



O -

SYDNEY

2012

«

2 (

) ».

. 5343/32,

202,

Ημερομηνία αίτησης της κ Γαζή Σοφίας: 9-2-2004

Ημερομηνία ορισμού Τριμελούς Συμβουλευτικής Επιτροπής: 529^α/23-3-2004

Μέλη Τριμελούς Συμβουλευτικής Επιτροπής:

Επιβλέπων

Στεφάνου Δημήτριος Αναπληρωτής Καθηγητής Παθολογικής Ανατομίας Ιατρικής Σχολής Πανεπιστημίου Ιωαννίνων

Μέλη

Αγνάντη Νίκη Καθηγήτρια Παθολογικής Ανατομίας Ιατρικής Σχολής Πανεπιστημίου Ιωαννίνων

Λεβειδιώτου –Στεφάνου Σταματίνα Επίκουρος Καθηγήτρια Μικροβιολογίας Ιατρικής Σχολής Πανεπιστημίου Ιωαννίνων

Ημερομηνία ορισμού θέματος: 1-4-2004

«Μοριακή ανίχνευση σε αρχαιακό υλικό ανθεκτικών στις μακρολίδες στελεχών ελικοβακτηριδίου του πλωρού και συσχετισμός με ιστολογικά δεδομένα ταξινόμησης κατά sydney»

ΔΙΟΡΙΣΜΟΣ ΕΠΤΑΜΕΛΟΥΣ ΕΞΕΤΑΣΤΙΚΗΣ ΕΠΙΤΡΟΠΗΣ : 726^α/17-1-2012

Αγνάντη Νίκη	Ομότιμος Καθηγήτρια Παθολογικής Ανατομίας, Ιατρικής Σχολής Πανεπιστημίου Ιωαννίνων
Ευαγγέλου Άγγελος	Καθηγητής Φυσιολογίας, Ιατρικής Σχολής Πανεπιστημίου Ιωαννίνων
Στεφάνου Δημήτριος	Καθηγητής Παθολογικής Ανατομίας, Ιατρικής Σχολής Πανεπιστημίου Ιωαννίνων
Λεβειδιώτου –Στεφάνου Σταματίνα	Αναπληρώτρια Καθηγήτρια Μικροβιολογίας, Ιατρικής Σχολής Πανεπιστημίου Ιωαννίνων
Μπατιστάτου Άννα	Αναπληρώτρια Καθηγήτρια Παθολογικής Ανατομίας, Ιατρικής Σχολής Πανεπιστημίου Ιωαννίνων
Γούσια Άννα	Επίκουρη Καθηγήτρια Παθολογικής Ανατομίας, Ιατρικής Σχολής Πανεπιστημίου Ιωαννίνων
Γκαρτζονίκα Κωνσταντίνα	Λέκτορας Μικροβιολογίας, Ιατρικής Σχολής Πανεπιστημίου Ιωαννίνων

Έγκριση Διδακτορικής Διατριβής με βαθμό «ΑΡΙΣΤΑ» στις 27-3-2012

ΠΡΟΕΔΡΟΣ ΤΗΣ ΙΑΤΡΙΚΗΣ ΣΧΟΛΗΣ

Μαργαρίτα Τζαφλίδου

Καθηγήτρια Ιατρικής Φυσικής

Η Γραμματέας της Σχολής



ΜΑΡΙΑ ΚΑΠΙΤΟΠΟΥΛΟΥ

1982 *Perth*,
 Marshall Warren $\div \emptyset$,
Cambylobacter.

1875,
 Giulio Bizzozero 1893

Jaworski 1899

1982 Marshall Warren
 1987

Thomas Borody
Cambylobacter pyloridis *Cambylobacter pylori*,
 16S RNA 1989,

Helicobacter
 \emptyset *Helicobacter*
 \emptyset *Helicobacter*
 58.000

1), 22

Nobel

2005

Warren

Marshall ⁽¹⁻³⁾ (

(),

Robin Warren

: ÷



1: Marshall () Warren ()
 Nobel 2005

í . 7-79

- 1. () í ..í í í í í í í í ..í í 9
 - í 9
 - í 9
 - í í í í í í í í í í í í í í í í í 9
 - í í í í í í í í í í í í í í í í íí í í í 11
 - í ..í ..í ... 11
- 2. í í í í í í í .í í í í í ..í í .í 13
 - í ... 13
 - - í . 14
 - í .. 15
 - í í í í ..í í í í ..í í í í í í í í í í í í í í í í í 17
 - ...í í í í .í í í í í í í í í í í í í í í í í í ..í 17
 - CO₂ (Breath test) í í í í í í í í í í í í í í í í í 19
- 3. í í í í í í í í í í í í í í í í .í í í í í í í .í í í í í . 21
 - í í .í í í í í í í í í í í í í í í í í í ..í í í 21
 - (BabA2, SabA) í í í í í í í í í í í í í í í .í . 22
 - IV (cag) í í í í í í í í í í í . 22
 - cagA vacA í í í í í í í í í í í í í í í í í í í .. 23
 - cag vac í ...í í í í íí .. 28
 - í í í í í í í í í í .. 30
 - í í í ..í í ..í í í í ..í í í í í í í í í 30
- 4. í í í í í í í í í í í í í í í í .í í í í í í . 32
 - í ... 32
 - í 34
 - í .. 35
 - í ... 36
- 5. í í í í í ..í í 37
 - í . 37
 - í í í í í í í í í í í 37

- (PCR) í í í í í í í í í í í í í í ... 38
- ...í .í í í í í í í í í í í í í . 39
- í ..í í í í í í í í 39
- 6. í í í í í í í .í í í 40
- 7. .í í ...í í í í í í í ..í í .. 45
- 8. í .í í í í ...í í í í í í í í 45
- 9. í í í í í í í í í í í í .í 47
- í í í í í í í í í í í í í í í í í 47
- í .í í í í í í í í í í í í í í í í í ... 48
- í í í í í í í í í í í í í í í í í 48
- 10. í í í ...í í í í í í í í í í í í í í í í í .. 49
- 11. ó -
- Sydney í í í í í í í í í í í .í í í í í í í í í 50
- í í í í í ...í í í í í í í í í í í . 51
- í í í í í í í í í í í í í í í í í ... 52
- í í í í í í í í í í í í í í í í í .. 55
- Sydney í ..í 55
- í í í í í í í í í í í í .í í í í í í í í í í .. 56
- ()í í í í í í í í í í í í í í í í í 56
- í 56
- í . 57
- í 58
- 12. í 60
- í 60
- í í í í í í í í í í í í í í í í í í 60
- í .. 60
- í ... 60
- 13. í í í í ...í í í í í í 61
- 14. í . 62
- 15. í 64
- í í í í í í í í í í í 64
- í í í í í í í í í í . 64

1. _____ ()

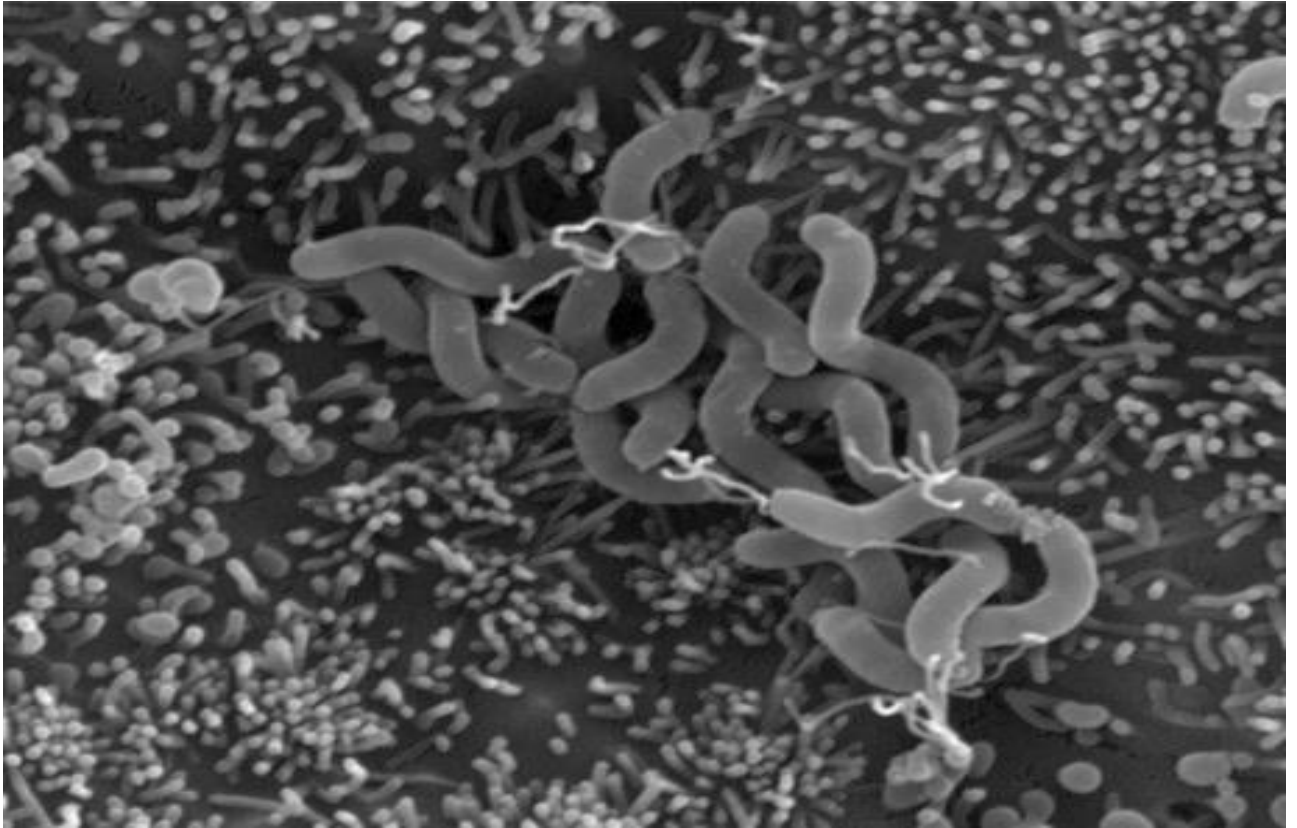
Gram (-), (4)
Campylobacter (
Campylobacter jejuni) (3;4). *Helicobacters*
 (1). , , 2,5-5 m
 0,75-1 m (3). 4-6
 (4).
 (5-7).
Campylobacters (8;9).
 :
 (10). , ,
 - .
 (11).
 : (C)
 (G) DNA 36-38 mol% C+G
Campylobacter (*C. jejuni* 30-32 mol% C+G). 16S
 RNA ,
 RNA (+) *Flexispira rappini* *Wolinella succinogenes* (12-16).
 :
Campylobacters.
 (>35%) (14:0) (16:0)
 (<8%), 3- - (3- -14:0),
 (3- -18:0) 19- - (19:0 cyc) (17-21).

Helicobacter

	<i>Helicobacter pylori</i> (type species)	<i>Helicobacter nemevstrinae</i>
	<i>Helicobacter mustalae</i>	<i>Helicobacter acinonyx</i>
<i>Helicobacters</i>	<i>Helicobacter felis</i>	<i>Gastrospirillum hominis</i>
	<i>Helicobacter fennelliae</i>	
	<i>Helicobacter cinaedi</i>	
<i>Helicobacters</i>	<i>Helicobacter muridarum</i>	

1.

(Lee O'Rourke, 1993⁽²²⁾).



3.

(23)

:

39, 257 21

19 kilodaltons

ø

Cambylobacters⁽¹⁷⁻²⁰⁾

62, 53, 50,

:

(24)

(25;25)

DNA

(26)



4.

2. _____

(27)

2.

	(%)	(%)	*
-	77-92	100	+++
-	93-99	95-99	+++
-	88-99	86-95	+
-CLO-test	89-98	93-98	+
- ¹³ C	90-100	98-100	+++
- ¹⁴ C	90-97	89-100	++

: +++ = , ++ = , + =

*

2.

(Brown Peura⁽²⁸⁾).

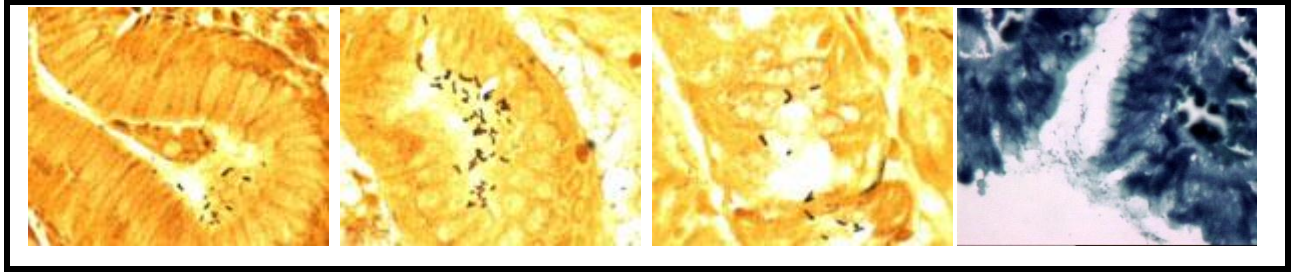
To

(29)

(30-32)

(29:30)

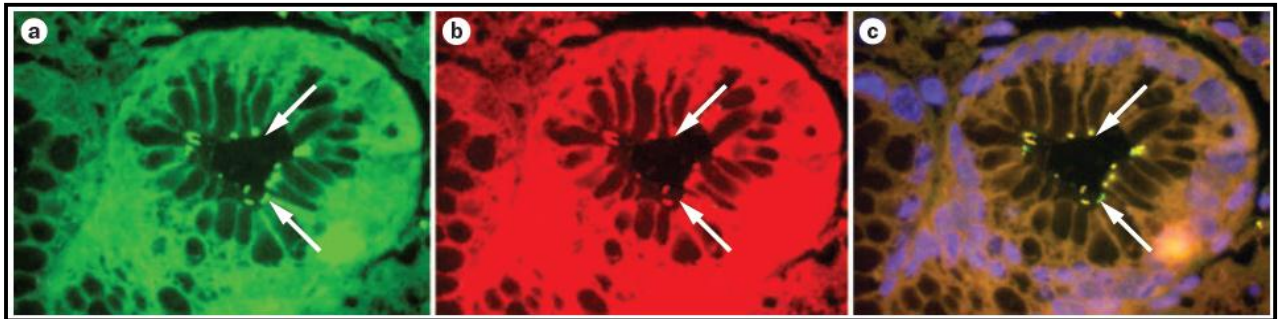
ø (33)
 4°C.
 (4)
 (24)
 Stuart Portagerm[®]
 BioMerieux⁽³⁴⁾
 GAB-CAMP Wilkins-Chalgren[®] (35)
 3-5
 37°C.
 Gram
 (36)
 90%, 100%.
 (Warthin-Starry)
 (5) (37)
 Gram, Giemsa, Gimenez
 Acridine-Orange.
 (38) Giemsa
 Warthin-Starry.
 (37)
 Wright-Giemsa
 (39)
in situ (FISH).
 (probes),
 (6).



5. Warthin-Starry ()

Giemsa .

Ortiz-Martinez . (37) .



6. FISH. (b).

Rimbara . (40)

IgM IgA ,
IgG (41) .

(28;42-45) .

test .

(46) .

screening ,

40

(47-49)

(ELISA)

(50)

kits

kits

cut-off

cut-off

(51-56)

• « »

•

•

120.

shock

kit.

kits

90%

(57-62)

(63)

(60;62)

IgG

(64)

6

6

IgG

(65-69)

(41;70)

FDA.

(71-73)

IgA

IgG

IgG

(immunoblotting) (50;74;75)

cagA vacA
(50;74-77)

CLOtest® (Delta West

Ltd.Canning Vale, Western Australia) (78).

pH.

(-)

(79)

(7).

test. 5, 20,

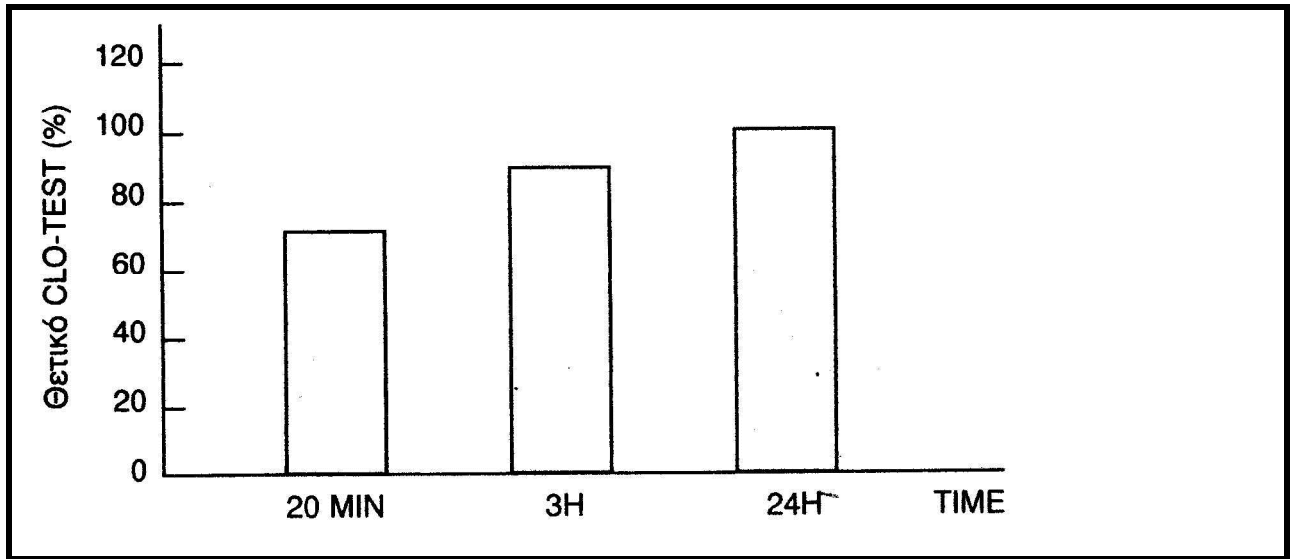
3, 24 (81), 100% CLOtest[®] 24 (8).

(80)

89-98%.



7. : CLO test[®] 12 ()⁽⁷⁹⁾



8. CLO-test, Rokkas 1999⁽⁸¹⁾.

CO₂ (Breath test)

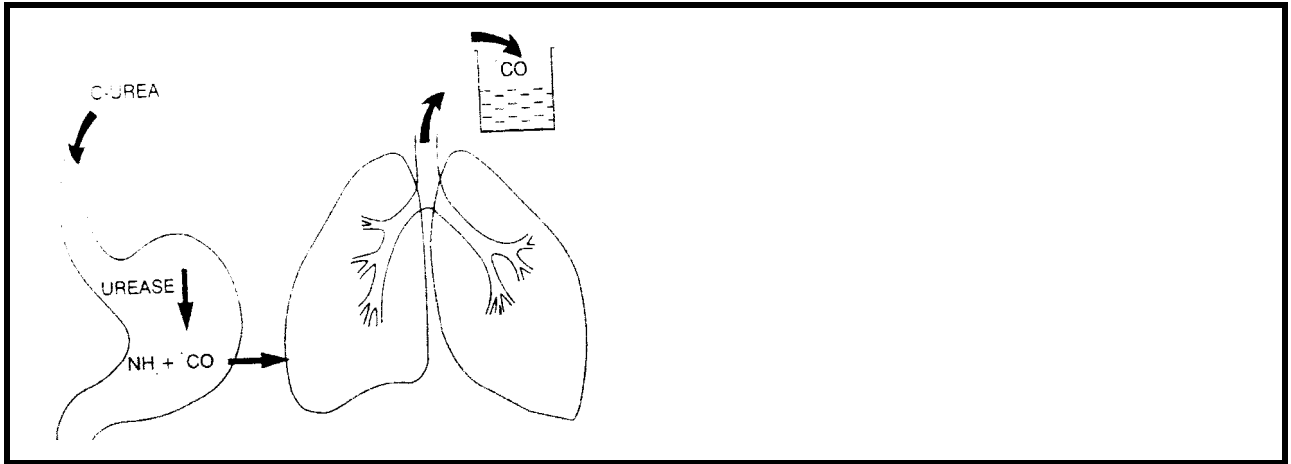
Graham⁽⁸²⁻⁸⁴⁾
 NH₃ CO₂ CO₂
 (

9). CO₂ beta counters, ¹³C ¹⁴C⁽³⁶⁻⁴¹⁾.

20 (10).

