

Quarta esercitazione pratica

MA 10-06-2014

(domande a cui si vuole rispondere con questo studio)

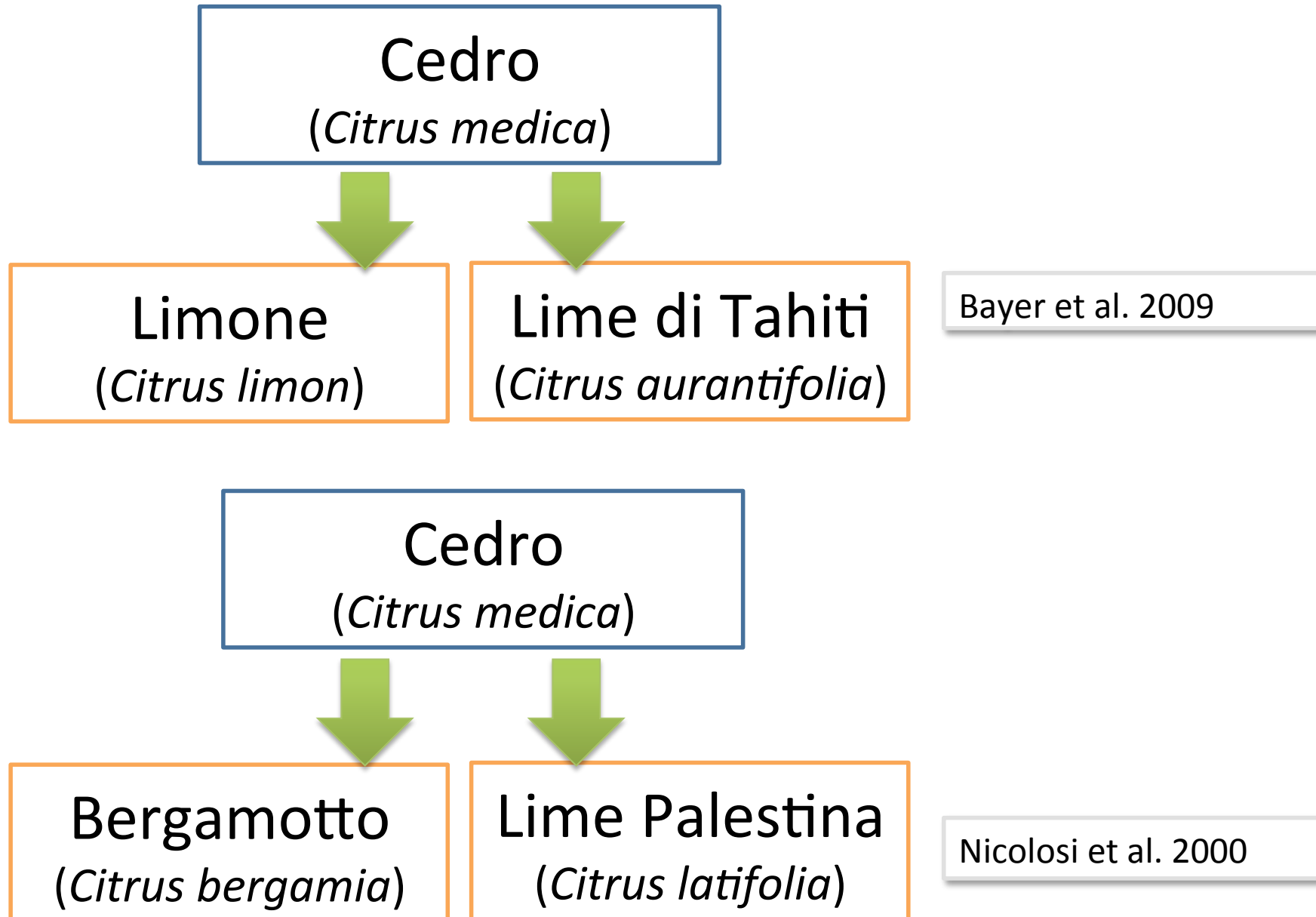
E' possibile ricavare delle relazioni di parentela tra genotipi sulla base di modelli suggeriti dalla bibliografia?

L'individuo sconosciuto "X" è assimilabile a qualcuno dei genotipi noti?

Qual è il livello di distanza genetica tra i sei genotipi analizzati?

Quarta esercitazione pratica
(parentele ipotetiche nel genere *Citrus*)

MA 10-06-2014



Theor Appl Genet (2000) 100:1155–1166

**E. Nicolosi · Z.N. Deng · A. Gentile · S. La Malfa
G. Continella · E. Tribulato**

Citrus phylogeny and genetic origin of important species as investigated by molecular markers

Nicolosi et al. 2000

American Journal of Botany 96(3): 668–685. 2009.

A MOLECULAR PHYLOGENY OF THE ORANGE SUBFAMILY (RUTACEAE: AURANTIOIDEAE) USING NINE cpDNA SEQUENCES¹

**RANDALL J. BAYER,^{2,7} DAVID J. MABBERLEY,³ CYNTHIA MORTON,⁴ CATHY H. MILLER,²
ISH K. SHARMA,⁵ BERNARD E. PFEIL,² SARAH RICH,² ROBERTA HITCHCOCK,² AND STEVE
SYKES⁶**

