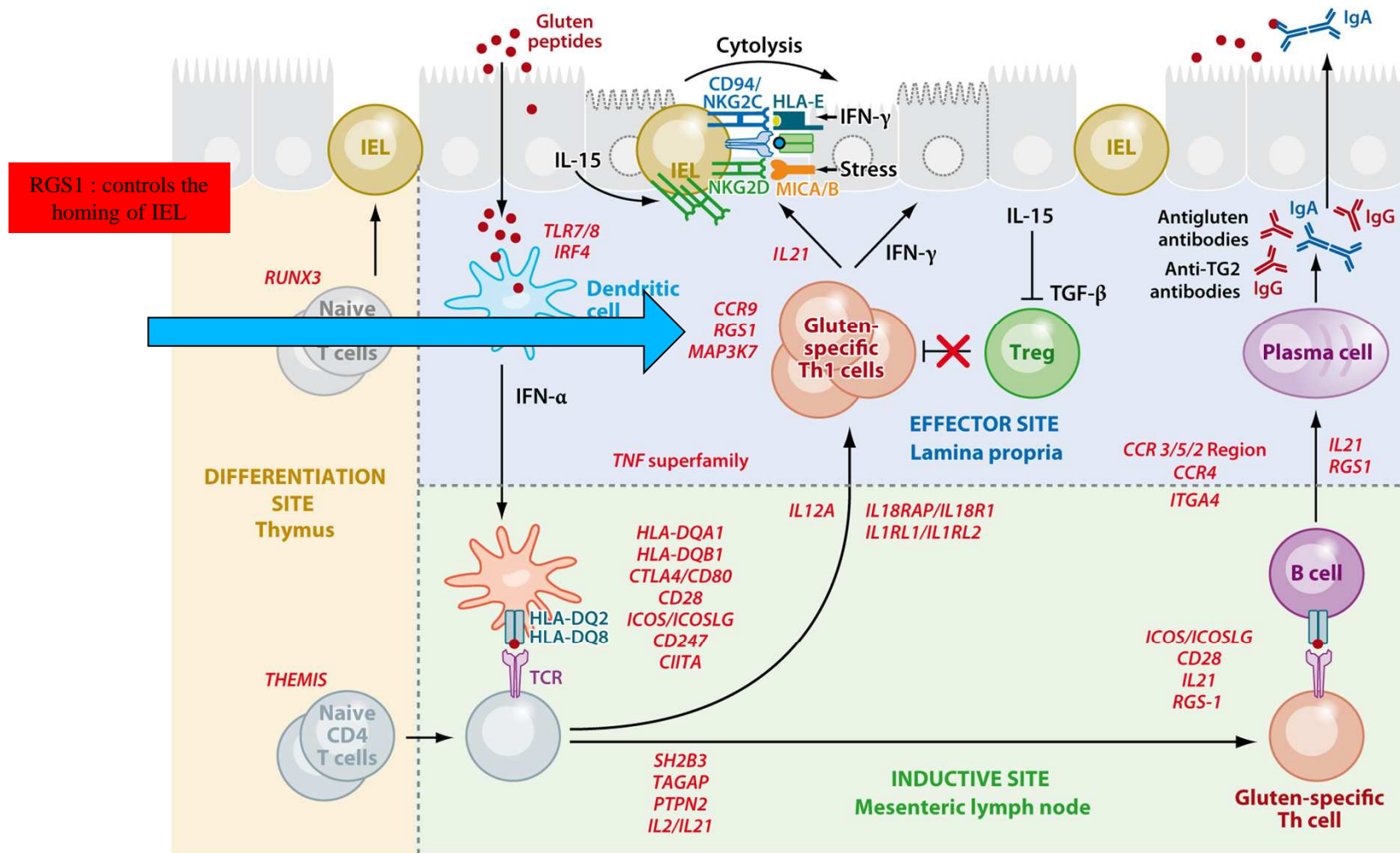
Chr: chromosome; A1: major allele; A2: minor allele; MAF: minor allele frequency; OR: odds ratio; CI: confidence interval; χ^2 : χ -square test; p-value was calculated by 2x2 two-sided χ -square test; bold indicates p-value < 0.05

372 CD-Cases vs 451 Controls

Pathway of c-Rel in NF-KB

GLUTINE ?





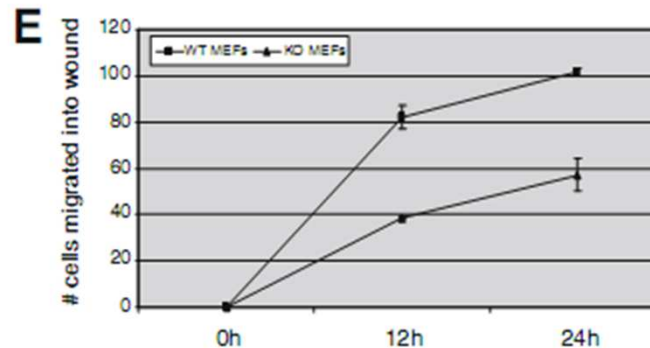
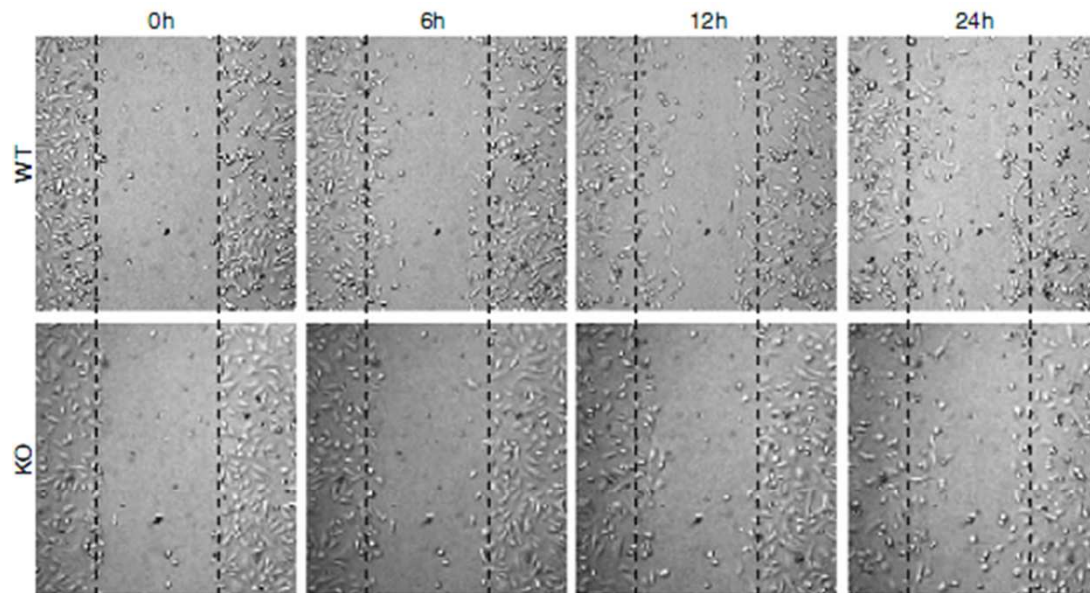
Abadie V, et al. 2011.
 Annu. Rev. Immunol. 29:493–525