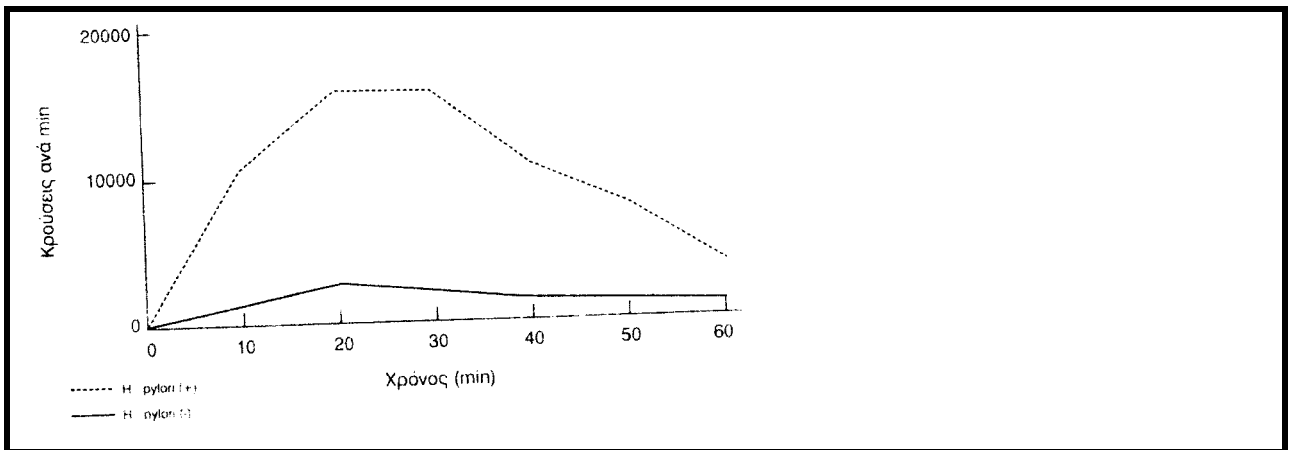
(90-100%) (89-100%).

spectroscopy) ¹⁴C ¹³C (mass
 (2-5 Ci)^(82;85;86).



9.

¹⁴CO₂



10.

¹⁴CO₂

3. _____

/ , (87-90)

20

DNA ⁽⁹¹⁾.

Associated Lymphoid Tissue-lymphoma)

MALT-

(Mucosa-
(92-95)

•

•

•

•

« »

:

•

BabA2 SabA

⁽⁹⁶⁾,

•

cag

IV ⁽⁹⁷⁾

•

cagA vacA

(54)

(BabA2, SabA)

,

Lewis b⁽⁹⁸⁾

Lewis x

Lewis a,

(99-101)

Lewis x

SabA,

BabA

Lewis b⁽¹⁰²⁾

Lewis b

Lewis b

BabA2

BabA,

(103)

IV (

cag)

cag

31

IV

,

cagA (

cag)

(104)

cagA,

cag

Nod

NF-kB

8 (IL-8)^(105;106)

cag

(90;107)

Hp-NAP (H.pylori-Neutrophile Activating Protein)

(108;109)

cagA vacA

cagA

vacA

(97)

cagA

vacA

in vitro

(104)

in vitro

«

» (hummingbird phenotype)

cagA (110-113)

cagA

(114)

cagA

Src

()

P

(

-

-

-

-

) (115-118)

P

-

, P

-

EPIYA-C (119-121)

(95%)

cagA-

3-4

EPIY

-

cagA

,

ABC

ABCC.

,

3-5%

EPIYA-C

1-4

cagA

(122-125)

EPIYA-C

Pasteur

135

3

EPIYA-C

(117;122;123)

EPIYA-C

cagA

EPIYA cagA

cagA

cagA

ZO-1 (epithelial tight-junction scaffolding protein) JAM (junctional adhesion molecule)

(126-131)

vacA,

50%

(vacuoles).

vacA

(m

region)

s (s region)

m1, m2

s1, s2

(132-138)

s1m1,

s1m2

s2m2,

s2m1

«

»

cagA,

vacA

s1m1,

cagA

vacA (s2m2

)⁽¹³²⁻¹⁴³⁾

vacA

()

()

vacA

p38/ATF-2

C

-9, -3, -6 -7⁽¹⁴⁴⁻¹⁴⁹⁾. , vacA

(150-152)

NFAT,

-2⁽¹⁵³⁻¹⁵⁵⁾.

vacA,

-a (Tumor Necrosis Factor-a,

TNF-a)

-6

-2 (Cyclooxygenase-2)^(156;157).

(11).

BabA

(158-161)

÷

∅

cagA

-8

(162-165)

cagA

vacA

vacA

C,

-a^(166;166;167).

12

(168-171)

vacA

cagA

vacA

cagA

vacA

(172-174)

.

(175)

,

(176-178)

,

«

»

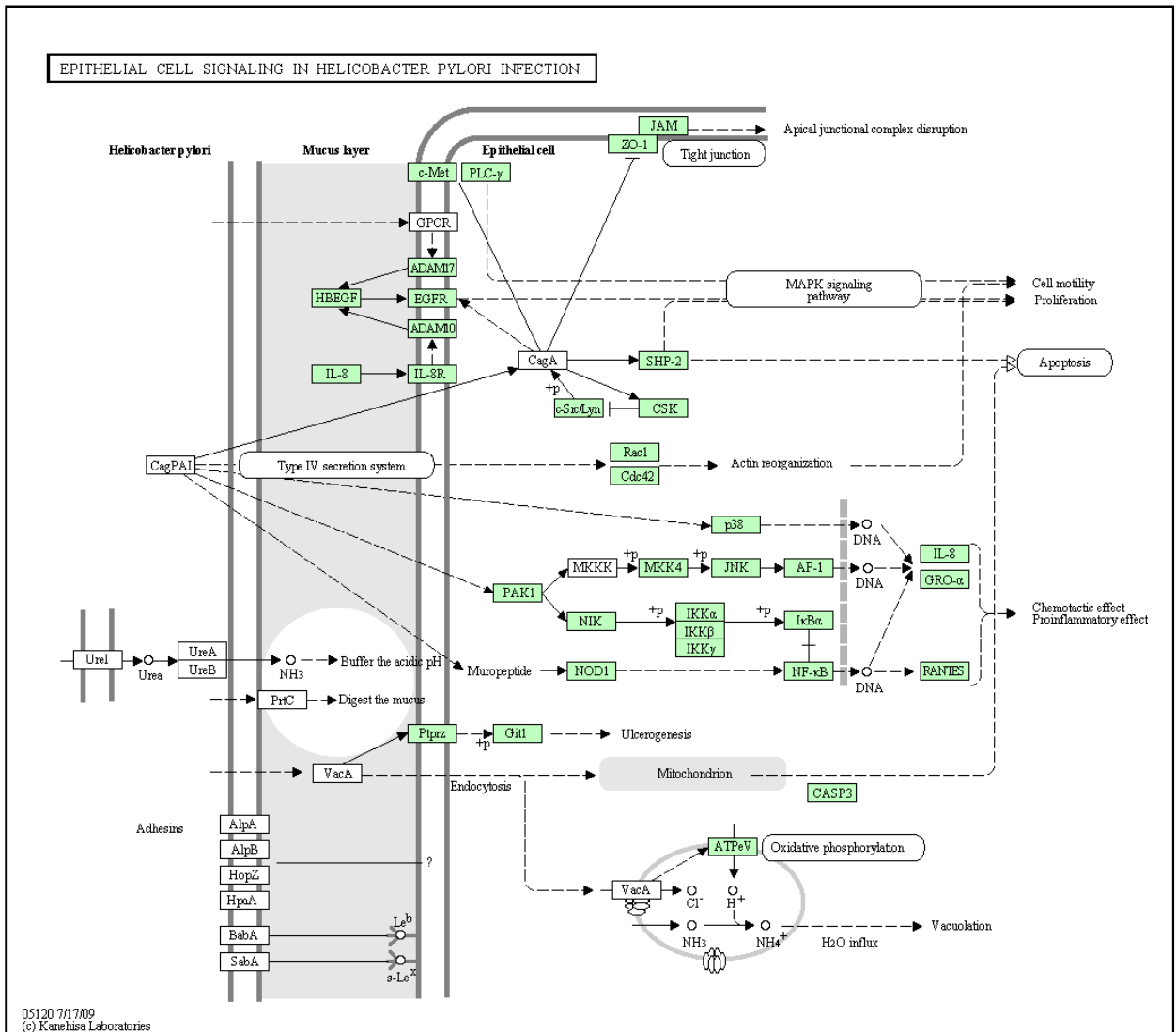
,

,

.

,

.



11.

(

Nature

Reviews in Microbiology 2004;2:747-765)

cag vac

cag vac
(PCR),

A

DNA

(primers)

cagA vacA

PCR

(179-184)

Western blot

Elisa

cagA

vacA^(185;186)

(Western blot

Immunoblotting,

12)

(-IgG)

(. . .)

Elisa

cagA

IgG

(. . .).

(187-190)

cagA

vacA

cag

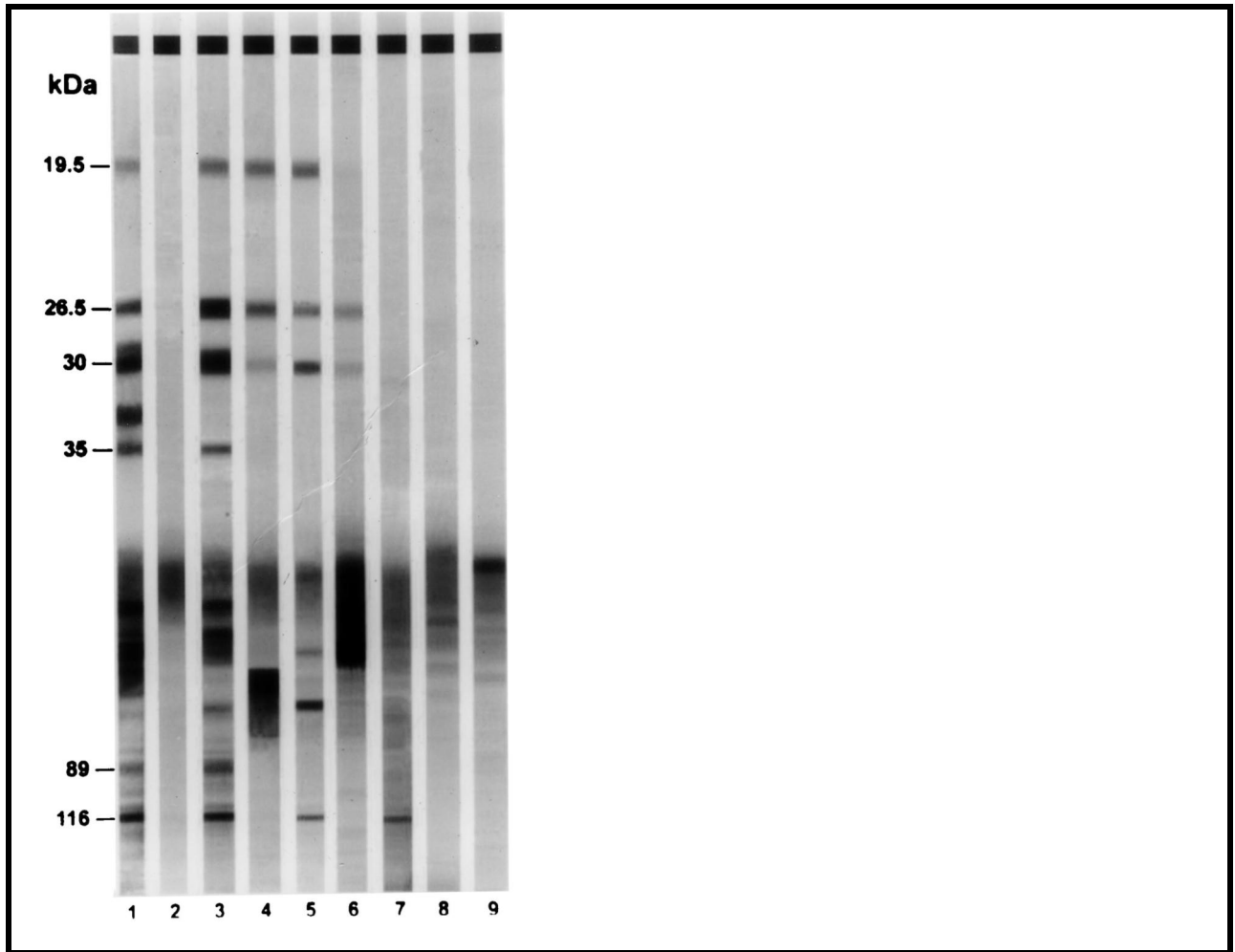
cag

(187-191)

()

<http://www.tigr.org>

DNA



12.

cagA

(immunoblotting).

control, 1 control, 2
control, 3 12 , 4-7
8-9 ()
Pasteur, ø Dr.)

.
 .
 , /
 ,
 (192-195)
 1.7
 1550 ,
 ,
 .
 ()
 ,
 .
 ()
 (196-202),
 MHC II
 (202).
 cag-PAI cagA.
 (203-207)
 1 , 2, 6 8
 -a P78 (Epithelial Neutrophil Activating Peptide 78)
 (208-214). 8,
 ,
 cag-PAI 8 cag- ,
 NF-
 AP-1 (163;215-218).

$^{+}/K^{+}ATP$

(+)

(219-224)

(T helper Th)

CD4

: 1) Th1
(168;208;225;226)

2) Th2

1

4, 5
Th1

10 (227-230)

(231;232)

(233-236)

(237;238)

pH-

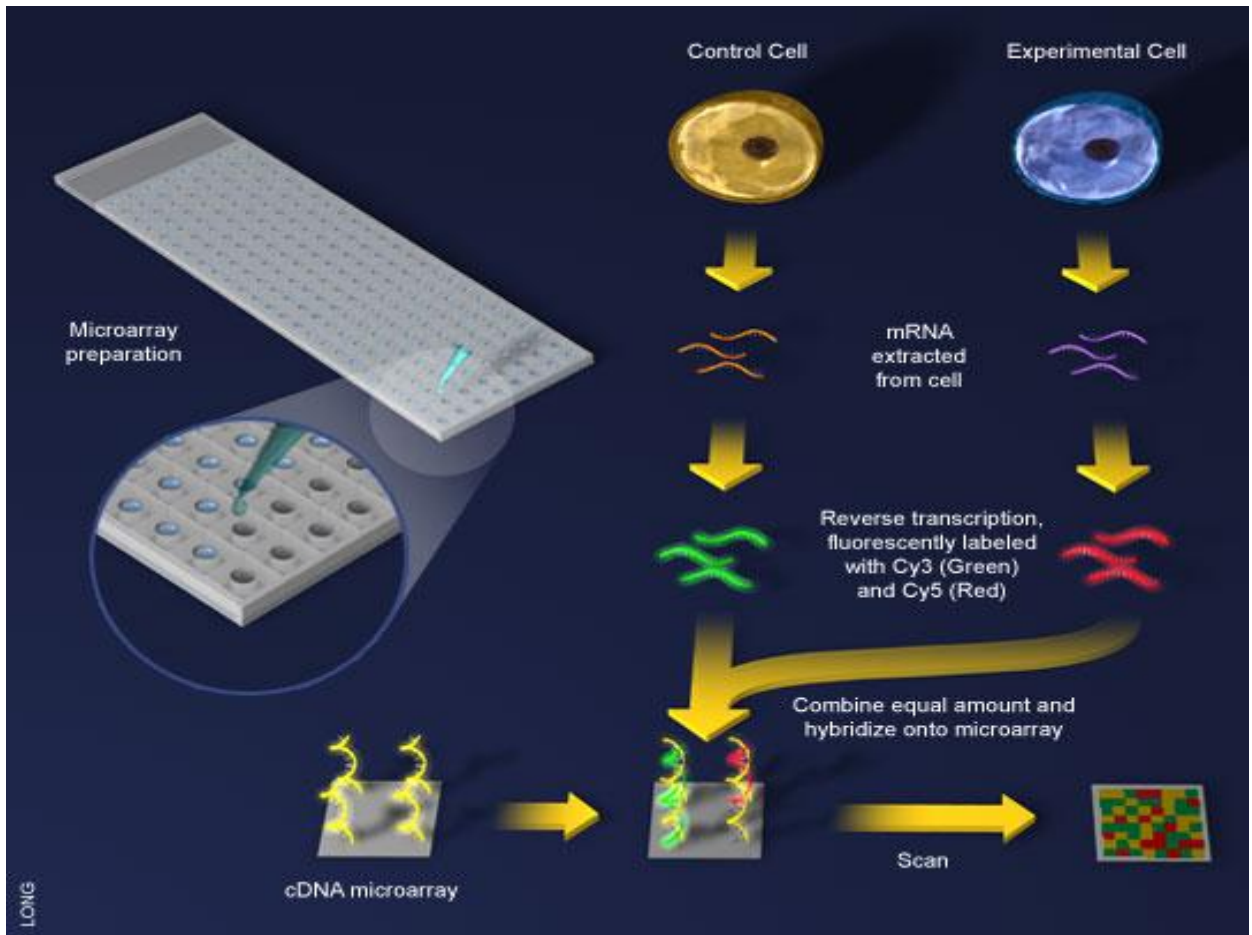
4. _____

microarrays, **13).** DNA DNA (DNA DNA
) (239;240).

PCR DNA *in situ*
 (> 280.000 /) (241-243).

- mRNA
- DNA
-

- mRNA, cDNA
- DNA
- DNA cDNAs.



13. DNA

(),

(),

DNA

1997 1999 (244;245) j99 26695,
 , 2/3 1590
 6%

:

stress,

1590

pH

pH

pH.

DNA 1534 «open reading frames» (ORFs)

26695 (243;246-251)

(39

, 80

11

),

6 (252;253)

j99

6

DNA

j99 26695

DNA

«

(constant genetic flux)»

DNA ()

ó

« »

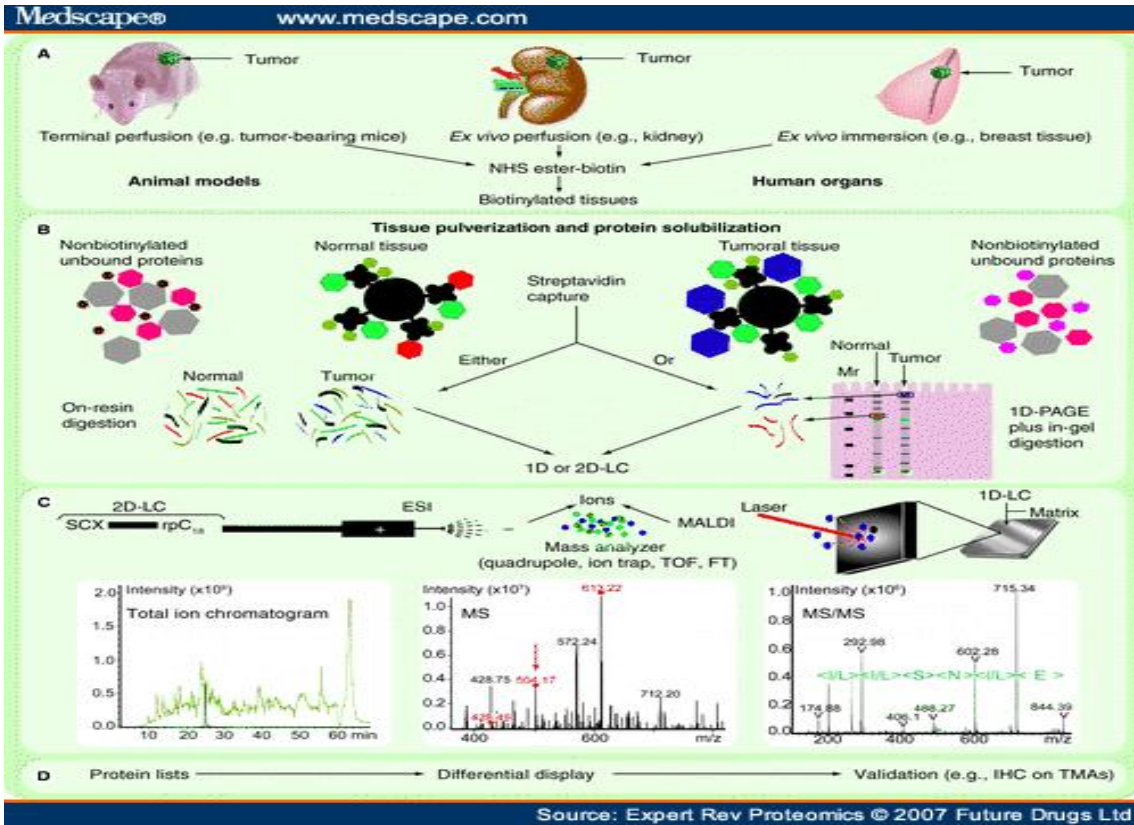
1995 ^(246;254;255)
dimension)

2-D (two

femtomole.

3-D (-three dimensional)

(14).



14. (Exper.Rev.Proteomics 2007)

To

(248;256;257)

1200 (interactions)

46,6%

•

2/3

1500

•

•

•

2-D (-two dimensional)

(254;258)

(2-DE)

(259;260)

5.

(PCR).

(261-263)

Brucella broth + 20% glycerol, cysteine,
Albimi broth + 20% glycerol, Stuart transport medium, Portagerm pylori medium . .

-20°C -70°C.

Brain heart infusion agar

Brucella

agar

7%
10 mg/lit,

,
B 10 mg/lit

5 mg/lit.

(N₂ 80-90%, CO₂ 5-10%, O₂ 5-10%) 5-7

:

• (, , 1-2 mm,
,)

• Gram (Gram
) ,

• (, ,
)

100%. 70-98%,

(PCR)

1997

(264)

DNA

PCR

(265)

PCR

(73%) (266;267) PCR

PCR

1997

(268;269)

88-100%

83-100%

(98%)

IgG,

(ELISA)

86-100%

76-98%

IgG

(4-10min) ELISA

ELISA

IgG

IgG

>25%

4-6

IgG

-cagA

cagA

IgA

39-82%.