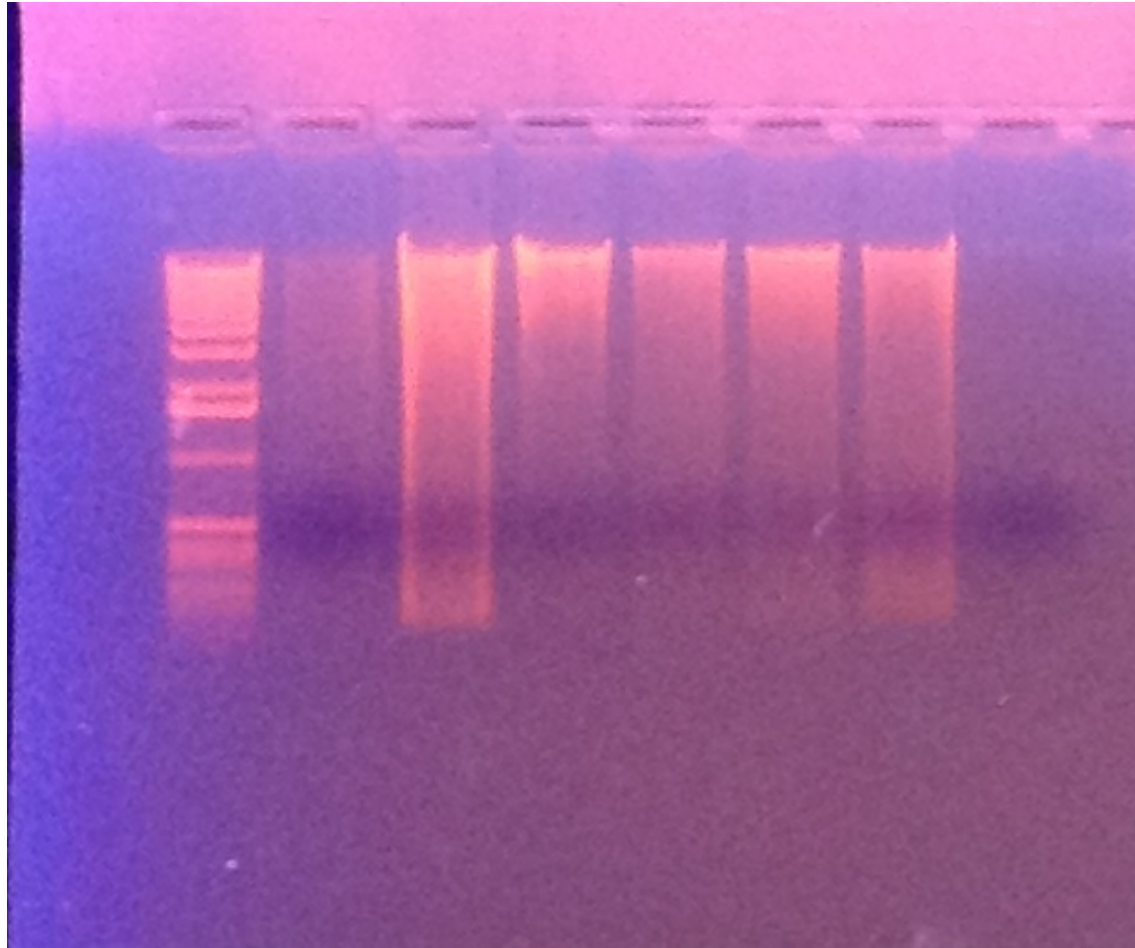
Bayer et al. 2009

Seconda esercitazione

ME 04-06-2014

(separazione elettroforetica su agarosio dei DNA genomici estratti)

- Primo turno -

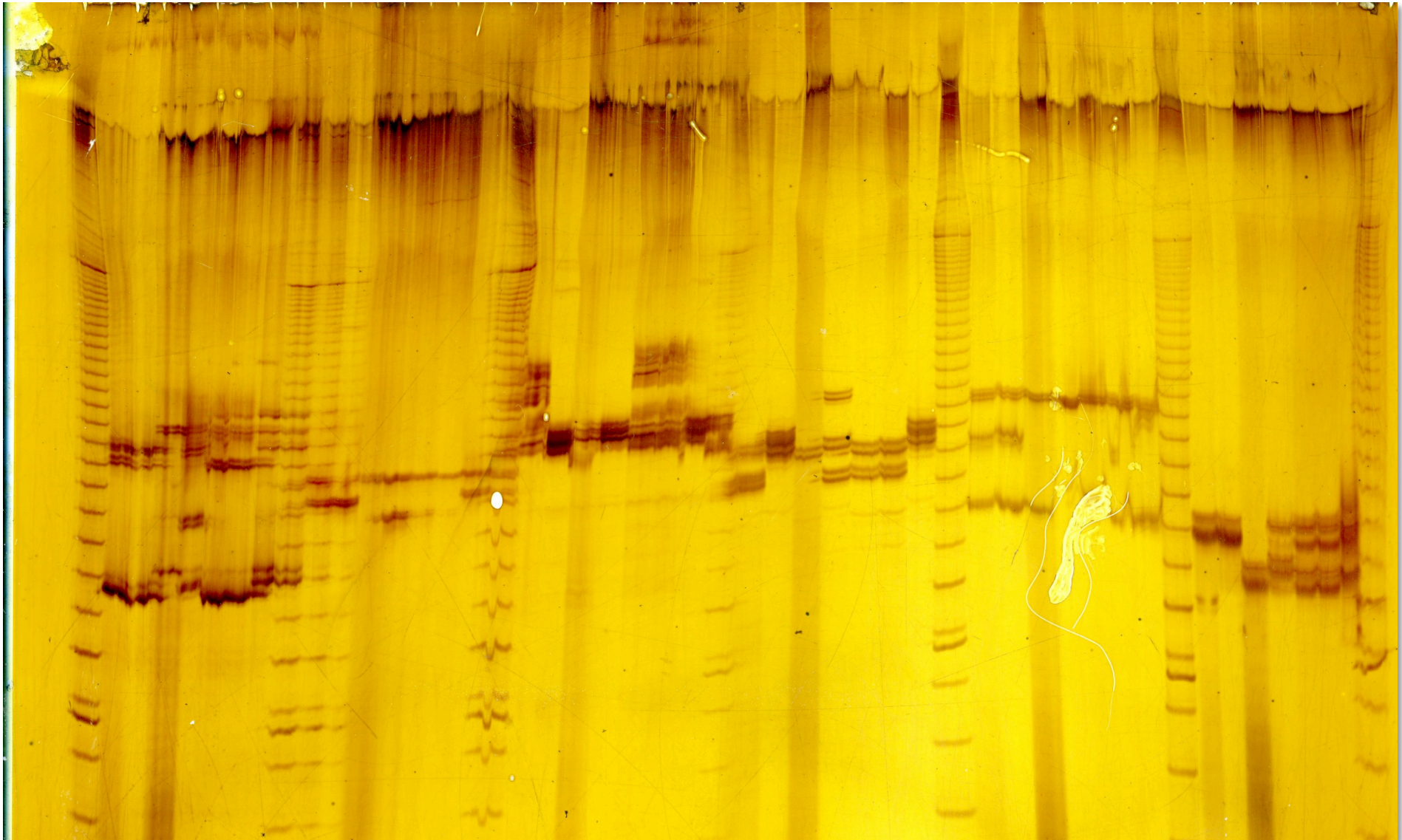


Terza esercitazione

GI 05-06-2014

(separazione elettroforetica PAGE dei prodotti di PCR)