Integration of immunological pathways and celiac disease (CD)-associated genes into a model of CD pathogenesis. The figure is subdivided into three distinct anatomical regions in which T cell differentiation (thymus), T cell polarization (inductive site), and effector immune response (effector site) take place. Genes associated with CD by genome-wide association studies are listed in red according to their potential implication in distinct immunological pathways. *THEMIS* and *RUNX3* are involved in the thymic differentiation of CD4 and CD8 T cells, respectively. Dendritic cells located in the lamina propria acquire a proinflammatory phenotype upon viral recognition (*TLR7/8* and *IRF4*) and migrate to the mesenteric lymph nodes (inductive site). There, they present gluten peptides (*HLA-DQA1*, *HLA-DQB1*, and *CIITA*) to naive CD4 T cells and promote T cell activation (e.g., *CD28*, *CD80*, *CTLA4*, *CD247*, *PTPN2*, *SH2B3*, *TAGAP*, *IL2*, and *FASLG*) and differentiation into inflammatory effector T cells (*IL12A*, *IL18R1*, *IL18RAP*, *IL1RL1*, and *IL1RL2*). In addition, transglutaminase 2 (TG2) and gluten-specific B cells (that have internalized gluten-TG2 complexes) receive help from gluten-specific T cells, become activated, and differentiate into immunoglobulin (Ig)A- and IgG-producing plasma cells (*ICOS*, *ICOSLG*, *IL21*, and *RGS1*). Other genes regulate activation and migration of cytotoxic intraepithelial lymphocytes (IELs) (*MAP3K7*, *IL-21*, *CCR9*, and *RGS1*). Finally, some genes are involved in cell migration [e.g., genes coding for chemokine receptors (*CCRs*) and *ITGA4*], and others regulate tumor necrosis factor (TNF)-dependent pathways (*TNFAIP3*, *TNFSF4*, *TNFSF18*, *TNFRSF9*, and *TNFRSF14*). Even though their genes have not been identified by genetic studies, interleukin (IL)-15 and interferon (IFN)- α play a critical role in orchestrating the immune responses that lead to CD pathogenesis. IL-15 upregulates activating natural killer cell (NK) receptors and licenses IELs to kill epithelial cells, whereas IFN- α promotes the differentiation of proinflammatory dendritic cells. Abbreviations: HLA, human leukocyte antigen; TGF, transforming growth factor; Th, T helper cell.

Lpp ^{-/-} mouse model

Lpp ^{-/-} mouse embryonic fibroblasts exhibited reduced migration capacity, reduced viability, and reduced expression of some Lpp interaction partners.