IgG

÷ ∅

()

,

.

,

,

.

,

,

.

,

in vitro

,

,

,

(291;292)

,

(293;294)

:

•

•

.

,

.

(-MIC),

(295-297)

,

(Kirby-Bauer[®]) E-test[®] (Cambridge Diagnostics Services, Cambridge, UK) ⁽²⁹⁸⁻³⁰⁰⁾ *in vitro*

(E-test[®]),

E-test[®]

E-test[®],

E-test[®]

4

(301;302)

5,

(283;286)

	(%)	
E-test [®]	28 (31.1)	4 (4.4)
	9 (10)	0

4.

(=90)

	(g/ml)	(%)
	<1	0,8
	<2	9,9
	<8	33,1

5.

1991 (6)

			MTZ	CLA	AMO
	1991	70	MIC ₅₀ =2	-	-
			MIC ₉₀ =32		
Cluczynski	1991	50	49%	-	-
ACT-10	1997	35	54%		
	1998	43	46%	2.3%	-
	2000	66	47	10%	1.5%
	1994	16	75%	-	-
	2002			48%	-

6.

45-50%, 75%.

OMC, 75%,
(303-306).

1998
10%,
48%.

OAC, 50%,
1,5% (307-309).

(7),
(.. , 2002)

E-test[®],
(287).

(287;310;311)

(futile cycling) ^(312;313)

∅ (loss of function

mutations)

RdxA

FrxA

^(314;315)

(128mg/L)

RdxA

FrxA

				CLA	AMO
1997	12	20%		8,3%	-
1998	21	24%		4,8%	-
2000	36	28%		5,5%	27%
2002	28	12(42%)		4 (14,6)	1 (3,5%)

7.

(

1997-2002)

RdxA

RdxA

32-

64mg/L)

(8mg/L)

FrxA

RdxA ^(314;316;317)

(273)

V

23S rRNA

A2143G (44.1%), A2142G (32.6%) A2142C (3.8%),
A2142G

(318-320)

-4,

7. _____

RFLP (Restriction Fragment Length Polymorphism), RT-PCR (Real Time-PCR), FISH (Fluorescence *in situ* Hybridization), PCR-line probe assay, 3ø mismatched reverse primer PCR Double Gradient-Denaturing Electrophoresis (DGDE).

(agar dilution),	(disk dilution)	E-test [®] (321).
	9.86\$ (
)	controls,	13,98\$ (ClariRes [®] kit
Ingenetix		650\$ 50
	controls),	24 (ø
),
	8,66\$	2-2 ½
	E-test [®]	6,90\$

8. _____

K

(PPis)

(322)

(323)

,
 20%.
 (90%),
 70%.⁽³²⁴⁾
 (5 , 5
),
 ()⁽³²⁵⁾.
 2 (),
 . (, ,
) ,
 2 , ,⁽³²⁶⁾
 70% , ,
 .
 ,
 ,
 ,
 (. .
 ,
). ,
 (. . ,
)
 , ,
 .
 100%
 .
 (327),
 , Ø
 (328).

(328)

(329)

9.

DNA

() 8-31% ⁽³³⁰⁾

() 10

76,2% ,
)

(

92%

(331)

(

)

(17%),

()

(332)

(100%)

33% ⁽³³³⁾

.pylori DNA (). -S,

(334)

()

in vitro (335)

450 mg

32,1%

41,6%

(336) (

2

3

).

Gram

(337)

10. _____

- . :
 - Lactobacillus spp
 (), (338)

- ,
) , FDA

,
 () ()
), (339)

3 , ()
 () (340)

6). 7 (

. (99%)
 91% (328)

11.

6

6

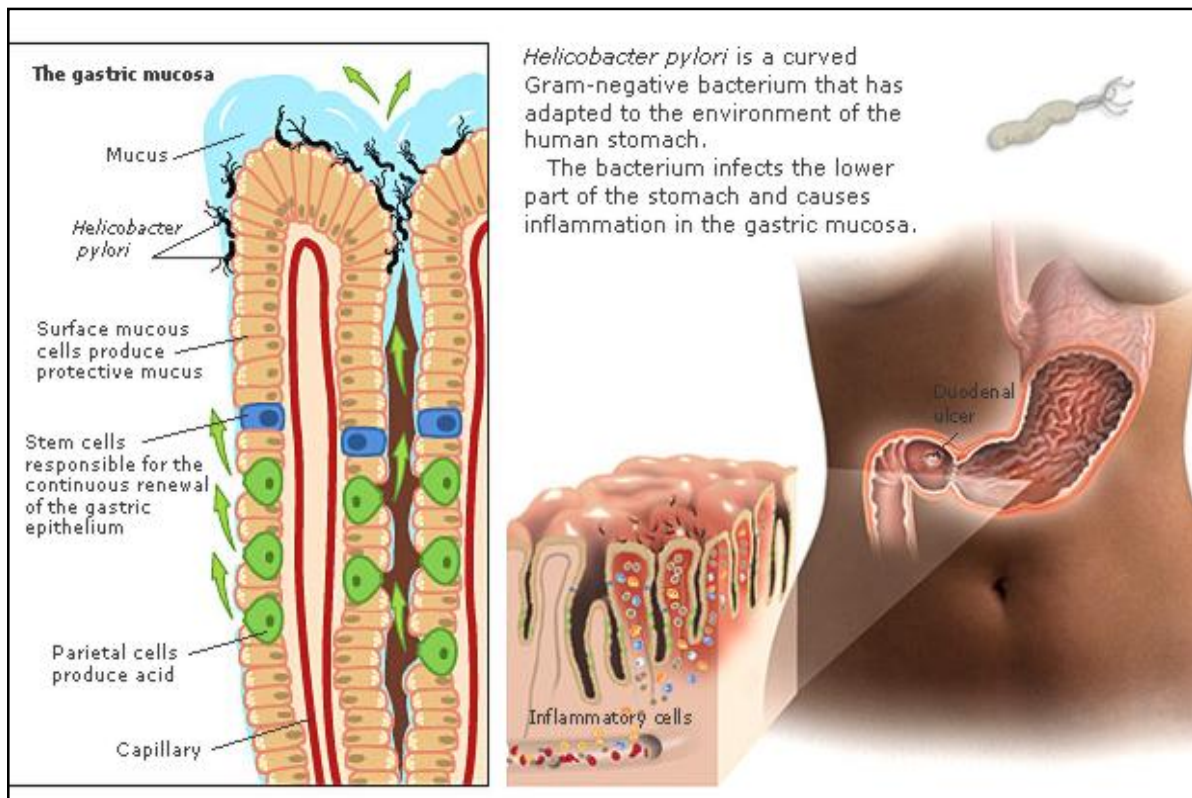
Sydney

(15).

(341)

(342;343)

(344)



15.

To

(345;346)

(347-350)

vacA,

(351)

(352;353)

(mast cells)

(354;355)

-8 (IL-8),

-a (Tumor Necrosis Factor-a)

-1 (L-1)

(356;357)

(

),

(

)

(358;359)

(360;361)

(362;363)

(332).

TNF-a IL-1

(330)

IgM

(364;365)

IgA

(366-368)

- (Th) :

- Th1 , CD8+ T

, ,

- Th2 ,
(369;369-371)

, Th1 ,

Th1 Th2

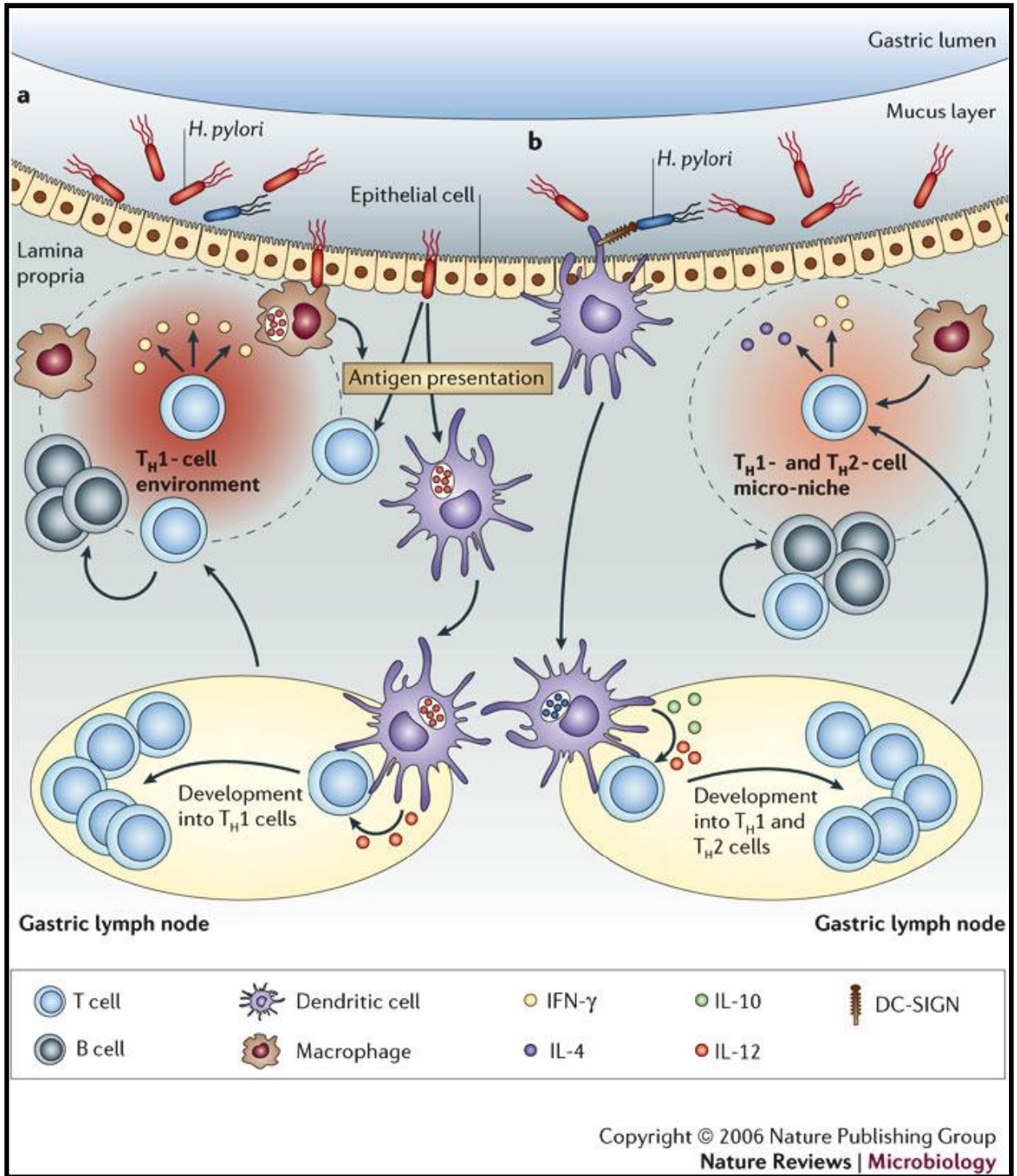
(372) ,

(16).

cagA+ vacA+

(373-375) . ∅ ,

(376) .



16.

(MHC)

II

T

1 (Th1)

2 (Th2).

« »

(DCs),

(Nature Reviews, 2006)

. 1990 Sydney ,
,

(377)

(1994) Houston Texas,

Sydney ⁽³⁷⁸⁾.

(. .

).

, (2)

(2 3

) (2)

(8

),

(358;379;380)

Giemsa,
Steiner/Hematoxylin-eosin/Alcian blue,
blue/Hematoxylin- osin

(Warthin Starry, Steiner .),
Carbon fuchsin/Alcian
(381-383)

(

/

)

Sydney

: 1)

, 2)

, 3)

, 4)

, 5)

(**8**).

6) : 1) , 2)
 , 3) , 4) , 5) ,
 7) .

(1) 1/3
 3,
 2/3

2
 2). ()

1/3 2/3.

CD4+ CD8+

(384;385).

>5/100

(grades):

- 1,
 - 2,
 - 3, 25%
 - 4 25-50%,
 - 5 >50% ,
 - 6
- 1 2 , 3 4 5 6

()
,

(**Intestinal Metaplasia-IM**)

(386)

1/3, 1/3-2/3 >2/3

1,

2

3,

4,

5

>50%

6,

()

(386-389)

(390)

AB/PAS HID/AB :

• (,):

Paneth.

• ():

Paneth.

(,):

Paneth

EM

		, ()
		<1/3 / = 1/3-2/3= , >2/3=
	/	,
		<1/3 = 1/3-2/3 = , >2/3 =
		<1/3 = , = >2/3 =

8:

ó

Sydney,

Houston ⁽³⁵⁴⁾.

12. _____

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:

()

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100%.

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,

,

.

13. _____

(391-393)

(1-2%)⁽³⁹⁴⁻³⁹⁶⁾

(397-399)

()

(400-402)

> 95%

(403;404)

14. _____

(379;405;406)

(antral-predominant chronic gastritis).

-PPis)

(. .

(407-409)

cagA+

cagA

cagA-

(410)

(411-414) TNF-a

G

(415)

(

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,

(corpus-predominant)

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s1 m1

vacA

cagA⁽⁴¹⁶⁻⁴¹⁸⁾.

,

-

,

(419-421).

,

-

(422;423)

15. _____

50%

(424)

(425)

(reservoir-

). A

(426)

H

(. , .)

(427-429)

(80%-90%)

(17).

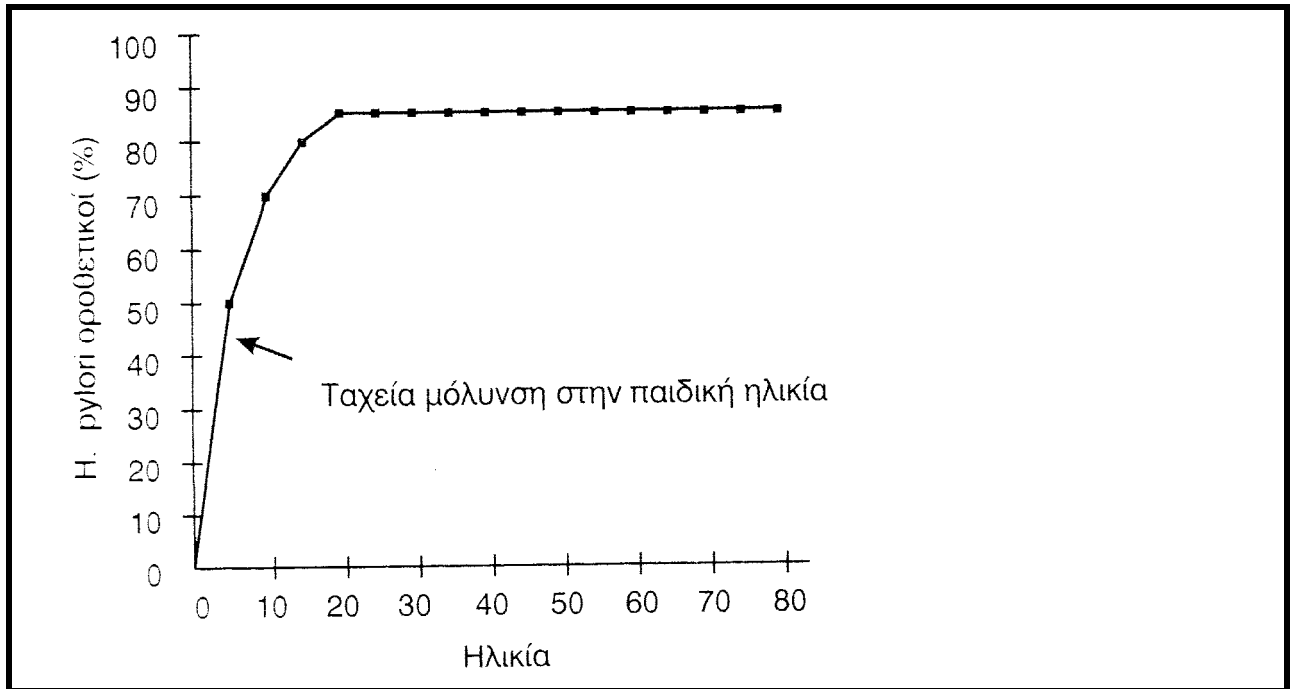
(, ,)

)

50%-60%

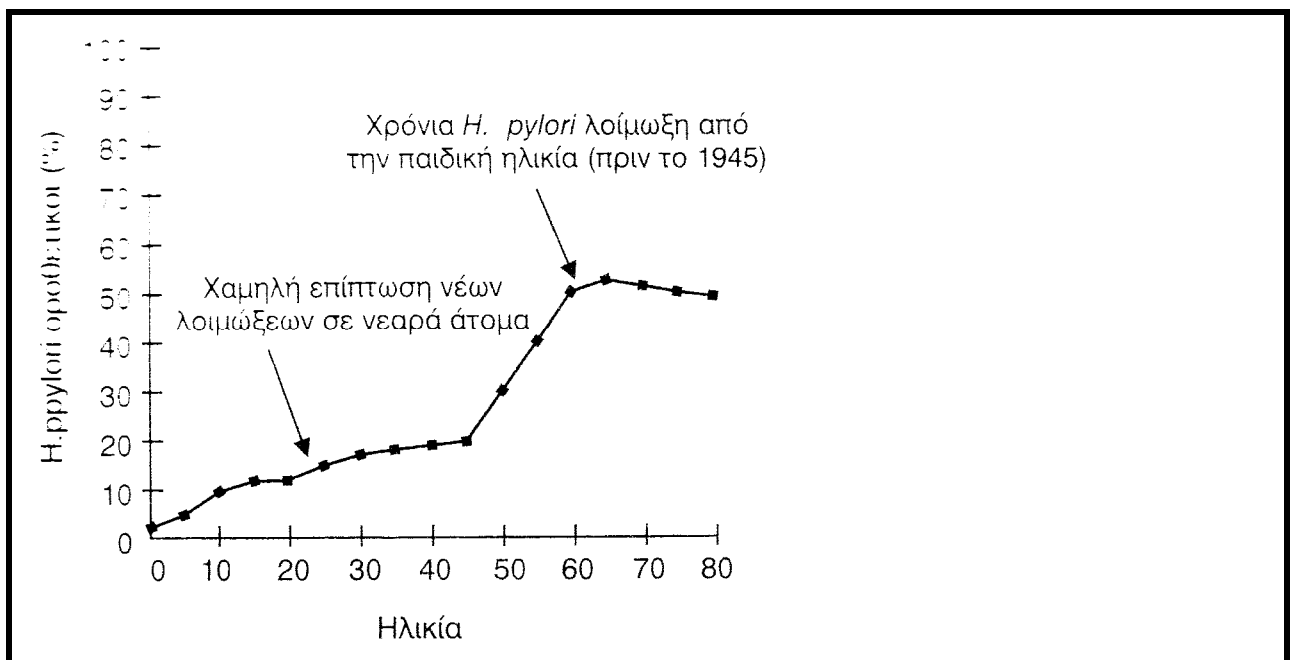
50 (18) (427;428;430;431)

20%, 50% 80% (19).



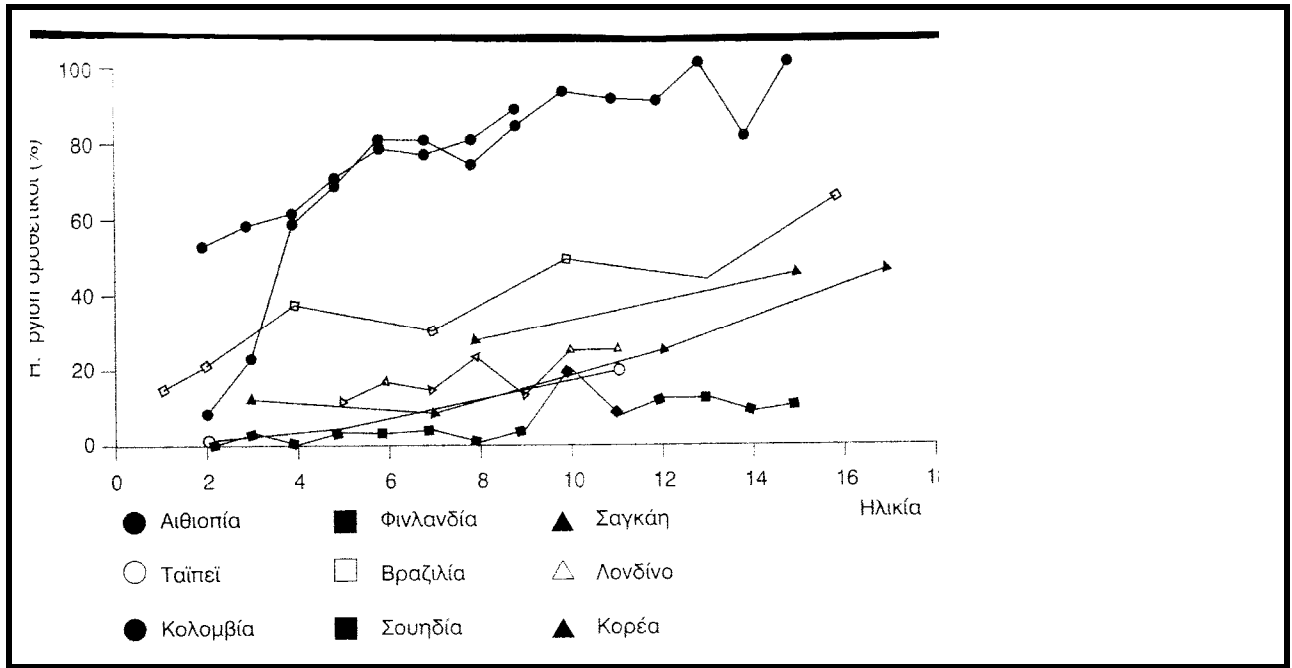
17.

vs.