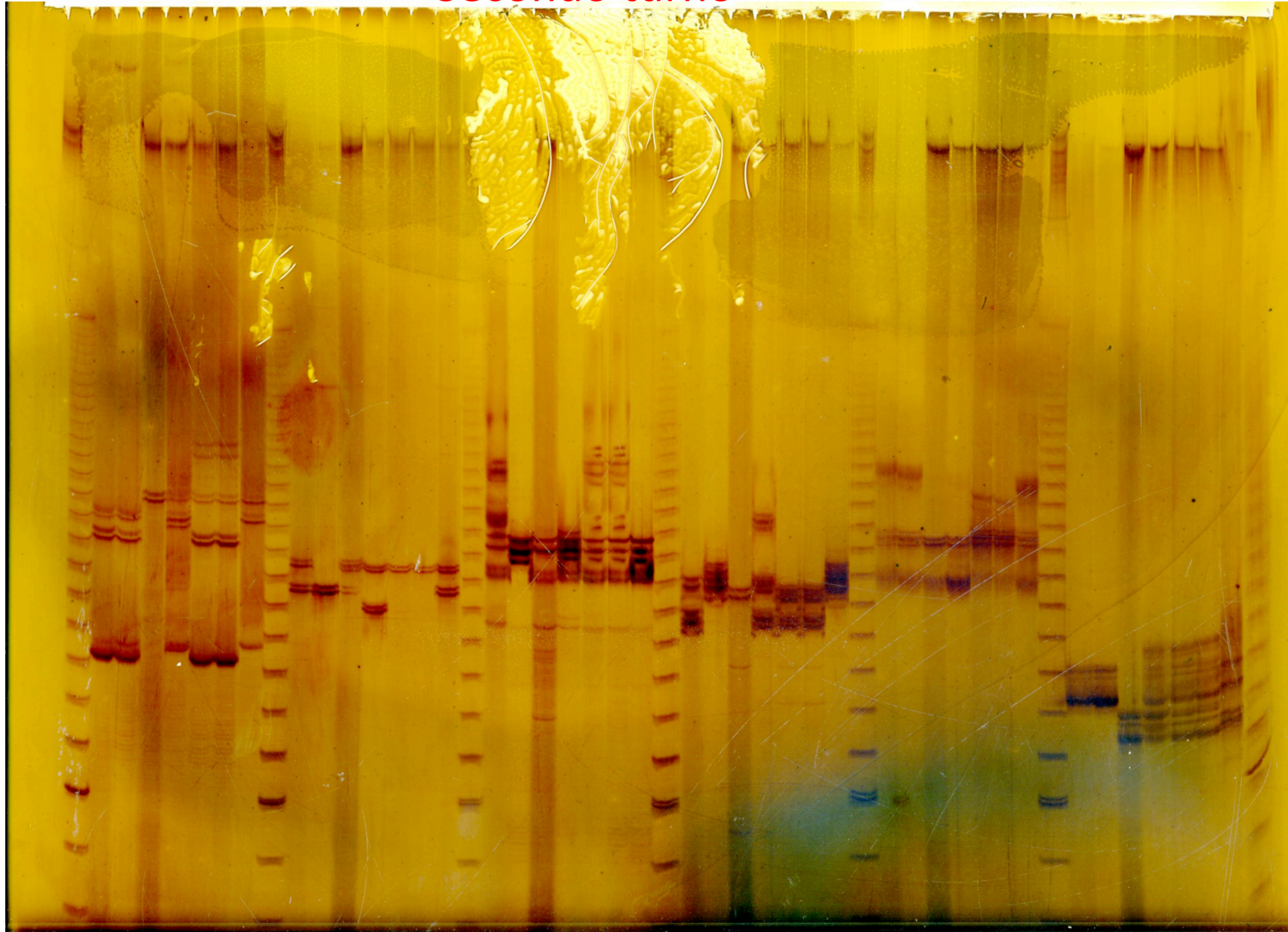
- Primo turno -



Terza esercitazione
(separazione elettroforetica PAGE dei prodotti di PCR)

ME 11-06-2014

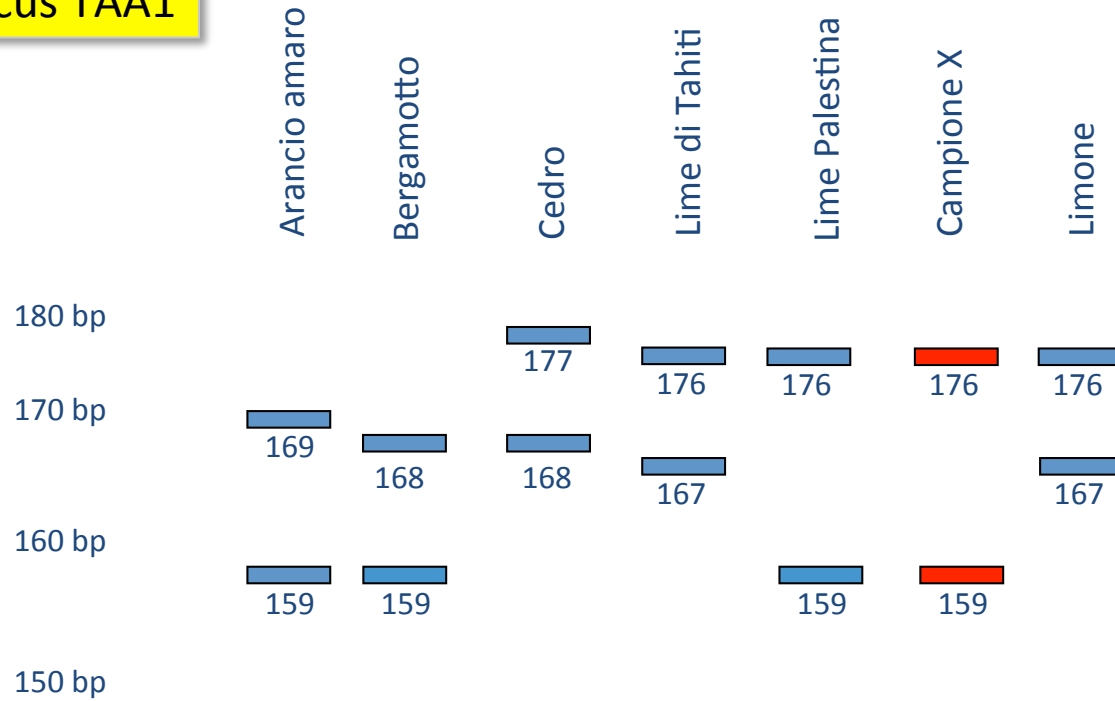
- Secondo turno -



Quarta esercitazione pratica (Raccolta e analisi dei dati)