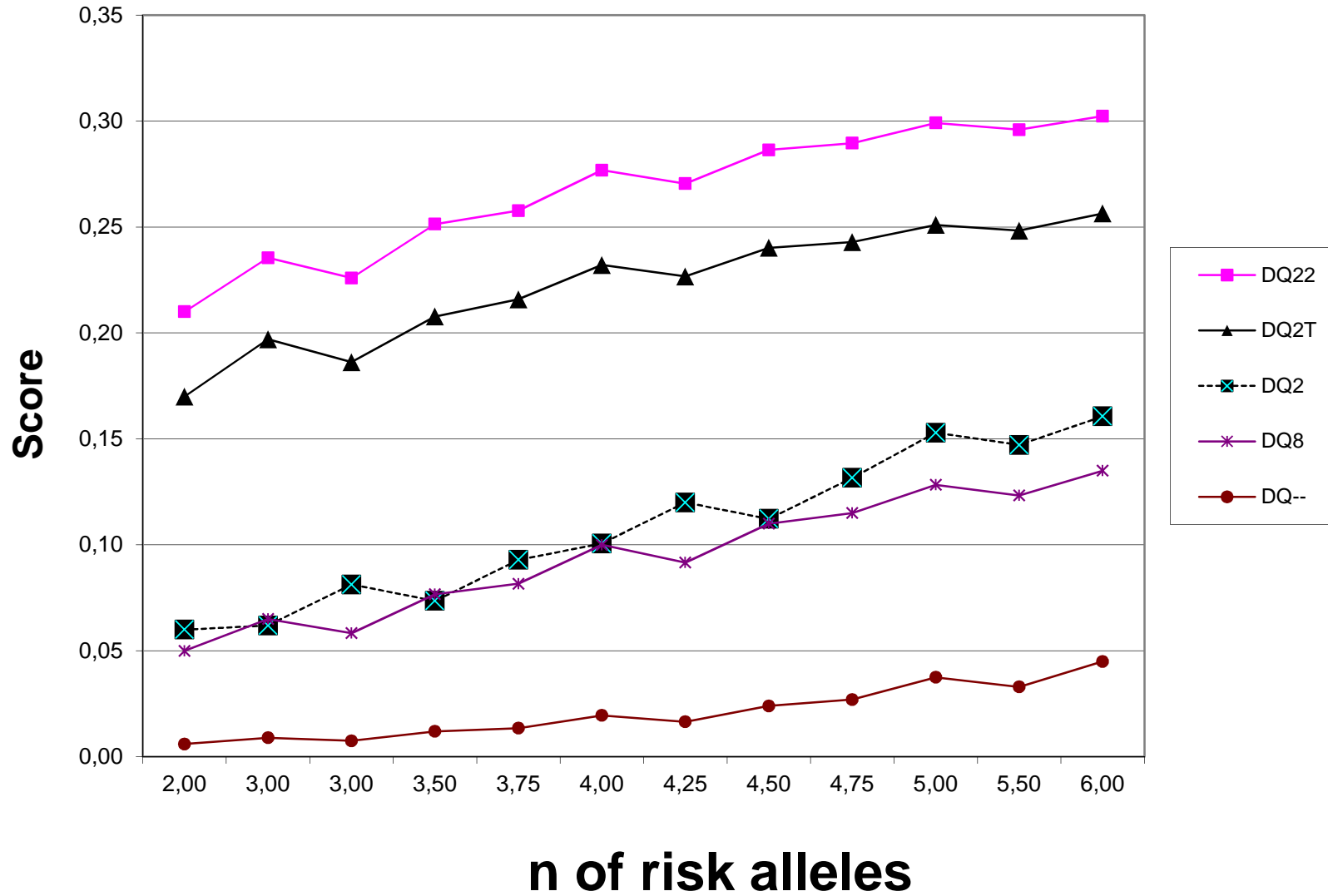
Vervenne et al., 2009



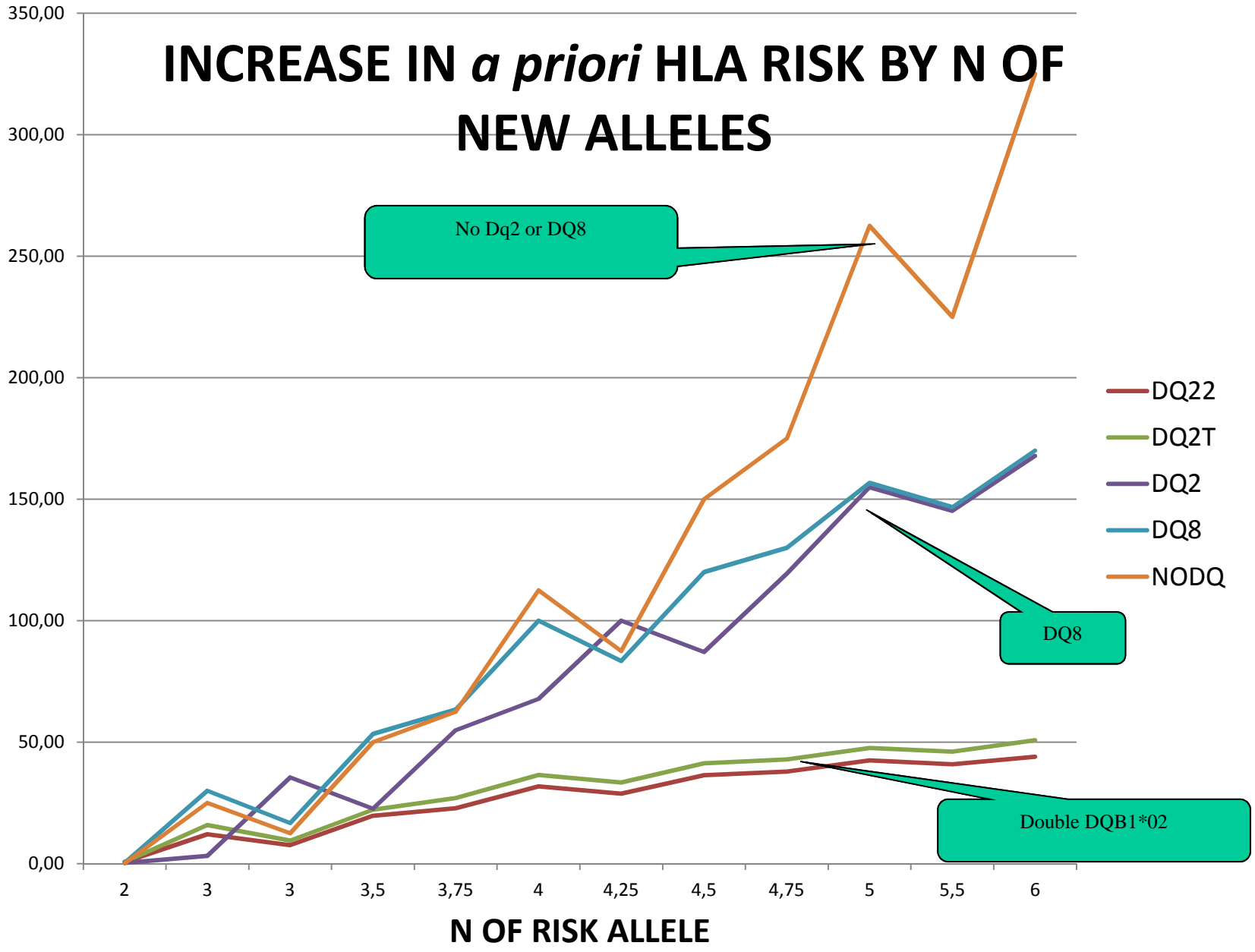
Increase of the a priori HLA Risk by adding LPP, c-REL, RGS1