18.

vs.



19.

, ()
 :
 • () (1,9%-2,7%)
) ∅ (0,3%-0,5%))
 •
 • (3/) (.
) ,
 • (birth cohort effect)
 ,
 (generation or cohort phenomenon).

, ,

15 ,
(21% 10%, p=0.01) ^(432;433) .
(
) ,

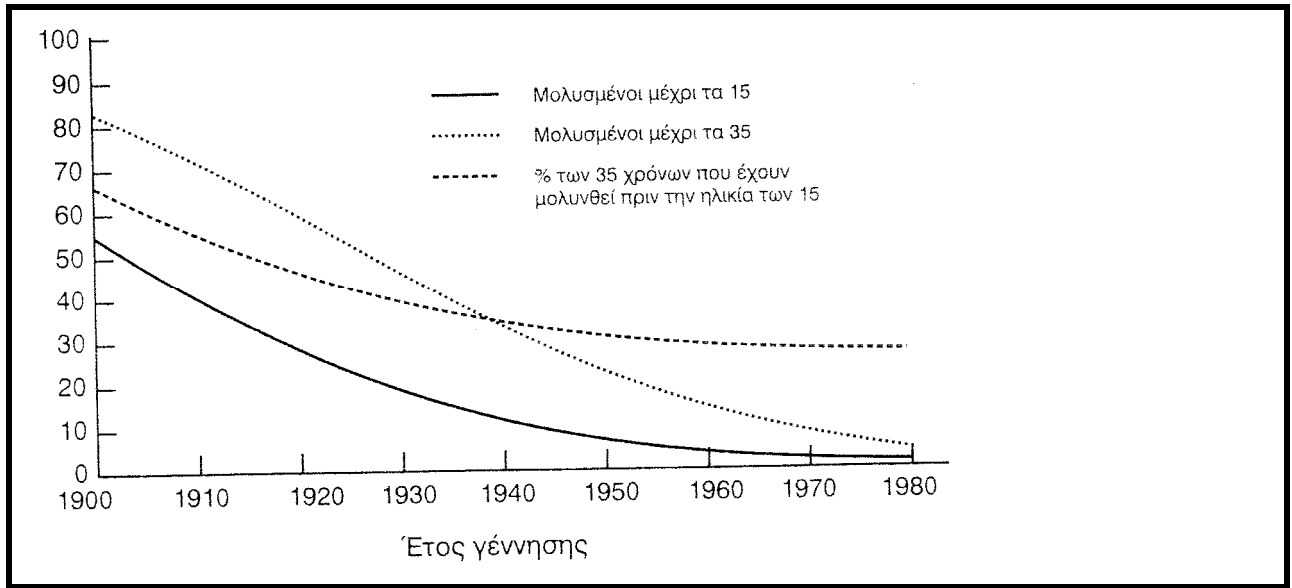
(20).

^(434;435) .

(
(0,5%-3,2%))
(3,7%-4,2%),
> 80%
6-12 ⁽⁴³⁶⁻⁴³⁹⁾ Rowland .
1-16 10,9%
2 , 16,33
5 ,
(1,95%) ⁽⁴⁴⁰⁻⁴⁴²⁾ .

(susceptibility)

(,).



20.

()

16. _____

∅

(human pathogens)

(zoonotic pathogens)

∅

(443;444)

West

pH (3-10)

2

(445;446)

(buffering capacity)

pH,

(445;446)

(447-449)

, Klein

(450)

()

12

(33%

5%

).

(60%)

, Hopkins

(451)

(odds ratio=3.25,95%,

(97%

CI:1.94-5.71).

5)

(38%)

ø

2

C-UBT

48%

17%

(452;453)

1

DNA

PCR
 (,) (454-457). , DNA
 Shahamat . ,
 DNA [³] ,
 4° C,
 4 10⁸ 0
 CFU/ml 20 25 . [³]
 (458).

(459-462)

(. .),

PCR

(463;464)

(person to person) (346;465).

(close contact).

(. .

, ,)

(466;467)

, , , , ,

(sanitation)

(overgrowing) (468;469)

, , .

) (

) (470-473)

(73,6%)

(82%)

(24,2%

14%

).

(470;471;474;475)

(471)

Mitchell

(476;477)

Malaty

(478;479)

Perez-Perez

(478-480)

Parente .

∅

(

)

71%

58%, p<0.05) ⁽⁴⁷⁸⁻⁴⁸¹⁾.

DNA

(fingerprinting) ⁽⁴⁸²⁻⁴⁸⁵⁾.

RNA ()

8

(44.4%)

10 (55.6%) ⁽⁴⁸⁴⁻⁴⁸⁷⁾.

RFLPóPCR

50%

(+)

27,6%

72,4%

⁽⁴⁸⁸⁾.

Nwokolo .

^(488;489) .

:

•

•

•

,

.

,

.

,

(+)

(490-492)

(469)

(+)

,

,

(492;493)

()

o

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).

•

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.

(route)

:

-

(feco-oral),

-

(oro-oral)

-

(gastro-oral).

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-

:

,

,

(. .

)

(494-496)

.

,

(497)

.

(9).

(453) Kelly (498)
 12 (25) (+)

:)

,)
)

(transit time)

()

(0%-90%)

, DNA , PCR

(9).

	(+)	/ / (%)	PCR (%)	(primers)
**23	9/23	(41,7%)	-	-
1	1/1			
25	12/25	(48%)	3/8 (37,5%)	Urease A cag A
8	0/8	(0%)	-	-
****22	0/44	(0%)	-	-
15	1/15	(6.7%)	1/15 (6.7%)	16SrRNA
31	-		28/31 (90%)	16SrRNA
24	-		0/24 (0%)	16SrRNA
61	-		15/61 (25%)	0.86KbDNA
79	-		1/79 (1.3%)	Urease A

9. (/) PCR

: (+) , ** 1 . ***

(12 40mg x1)

PCR

(inhibitors)

(499-501)

(502-506)

(. . . , *E.coli*)

(346)

Barrett,

(507;508)

« »

PCR

(**10-11**)⁽⁵⁰⁹⁻⁵¹¹⁾

(512-515)

, *in situ*

(CMV),

(516)

PCR,

(517)

,
÷

∅

(. .

)

(518-520)

PCR

(, , , ,)

(521;522)

PCR (523;524)

(525;526)

Epstein-Barr

(527;528)

(529-531)

	(+)	PCR (%)	(Primers)
	/ / (%)		
16	1/16 (6.3%)	A	-
71	1/71 (1,4%)		.
	0/71 (0%)		
81	12/81 (14,8%)		.
	0/81 (0%)		
94	0/94 (0%)		. &
52	0/52 (0%)		. &
31	1/31 (3,2%)		.
21	0/21 (0%)		.
	1/21 (4,8%)		/
54	0/54 (0%)	39/54 (72,2%)	.
15	0/15 (0%)	0/15 (0%)	.
62	0/62 (0%)	1/62 (1/6%)	.
**15	2/15 (13.3%)	3/15 (20%)	. .
6	A	5/6 (83.3%)	.
25	A	7/25 (28%)	O .
29	A	8/29 (27.6%)	.
21	A	5/21 (2/21%)	. &
14		0/14 (0%)	.
68	A	56/68 (82/4%)	
56	A	33/56 (58/9%)	
27	A	9/27 (33.3%)	
103	A	25/103 (24.3%)	

10.)

(/) PCR

*

40	40/40 (100%)		.	-
170	12/170 (7,1%)		.	-
55	0/55 (0%)		.	-
19	0/19 (0%)	11/19 (57,9%)	.	Urease A
336	A	0/336 (0%)	.	Urease A
124	A	2/124 (1/6%)	.	Urease A
		12/124 (9/8%)	&	26KDa p

11.) (/) PCR

*

:

: , 26KDA p : 26KDa, 0.86 KbdNA : DNA, 0,86 Kbase,

* (+)

** / (+) : , , , ó PCR(+): , ,

- :

pHó

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-

. Ø

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-

-

,

,

.

Osler

(532;534)

(. .)

(535;536)

(33;537)

(538;539)

(432;540)

23S rRNA

A2142G, A2142C

A2143G

23S rRNA

Sydney (

Houston)

1. _____

75

25

50

_____ /

LIS (Laboratory Information System)

10% (buffered formalin)

2005-2010.

150 : 50

100

Leica, RM2255,

2 m :

-
- Giemsa ()
- High Iron Diamine (HID) /

5-10 m (RT-PCR,

(wild type)

() 13 12
 65 , () 26 24
 61 (39 36).

		%	%	%
(X2)	78 (39 2)	52.3	52.7	52.7
(X2)	72 (36 2)	47.0	47.3	100.0
	150	99.3	100.0	100.0

12.

ó

3-5

, ,
 (ø
 /).

		%	%	%
-	71	47.0	47.7	47.7
-	2	1.3	1.3	49.0
	48	31.8	32.2	81.2
-	4	2.6	2.7	83.9
-	3	2.0	2.0	85.9
	14	9.3	9.4	95.3
-	5	3.3	3.4	98.7
	2	1.3	1.3	100.0
	150	98.7	100.0	

13.

LIS

, (,
 ,)
 , ()
).
 / (PPis) / ,

-

Houston (1994), **31.** Sydney
 Sydney

()

(SPSS

Statistics Data Editor V.19),

(3-5 /).

Sydney

/

Giemsa.

0= , 1= , 2= 3= .

(0= , 1= , 2= , 3=).

0 , 1 <1/3

, 2=1/3-2/3 3>2/3 .

0= , 1= / ,

2= 3= ,

: 1= - , 2= - , 3= , 4= -

, 5= - , 6= , 7= - 8= .

Q-RT-PCR

(.17683 18000).

(1 5) ()

« » (missing

values) SPSS.

/			
1	74		-
1	74	«	-
2	41		-
2	43	«	-
3	81		-
3	82	«	-
4	67		-
4	67	«	-
5	71		-
5	74	«	-
6	45		A -
6	46	«	-
7	48		
7	49	«	
8	45		-
8	46	«	-
9	68		
9	68	«	
10	60		-
10	61	«	-
11	52		-
11	53	«	
12	78		
12	79	«	-
13	46		-
13	47	«	-
14	75		-
14	76	«	
15	71		-
15	72	«	
16	76		-
16	76	«	-
17	55		-
17	55	«	-
18	68		
18	68	«	
19	47		-
19	52	«	-
20	91		
20	91	«	
21	62		
21	62	«	
22	76		
22	78	«	
23	61		
23	61	«	-
24	69		-
24	71	«	-
25	74		
25	75	«	

14.

, ,

:

:

<i>l</i>			
1	65		
1	65	«	
2	49		
2	49	«	-
3	46		
3	51	«	-
4	62		
4	65	«	
5	55		
5	55	«	
6	53		
6	53	«	
7	68		
7	71	«	-
8	60		
8	61	«	-
9	66		-
9	67	«	
10	60		
10	63	«	
11	47		-
11	51	«	
12	60		-
12	65	«	-
13	82		
13	84	«	
14	56		-
14	61	«	
15	80		
15	82	«	
16	45		-
16	47	«	-
17	63		
17	64	«	-
18	36		
18	38	«	-
19	72		-
19	73	«	
20	57		-
20	60	«	
21	66		-
21	66	«	
22	59		
22	61	«	
23	69		-
23	71	«	
24	64		± -
24	65	«	-
25	79		
25	79	«	
26	28		-
26	28	«	-
27	60		
27	63	«	-
28	59		-

28	62	«	-
29	48		-
29	51	«	
30	54		-
30	55	«	-
31	50		
31	51	«	-
32	75		
32	76	«	-
33	65		-
33	67	«	
34	82		
34	84	«	-
35	58		-
35	60	«	-
36	64		-
36	65	«	-
37	73		-
37	80	«	
38	66		-
38	66	«	-
39	60		-
39	65	«	-
40	49		-
40	49	«	-
41	52		-
41	54	«	
42	52		-
42	54	«	
43	63		
43	67	«	-
44	56		-
44	57	«	-
45	64		-
45	67	«	
46	58		-
46	59	«	
47	65		-
47	65	«	
48	46		
48	46	«	-
49	52		-
49	52	«	-
50	61		-
50	64	«	-

15.

, ,

,

:

:

÷ **ø (biprobe)** **Real Time PCR**

(biprobe) ClariRes Assay[®] *in vitro* (IVD) ÷ ø⁽⁵⁴¹⁾

(**22**). ,
 (transition A-to-G)

2142 2143 - - (A-to-C) 2142
 23S rRNA. ÷ ø (biprobe)
 Cy5.

- , Cy5 ÷ ø
 SybrGreen I, .

(**23**). DNA

Nucleospin
 Tissue XS[®] (Extra Small)⁽⁵⁴²⁾ Macherey-Nagel, Duren, Germany.

H. pylori CCUG38771 wild type 23S rRNA *H. pylori* 825,
 683 677 2142C, A2142G A2143G 23S rRNA
⁽⁵⁴³⁾. 20 1 PCR

RT-PCR, 2 1 LightCycler FastStart DNA
 Master SYBR green I (Roche Molecular Biochemical, Mannheim, Germany), 2.4 1 4 mM
 MgCl₂, 12.1 1 , 0.5 1 *H. pylori* ClariRes[®] Assay solution (Ingenetix, Vienna,
 Austria), 1 1 (<1) control (Ingenetix, Vienna, Austria) 2
 1 0.075

23S-F (5øAGATGGGAGCTGTCTCAACCAG-3ø 2437-2458,
 GeneBank U27270, 0.25 23S-R (5øTCCTGCGCATGATATTTCCC-3ø),
 2573-2555, GeneBank U27270 0.2 mM
 23S-S (5øCy5-AAGACGGAAAGACCCCGT-biotin-3ø), 2507-2524,
 GeneBank U27270.

primers probes kit.
 (melting curves) (software) Roche LightCycler, version
 3.5.3 LightCycler 2.0 (21)



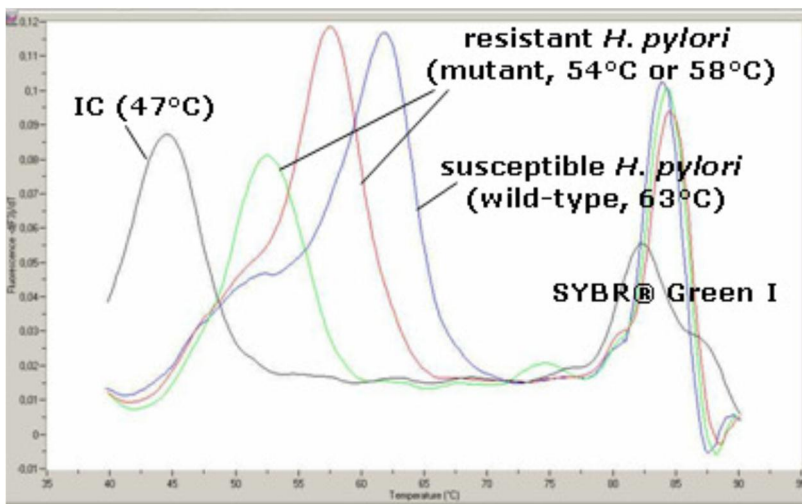
21. LightCycler[®] 2.0 Roche Real Time-PCR



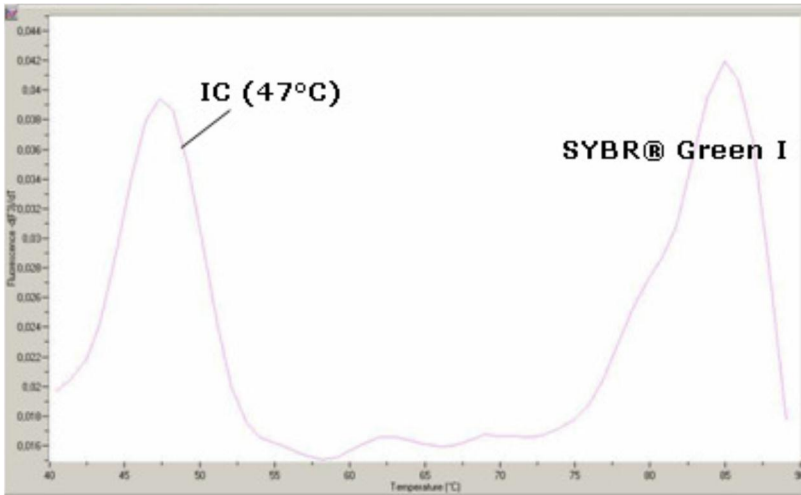
22. ClariRes[®] Assay kit Ingenetix, Austria,

/
 (denaturation) 95⁰C 10
 , 70
 20⁰C/
 65⁰ C 10 95⁰C 5 (annealing)
 (extention) 72⁰C 6 ,
 (melting point)

(product duplex) PCR : 95°C 5
 60 40°C,
 95°C, 0.2°C/
 40°C 10
 F1 Roche LightCycler®
 Cp.
 (software Roche LightCycler® version 3.5.3) F3.
 kit,
 23 24. Ingenetix, (specificity) kit
 100%
 (sensitivity) 82% ().



23.
 54-58°C, (wild type)
 63°C control (internal positive control), F1
 (Roche LightCycler®, software version 3.5.3)



24. control (internal positive control) 47°C
 F3 (Roche LightCycler[®], software version
 3.5.3)

Q-RT-PCR (quantitative RT-PCR)

()

LightCycler 2.0

10 1 1 1 Faststart DNA Cybergreen I (Roche Molecular Biochemicals),
 1.5mM MgCl₂, 0.5 mM primer (HP-FOR, 5'-TTATCGGTAAAGACACCAGAAA-3'
 HP-REV, 5'-ATCACAGCGCATGTCTTC-3) 5 1 (1-25 ng).
 10 95°C,
 (20°C/s), 40
 94°C 10 seconds (20°C/s), 54°C 5
 seconds (20°C/s), 72°C 8 seconds (20°C/s)
 77°C 5 seconds (20°C/s). 4°C 1 .

Cp (Crossing point)

(.

)

DNA

(**29**).

SPSS 19.0 Windows 7.0 (Statistical Package for Social Sciences,
Inc. Chicago, IL, USA)

- χ^2 : Fischer exact test
- t (t-test)

(p)
0,05 (p value <0.05)

. Post hoc

2. _____

**Real Time PCR/Q-Real Time PCR
RT-PCR/Q-RT-PCR**

(- 29). ,

/ . ,

(28, , 1).

(),

25 26

52-54⁰C A2142G A2143G,

61-63⁰C (melting point

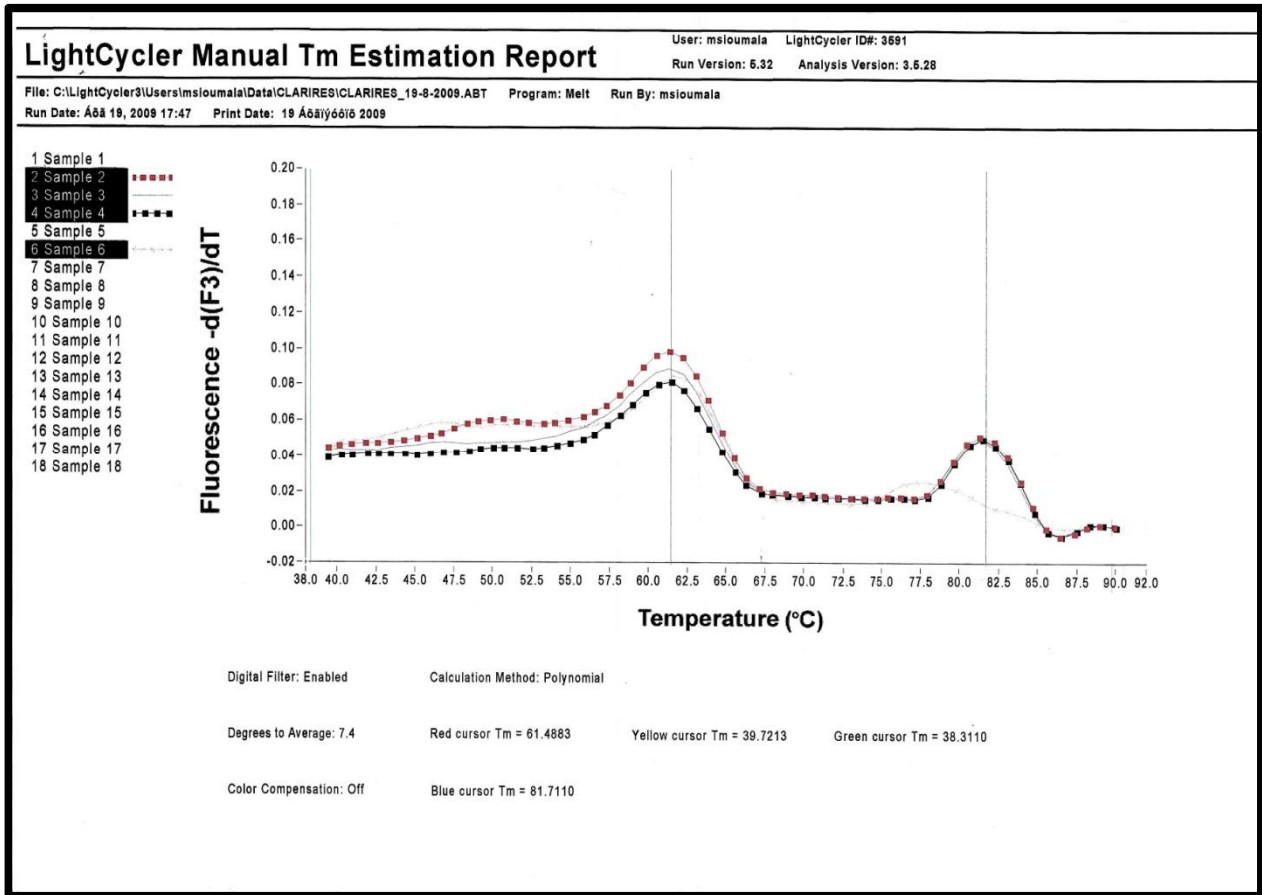
), 23.