MA 10-06-2014

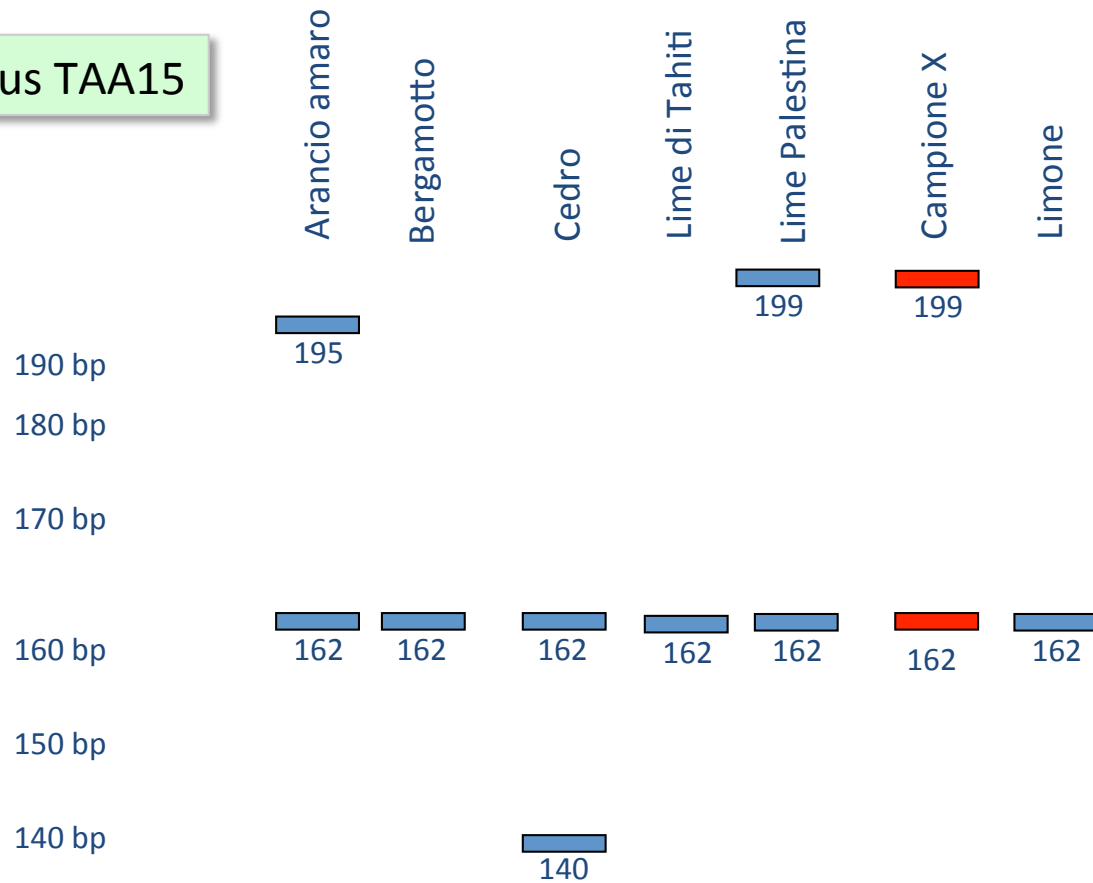
Locus TAA1



Quarta esercitazione pratica (Raccolta e analisi dei dati)