LPP	c-REL	RGS1	DQ22	DQ2T	DQ2	DQ8	DQ--
CC	AG+GG	AC+CC	0,21	0,17	0,06	0,05	0,01
CC	AA	AC+CC	0,24	0,20	0,06	0,07	0,01
CC	AG+GG	AA	0,23	0,19	0,08	0,06	0,01
CC	AA	AA	0,25	0,21	0,07	0,08	0,01
AC	AG+GG	AC+CC	0,26	0,22	0,09	0,08	0,01
AC	AA	AC+CC	0,28	0,23	0,10	0,10	0,02
AC	AG+GG	AA	0,27	0,23	0,12	0,09	0,02
AC	AA	AA	0,29	0,24	0,11	0,11	0,02
AA	AG+GG	AC+CC	0,29	0,24	0,13	0,12	0,03
AA	AA	AC+CC	0,30	0,25	0,15	0,13	0,04
AA	AG+GG	AA	0,30	0,25	0,15	0,12	0,03
AA	AA	AA	0,30	0,26	0,16	0,14	0,05

A posteriori Risk adding each new allele to HLA



INCREASE IN *a priori* HLA RISK BY N OF NEW ALLELES

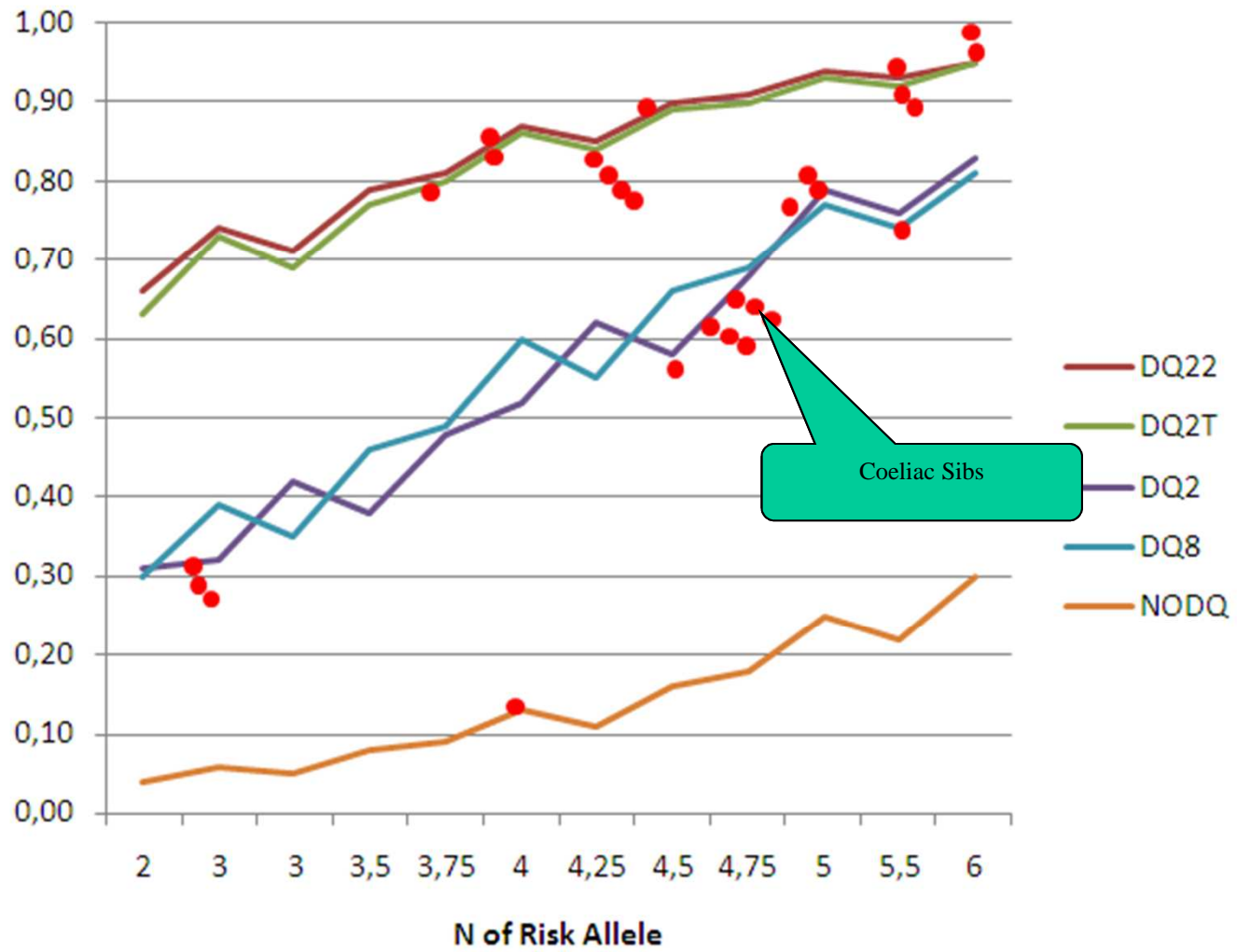


No Dq2 or DQ8

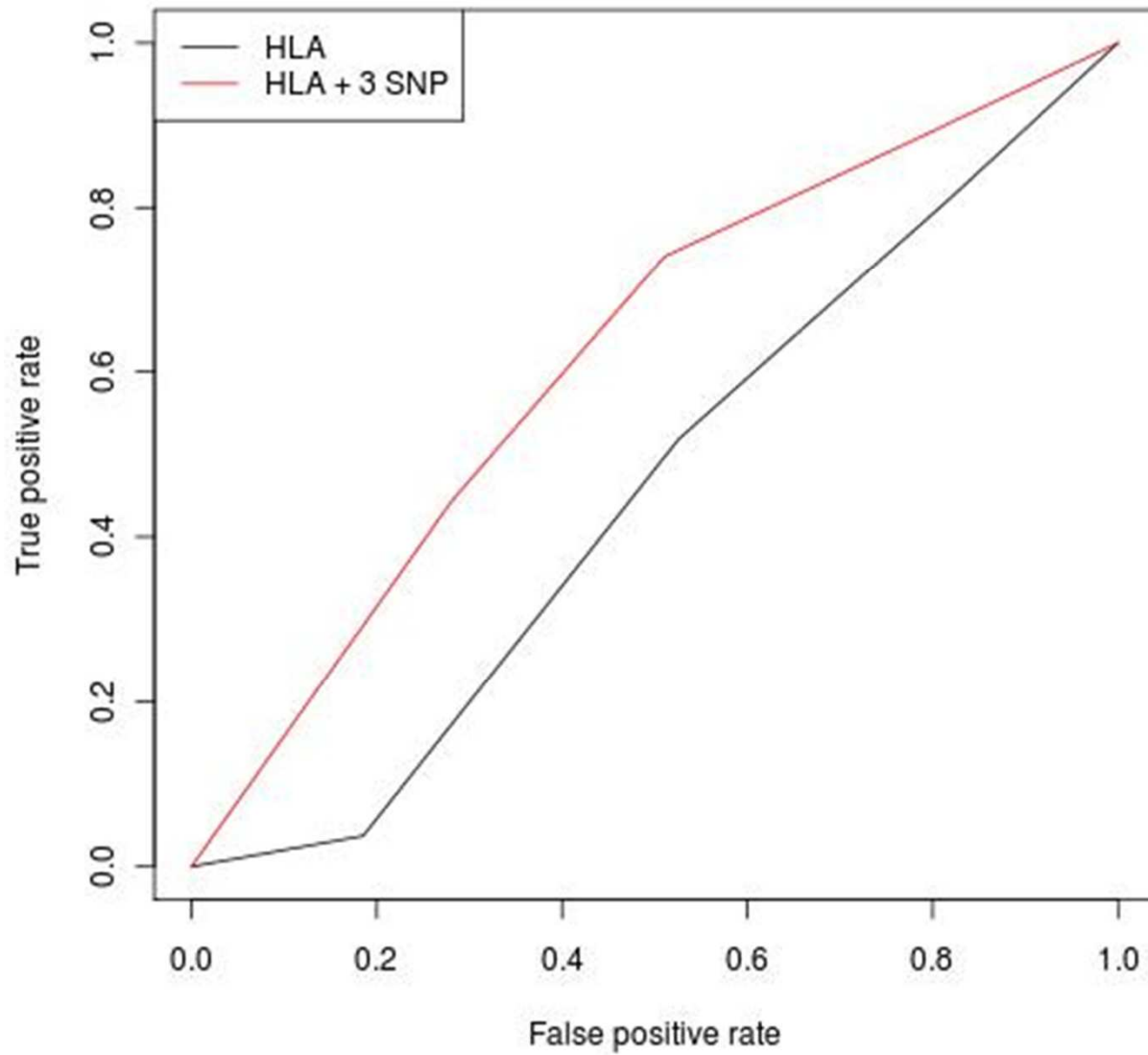