47⁰C control (24).

()

, ø

1/10.



25.

14,

16, 17,

18.

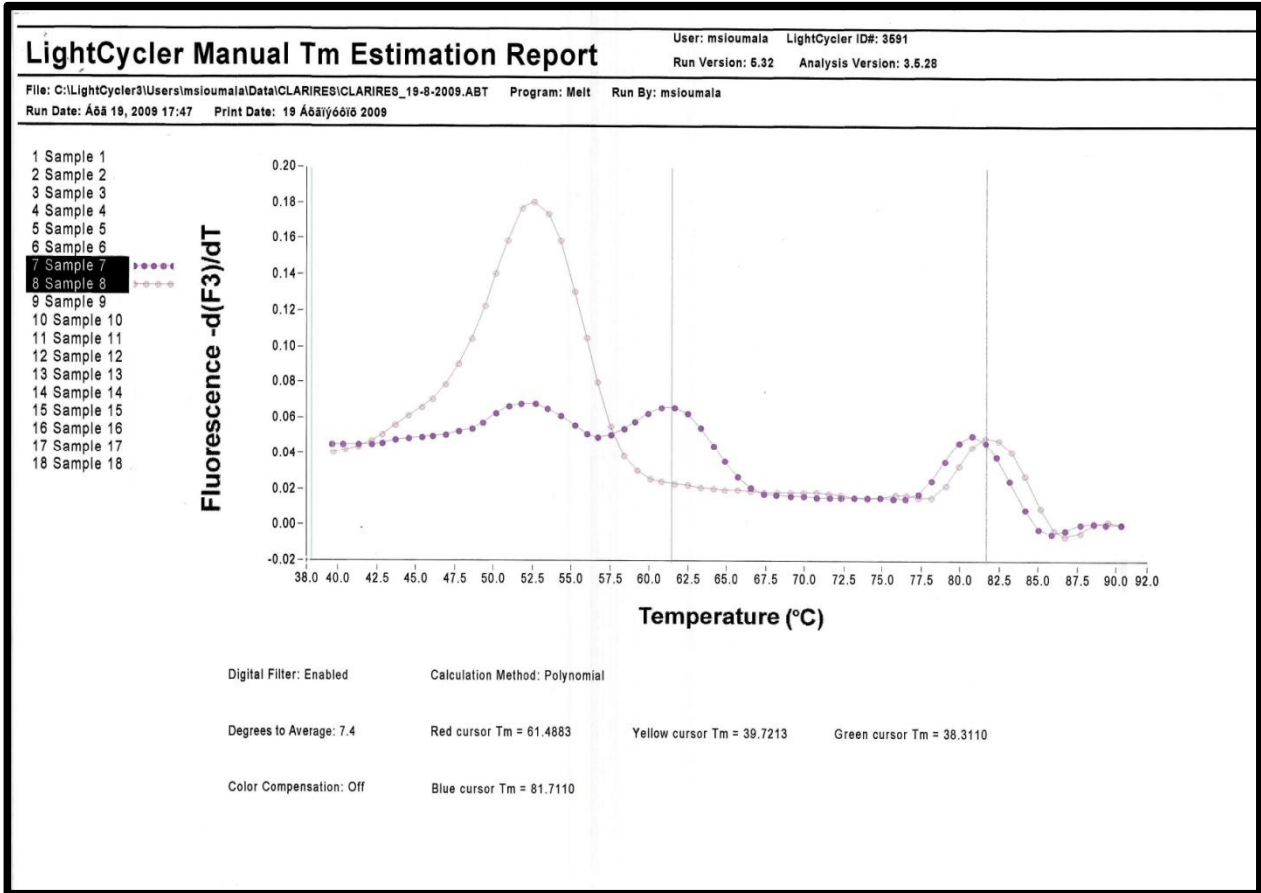
(wild type)

, Melting point

61°C (

Roche LightCycler®,

software version 3.5.3)



26.

14,

24

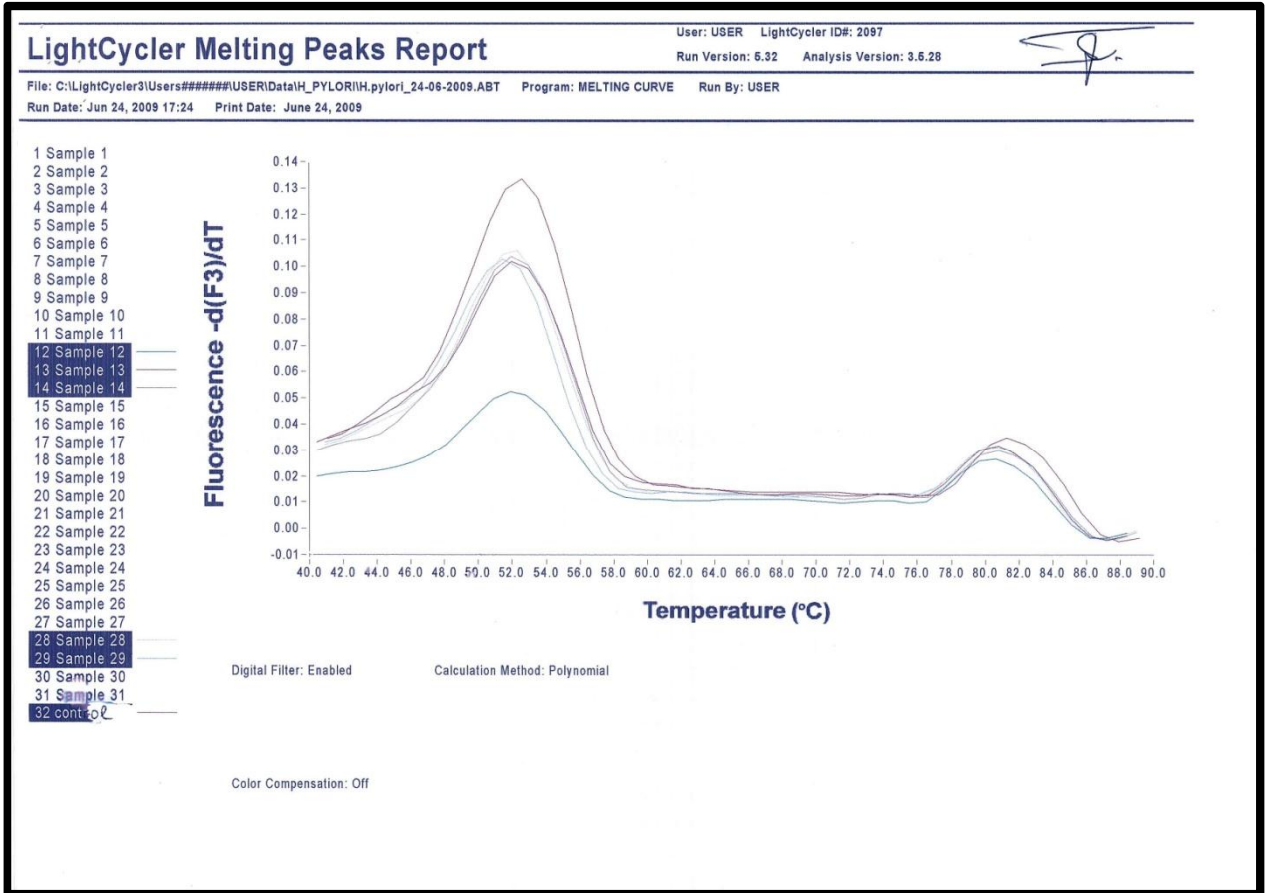
24 .

. Melting point 52,5° C

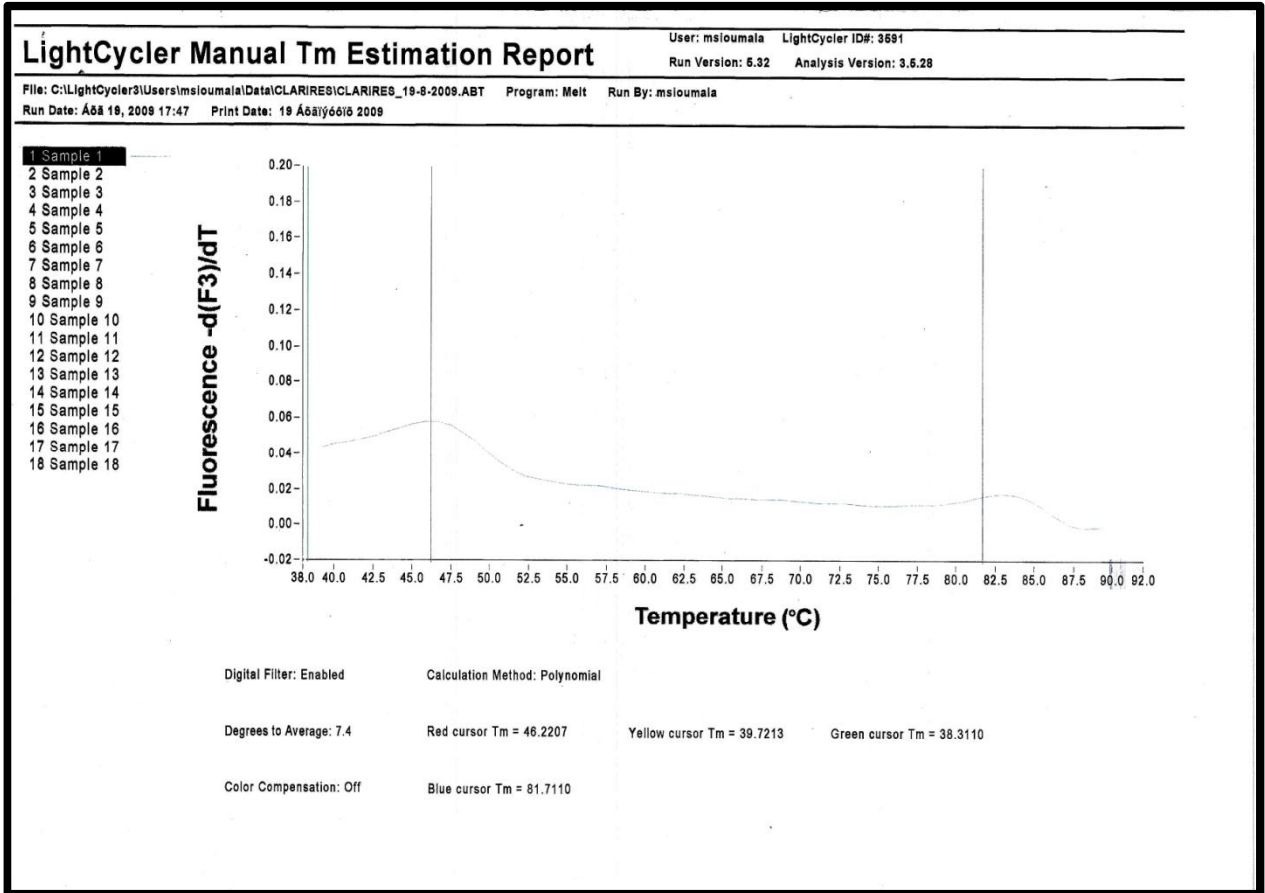
61° C

. (Roche LightCycler®,

software version 3.5.3)



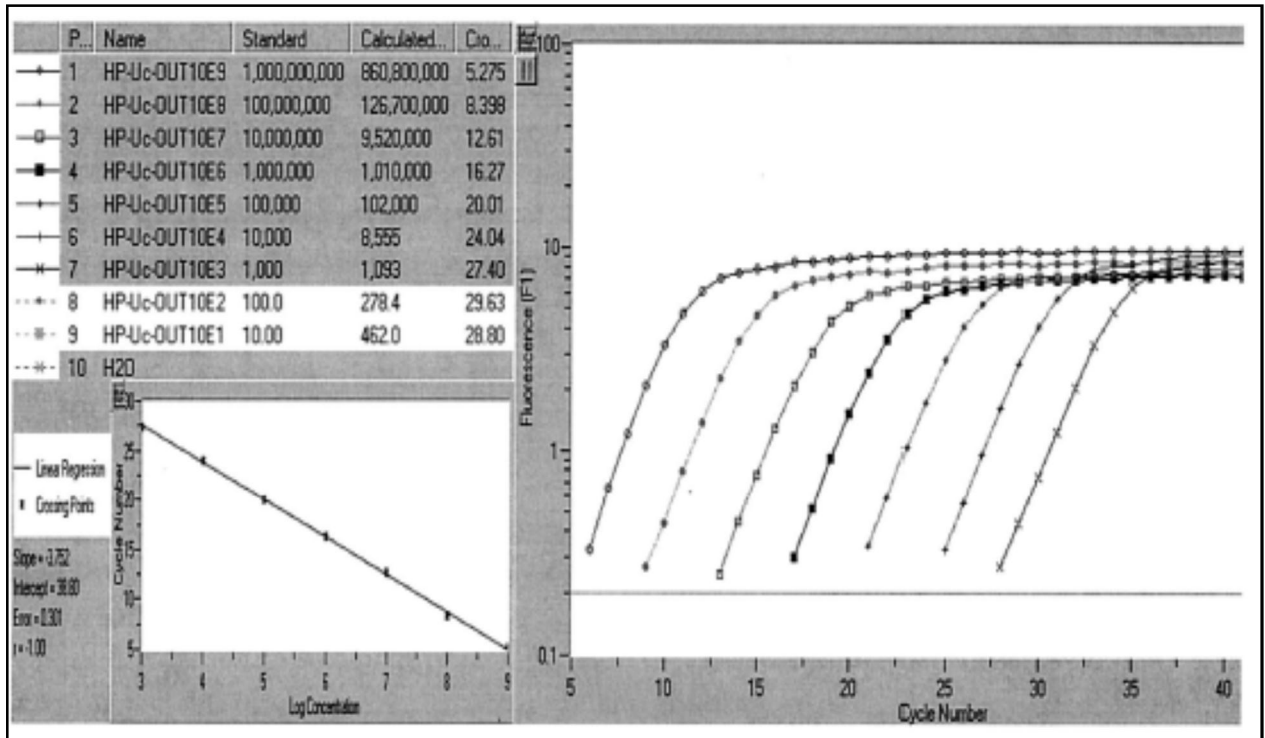
27. 14, 15 21.
 2142G - 2143G, melting point 52-
 54° C. (Roche LightCycler®, software version 3.5.3)



28.

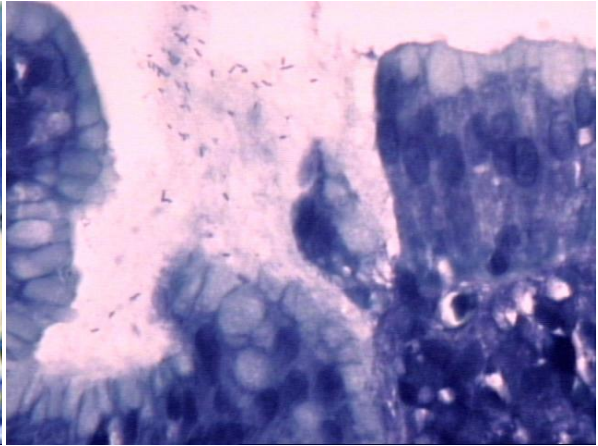
14,

1 .



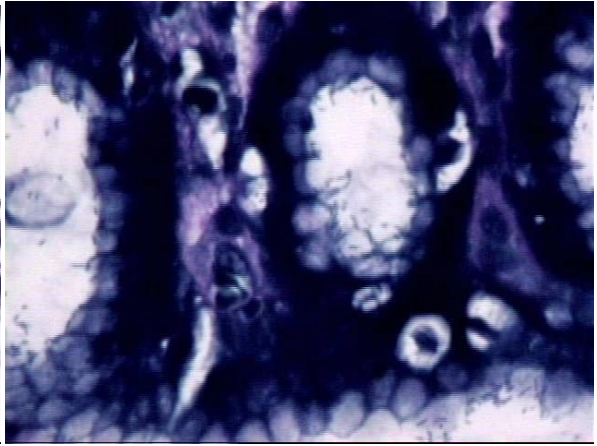
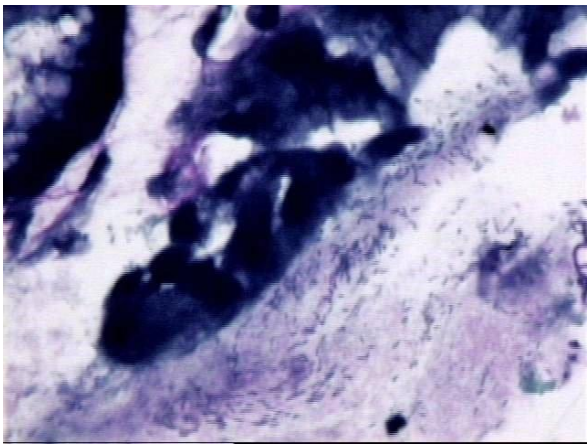
29.

) Quantitative Real Time PCR



30.

(Sydney 1,1,1,0, 1), GiemsaX100

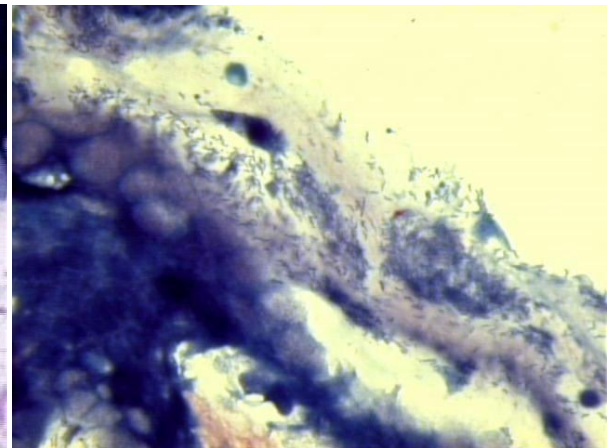
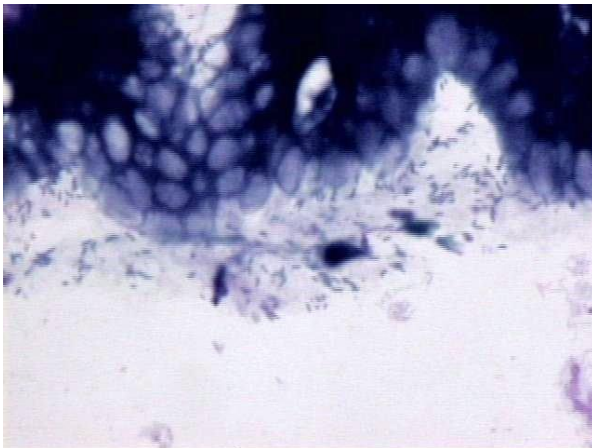


31.

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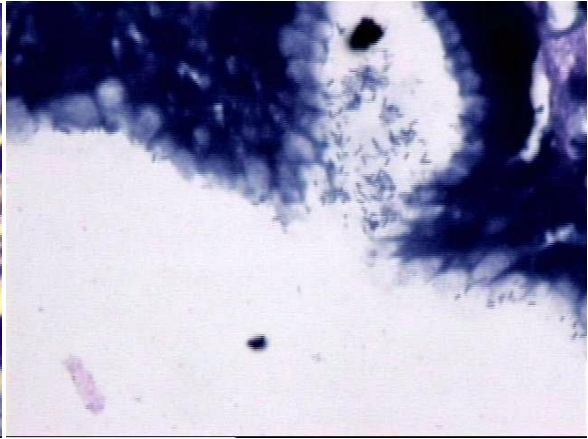
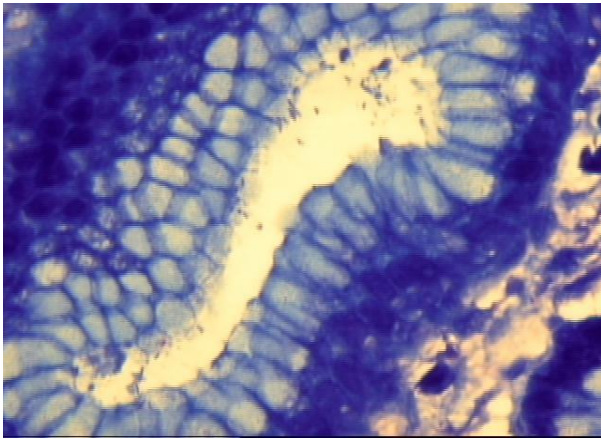
(Sydney 2,1,1,0,2-3), GiemsaX100



32.