MA 10-06-2014

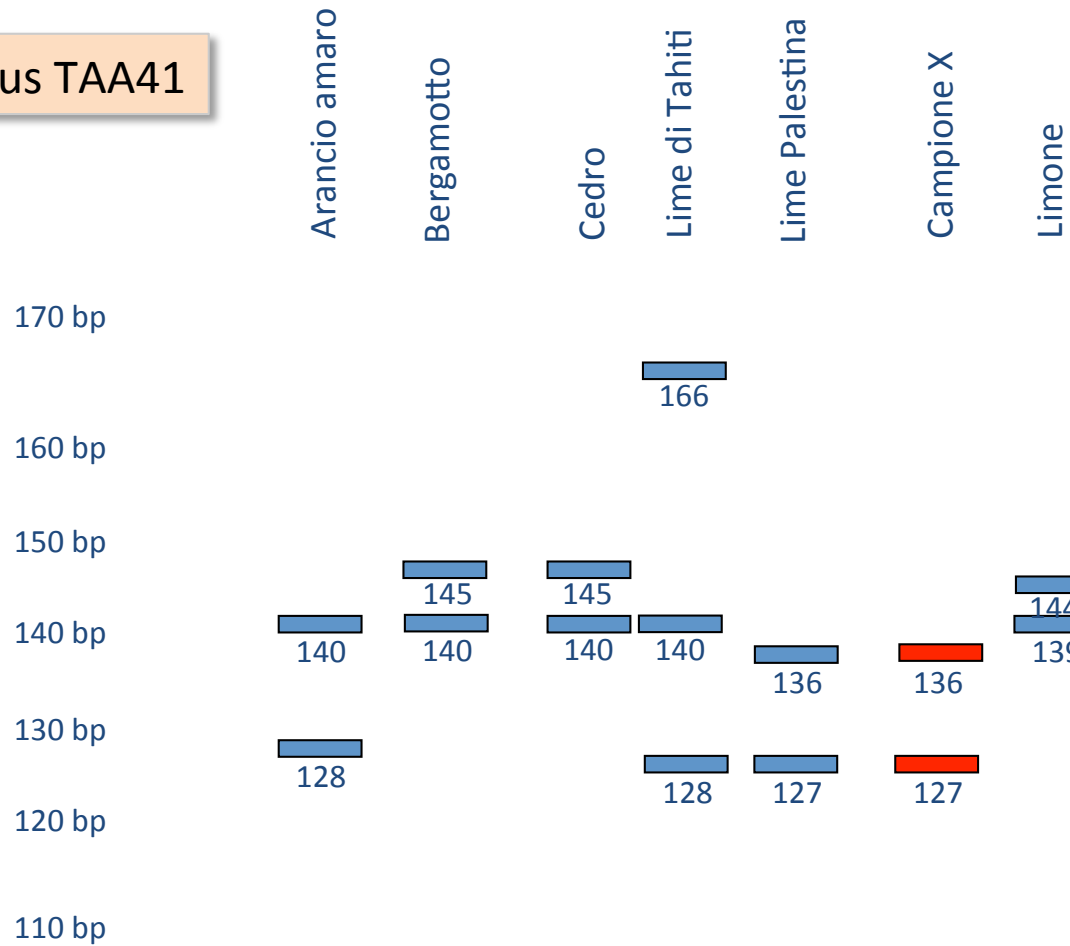
Locus TAA15



Quarta esercitazione pratica (Raccolta e analisi dei dati)

MA 10-06-2014

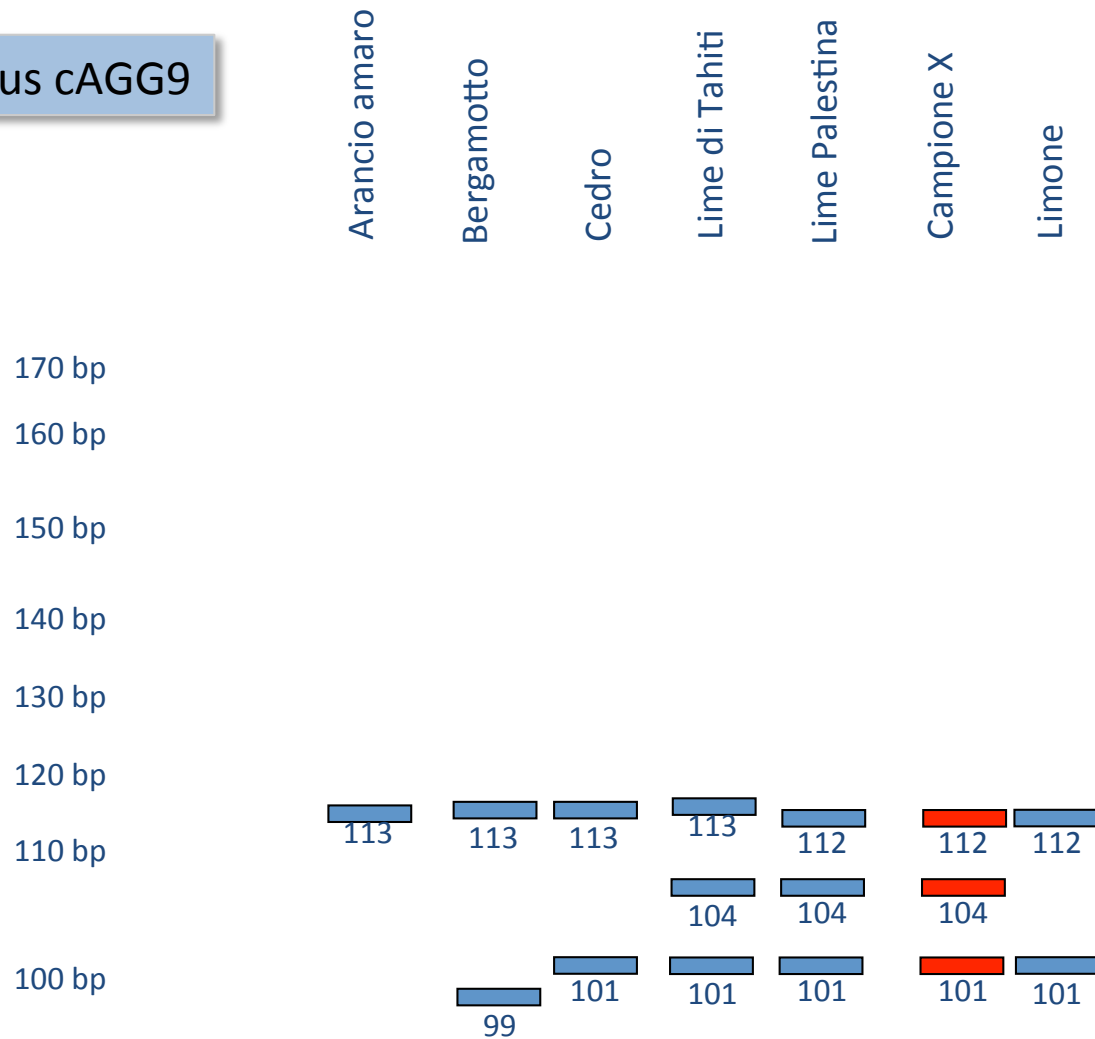
Locus TAA41



Quarta esercitazione pratica (Raccolta e analisi dei dati)