DQ8

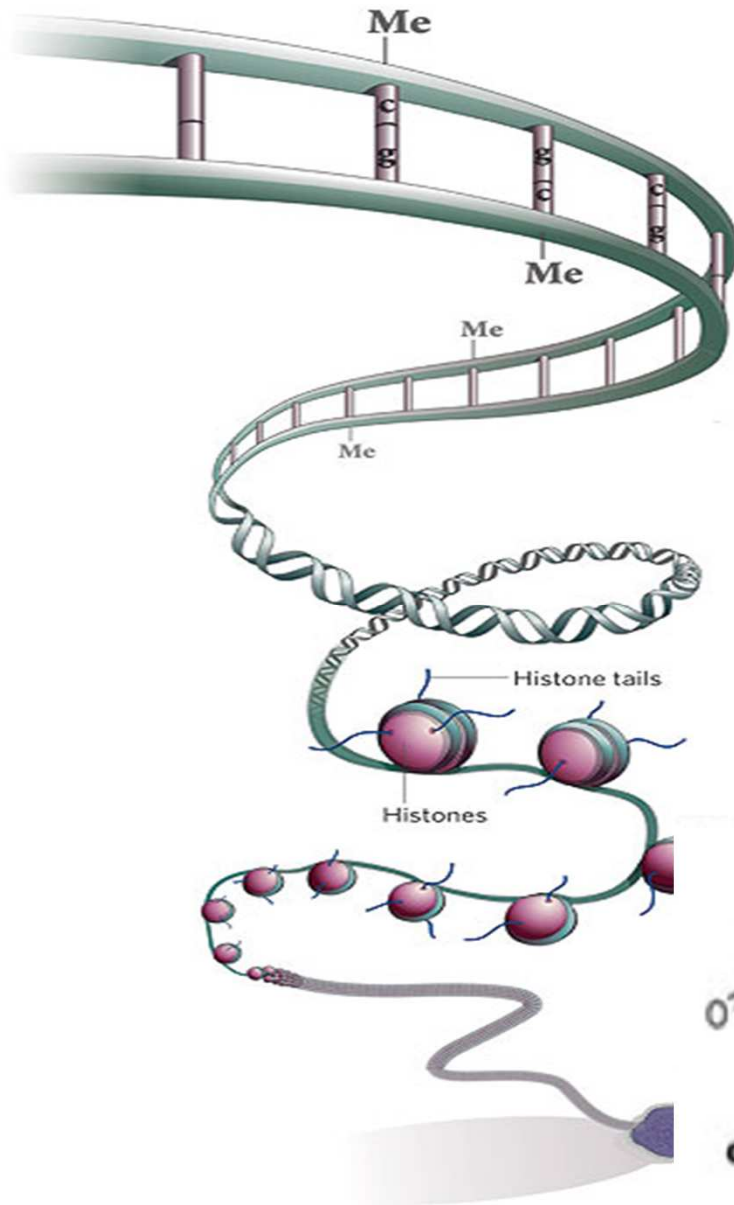
Double DQB1*02

RELATIVE RISK OF HLA + 3 SNPs



ROC - Performance of the predicting model

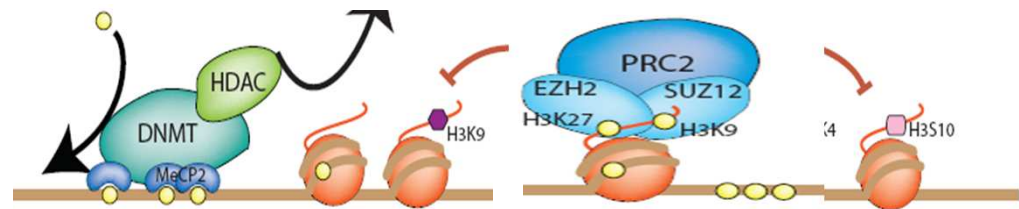




The two main components of the epigenetic code

DNA methylation

Methyl marks added to certain DNA bases repress gene activity.



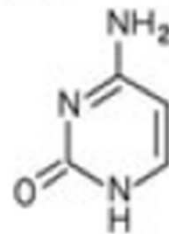
DNA Methylation
Recruitment of HDACs

Histone Deacetylation
H3K9 deacetylation

Histone Methylation
H3K9 and K27 methylation by G9a
Competition between H3 tail modifications

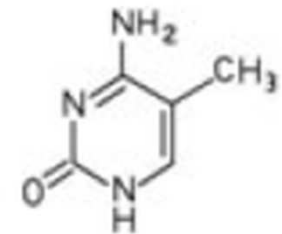
Histone modification

A combination of different molecules can attach to the 'tails' of proteins called histones. These