GiemsaX100

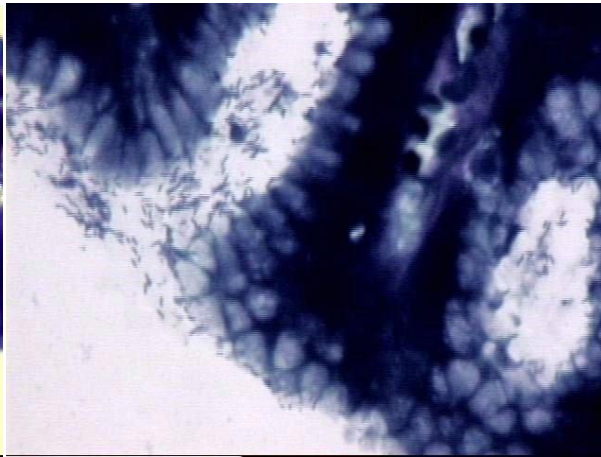
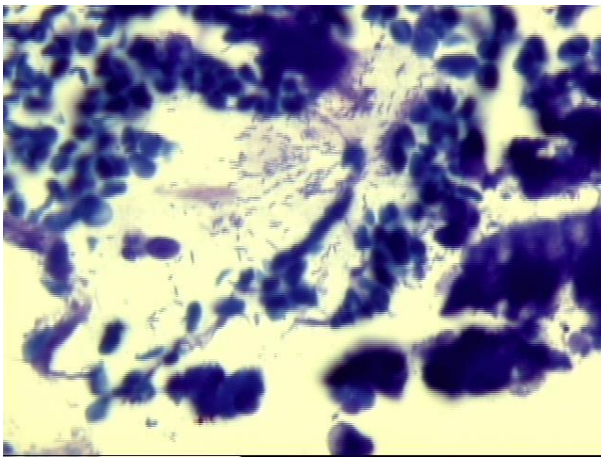
(Sydney 2,1,1,0,3),



33. ()

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(Sydney 1,1,1,0,1) GiemsaX100

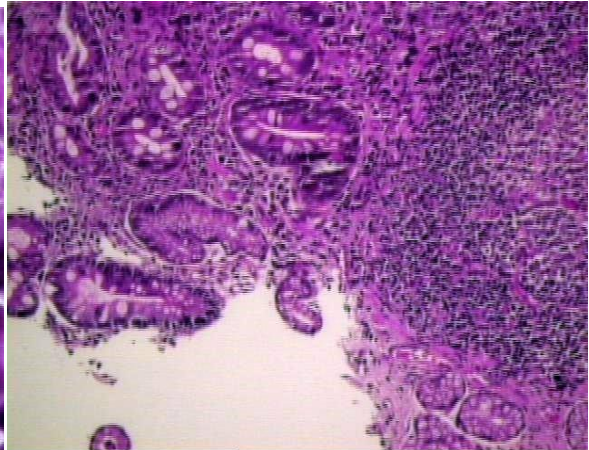
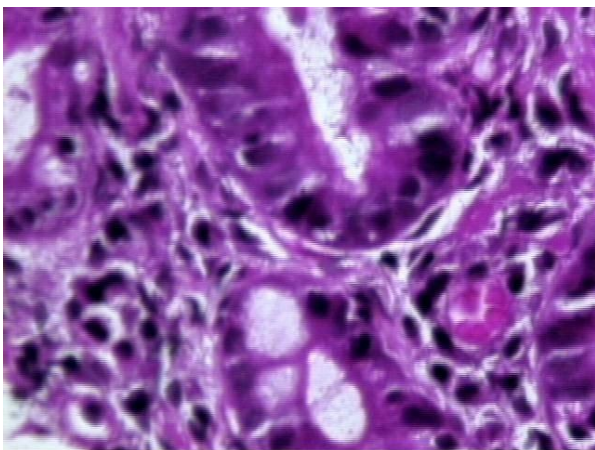


34.

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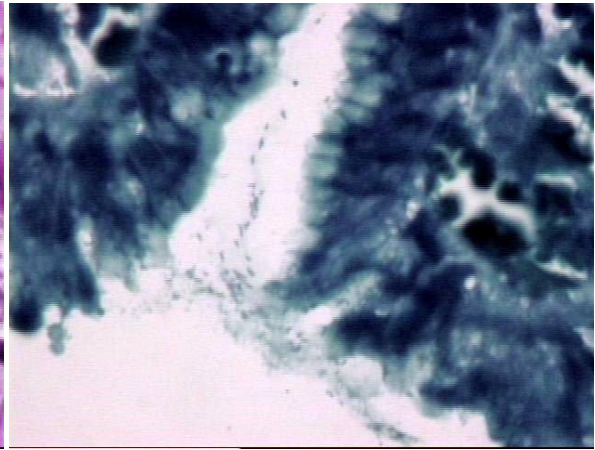
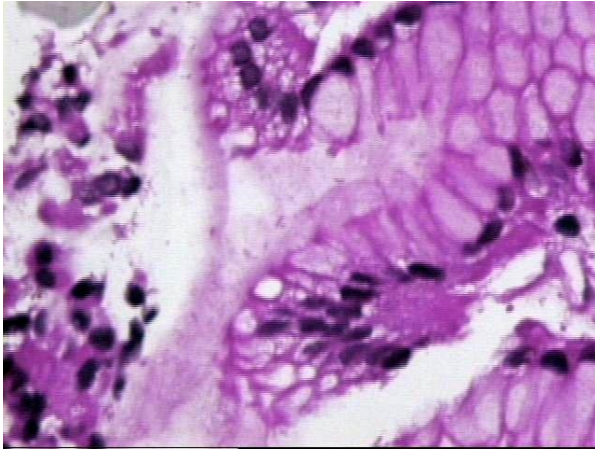
, Sydney 1,2,1,0,2, GiemsaX100



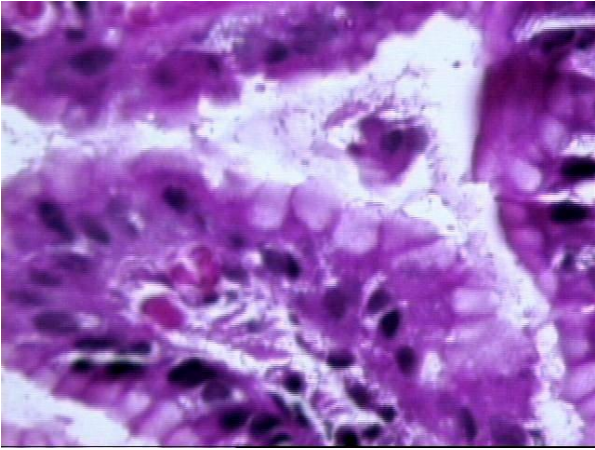
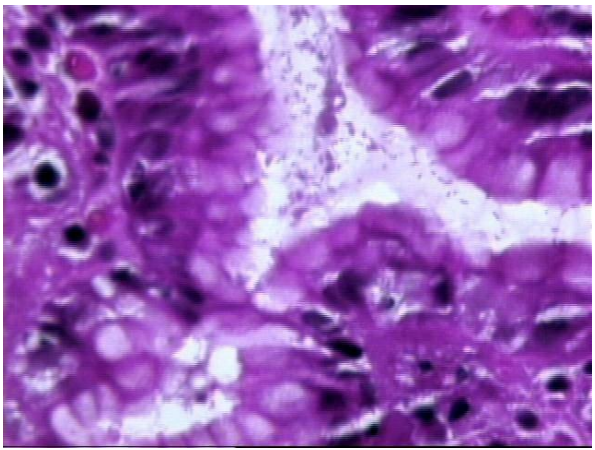
35. ()

(Sydney 2,2,1,2,1),

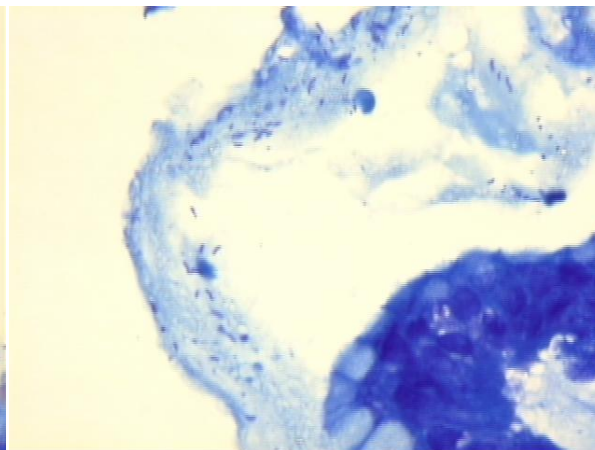
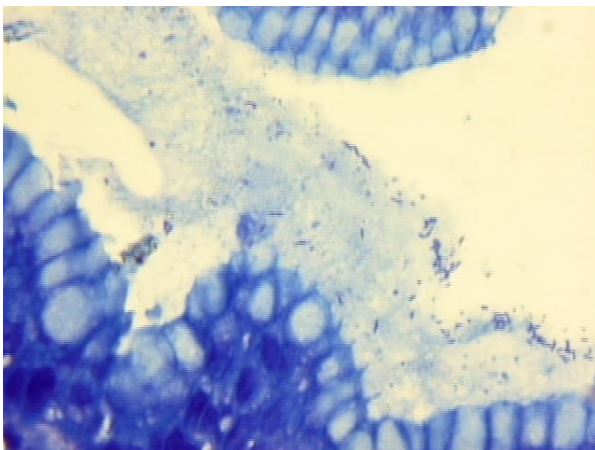
- , 100-X20 ()



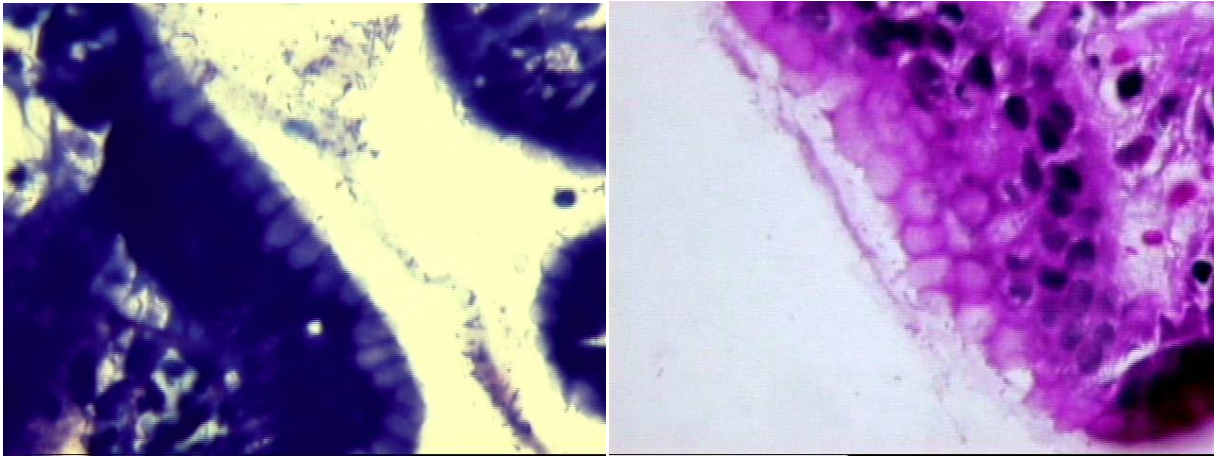
36. () ()
, (Sydney 1,1,1,0,1) 100
GiemsaX100,



37. (- X100)





38. (GiemsaX100)





39. GiemsaX100 , (100)

Sydney :

- : 10 ,
 (80 (53,3%), 53 (35,1%)
 7 (4,6%)



		%	%	%
0	10	6.6	6.7	6.7
	80	53.0	53.3	60.0
	53	35.1	35.3	95.3
	7	4.6	4.7	100.0
	150	99.3	100.0	

• :
 (,) 20 , ,
 87 (57,6%), 37 (24,5%)
 6 (4%)

		%	%	%
0	20	13.2	13.3	13.3
	87	57.6	58.0	71.3
	37	24.5	24.7	96.0
	6	4.0	4.0	100.0
	150	99.3	100.0	

17.

• : 4 (2,6%),
 97 (64,2%), 48 (31,8%)
 1 (0,7%)

		%	%	%
0	4	2.6	2.7	2.7
	97	64.2	64.7	67.3
	48	31.8	32.0	99.3
	1	.7	.7	100.0
	150	99.3	100.0	

18.

• :
 (83 , 55%).
 40 (26,5%), 19 (11,9%) 8
 (5,3%)

IM

	Frequency	Percent	Valid Percent	Cumulative Percent
IM	83	55.0	55.7	55.7
	40	26.5	26.8	82.6
	19	11.9	12.1	94.6
	8	5.3	5.4	100.0
	150	98.7	100.0	

19.

• - : 48
 (31,8%) . 62
 (41,1%), 29 (19,2%)
 11 (7,3%)

		%	%	%
	48	31.8	32.0	32.0
	62	41.1	41.3	73.3
	29	19.2	19.3	92.7
	11	7.3	7.3	100.0
	150	99.3	100.0	

20.

Giemsa

SPSS Statistics 19.

()

Sydney

31.

75 (25+50)

(2 75=150 block)

31, 75 , 7

(9,33%) (wild type) , 9

(12%) wild type ,

7 (9,33%) .

, 3

, 2

(

p value<0,05) profile

Sydney,

/

Q-Real Time PCR.

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Giemsa,

(

),

Sydney

21.

	150	0	3	207	1.38	.682	.465
	150	0	3	179	1.19	.711	.506
	150	0	3	196	1.31	.530	.281
	150	0	3	100	.67	.889	.790
	150	0	3	153	1.02	.901	.812
	148	1	3	294	1.99	.495	.245
(1= ,2=WT,3= +WT) *	148	30	67000	2954712	19964.27	19091.672	3.645E8
(1= ,2=)	150	1	2	221	1.47	.501	.251
	150	28	91	9286	61.91	11.906	141.763
(+ =1, + =2, =3, + =4, + =5, =6, + =7, =8)	150	1	8	385	2.58	1.896	3.596

21.

()

* (Gauss)

(p<0,05)

1.

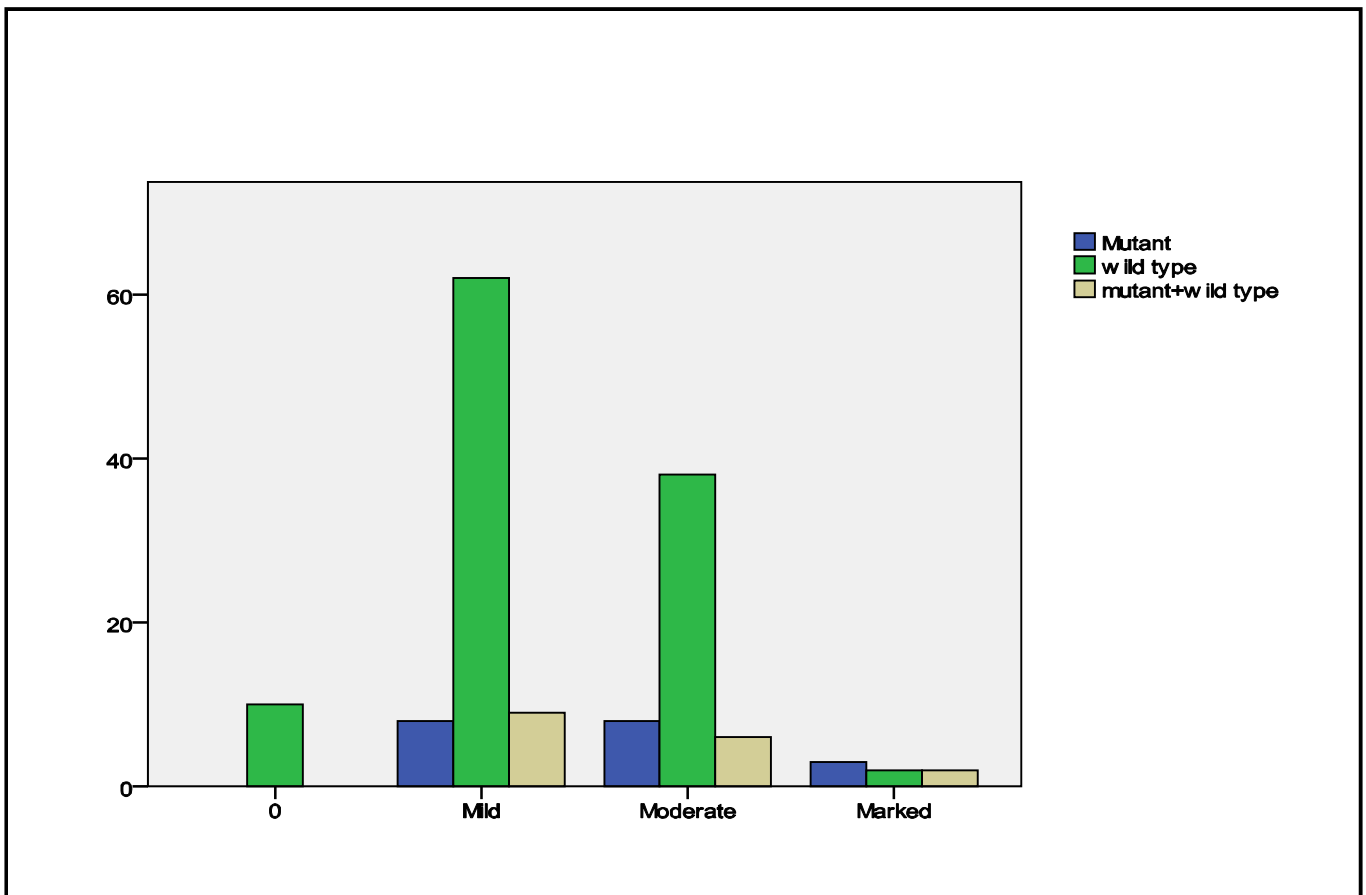
(22

40)

		df	. (2-sided)
Pearson Chi-Square	12,804 ^a	6	,046
Likelihood Ratio	13,420	6	,037
Linear-by-Linear Association	,625	1	,429
N of Valid Cases	148		

22.

2



40.

40,

wild type

(0)

2.

41)

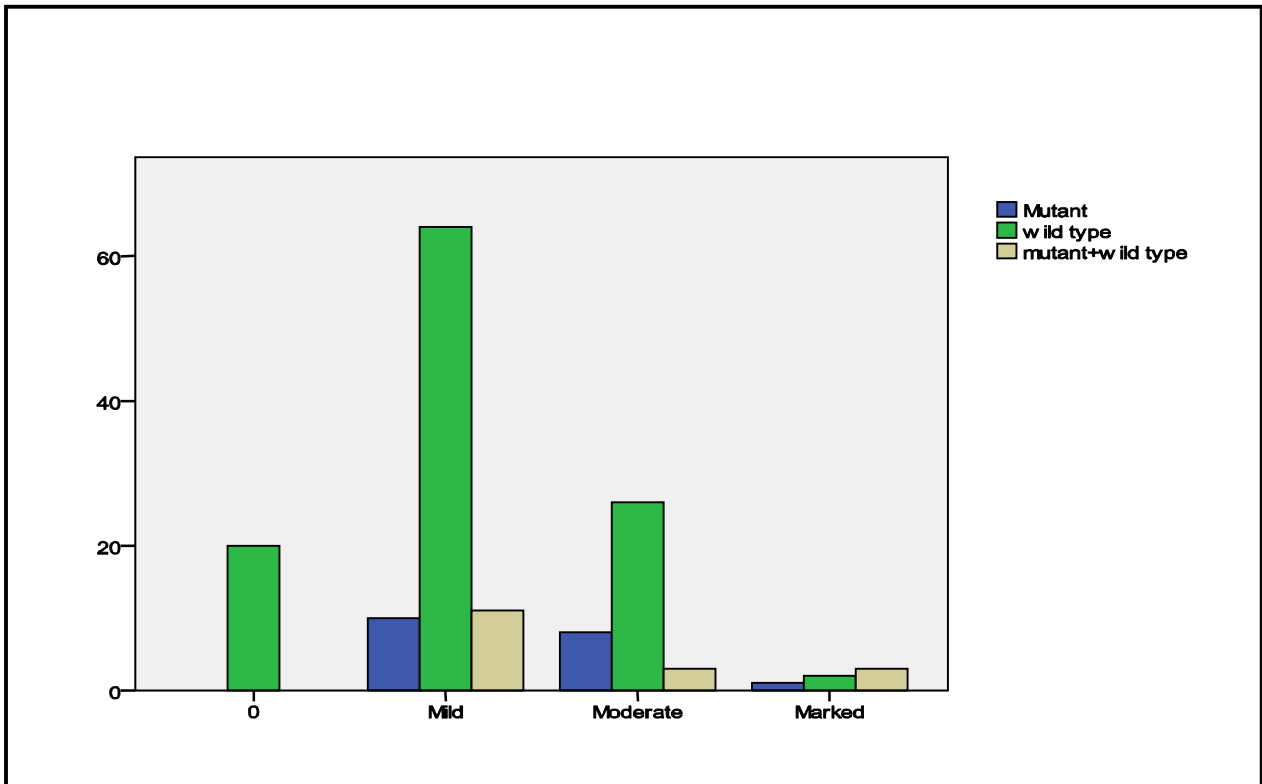
(

23

		df	(2-sided)
Pearson Chi-Square	18,635 ^a	6	,005
Likelihood Ratio	19,844	6	,003
Linear-by-Linear Association	,020	1	,887
N of Valid Cases	148		

23.