MA 10-06-2014

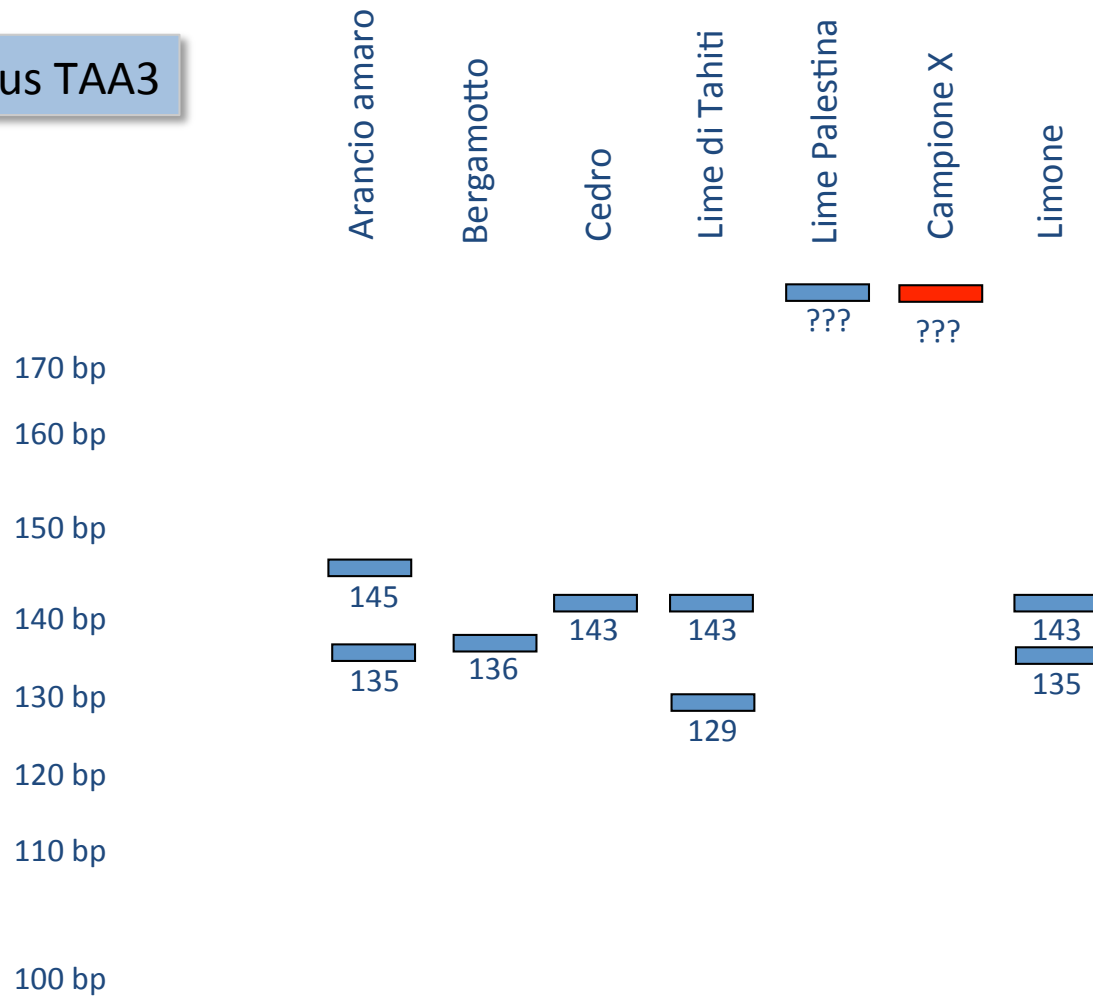
Locus cAGG9



Quarta esercitazione pratica (Raccolta e analisi dei dati)

MA 10-06-2014

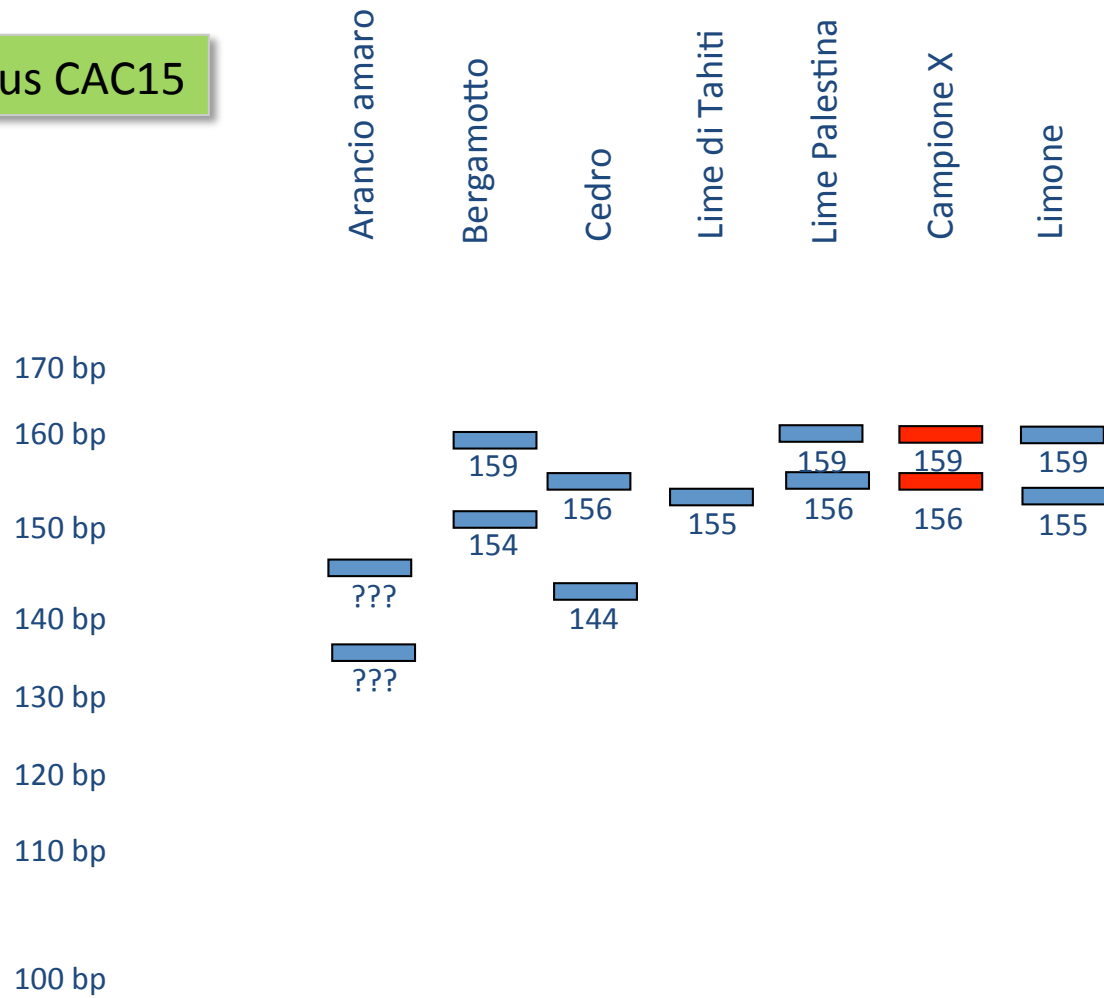
Locus TAA3



Quarta esercitazione pratica (Raccolta e analisi dei dati)