Cytosine

DNA Methyltransferase Enzymes



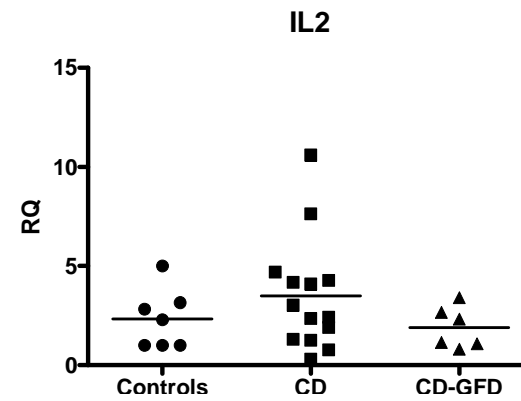
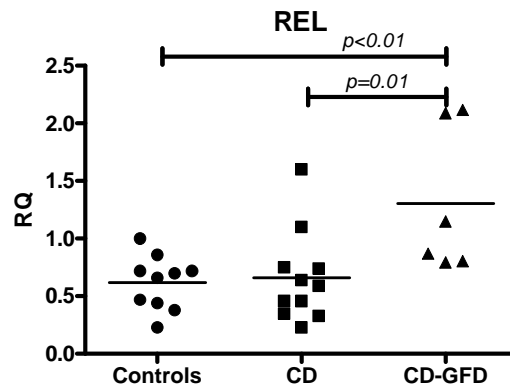
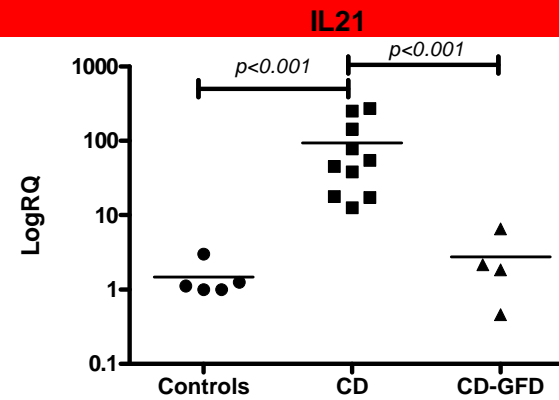
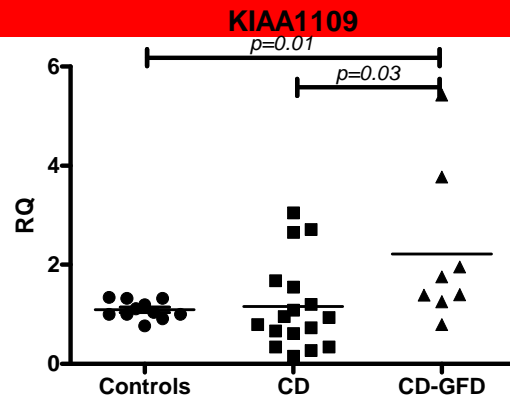
5-Methylcytosine

But the GENOMA is a written book : Life is the EXPRESSION of Genes

di Napoli "Federico II"



EXPRESSION Biopsie intestinale - 1



4q27

Discriminant Analysis between Coeliacs and Controls by the Expression of Candidate Genes in Intestinal Mucosa

		Wilks' Lambda	df1	Exact F
1	TNFAIP3	,404	1	59,002
2	IL21	,300	2	45,521
		,000		
3	REL	,261	3	35,809
4	RGS1	,235	4	30,143
		,000		
		,222	5	
		,000		