2



41.

41,

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(0)

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40

41,

3.

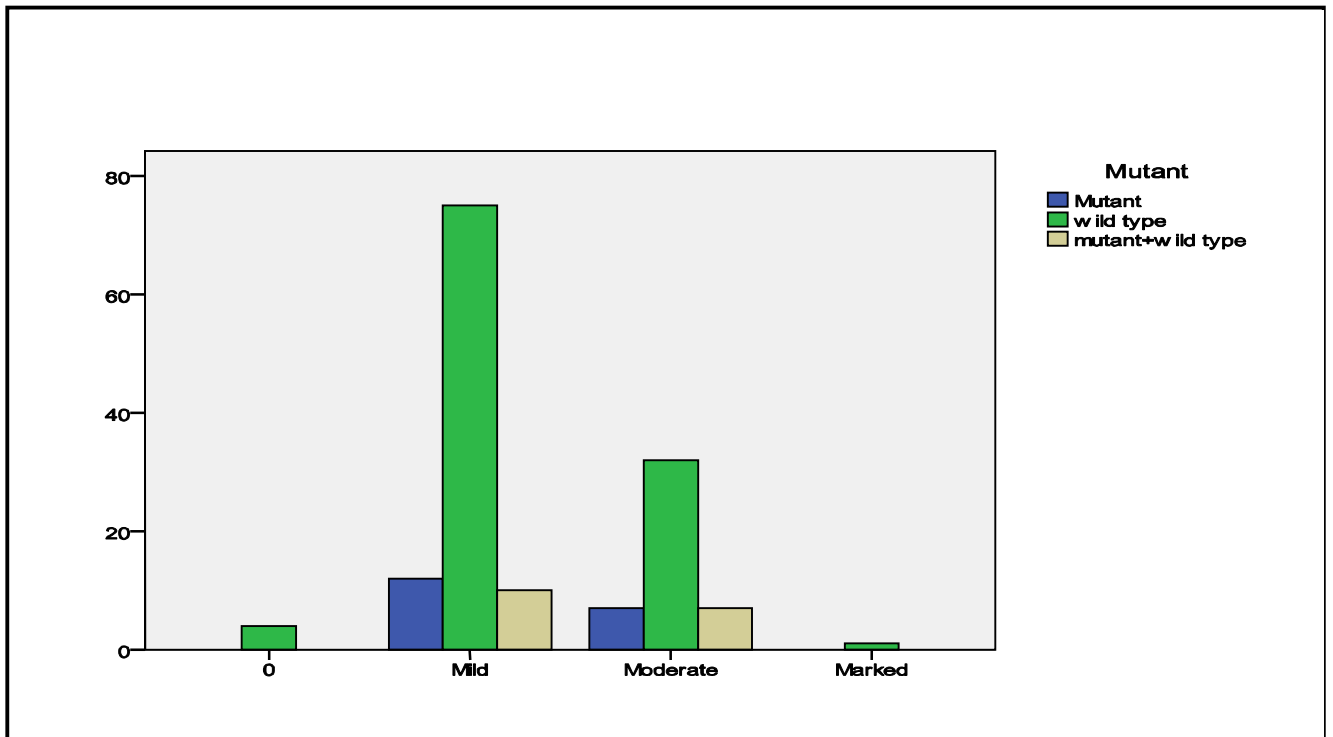
(24

42)

		df	. (2-sided)
Pearson Chi-Square	2,763 ^a	6	,838
Likelihood Ratio	3,889	6	,692
Linear-by-Linear Association	,035	1	,851
N of Valid Cases	148		

24.

2



42.

42

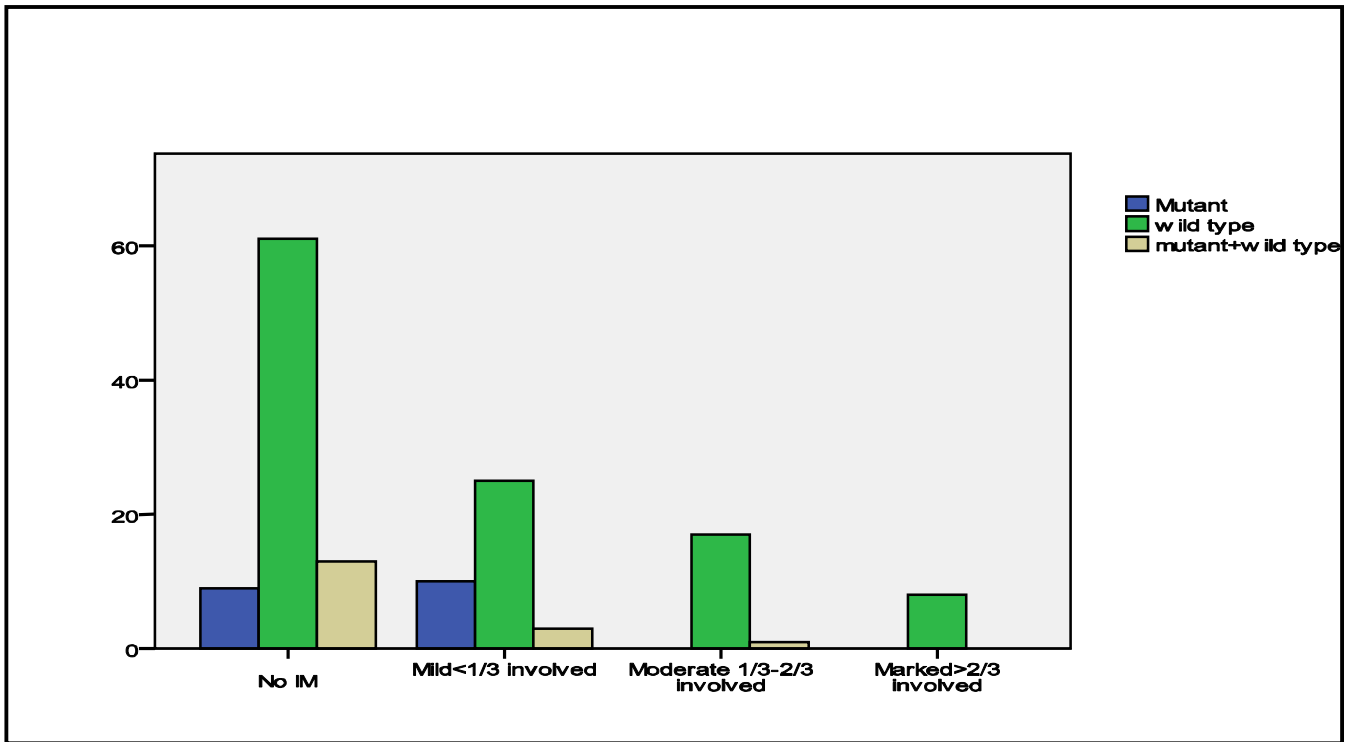
4.
43)

(25

		df	. (2-sided)
Pearson Chi-Square	14,056 ^a	6	,029
Likelihood Ratio	17,098	6	,009
Linear-by-Linear Association	,468	1	,494
N of Valid Cases	147		

25.

2



43.

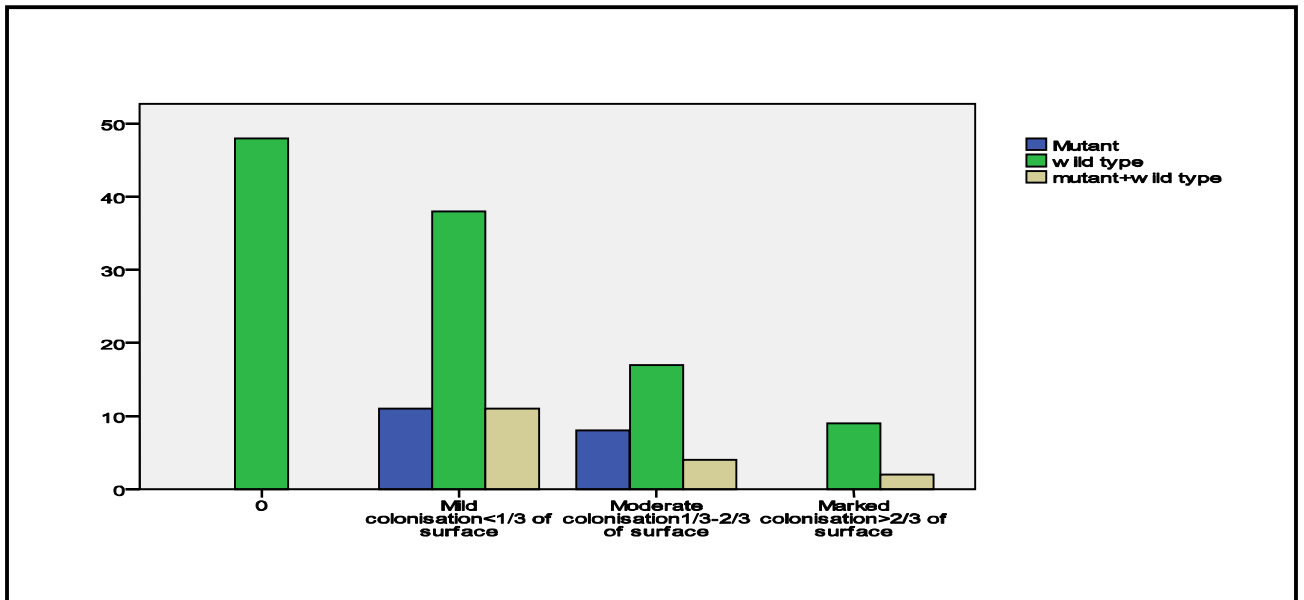
43,

>2/3

5. (26 44)

		df	. (2-sided)
Pearson Chi-Square	28,555 ^a	6	,000
Likelihood Ratio	39,612	6	,000
Linear-by-Linear Association	,000	1	,994
N of Valid Cases	148		

26. 2



44.

44,

(0),

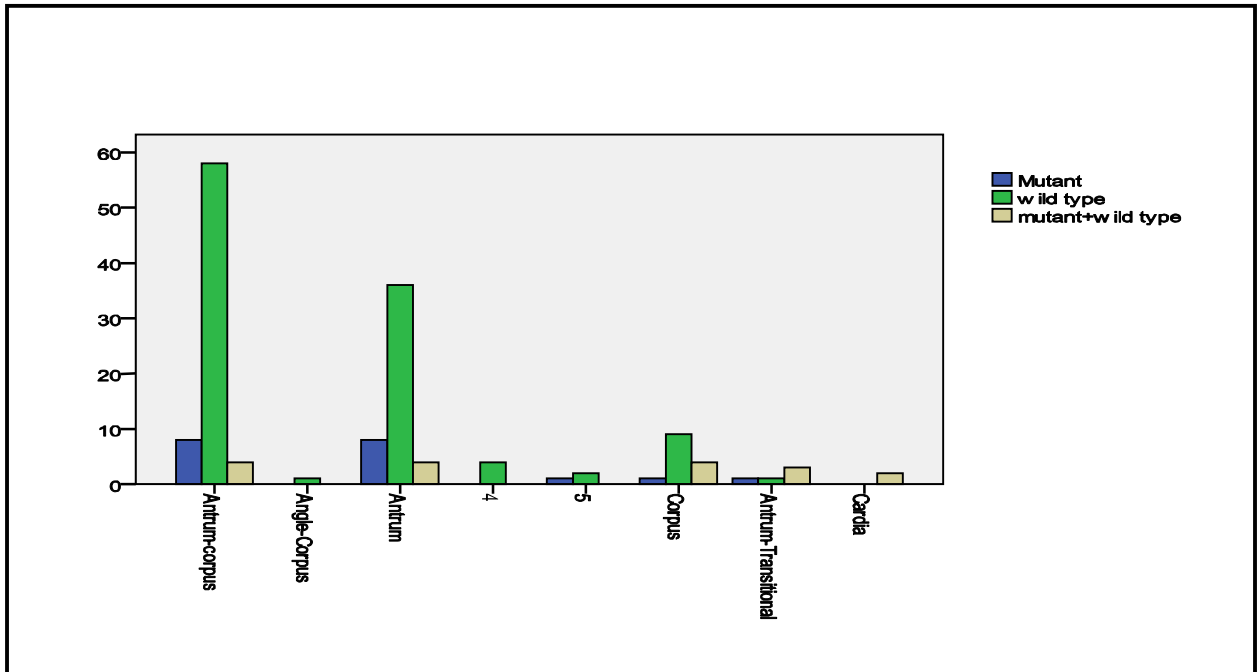
(

)

6. (27 45)

		df	. (2-sided)
Pearson Chi-square	38,383	14	,000
Likelihood Ratio	28,202	14	,013
Linear-by-linear Association	7,949	1	,005
N of Valid Cases	147		

27. 2



45.

45,

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7.

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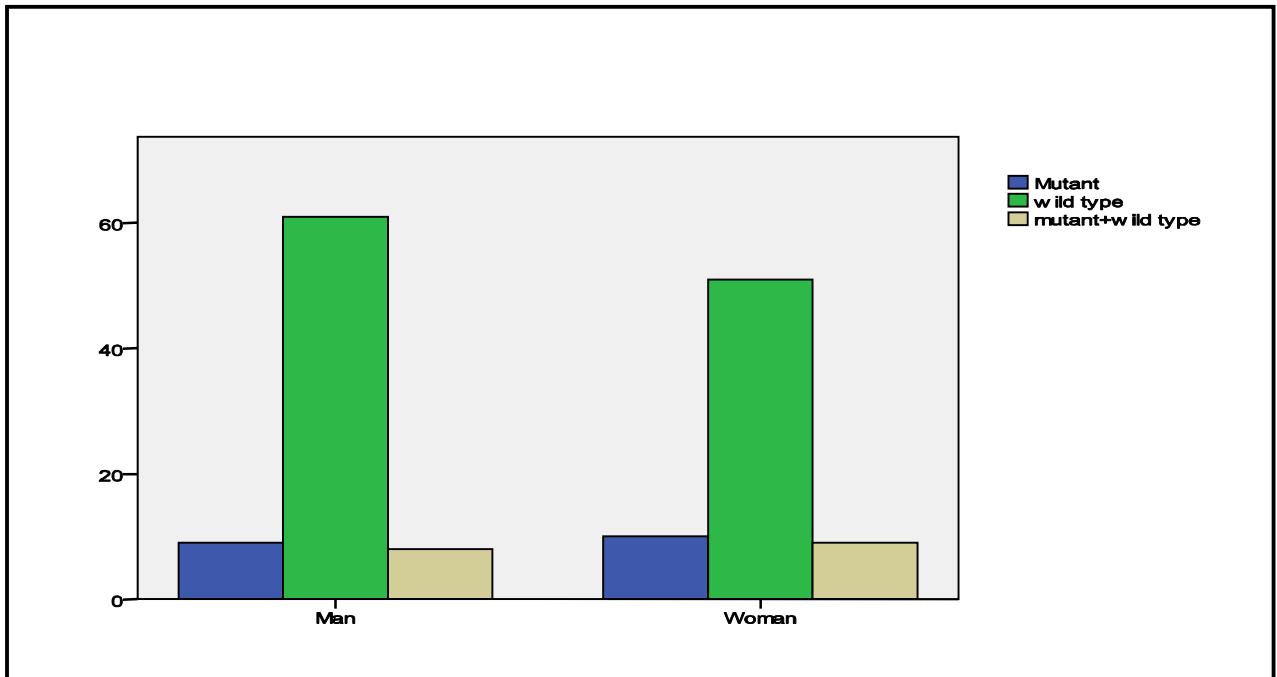
28

46)

		df	. (2-sided)
Pearson Chi-Square	,574	2	,751
Likelihood Ratio	,573	2	,751
Linear-by-Linear Association	,000	1	,986
N of Valid Cases	148		

28.

2



46.

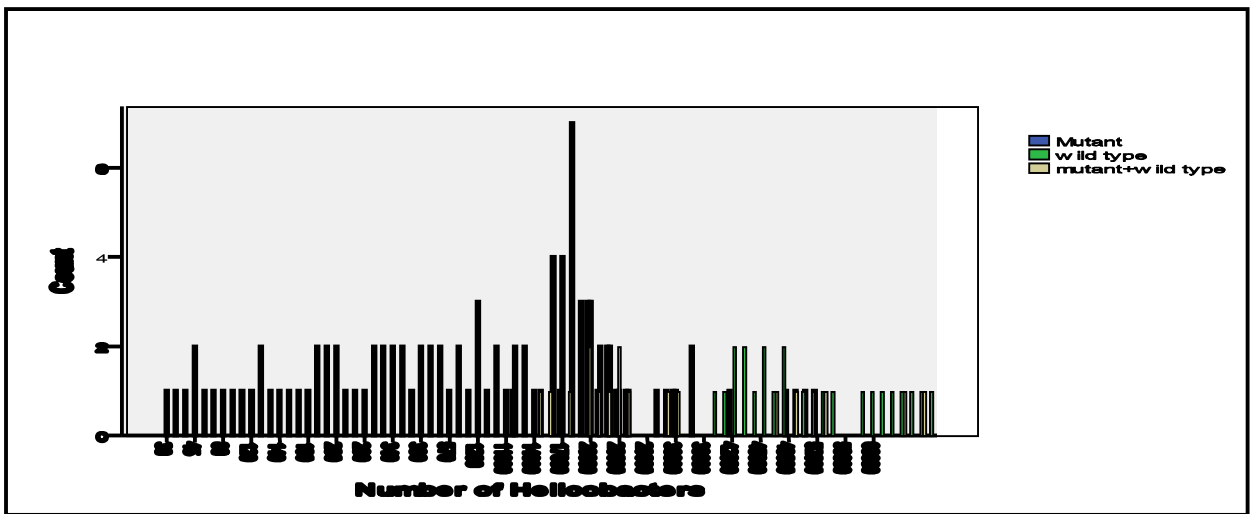
28

46,

8. (29 47) ()

		df	(2-sided)
Pearson Chi-Square	119,467 ^a	154	,982
Likelihood Ratio	110,381	154	,997
Linear-by-Linear Association	,122	1	,726
N of Valid Cases	148		

29. 2



47. ()

29

(). 47,
11000-23000 ,
(30-1200)

)

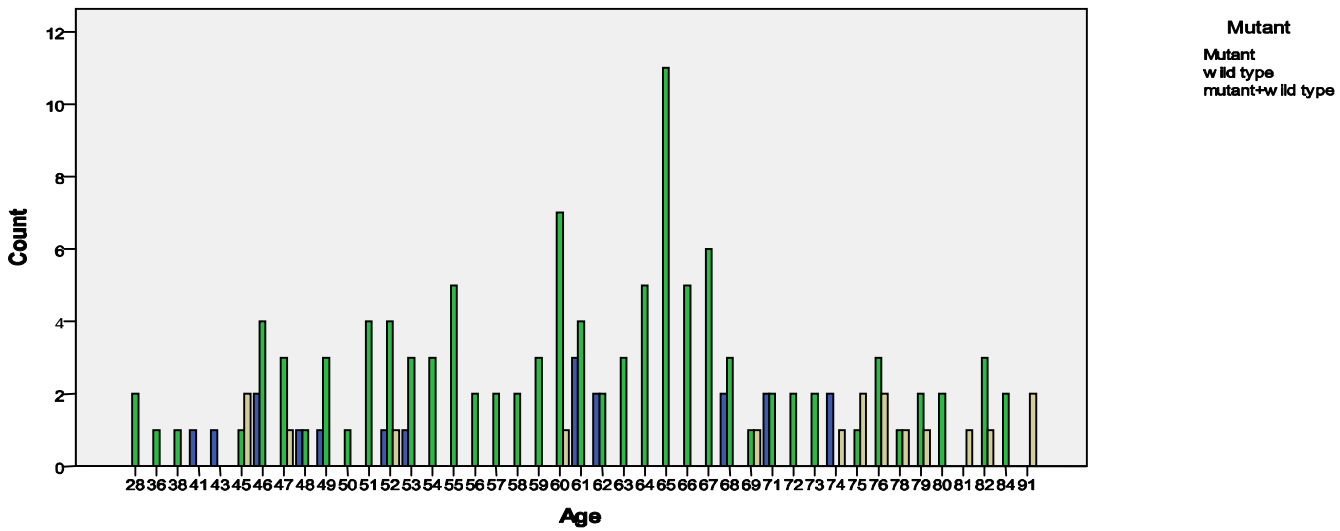
9.