MA 10-06-2014

Locus CAC15



Quarta esercitazione pratica

ME 11-06-2014

(visualizzazione cluster Neighbor-Joining con software Neighbor)

- Comune ai due turni -

6-1(NJ).neighbor

6 Populations

Neighbor-Joining/UPGMA method version 3.69

Neighbor-joining method

Negative branch lengths allowed

```
graph TD
    A[+ARANCIOAMA] --- B[+LIMEPALEST]
    B --- C[+LIMETAHITI]
    C --- D[+LIMONE]
    C --- E[+CEDRO]
```

remember: this is an unrooted tree!

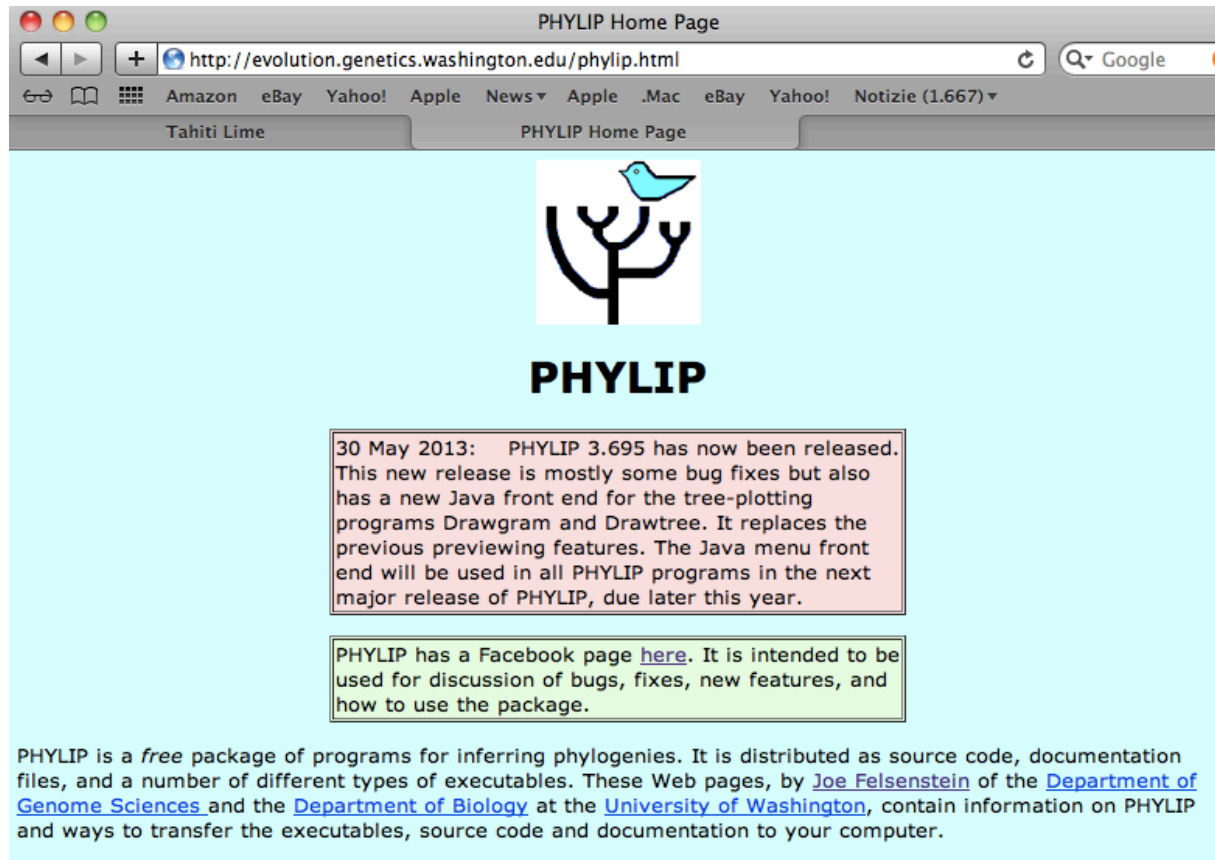
Between	And	Length
1	BERGAMOTTO	1.00000
1	2	7.00000
2	LIMEPALEST	-0.00000
2	3	8.00000
3	CEDRO	2.00000
3	4	0.00000
4	LIMETAHITI	0.00000
4	LIMONE	0.00000
1	ARANCIOAMA	0.00000

6-1.txt

```
6
ARANCIOAMA0
BERGAMOTTO1      0
CEDRO      17      18      0
LIMETAHITI15     16      2      0
LIMEPALEST7      8      10     8      0
LIMONE      15     16      2      0      8      0
```

Quarta esercitazione pratica (il pacchetto PHYLIP e la documentazione relativa)