Wilk's Lambda shows the ability to discriminate between Coeliac and Controls



1-----0

Wilks' Lambda

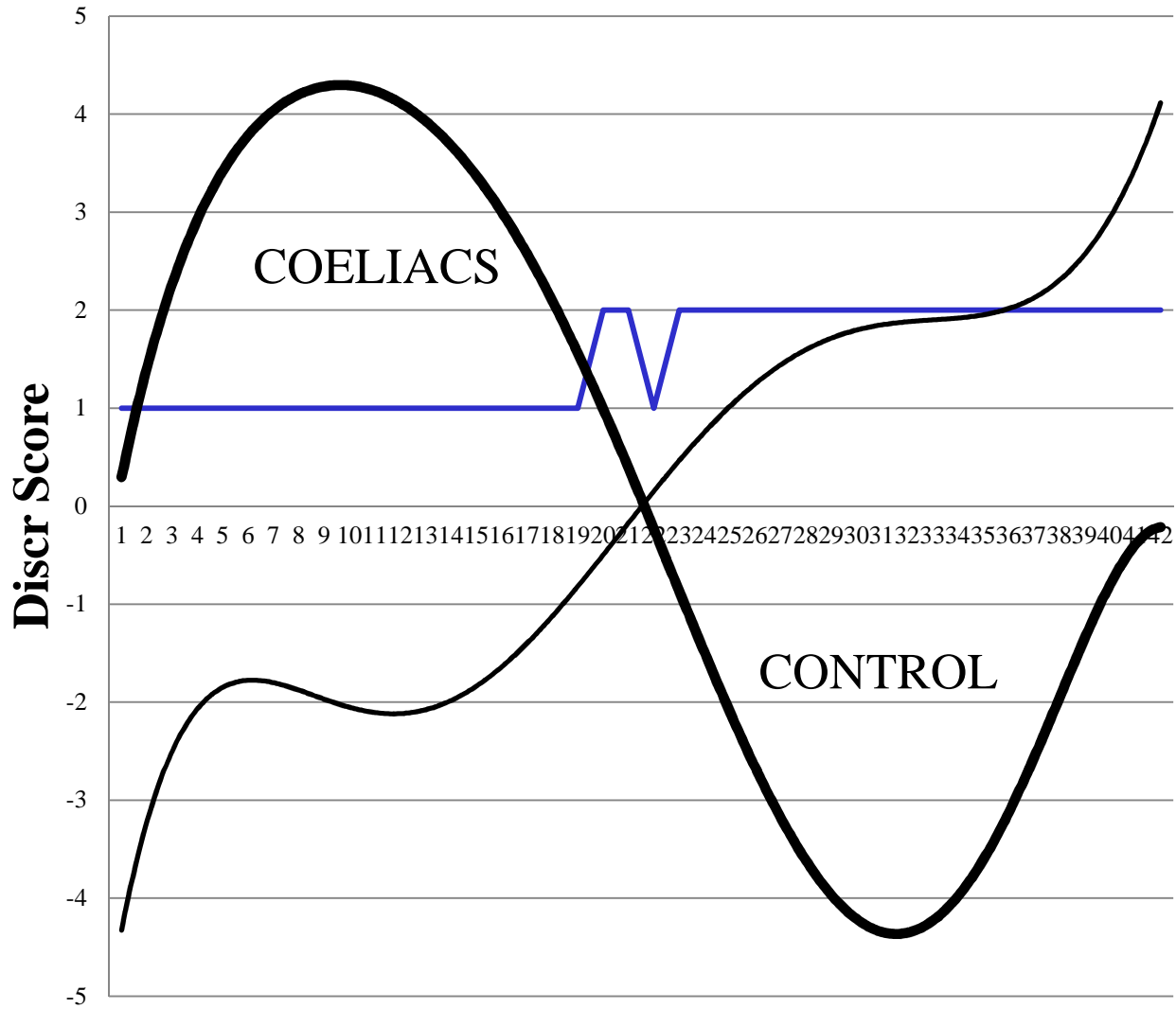


Classification results

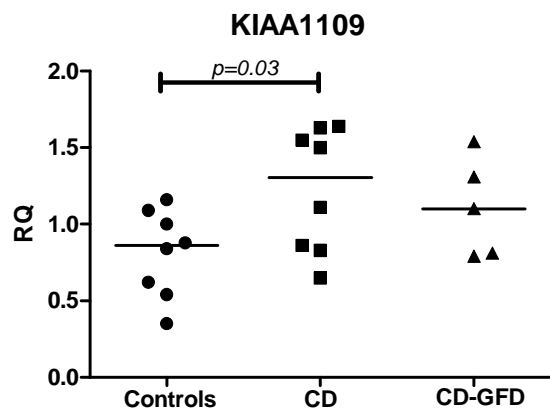
		Predicted Group Membership		Total
	STATUS	Control	Celiac	
Count	Control	19	1	20
	Celiac	2	20	22
%	Control	95	5	100
	Celiac	10	90	100

92,9% of original grouped cases correctly classified.