(30 48)

		df	. (2-sided)
Pearson Chi-Square	128,422^a	84	,001
Likelihood Ratio	114,236	84	,016
Linear-by-Linear Association	8,506	1	,004
N of Valid Cases	148		

30.

2



48.

(count)

48,

: 45 53 69 91 .

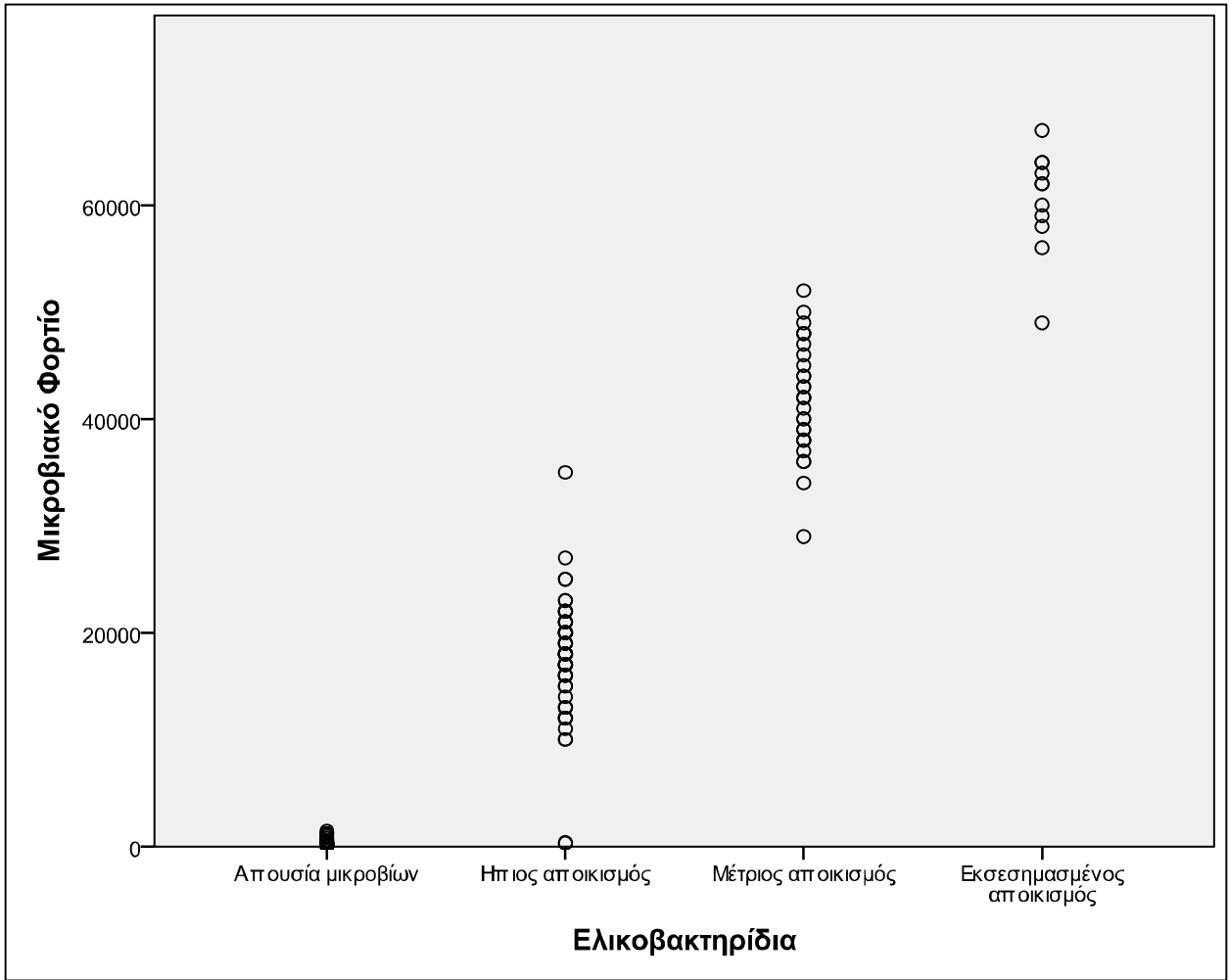
54-68

(60-62)

49

Sydney.

Q-RT-PCR



49.

Q-RT-PCR

Sydney

cut-off points 30.000 50.000

Q-RT-PCR

1	1	1	2	1	1	No DNA	
1	2	2	2	1	2	M	50000
2	1	2	2	0	1	M	20000
2	2	2	2	0	1	M	25000
3	1	2	2	0	2	W-T/M	45000
3	1	1	2	0	3	W-T/M	62000
4	1	1	1	0	2	W-T	40000
4	1	1	2	0	3	W-T	60000
5	2	1	2	1	1	No DNA	
5	2	1	2	1	2	M	48000
6	1	1	1	0	1	W-T/M	18000
6	1	1	1	0	1	M	20000
7	1	1	1	1	2	M	49000
7	1	1	1	1	1	M	22000
8	2	3	2	1	2	W-T/M	43000
8	3	2	2	1	2	M	38000
9	2	1	1	1	1	M	15000
9	1	1	1	0	1	M	17000
10	2	2	2	0	3	W-T	64000
10	2	3	2	0	2	W-T	42000
11	1	2	1	1	2		36000
11	3	2	2	1	2		38000
12	2	2	2	3	1	W-T	16000
12	2	1	2	2	1	W-T	14000
13	2	1	2	2	3	W-T	56000
13	1	1	2	0	1	W-T	20000
14	3	3	2	0	1	W-T / M	12000
14	2	1	2	0	1	W-T / M	17000
15	2	1	1	0	1		21000
15	2	2	1	0	1	M	18000
16	2	2	1	2	1	W-T	18000
16	1	2	2	3	3	W-T	49000
17	2	1	1	1	1	W-T	10000
17	2	1	1	0	1	W-T	13000
18	2	1	1	0	1	W-T	10000
18	1	1	1	0	1	W-T	12000
19	1	1	1	0	1	W-T/M	13000
19	1	1	2	0	1	W-T/M	15000
20	1	1	1	0	1	W-T/M	17000
20	2	2	1	0	2	W-T/M	48000
21	2	2	1	0	2		52000
21	1	1	1	0	1		12000
22	2	1	1	2	1	W-T/M	20000
22	2	2	1	0	1	W-T/M	20000
23	3	2	1	1	1		23000
23	1	1	1	1	1	M	22000
24	3	3	2	0	3	W-T/M	64000
24	2	1	1	0	1		20000
25	2	1	1	1	2	W-T/M	29000
25	1	1	1	1	1	W-T/M	27000
26	2	2	1	0	2	W-T	48000
26	1	1	1	0	0	W-T	350
27	2	1	2	0	1	W-T	17000
27	1	0	1	0	0	W-T	180
28	2	2	1	1	1	W-T	20000
28	0	0	1	0	0	W-T	230
29	2	1	1	0	1	W-T	18000
29	1	1	1	0	0	W-T	36
30	2	2	1	0	2	W-T	43000
30	1	0	1	0	0	W-T	60

31	2	1	1	0	3	W-T	63000
31	1	1	1	2	0	W-T	175
32	2	2	2	1	2	W-T	39000
32	1	1	2	2	0	W-T	45
33	1	1	1	0	1	W-T / M	21000
33	1	1	1	0	0	W-T	1200
34	2	1	1	3	2	W-T	46000
34	1	1	1	2	0	W-T	570
35	2	2	1	0	1	W-T	16000
35	1	0	1	0	0	W-T	250
36	2	2	1	2	3	W-T	58000
36	1	1	1	3	0	W-T	136
37	1	1	1	0	1	W-T	17000
37	0	0	1	0	0	W-T	35
38	2	2	1	0	3	W-T	67000
38	1	1	1	0	0	W-T	450
39	2	2	1	1	2	W-T	47000
39	1	0	2	1	0	W-T	310
40	1	2	1	1	2	W-T	38000
40	1	0	2	0	0	W-T	45
41	2	2	1	0	1	W-T	13000
41	1	0	1	0	0	W-T	200
42	2	1	1	1	1	W-T	19000
42	1	1	1	3	0	W-T	100
43	3	1	2	0	1	W-T	16000
43	1	0	1	0	0	W-T	30
44	1	1	1	1	1	W-T	18000
44	1	1	2	2	0	W-T	140
45	1	1	2	0	1	W-T	18000
45	2	2	2	0	0	W-T	90
46	2	2	2	0	2	W-T	44000
46	1	1	1	0	0	W-T	130
47	2	2	2	0	2	W-T	35000
47	1	1	1	0	0	W-T	190
48	1	1	1	1	1	W-T	21000
48	1	1	1	0	0	W-T	200
49	2	2	3	3	2	W-T	44000
49	1	1	1	1	0	W-T	280
50	1	1	1	0	1	W-T / M	19000
50	1	1	1	0	0	W-T	1200
51	2	2	2	0	3	W-T	62000
51	1	1	1	0	0	W-T	1450
52	2	3	2	2	3	W-T	59000
52	1	1	2	2	0	W-T	190
53	1	1	1	1	1	W-T	17000
53	0	0	1	0	0	W-T	290
54	1	1	1	1	2	W-T	36000
54	0	0	1	0	0	W-T	800
55	2	1	2	2	1	W-T	16000
55	0	0	1	0	0	W-T	310
56	1	1	1	3	2	W-T	40000
56	1	1	2	2	0	W-T	360
57	2	2	2	0	2	W-T	42000
57	0	0	1	0	0	W-T	160
58	1	1	2	1	1	W-T	11000
58	1	1	1	1	0	W-T	70
59	1	1	1	0	1	W-T	18000
59	1	1	1	0	0	W-T	340
60	2	2	2	1	2	W-T	42000
60	0	0	1	0	0	W-T	380
61	2	2	2	3	2	W-T	39000
61	1	1	1	2	0	W-T	230
62	2	1	2	0	1	W-T	17000
62	2	2	1	0	0	W-T	240

63	2	2	1	1	1	W-T	19000
63	1	1	1	1	0	W-T	560
64	1	1	1	1	2	W-T	34000
64	1	1	0	0	0	W-T	450
65	1	1	1	0	1	W-T	18000
65	1	1	1	0	0	W-T	440
66	1	1	1	1	1	W-T	21000
66	1	0	1	1	0	W-T	1200
67	1	1	1	0	1	W-T	20000
67	0	0	0	0	0	W-T	120
68	1	1	1	2	1	W-T	23000
68	1	1	1	1	0	W-T	290
69	1	1	2	0	1	W-T	25000
69	1	1	2	0	0	W-T	1000
70	2	2	2	1	2	W-T	37000
70	1	1	1	0	0	W-T	800
71	1	1	1	0	1	W-T	22000
71	0	0	0	0	0	W-T	350
72	1	1	1	2	1	W-T	19000
72	0	0	1	1	0	W-T	130
73	2	1	1	0	1	W-T	22000
73	1	1	1	0	0	W-T	560
74	3	3	2	2	2	W-T	41000
74	1	1	1	0	0	W-T	380
75	1	1	1	0	1	W-T	12000
75	1	0	0	1	0	W-T	80

31. Sydney,

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(wild type)

3. _____

÷ ø (biprobe) Real Time PCR

(544;545)

Sydney,

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Giemsa),

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Real Time-PCR (Q-RT-PCR).

Sydney

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Giemsa),

Q-RT-PCR

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1200

1993

Chan

(546)

(546;547)

DNA

(548)

Maastricht

(guidelines)

(322)

(PPIs)

(549)

pH

(550)

()

12

(40,9%)

(551)

9.9-43.5%.

(552)

12 48%.

(553)

10-15% (326).

4%,

MIC

pH,

(554)

23S rRNA

(555)

V 23S rRNA.

23S rRNA

(transition)

-

(A-G)

2143 (2143G),

(-point)

A2142G, A2142C, A2144G

T2182C.

A2115G, G2141C, C2147G,

T2190C, C2195T, A2223G C2694A,
(556)

÷ ø (active efflux
pump mechanism) (557). ClariRes[®] assay

A2142C, A2142G A2143G.
(A2143G),
85%

(558)

92%. (7)

«efflux pump mechanism». Agudo

(559)

: 44 53

, 60 62 68 77 .

Alarcon 4 18 ,
8 .

(560)

Bremon

8% 1987 18% 1997 (561)

3 , (44-

53)

Real Time PCR

Oleastro (562)

10%

(2)

test GenoType Helico DR[®]

Cambau

30%

(563)

Noguchi

(564)

(2)

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Lascols

(
Sydney),
(565)

crosstabulation

Giemsa,

in situ,

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Lu

(566)

(40 41)

Sydney

(12/2011)

17

: 1)

2)

2

(p=0.169).

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12

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Ca

Sydney

(567-570)

(

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(p=0,838).

(571-575),

(=1)

Scholte

cac vag

(576).

vacA s1, cagA+

vacA s2/cagA

Sydney

(577),(578),

(. active efflux pump mechanism).

Chu

(double-layer vacuoles)

(579). ()

;))

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Ribeiro

Sydney,

(584:585)

Sydney

RNA

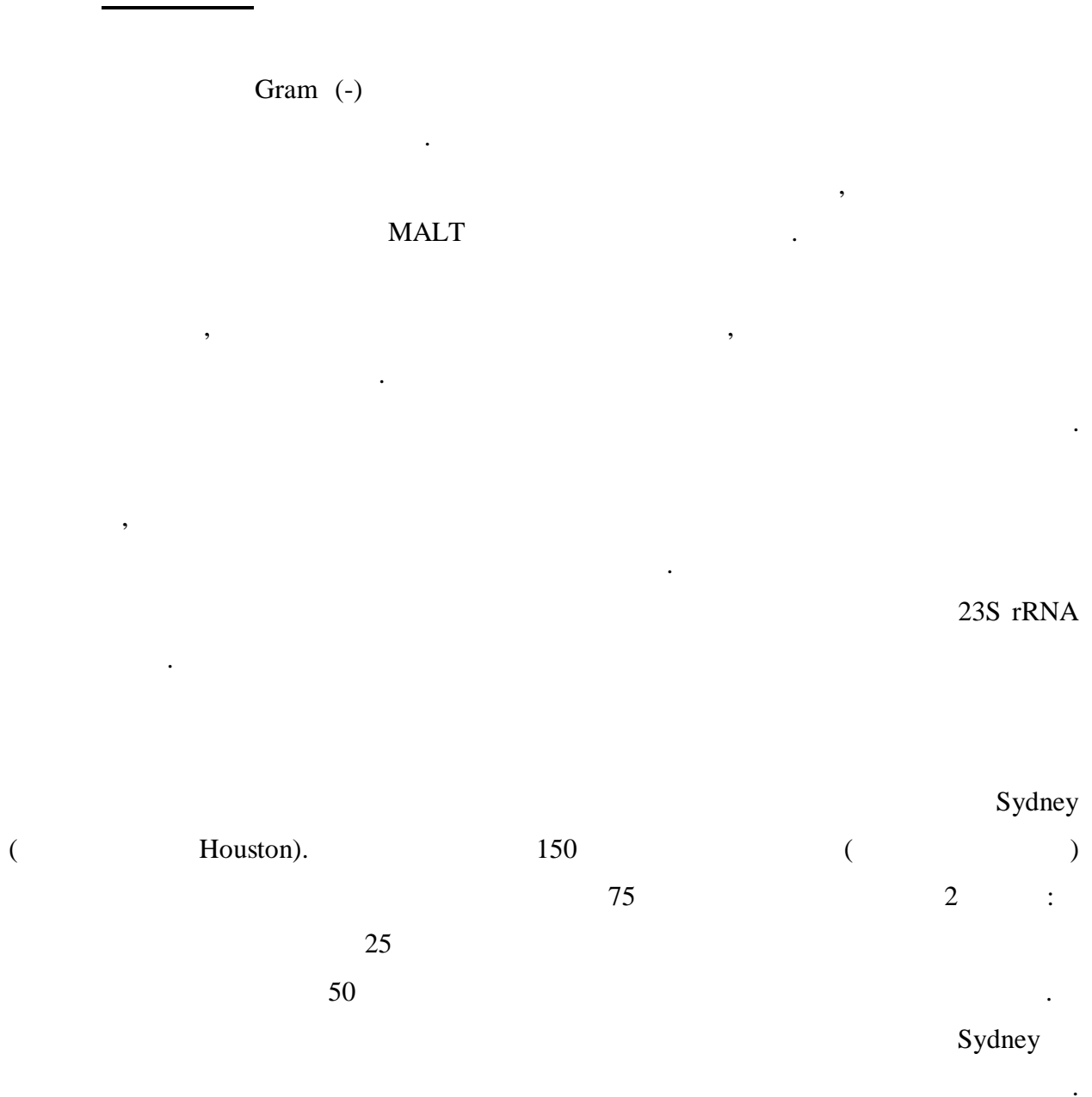
Sydney.

(in situ)

12.

Sydney

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Roche LightCycler[®] Real Time PCR kit *H.pylori* ClariRes[®]
 Ingenetix, Vienna, Austria.

Quantitative-RT-PCR.

(16/25)

A2142C, A2142G / A2143G 23S rRNA (7)

(p<0,005)

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Q-RT-

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ABSTRACT

Molecular detection of *H. pylori* macrolides-resistance strains in archival material and correlation with histological data according to Sydney classification

Sofia Gazi, Biologist, PhD thesis

Introduction. *Helicobacter pylori* (*Hp*) is a spiral, microaerobic, gram negative bacterium that infects gastric mucosa with a prevalence rate more than 50% and is associated with different digestive diseases such as gastritis, peptic ulcer and neoplasia as MALT lymphoma and gastric carcinogenesis. The progression of these diseases is affected by the genotype of the organism, the immune response of the host, as well as by genetic and environmental influences. As a consequence, all consensus guidelines recommend eradication of *Hp* for patients with symptoms. Standard therapy combines a proton pump inhibitor (PPI), or ranitidine bismuthe citrate and two antibiotics chosen among Amoxicillin, Clarithromycin and Metronidazole. Many factors have been implicated as causes of treatment failure, and among them are certain genetic changes in terms of point mutations in the peptidyltransferase region of the domain V of the 23S rRNA of *Hp*, connected particularly with Clarithromycin resistance.

Aim. The focus of this study was to evaluate these genetic changes in formalin-fixed paraffin embedded biopsies of *Hp*⁺ patients and to correlate them with various phenotypic changes expressed by Sydney's classification parameters.

Material and Methods. A total of 150 *Hp*(+) gastritis cases (biopsies-paraffin blocks) were studied, taken from 75 patients divided in 2 groups: group A consisted of 25 Clarithromycin-resistant *Hp*(+) gastritis patients and group B consisted of 50 *Hp*(+) gastritis patients where successful eradication was achieved. Histologic classification was done according to Sydney criteria in biptic material obtained before and after *Hp*(+) gastritis therapy. In most of the cases adequate quantity of DNA was extracted from archival biptic material and analyzed in a Roche LightCycler[®] RT-PCR thermocycler, using the recently introduced *Hp* ClariRes[®] kit (Ingenetix, Vienna, Austria), for the determination of point mutations in the 23S rRNA gene, responsible for Clarithromycin resistance. At the same time, a Real Time Quantitative PCR was also performed using the same cyler at the same DNA, in order to determine the absolute number of *Hp* bacteria per clinical sample.

Results. Our results revealed that in most of the Clarithomycin resistance cases of group A (16/25), certain point mutations at sites A2142C, A2142G and A2143G of the 23S rRNA had occurred. In some cases among group A patients, it was shown that mixed infections with both susceptible and resistant *Hp* strains had also occurred. Seven (7) cases from group A patients showed no mutations at all. A coexistence of mutated and wild type cases in 3 out of 50 *Hp*+ patients before therapy were observed in group B. A statistically significant association among almost all Sydney classification parameters (except atrophy) and genetic alterations in 23S rRNA of *Hp* were noticed. Furthermore, a strong correlation between genetic alterations and age of the patients was revealed, as well as between genetic alterations and the sites from where the biopsies were obtained (antrum, corpus, cardia, angle, and fundus). No correlation was observed between genetic status and absolute number of bacteria per clinical case as defined by Q-RT-PCR. *Hp* quantity correlates well with bacterial colonization as described histologically in Sydney classification.

Conclusion. In conclusion, it seems that *Hp* is a rather genetically complicated microorganism, the biological and clinical behavior of which is largely affected by the host. Enhanced risk may be related to differences in expression of specific bacterial products, to variations in the host inflammatory response to the bacteria, or to specific interactions between host and microbes. Genes that are heterogeneously represented among *Hp* strains, however, may encode candidate virulence factors that influence the pathological course. *Hp* genome is largely characterized by genetic variability that permits the survival of the bacterium in a quite hostile environment. This genetic diversity affects the response of *Hp* in the followed treatment strategies, and alters the phenotype of the gastric mucosa environment, as this reflected in Sydney classification. So our findings in this study confirm the relevance of the *Hp* genotypes for the severity of gastric disease and the efficacy of antibiotic therapy to further prevent the (possible) progression to carcinogenesis or lymphomatogenesis.

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