MA 10-06-2014



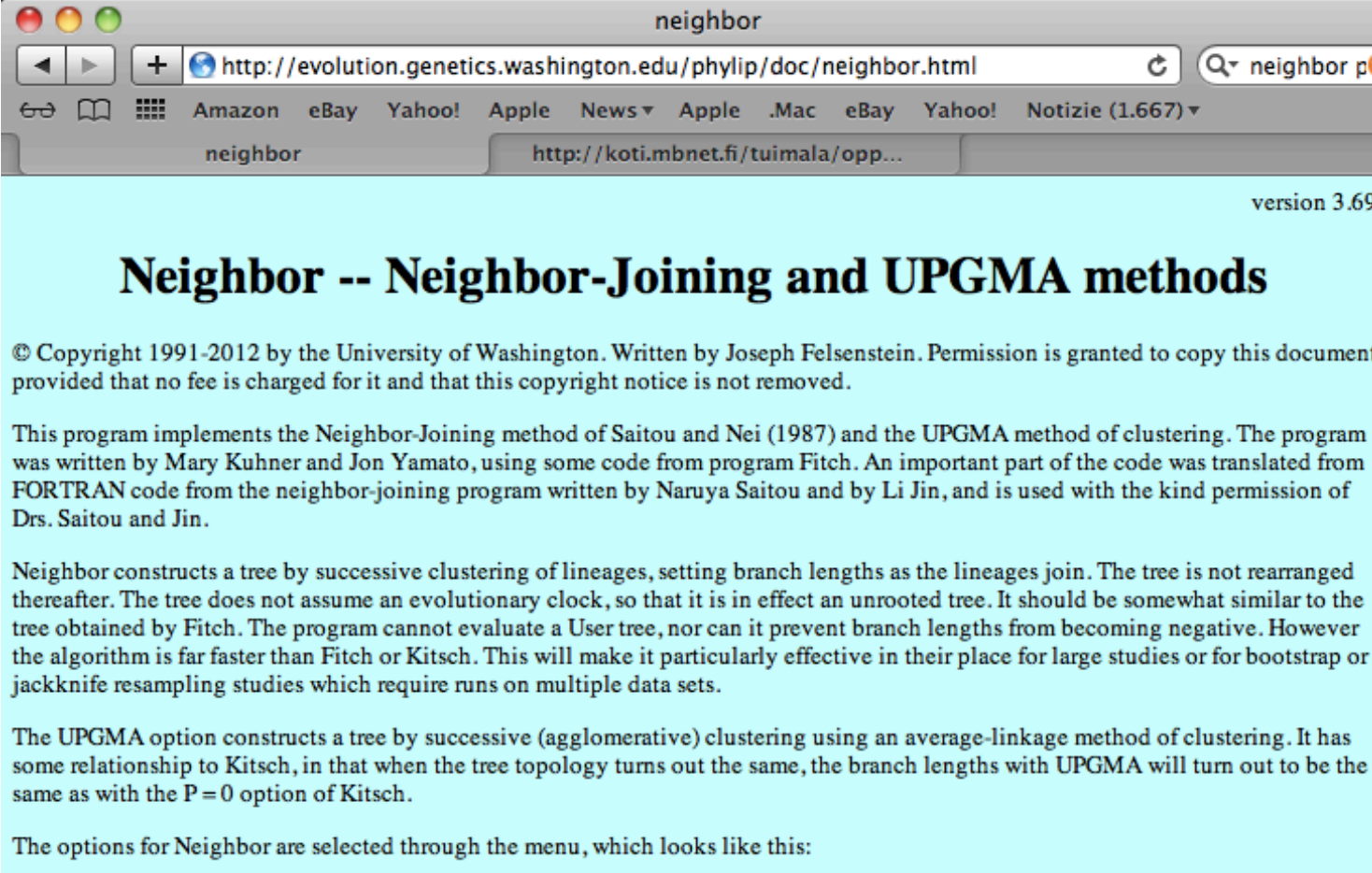
<http://evolution.genetics.washington.edu/phylip.html>

**A primer to phylogenetic analysis using
the PHYLIP package**

Jarno Tuimala - Fifth Edition

<http://koti.mbnet.fi/tuimala/oppaat/phylip2.pdf>

(creazione del dendrogramma con “Neighbor” del pacchetto PHYLIP)



The screenshot shows a web browser window with the title "neighbor". The address bar contains the URL "http://evolution.genetics.washington.edu/phylip/doc/neighbor.html". The browser's search bar contains "neighbor p". The page content is as follows:

version 3.69

Neighbor -- Neighbor-Joining and UPGMA methods

© Copyright 1991-2012 by the University of Washington. Written by Joseph Felsenstein. Permission is granted to copy this document provided that no fee is charged for it and that this copyright notice is not removed.

This program implements the Neighbor-Joining method of Saitou and Nei (1987) and the UPGMA method of clustering. The program was written by Mary Kuhner and Jon Yamato, using some code from program Fitch. An important part of the code was translated from FORTRAN code from the neighbor-joining program written by Naruya Saitou and by Li Jin, and is used with the kind permission of Drs. Saitou and Jin.

Neighbor constructs a tree by successive clustering of lineages, setting branch lengths as the lineages join. The tree is not rearranged thereafter. The tree does not assume an evolutionary clock, so that it is in effect an unrooted tree. It should be somewhat similar to the tree obtained by Fitch. The program cannot evaluate a User tree, nor can it prevent branch lengths from becoming negative. However the algorithm is far faster than Fitch or Kitsch. This will make it particularly effective in their place for large studies or for bootstrap or jackknife resampling studies which require runs on multiple data sets.

The UPGMA option constructs a tree by successive (agglomerative) clustering using an average-linkage method of clustering. It has some relationship to Kitsch, in that when the tree topology turns out the same, the branch lengths with UPGMA will turn out to be the same as with the P = 0 option of Kitsch.

The options for Neighbor are selected through the menu, which looks like this:

<http://evolution.genetics.washington.edu/phylip/doc/neighbor.html>

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n.	accessione	TAA1 HEX	TAA15 FAM	TAA41 FAM	cAGG9 HEX
01	Chinotto Savona	158	163 – 195	129	113
02	Chinotto comune	158-168	161-194	---	113
03	Arancio dolce polpa bionda ombelicato	159-163	162-185	128-132-140 -150	99-112
04	Cedro (Pietra Ligure)	168-177	161	140-145	101-113
05	Mandarino	158-161	188-201	142	112
06	Chinotto Savona	158-168	188-199	128-140	113
07	Arancio amaro	159-169	162-193	128-140	114
08	Bergamotto	159-168	161	140-145	99-113

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n.	accessione	TAA1 HEX	TAA15 FAM	TAA41 FAM	cAGG9 HEX
04	Cedro (Pietra Ligure)	168-177	161	140-145	101-113
09	Cedro Etrog	177	161	136	88-101
11	Lime di Tahiti (Bearss)	167-176	162	127-140-166	101-104-113
12	Lime dolce della Palestina	157-176	161-199	127-136	101-104-112
16	Limone Zagara	167-176	162	139-144	101-112

Il programma di PCR è MEDSSR modificato; questi sono i cicli

<u>Step</u>	T°C	tempo
1	94	120
2	94	30
3	55	60
4	72	60
5 torna a 2 e ripeti fino a 4 per 34 volte		
6	72	10
7	10	∞