Discriminant Score and Diagnostic Probability from expression in Biopsies



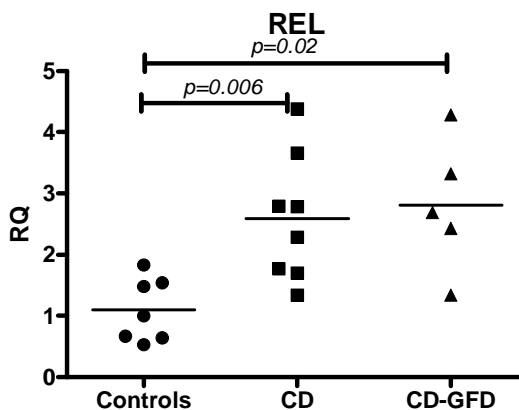
EXPRESSION Monociti da Sangue Periferico



□ Endopeptidasi

□ Si suppone che nei mammiferi abbia un ruolo nella regolazione della crescita delle cellule epiteliali e nella differenziazione e sviluppo tumorale

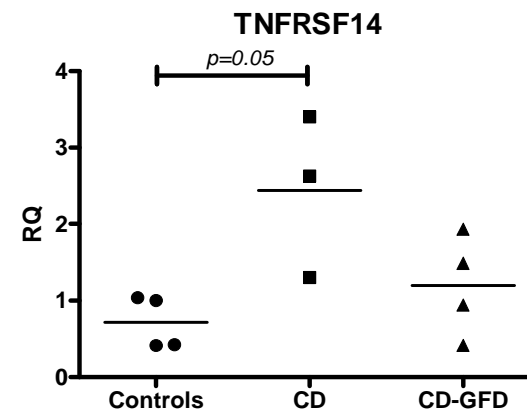
(Kuo et al., 2006)



□ Subunità del complesso NF-kB

□ Può innescare ma anche terminare (feedback -) i meccanismi di azione pro-infiammatoria di NF-kB

(Bonizzi et al, 2004, Lawrence et al, 2005).

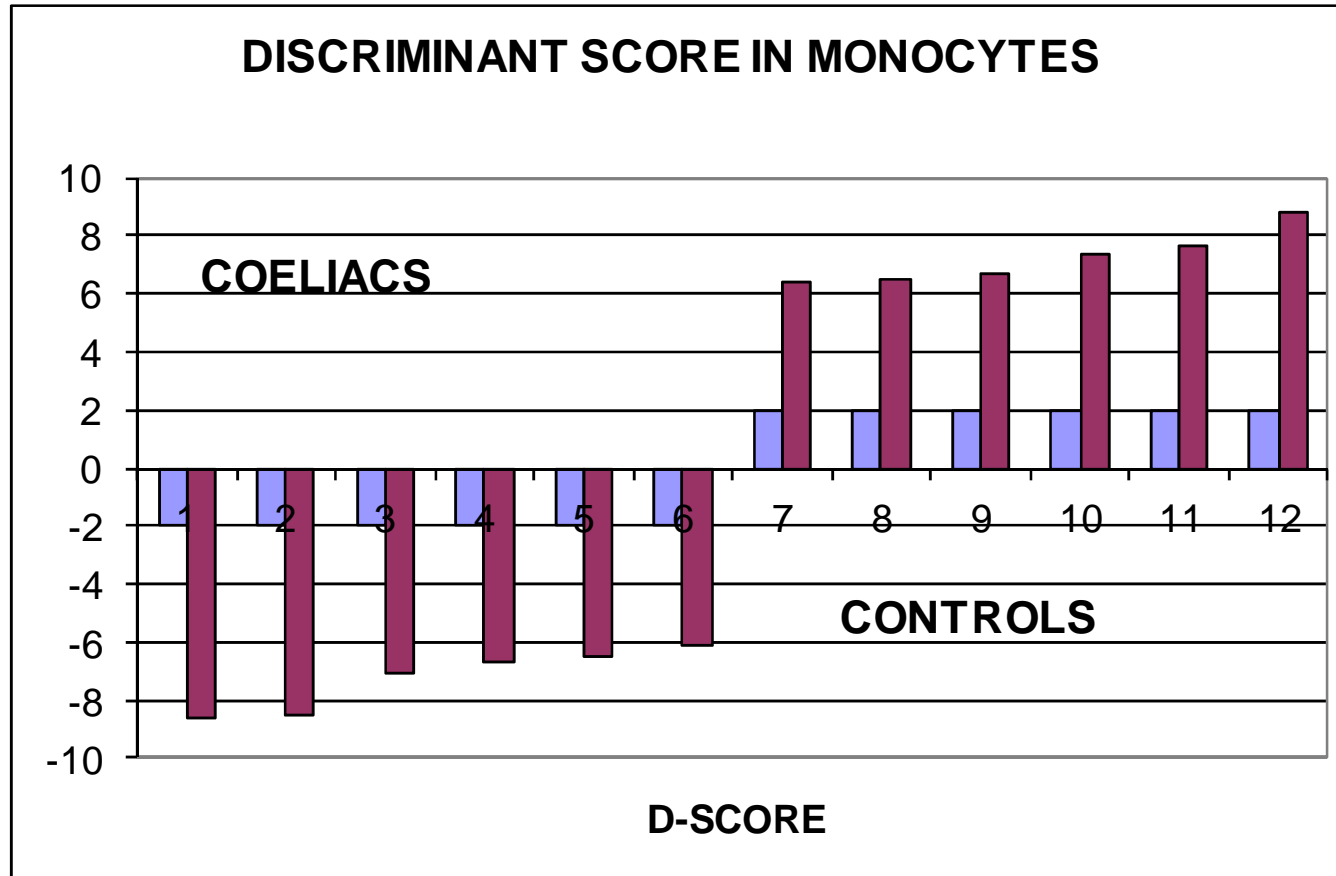


□ Conosciuto anche come Herpesvirus Entry Mediator (HVEM).



**Interessamento infiammatorio
a livello periferico**

Classification based on the expression of 4 gene in blood leucocytes



Diseases in symptomatic cases

Regions	GI Symptoms	Anaemia	Osteopenia	Abnormal Liver	Short Stature Children
<i>North</i>	214.069	100.738	75.554	25.185	10.047
<i>N.East</i>	18.557	8.733	6.550	2.183	927
<i>M.East</i>	123.447	58.093	43.570	14.523	8.849
<i>East</i>	52.903	24.896	18.672	6.224	4.535
<i>South</i>	252.846	118.986	89.240	29.747	21.125
MED tot	657.119	309.232	231.924	77.308	41.609

Possiamo prevenirne almeno una parte ????